



IBD2025

BOOK OF ABSTRACTS

INTERNATIONAL CONFERENCE ON BIODIVERSITY 2025

Biodiversity and Humanity in Global Crisis



5 - 7 November 2025, Queen Sirikit National Convention Center (QSNCC), Bangkok, Thailand



ด้วยสำนึกในพระมหากรุณาธิคุณ
สมเด็จพระกนิษฐาธิราชเจ้า กรมสมเด็จพระเทพรัตนราชสุดา ฯ
สยามบรมราชกุมารี
เสด็จพระราชดำเนินทรงประกอบพิธีเปิดงานและทรงบรรยายพิเศษ
ในการประชุมวิชาการนานาชาติด้านความหลากหลายทางชีวภาพ ๒๕๖๘
วันพุธที่ ๕ พฤศจิกายน พ.ศ. ๒๕๖๘
(เป็นการส่วนพระองค์)

With sincere gratitude to
HER ROYAL HIGHNESS PRINCESS MAHA CHAKRI SIRINDHORN
For presiding over the opening ceremony and delivering a special address
of THE INTERNATIONAL CONFERENCE ON BIODIVERSITY 2025
on Wednesday 5 November 2025
BANGKOK, THAILAND





**INTERNATIONAL CONFERENCE ON
BIODIVERSITY 2025 : IBD2025**
"BIODIVERSITY AND HUMANITY IN GLOBAL CRISIS"

November 5-7 2025
Queen Sirikit National Convention Center,
Bangkok, Thailand

Organized by
Kasetsart University
National Research Council of Thailand
Thai Beverage Public Company Limited

Co-Organized by
Chitralada Technology Institute
National Science and Technology Development Agency (NSTDA)
Biodiversity-Based Economy Development Office (BEDO)
Suan Luang Rama IX Foundation

Supported by
Thailand Science Research and Innovation
PTT Public Company Limited
Electricity Generating Authority of Thailand
B.Grimm Power Public Company Limited
Electricity Generating Public Company Limited



IBD2025

WELCOME MESSAGE

INTERNATIONAL CONFERENCE ON BIODIVERSITY (IBD2025)

5-7 November 2025 | Bangkok, Thailand



On behalf of the IBD2025 Organizing Committee, we are delighted to extend a warm welcome to the International Conference on Biodiversity 2025 (IBD2025). This event is organized to honor the auspicious occasion of the 70th birthday of Her Royal Highness Princess Maha Chakri Sirindhorn on April 2, 2025.

The conference will be held at the Queen Sirikit National Convention Center (QSNCC) in Bangkok, Thailand, from November 5 to 7, 2025. This prestigious event is organized by Kasetsart University, the National Research Council of Thailand (NRCT) and the Thai Beverage Public Company Limited with the support of key collaborators, including the Chitralada Technology Institute, the National Science and Technology Development Agency (NSTDA), the Biodiversity-Based Economy Development Office (BEDO), the Suan Luang Foundation Rama IX, Thailand Science Research and Innovation, PTT Public Company Limited, Electricity Generating Authority of Thailand, B.Grimm Power Public Company Limited, Electricity Generating Public Company Limited

This year's conference theme, "Biodiversity and Humanity in Global Crisis," reflects the urgent need for collective action and collaboration to address the intertwined challenges of biodiversity loss, climate change, environmental degradation, and the sustainable utilization of biodiversity without disturbing the natural ecosystem. It presents a unique opportunity for experts from various biodiversity-related communities to exchange knowledge, share research, and explore innovative solutions. Sessions will focus on vital topics such as ecosystem conservation and services, the integration of biodiversity into the BCG (Bio-Circular-Green) economy model, international collaboration, and addressing global crises through sustainable practices.

We wish all IBD2025 guests and participants a fruitful opportunity to communicate, share their expertise, and expand their networks among friends and colleagues interested in biodiversity. We look forward to welcoming you to IBD2025 in Bangkok, Thailand, in November 2025.

Prof. Sanit Aksornkoae, Ph.D.

Chairman, IBD2025 Organizing Committee

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About The Conference

Background

The year 2025 marks a momentous occasion as Her Royal Highness Princess Maha Chakri Sirindhorn celebrates her 70th birthday. To commemorate this auspicious event, organizations dedicated to biodiversity conservation in Thailand have initiated the International Conference on Biodiversity 2025 (IBD2025). This conference serves as a global platform for Thai and international researchers to exchange knowledge and insights on biodiversity from multiple perspectives, including scientific research, conservation, prevention, restoration, and sustainable utilization.

The event will be held at the Queen Sirikit National Convention Center from November 5 to 7, 2025. It is a great privilege that Her Royal Highness Princess Maha Chakri Sirindhorn has graciously accepted the invitation to preside over the opening ceremony on November 5, 2025.

The National Research Council of Thailand (NRCT) and Kasetsart University will serve as the primary hosts, with support from Chitralada Technology Institute, National Science and Technology Development Agency (NSTDA), Biodiversity-Based Economy Development Office (BEDO), Suan Luang Rama IX Foundation, Thai Beverage Public Company Limited and other key stakeholders. The conference aims to foster academic exchange among researchers and professionals while advancing biodiversity research, conservation, and sustainable development.

Date and Venue:

5-6 November 2025

Conference: Ballroom 1, 1st Floor Queen Sirikit National Convention Center, Bangkok, Thailand
(For all participants)

Exhibition: Ballroom 2, 1st Floor Queen Sirikit National Convention Center, Bangkok, Thailand

Poster: Ballroom 2, 1st Floor Queen Sirikit National Convention Center, Bangkok, Thailand

7 November 2025

Excursion:

Program 1: Suan Luang Rama IX Royal Botanic Garden, Prawet District, Bangkok, Thailand

Program 2: PTT Metroforest Learning Center Venue, Lat Krabang District, Bangkok, Thailand

(For registered excursion participants only)

Main Topics:

Session 1: Biodiversity and Food Security

Session 2: Biodiversity and Health

Session 3: Biodiversity and Tourism

Session 4: Biodiversity and Environmental Rehabilitation

Session 5: Biodiversity and Cultural Conservation

Session 6: Biodiversity Management to Overcome Global Crisis (Panel Discussions)

Organizing Committee

1	Dr.Sumet Tantivejkul The Chaipattana Foundation	Advisor
2	Mr. Dnuja Sindhvananda Suan Luang Rama IX Royal Botanic Garden	Advisor
3	Associate Professor Dr. Khunying Suchada Sripen Suan Luang Rama IX Royal Botanic Garden	Advisor
4	Associate Professor Dr. Khunying Sumonta Promboon Chitralada Technology Institute	Advisor
5	Professor Dr. Sanit Aksornkoe Office of National Economics and Social Development Council	Chairman
6	President of Kasetsart University	Vice Chairman
7	Director of the National Research Council of Thailand	Vice Chairman
8	Vice President for Academic Affairs and Lifelong Learning at Kasetsart University	Committee
9	Dr. Weerachai Nanakorn Suan Luang Rama IX Royal Botanic Garden	Committee
10	Mr. Pornchai Jutamas Plant Genetic Conservation Project Under the Royal Initiative of H.R.H. Princess Maha Chakri Sirindhorn	Committee
11	Professor Dr. Khanjanapat Lewmanomont Kasetsart University	Committee
12	Professor Dr. Morakot Tanticharoen King Mongkut's University of Technology Thonburi	Committee
13	Professor Dr. Savitree Limtong Kasetsart University	Committee
14	Professor Dr. Siriwat Wongsiri Chulalongkorn University	Committee
15	Professor Dr. Somsak Panha Chulalongkorn University	Committee
16	Associate Professor Dr. Napavarn Noparatnaraporn National Research Council of Thailand	Committee
17	Dr. Damrong Sripraram Kasetsart University	Committee
18	Associate Professor Dr. Thamasak Yeemin Ramkhamhaeng University	Committee
19	Assistant Professor Dr. Chanawat Bunnag Chitralada Technology Institute	Committee
20	Dr. Tanit Changthavorn Biodiversity-Based Economy Development Office	Committee
21	Miss Saowanee Mungsujaritkran National Research Council of Thailand	Committee
22	Mr. Thapana Sirivadhanabhakdi Thai Beverage Public Company Limited	Committee
23	Associate Professor Dr. Kornson Srikulnath Kasetsart University	Committee
24	Representative of the Secretary General of the National Economic and Social Development Council	Committee
25	Representative of the President of the National Science and Technology Development Agency	Committee
26	Representative of the secretary-general of the Office of the Royal Development Projects Board	Committee
27	Representative of the Governor of Bangkok	Committee
28	Representative of the Secretary General of the Office of Natural Resources and Environmental Policy and Planning	Committee

29	Representative of the Director General of the Department of National Parks, Wildlife and Plant Conservation	Committee
30	Representative of the Director General of the Royal Forest Department	Committee
31	Representative of the Director General of the Department of Marine and Coastal Resources	Committee
32	Representative of the Director General of the Department of Fisheries	Committee
33	Representative of the President of Thailand Environment Institute	Committee
34	Representative of the Director General of Biodiversity-Based Economy Development Office (Public Organization)	Committee
35	Representative of the President and Chief Executive Officer of the PTT Public Company Limited	Committee
36	Representative of the Governor of the Electricity Generating Authority of Thailand	Committee
37	Representative of the President & CEO of the Siam Cement Public Company Limited	Committee
38	Representative of the Executive Director of the Bangchak Corporation Public Company Limited	Committee
39	Assistant Professor Buarong Lewchalermwongse Chitralada Technology Institute	Committee and secretary
40	Mrs. Rungsima Tanthalakha National Science and Technology Development Agency	Committee and secretary
41	Miss Kannika Durongkadej National Research Council of Thailand	Committee and secretary
42	Dr.Ubon Thongpanya Kasetsart University	Committee and secretary
43	Miss Weeraya boontia Suan Luang Rama IX Royal Botanic Garden	Committee and assistant secretary
44	Miss Sunthari Sueakham National Science and Technology Development Agency	Committee and assistant secretary
45	Miss Rungrawee Taweasuk National Science and Technology Development Agency	Committee and assistant secretary

Scientific Committee

1	Associate Professor Dr. Khunying Sumonta Promboon Chitralada Technology Institute	Advisor
2	Associate Professor Dr. Khunying Suchada Sripen Suan Luang Rama IX Royal Botanic Garden	Advisor
3	Professor Dr. Sanit Aksornkoae Office of National Economics and Social Development Council	Advisor
4	Professor Dr. Morakot Tanticharoen King Mongkut's University of Technology Thonburi	Advisor
5	Professor Dr. Dokrak Marod Kasetsart University	Advisor
6	Professor Dr. Savitree Limtong Kasetsart University	Chairman
7	Professor Dr. Somsak Panha Chulalongkorn University	Vice Chairman
8	Professor Dr. Khanjanapat Lewmanomont Kasetsart University	Committee
9	Professor Dr. Siriwat Wongsiri Chulalongkorn University	Committee
10	Dr. Weerachai Nanakorn Suan Luang Rama IX Royal Botanic Garden	Committee
11	Dr.Kongkanda Chayamarit Suan Luang Rama IX Royal Botanic Garden	Committee
12	Miss Saowanee Mungsujaritkran National Research Council of Thailand	Committee
13	Associate Professor Dr. Thamasak Yeemin Ramkhamhaeng University	Committee
14	Associate Professor Dr. Sirintornthep Towprayoon King Mongkut's University of Technology Thonburi	Committee
15	Associate Professor Dr. Warapa Mahakarnchanakul Kasetsart University	Committee
16	Associate Professor Dr. Naruemon Arunothai Chulalongkorn University	Committee
17	Associate Professor Dr. Kornorn Srikulnath Kasetsart University	Committee
18	Assistant Professor Buarong Lewchalermwongse Chitralada Technology Institute	Committee
19	Dr. Tanit Changthavorn Biodiversity-Based Economy Development Office	Committee
20	Mrs. Pattarin Thongsima Office Of Natural Resources and Environmental Policy and Planning	Committee
21	Mr. Sissades Tongsima National Center for Genetic Engineering and Biotechnology	Committee
22	Mr. Virulh Huttawattana Chitralada Technology Institute	Committee
23	Mrs. Thidawan Sawaengkan Electricity Generating Authority of Thailand	Committee
24	Mrs. Rungsima Tanthalakha National Science and Technology Development Agency	Committee and secretary
25	Miss Sunthari Sueakham National Science and Technology Development Agency	Committee and assistant secretary
26	Miss Rungrawee Taweasuk National Science and Technology Development Agency	Committee and assistant secretary
27	Miss Weeraya Boontia Suan Luang Rama IX Royal Botanic Garden	Committee and assistant secretary
28	Miss Sasiwimon Boonanunt National Science and Technology Development Agency	Committee and assistant secretary



CONFERENCE PROGRAM

Venue: Ballroom 1, 1st floor,
Queen Sirikit National Convention Center (QSNCC)
Bangkok, Thailand

Day 1: Wednesday 5 November 2025

07.00 – 08.30	Registration
08.30	All distinguished guests and participants be seated in the Hall
09.00 – 12.00	Arrival of HRH Princess Maha Chakri Sirindhorn
	Address by Professor Dr. Sanit Aksornkoe, Chairman, IBD 2025 Organizing Committee
	Commemorative Video in Honor of HRH Princess Maha Chakri Sirindhorn
	Inaugural Speech by HRH Princess Maha Chakri Sirindhorn
	Keynote Lecture by HRH Princess Maha Chakri Sirindhorn
	HRH Princess Maha Chakri Sirindhorn visits the Exhibitions
	Departure of HRH Princess Maha Chakri Sirindhorn
12.00 – 13.00	Lunch

Session 1: Biodiversity and Food Security

Chairman: **Professor Emeritus Dr. Savitree Limtong**, Kasetsart University and The Royal Society of Thailand

Co-Chairman: **Dr. Tanit Changthavorn**, Biodiversity-Based Economy Development Office, Thailand

13.30 – 13.55	Invited Speaker 1-1: Biodiversity for Sustainable Agrifood Systems: Pathways to Food Security in Asia and the Pacific by: Mr. Robert Simpson, Deputy Regional Representative, FAO Regional Office for Asia and the Pacific, Thailand
13.55 – 14.10	Oral Presentation O1-01: Designing Food Systems for Biodiversity and Regenerative Development by Aracha Krasae-in, Kasetsart University, Thailand
14.10 – 14.25	Oral Presentation O1-02: Composition and Diversity of Bacterial Communities in the Gut of Black Soldier Fly Larvae (<i>Hermetia illucens</i> L.) Reared on Organic Wastes by Sutinee Plodprong, Thammasat University, Thailand
14.25 – 14.40	Oral Presentation O1-03: Ethnobotanical Knowledge and Nutritional Evaluation of Wild Leafy Vegetables Used by the Munda Tribe in Khunti District, Jharkhand (India) by Geetanjali Singh, Dr. Shyama Prasad Mukherjee University, India
14.40 – 14.55	Oral Presentation O1-04: Orthoptera as Pollinators: Assessing Their Role in Pollination Ecology by Sheryl A. Yap, University of the Philippines Los Banos, Philippines
14.55 – 15.10	Oral Presentation O1-05: Identification of Bacteria in the Gut of Black Soldier Fly Larvae (<i>Hermetia illucens</i> L.) from Breeding Farms and its Application by Pongpan Phuengmun, Thammasat University, Thailand
15.10 – 15.45	Coffee Break

Session 2: Biodiversity and Health

Chairman: **Professor Emeritus Dr. Morakot Tanticharoen**, King Mongkut's University of Technology Thonburi, Thailand

Co-Chairman: **Professor Dr. Dokrak Marod**, Kasetsart University, Thailand

- 15.45 – 16.10 **Invited Speaker 2-1:**
Ethnobotany of the Thai Flora
by Professor Emeritus Dr. Henrik Balslev, Department of Biology, Aarhus University, Denmark
- 16.10 – 16.25 **Invited Speaker 2-2:**
Diversity of Plants, Animals and Minerals in Thai Traditional Medical Wisdom
by Professor Dr. Chayan Picheansoonthon, The Royal Society of Thailand
- 16.25 – 16.40 **Oral Presentation O2-01:**
Household Case-Bearing Moths (Lepidoptera: Tineidae, *Phereoeca uterella*) as Indicators of Microplastic Pollution in Buildings
by Punyisa Churboonmee, Kasetsart University Laboratory School Kamphaeng Saen Campus Educational Research and Development Center, Thailand
- 16.40 – 16.55 **Oral Presentation O2-02:**
Assessing Marine Plankton Community Assemblages in Selected Areas of Illana Bay, Celebes Sea, and Sangay - Paril Kalamansig, Philippines
by Rande Babac Dechavez, Sultan Kudarat State University, Philippines
- 16.55 – 17.10 **Oral Presentation O2-03:**
***Amblyomma* (Bont Ticks) of Southeast Asia: An Overview on its Diversity, Host Associations, and Associated Pathogens**
By Ace Kevin Amarga, National Taiwan University, Taiwan

17.10 – 18.30 Poster Presentation Session (presenters at posters) and exhibition

18.30 – 20.30 Welcome Reception

Day 2: Thursday 6 November 2025

08.30 – 09.00 Registration

Session 3: Biodiversity and Tourism

Chairman: **Professor Emeritus Dr. Khanjanapat Lewmanomont**, Kasetsart University, Thailand

Co-Chairman: **Associate Professor Dr. Naruemon Arunothai**, Chulalongkorn University, Thailand

- 09.00 – 09.25 **Invited Speaker 3-1:**
Nature Positive Tourism: A Turning Point, Not a Trend
by Mr. Weerasak Kowsurat, Bangkok Breathe Council, Thailand
- 09.25 – 09.40 **Oral Presentation O3-01:**
From Biodiversity to Business Value: A Multidimensional BEQI Approach to Sustainable Coastal Tourism
Miss Panichat Kitisittichai, Chulalongkorn University, Thailand
- 09.40 – 09.55 **Oral Presentation O3-02:**
Dragonflies as Narrative Ambassadors: An Interdisciplinary Approach to Promoting Education, Ecotourism and Conservation Engagement in Khao Yai National Park
by Tosaphol Saetung Keetapithchayakul, Duy Tan University, Vietnam
- 09.55 – 10.10 **Oral Presentation O3-03:**
Enhancing coral reef biodiversity through Novel Restoration Techniques for Nature-Positive Tourism in Thailand
by Dr. Wichin Suebpala, Ramkhamhaeng University, Thailand
- 10.10 – 10.25 Coffee Break

Session 4: Biodiversity and Environmental Rehabilitation

Chairman: **Dr. Weerachai Nanakorn**, Suan Luang Rama IX Royal Botanic Garden, Thailand

Co-Chairman: **Dr. Kongkanda Chayamarit**, Suan Luang Rama IX Royal Botanic Garden and The Royal Society of Thailand, Thailand

- 10.25 – 10.50 **Invited Speaker 4-1:**
The Restoration of Natural Forests and Biodiversity Based on Miyawaki Method for Human Life
by Professor Emeritus Dr. Kazue Fujiwara, Yokohama City University, Japan
- 10.50 – 11.15 **Invited Speaker 4-2:**
Adapting Miyawaki forests to tropical and other climates
by Professor Dr. Elgene O. Box, University of Georgia, USA
- 11.15 – 11.30 **Oral Presentation O4-01:**
Rebuilding Biodiversity on Tsunami-Devastated Land: A Decade of Miyawaki Forest Creation in Iwanuma and Minamisoma, Japan
by Teruko Sano, Morino Project Public Interest Incorporated Foundation, Japan
- 11.30 – 11.45 **Oral Presentation O4-02:**
Biodiversity Restoration based on the Miyawaki Method and Ecosystem Benefits in Thailand
by Sirin Kawlaierd, Chitralada Technology Institute, Thailand
- 11.45 – 12.00 **Oral Presentation O4-03:**
Mangrove Plantation at Abandoned Shrimp Ponds in Nakhon Si Thammarat: Restoring Biodiversity and Countering Climate Change
by Shigeru Kato, Seikei University, Japan
- 12.00 -13.00 Lunch

13.00 – 13.45 Poster Presentation Session (presenters at posters) and exhibition

Session 4: Biodiversity and Environmental Rehabilitation (continued)

Chairman: **Professor Dr. Somsak Panha**, Chulalongkorn University and The Royal Society of Thailand, Thailand

Co-Chairman: **Professor Dr. Kornsorn Srikulnath**, Kasetsart University, Thailand

- 13.45 – 14.00 **Oral Presentation O4-04:**
Understanding and Mitigating Human-Elephant Conflict in Thailand: An Interdisciplinary and Community-based Ecotourism Approach
by Chution Savini, Srinakharinwirot University, Thailand
- 14.00 – 14.15 **Oral Presentation O4-05:**
Haplotype Diversity of Wild Asian Elephants in Phu Khieo and Khao Ang Rue Nai Wildlife Sanctuaries, Thailand
by Supansa Rerkdee, Kasetsart University, Thailand
- 14.15 – 14.30 **Oral Presentation O4-06:**
Habitat Associations of Critically Endangered Big-Headed Turtles in Northern Thailand: A Study to Support Grassroots River Conservation
by Mark Herse, Kasetsart University, Thailand
- 14.30 – 14.45 **Oral Presentation O4-07:**
Flight Altitude of Bats and Associated Collision Risk at Wind Turbines in Central Thailand
by Supawan Srilopan, Prince of Songkla University, Thailand
- 14.45 – 15.00 **Oral Presentation O4-08:**
Population Density and Distribution of Great Hornbills (*Buceros bicornis*) During the Breeding Season on Koh Chang Island, Trat Province, Thailand
by Peerawut Rincam, Kasetsart University, Thailand
- 15.00 – 15.15 Coffee Break

Session 5: Biodiversity and Cultural Conservation

Chairman: **Professor Emeritus Dr. Siriwat Wongsiri**, The Royal Society of Thailand

Co-Chairman: **Associate Professor Dr. Thamasak Yeemin**, Ramkhamhaeng University, Thailand

- 15.15 – 15.40 **Invited Speaker 5-1:**
How Can the Flora of Thailand Contribute to Nature Conservation?
by Professor Dr. Peter van Welzen, Naturalis Biodiversity Center, Netherlands
- 15.40 – 16.05 **Invited Speaker 5-2:**
Bees and Biodiversity: A Symbiotic Relationship for Sustainable Futures
by Professor Dr. Chen Lihong, Asian Apiculture Association, China
- 16.05 – 16.20 **Oral Presentation O5-01:**
Biodiversity through a Child's Eyes: Learning with Culture, Environment, and Curiosity
by Ruetai Chongsrid, National Science and Technology Development Agency, Thailand
- 16.20 – 16.35 **Oral Presentation O5-02:**
Geospatial Artificial Intelligence (GeoAI) for Estimating Tree Covered Area and Number of Trees in Historical Sites: A Case of The Old Moat of Nakhonratchasima Municipality City, Thailand
by Yaowaret, Jantakat, Rajamangala University of Technology Isan, Thailand
- 16.35 – 16.50 **Oral Presentation O5-03:**
Investigating the Urgency of Regulating Digital Sequence Information (DSI) to Protect Traditional Knowledge of Indigenous People from Digital Biopiracy
by Sri Oktavia, Universitas Andalas, Indonesia

Session 6: Biodiversity Management to Overcome Global Crisis (Panel Discussion)

Chairman: **Dr. Wijarn Simachaya**, Thailand Environment Institute, Thailand

- 16.50 – 18.00 **Enhancing Biodiversity Conservation and Sustainable Tourism in Thailand through Local Government Financing Solution**
 - Ms. Niran Nirannoot, BIOFIN Project United Nations Development Programme (UNDP), Thailand**Biodiversity Management to Overcome Global Crisis from ACB perspective**
 - Dr. Jerome L. Montemayor, ASEAN Centre for Biodiversity, Philippines**Managing Biodiversity in Common Pool Resources: Insights from Experimental Economics to Address Global Crises**
 - Associate Professor Dr. Witsanu Attavanich, Kasetsart University, Thailand**How Youth Can Shape the Future of Biodiversity?**
 - Pasut To-ying, Community Engagement Team Lead, GYBN Thailand
- 18.00 – 18.15 **Closing Ceremony**
By Associate Professor Dr. Khunying Sumonta Promboon, President of Chitralada Technology Institute, Thailand

Paper Lists

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ABSTRACT



SESSION 1

BIODIVERSITY AND FOOD SECURITY



INVITED SPEAKER 1-1:



Biodiversity for Sustainable Agrifood Systems: Pathways to Food Security in Asia and the Pacific

Robert Simpson

FAO Regional Office for Asia and the Pacific, Bangkok, Thailand

ABSTRACT:

Biodiversity underpins sustainable agrifood systems, food security, nutrition, and climate resilience, yet it is declining at an alarming rate. This keynote explores the interdependence between biodiversity and food systems, drawing on global policy frameworks and scientific assessments. It situates biodiversity within the Kunming-Montreal Global Biodiversity Framework (CBD COP15, 2022), including Target 10 on biodiversity-friendly agricultural practices, and references major assessments such as FAO's State of the World's Biodiversity for Food and Agriculture (2019) and the IPBES Nexus Assessment (2024). The presentation highlights the Food and Agriculture Organization's efforts to mainstream biodiversity through its Strategy (2019) and Action Plan (2024–2027), regional commitments, and initiatives such as Food System Transformation and Globally Important Agricultural Heritage Systems (GIAHS), with examples from Thailand. The talk concludes with a call to action for interdisciplinary research, intergovernmental dialogue, and concrete action to advance resilient agrifood systems and the effective implementation of the KMGBF.

KEYWORD:

agrifood systems, food security, Globally Important Agricultural Heritage Systems

ORAL PRESENTATION SESSION 1



Designing Food Systems for Biodiversity and Regenerative Development

Aracha Krasae-in^{1,*}

¹Department of Architecture, Faculty of Architecture, Kasetsart University, Bangkok, 10900, Thailand

*Corresponding author, e-mail: aracha.kr@ku.th

ABSTRACT:

Design and creativity are emerging as transformative forces in rethinking global food systems. As industrial agriculture and intensive livestock farming continue to drive biodiversity loss and environmental degradation, the need for innovative, regenerative solutions becomes increasingly urgent. These extractive models not only erode ecological diversity but also jeopardize food security, nutrition, and the livelihoods of farming communities.

Food design offers a strategic entry point for reversing these trends. By applying circular economy principles—such as reducing waste, reusing resources, and restoring ecosystems—designers can catalyze systemic change. Ingredient selection is a crucial area: incorporating underutilized crops, wild edibles, and products from regenerative practices like agroforestry and crop rotation helps diversify ecosystems, improve soil health, and reduce reliance on harmful inputs.

Creativity also plays a key role in shifting public perception and consumer behavior. The Food Design Courses at the Faculty of Architecture of Kasetsart University, and KU–ELISAVA–FORK Food Design Workshop: Bangkok Food Uncensored exemplifies how design-led approaches can reimagine everyday foods to align with sustainability goals without sacrificing cultural relevance or sensory appeal. Similarly, distributed design frameworks empower local communities to co-create biodiversity-supportive solutions, often leveraging digital platforms and open-source tools to scale impact.

The benefits of biodiversity-friendly food design are profound. More diverse diets lead to better nutrition, while resilient food systems can better withstand climate and market shocks. Moreover, promoting biodiversity in food production safeguards critical ecosystem services like pollination and pest control. Importantly, it also preserves culinary heritage, as traditional foodways often reflect deep ecological knowledge.

Ultimately, embedding biodiversity and regenerative principles into food design offers a pathway toward more equitable, sustainable, and resilient futures. By designing with nature, not against it, food systems can become active contributors to planetary and human well-being.

KEYWORDS:

Food Design; Biodiversity; Regenerative Development; Circular Economy; Sustainable Food Systems

Composition and diversity of bacterial communities in the gut of black soldier fly larvae (*Hermetia illucens* L.) reared on organic wastes

Sutinee Plodprong^{1,*} and Jureemart Wangkeeree¹

¹Department of Agricultural Technology, Faculty of Science and Technology, Thammasat University
Rangsit Campus, Pathum Thani, 12120, Thailand

*Corresponding author, e-mail: sutinee.plod@dome.tu.ac.th

ABSTRACT:

The black soldier fly larvae (BSFL; *Hermetia illucens* L.) is gaining recognition as a protein-rich ingredient for animal feed. BSFL is also demonstrating a remarkable ability to efficiently bioconvert various organic waste streams into high quality biomass. However, the bacterial communities in the gut of BSFL reared on organic wastes that locally available in Thailand remains unexplored. This study was aimed to investigate effect of substrates on the gut bacterial communities of BSFL using both culture-dependent and culture-independent methods. BSFL were reared on food waste (FOW), a mixture of food waste and supermarket waste (FSM), fruit waste (FRW), a mixture of fruit waste and soybean residue (FSB) and chicken manure (CHM), compared with chicken feed mixed with soybean residue (control diet). In the culture-dependent method, bacteria were isolated and cultured on nutrient agar and brain heart infusion agar. Colonies with distinct morphologies were selected, with a total of 45 isolates were identified using 16S rRNA gene sequencing. The results revealed that the dominance phyla included Firmicutes (84.44%) and Proteobacteria (15.56%). At genus level, *Bacillus* (53.33%) was the most abundant genus. Moreover, *Lysinibacillus* (11.11%) was specific to FRW, FSB and CHM, *Klebsiella* (8.89%) was specific to FSM and FSB, *Priestia* (8.89%) was specific to FRW and CHM, *Enterococcus* (4.44%), *Cytobacillus* (2.22%), *Kurthia* (2.22%), and *Niallia* (2.22%) were specific only to control diet. *Proteus* (2.22%), *Providencia* (2.22%) and *Pseudomonas* (2.22%) were specific to FSB, FSM and FRW, respectively. For the culture-independent method, metagenomic technique was used to analyze the V3-V4 regions of the 16S rRNA gene. The results revealed that bacterial diversity ranged from 125 to 779 Operational Taxonomic Units (OTUs), with BSFL reared on CHM exhibit the highest numbers of OTUs. The dominant phyla were Proteobacteria (47.27%), Firmicutes (36.03%), Bacteroidota (12.29%) and Actinobacteriota (4.12%). At genus level, *Providencia* (16.52%), *Enterococcus* (16.12%) and *Klebsiella* (10.07%) were the most abundance. Additionally, *Enterobacter* was specific to FOW (7.55%) and FSM (11.38%), *Kineothrix* was specific to FRW (46.65%) and FSB (50.32%) and *Sphingobacterium* was specific to CHM (18.32%) and control diet (29.86%). Obtained result indicate that some species within the identified genera may be pathogenic to human, such as *Bacillus*, *Enterococcus*, *Klebsiella*, *Proteus* and *Providencia*. Therefore, the utilization of BSFL should be accompanied by appropriate biosafety measures and proper rearing practices to minimize the risk of pathogenic bacterial contamination.

KEYWORDS:

Bacterial community; black soldier fly larvae; gut microbiota; *Hermetia illucens* L.; organic waste

Ethnobotanical Knowledge and Nutritional Evaluation of Wild Leafy Vegetables Used by the Munda Tribe in Khunti District, Jharkhand (India)

Geetanjali Singh^{1,*}

¹University Department of Botany, Dr. Shyama Prasad Mukherjee University, Ranchi -9, Jharkhand, India.

*Corresponding author, Email: gsingh_8apr@yahoo.co.in

ABSTRACT:

The Munda tribe of Khunti district in Jharkhand sustains a rich tradition and time-tested ethnobotanical knowledge of utilizing wild leafy vegetables (WLVs) as an integral part of their daily sustenance and healthcare practices. This study documents the indigenous knowledge associated with the identification, collection, and usage of WLVs, evaluates their ethnobotanical relevance, and investigates their nutritional content. A total of 62 WLV species belonging to 35 families were recorded through ethnobotanical surveys and semi-structured interviews conducted in selected villages of Khunti district. Nutritional analyses of selected species revealed high contents of micronutrients such as iron, calcium, fibres, and vitamins, thereby contributing significantly to the dietary diversity and nutritional resilience of tribal households.

The findings emphasize the critical role of wild edible plants in achieving food and nutrition security, especially in tribal and rural ecosystems where access to market-based nutrition is limited. Moreover, the continued use of WLVs reflects a sustainable relationship with the environment and underscores the importance of conserving both biological and cultural diversity. The study advocates for integrating traditional ecological knowledge with modern nutritional science to enhance community health and promote biodiversity-based food systems.

KEYWORDS:

Wild leafy vegetables, Munda tribe, nutrition, biodiversity, food security

Orthoptera as Pollinators: Assessing Their Role in Pollination Ecology

Sheryl A. Yap^{1,*}, Jessica B. Baroga-Barbecho² and Ming Kai Tan^{3*}

¹Institute of Weed Science, Entomology and Plant Pathology, College of Agriculture and Food Science and Museum of Natural History, University of the Philippines Los Baños, Laguna, Philippines

²UPLB Bee Program, Office of the Vice Chancellor for Research and Extension, University of the Philippines Los Baños, Laguna, Philippines

³Lee Kong Chian Natural History Museum, Singapore, Singapore

*Corresponding author, e-mail: sayap3@up.edu.ph, orthoptera.mingkai@gmail.com

ABSTRACT:

Pollination is a critical ecological function typically attributed to bees, butterflies, and birds. However, recent observations suggest that certain Orthoptera species, including grasshoppers, katydids, and crickets, may contribute to pollination. This study aims to investigate the pollination potential of Orthoptera by identifying species that interact with flowering plants and evaluating their role in pollen transfer. Understanding these interactions could provide novel insights into alternative pollinators, particularly in ecosystems where traditional pollinators are declining. Pollinators decline due to several factors such as habitat loss, pesticide use, and climate change poses a serious threat to biodiversity. While insects like bees are well-documented pollinators, limited research exists on Orthoptera's potential role in pollination. Field observations were conducted across various floral habitats to document Orthoptera species feeding on flowers. Species were identified, including *Phaneroptera* sp. and *Tettigonia* sp., and their interactions with plants were recorded, focusing on feeding behavior and floral preferences. Several Orthoptera species were observed feeding on floral resources, particularly nectar and petals. Pollen adhered to different parts of their body, particularly their mouthparts, legs, and antennae, indicating passive pollen transfer. While not as specialized as bees, Orthoptera may serve as incidental pollinators, especially in nocturnal and understudied pollination networks. For beekeepers and conservationists, understanding alternative pollinators like Orthoptera can help mitigate the effects of pollinator loss. Encouraging habitat diversity may support Orthoptera populations, potentially enhancing overall pollination resilience.

KEYWORDS:

crickets, grasshopper, insect-plant interaction, katydids, plant-pollinator relationship, pollination

Identification of bacteria in the gut of black soldier fly larvae (*Hermetia illucens* L.) from breeding farms and its application

Pongpan Phuengmun^{1,*} and Jureemart Wangkeeree¹

¹Department of Agricultural Technology, Faculty of Science and Technology, Thammasat University, Rangsit Campus, Pathum Thani, 12120, Thailand

*Corresponding author, e-mail: pongpan.phuen@dome.tu.ac.th

ABSTRACT:

The black soldier fly larvae (*Hermetia illucens* L.) is represent a novel source of protein and serve as a sustainable alternative to conventional protein sources in animal feed. This species is capable of consuming various types of waste and organic matter, which influences the diversity of microorganisms in their gut, especially bacteria. This research aimed to identify the bacterial community in gut of black soldier fly larvae collected from rearing farms in Nakhon Pathom, Ratchaburi, Roi Et, Surin, Maha Sarakham, Chiang Mai, Chonburi, and Chumphon provinces. Bacterial classification was performed using a non-culture method through metagenomic techniques, targeting the V3 and V4 regions of the 16S ribosomal RNA (16S rRNA) gene. The bacterial diversity ranged from 98 to 400 Operational Taxonomic Units (OTUs), with Nakhon Pathom exhibiting the highest number at 400 OTUs. The dominant bacterial phyla identified were Proteobacteria, Firmicutes, Bacteroidota, and Actinobacteriota. The most common genera included *Providencia*, *Enterococcus*, *Klebsiella*, *Lachnoclostridium*, *Actinomyces*, *Proteus*, and *Dysgonomonas*. Most of these bacteria are considered core gut microbiota that play important roles in the development of the larvae. For the culture method, bacteria were isolated using three different culture media. Colony morphology was classified into 15 groups, and 16S rRNA gene sequencing identified 58 bacterial isolates. The bacteria isolates belonged to the phyla Firmicutes (96.55%) and Actinobacteria (3.45%). The identified genera included *Bacillus*, *Rummeliibacillus*, *Staphylococcus*, *Priestia*, and *Micrococcus*. Subsequently, selected cultured bacterial isolates were further studied for their ability to produce cellulase and amylase enzymes. *Bacillus subtilis* showed the highest cellulase production, while *Bacillus siamensis* exhibited the highest amylase production, with clear zone diameters of 2.06 ± 0.03 and 3.25 ± 0.07 mm, respectively. *B. subtilis* was selected as supplementation with feeding substrates and impact on growth performance was determined. The results of this research can serve as an information provided data on bacterial diversity from different locations in Thailand and can be utilized for selecting beneficial bacteria to supplement in black soldier fly larvae feed, promoting their growth and development.

KEYWORDS:

Alimentary tract; bacterial diversity; black soldier fly; *Hermetia illucens* L.

POSTER PRESENTATION SESSION 1



Effective method development for pesticide residues in soil and prevalence of pesticides in soils from conventional, chemical-stopping and organic farms in Thailand

Prapha Arnnok^{1,*}, Rodjana Burakham², Jitlada Vichapong³, and Thannathon Wonghiran¹

¹Department of Chemistry, Faculty of Science, Ramkhamhaeng University, Bangkok, 10240, Thailand

²Materials Chemistry Research Center, Department of Chemistry, Faculty of Science, Khon Kaen University, Khon Kaen, 40002, Thailand

³Department of Chemistry, Faculty of Science, Mahasarakham University, Mahasarakham, 44150, Thailand

*Corresponding author, e-mail: prapha.a@ru.ac.th

ABSTRACT:

An effective analytical method for the determination of pesticide residues in soil has been proposed. The QuEChERS (Quick, Easy, Cheap, Effective, Rugged, and Safe) method, recognized as a standard sample preparation approach for a broad range of pesticides in fruits and vegetables based on solvent and solid-phase extraction, has been modified. The ultrasonic-assisted QuEChERS method, utilizing an acid-modified extractant, provided efficient sample preparation by improving both matrix cleanup and extraction efficiency. The optimized conventional reversed-phase chromatography-diode array detection was coupled with the QuEChERS method for pesticide quantification. Among eight targeted pesticides which have been frequently reported in fruits and vegetables in Thailand, five pesticides were successfully extracted by the fabricated QuEChERS method, with percentages of recovery of 55.7% – 100.2% and relative standard deviations (RSD) below 7%. The method detection limit was in the range of 0.98 – 2.13 $\mu\text{g kg}^{-1}$ dry weight (dw). Application of the proposed method to soil samples collected from conventional, chemical-stopping, and organic farms; cultivating various crops including fruits, vegetables, rice, tobacco, and rubber; in different regions of Thailand revealed the presence of five pesticides across all farm types, with total pesticide residues ranging from 11 to 4,437 $\mu\text{g kg}^{-1}$ dw. Surprisingly, the frequency of pesticide detection in non-chemical farms was comparable to that in chemical farms. The most frequently detected pesticides were pyrimethanil, carbofuran, atrazine, isoprocarb, and prochloraz, in that order.

KEYWORDS:

Pesticide; residue; soil contaminant; QuEChERS; liquid chromatography

Heavy Metal Contamination, Crop Accumulation, and Remediation Potential in a Wetland Ecosystem: Implications for Biodiversity and Food Security

Munmun Kundu¹, Souparna Chakrabarty², Swati Chakraborty^{3*}

¹Faculty of Botany, Hiralal Mazumdar Memorial College for Women, Dakshineswar, Kolkata, West Bengal, India

² Research Scholar, Department of Chemical Biology, Memorial Sloan Kettering Cancer Center, New York, NY 10065, USA Orcid No. 0000-0002-6876-3034

³ Swati Chakraborty, Head of the Department, Department of Biotechnology, Guru Nanak Institute of Pharmaceutical Science and Technology, West Bengal, India

*Corresponding e-mail: swati.chakraborty@gnipst.ac.in

ABSTRACT:

East Kolkata Wetland (EKW), a designated Ramsar site supporting garbage-based and sewage-fed farming, faces severe Heavy Metal (HM) contamination from untreated wastes. This study assessed the selected HMs Cadmium (Cd), Lead (Pb), Chromium (Cr), Nickel (Ni) uptake efficiency and accumulation in two commonly cultivated crops, maize (*Zea mays* L.) and mustard (*Brassica juncea* L. Czern.), in Dhapa of EKW, exploring their potential as a cost-effective remediation strategy. Soil and plant samples were collected over two years. Atomic Absorption Spectrophotometric results revealed spatio-temporal differences of HM concentration in the soil of agricultural plots. Cd, Pb, and Cr concentrations in soil consistently exceeded WHO permissible limits, while Ni remained within limits. Ultrastructural elemental deposition was visualized via SEM - EDAX. Despite significant impacts on root tissue, both crops exhibited minimal translocation of selected HMs ($TF < 1$) to edible parts, especially for Ni and Cr. Both crops predominantly accumulated metals in roots, with maize showing limited phytoextraction potential, whereas mustard primarily supports phytostabilization. These findings highlight the vulnerability of wetland agro-biodiversity due to pollution and emphasize the need for sustainable use of land and crop selection strategies to maintain ecosystem resilience and play complementary roles in mitigating HM contamination. Although, the consumption of these crops appears feasible till now, but it will be worth monitoring these levels of HMs to track bioaccumulation patterns to avoid adverse effects on human health. This study is vital for both ecological rehabilitation and ensuring long-term food security in similar polluted agricultural landscapes.

KEYWORDS:

Heavy metals; phytoextraction; phytostabilization; agro-biodiversity; sustainable land use

People, Plants, and Survival: Ethnobotany of Edible Plants Utilized by the Mamanwa-Manobo Tribes of Surigao del Sur, Mindanao Island, Philippines

Dave P. Buenavista^{1,*}, Roxan Eupeña-Caray², Daniel I. Tacbas², and Arturo G. Gracia Jr.²

¹Institute of Biological Sciences, Central Mindanao University, Musuan, 8710 Bukindon, Philippines

²Department of Mathematics and Natural Sciences, North Eastern Mindanao State University, Tandag City, Surigao del Sur, Philippines

*Corresponding author, e-mail: davista.cmu@gmail.com

ABSTRACT:

Food plants sustain human life and the Philippine economy. However, many biocultural landscapes harboring rich biodiversity of cultural and spiritual significance are disappearing without being studied. Though few studies have been carried-out in Mindanao, many indigenous communities remain undocumented despite the pressing concern on food security and the imminent threat of loss of biocultural heritage. In this study, we explored the food system of one of the understudied and poorly known ethnic groups in the Philippines, the Mamanwa-Manobo tribes of Surigao del Sur. The results of the ethnobotanical analyses showed that most species-rich group in the Mamanwa-Manobo food system include Arecaceae, Cucurbitaceae, Myrtaceae, Araceae, Malvaceae, Moraceae, Poaceae, Rutaceae, Solanaceae, and Zingiberaceae. A total of 589 use-reports were accounted in all 9 FAO use-categories: 1 species (1.38%) were consumed as cereals, 8 species (11.11%) were white roots, tubers, and plantains, 2 species (2.77%) were Vitamin A-rich vegetables and tubers, 16 species (22.22%) were eaten as green leafy vegetables, 19 species (26.38%) were categorized as other vegetables, 9 species (12.5%) were Vitamin A-rich fruits, 24 species (33.33%) were considered as other fruits, 5 species (6.94%) were classified as legumes, nuts, and seeds, and 13 species (18.05%) were used as spices, condiments, and beverages. Using the statistical software R, we further calculated the ethnobotanical indices; use-report (UR), use-value (UV), number of use (NU), and fidelity level (FL) from 589 URs in all 9 food use-categories. The edible plant species with the highest use-reports (UR) and use-values (UV) (Figure 6) were *Ipomoea batatas* (L.) Lam. (UR=73; UV=2.21), *Musa acuminata* (UR=59; UV=1.78), *Xanthosoma sagittifolium* (L.) Schott. (UR=40; UV=1.21), *Manihot esculenta* Crantz (UR=33; UV=1.0), *Artocarpus heterophyllus* Lam. (UR=24; UV =0.72), *Colocasia esculenta* (L.) Schott. (UR=22; UV=0.66). This ethnobotanical wealth are important cultural keystone species that could potentially contribute to the Philippines' commitment to achieving the Sustainable Development Goals from food security and resilience, to human health, and well-being. Through respectful and culture-sensitive collaboration, the ancestral domain of the Mamanwa-Manobo tribe should be therefore safeguarded as it harbors the wealth of biodiversity and the associated knowledge systems and practices handed down through the generations.

KEYWORDS:

food security; economic plants; indigenous peoples; traditional knowledge; food plants.

Phenological Patterns and Wildlife Utilization of Selected Tree Species in Mahidol University Kanchanaburi Campus

Nareekarn Singkornrat^{1,*}, Pornwiwan Pothasin¹

¹Conservation Biology, Mahidol University Kanchanaburi Campus, Kanchanaburi, 71150, Thailand

*Corresponding author, e-mail: nareekarnsingkorn2546@gmail.com

ABSTRACT:

Climate change is altering plant phenology globally, particularly in seasonally dry ecosystems like deciduous forests. The Limestone Mixed Deciduous Forest at Mahidol University Kanchanaburi Campus, characterized by high environmental variability, is particularly sensitive to these shifts. Despite this vulnerability, current phenological data are limited, and no baseline information exists on the relationship between plant phenology and wildlife activity in this area.

This study aimed to investigate the phenological patterns of selected tree species in relation to climatic variables and to assess wildlife utilization during key reproductive phases. Six species from four plant families (24 individuals total) were monitored biweekly from March 2024 to February 2025. Leafing, flowering, and fruiting phenophases were recorded, and wildlife interactions were observed using focal animal sampling during peak flowering and fruiting stages. Results revealed that prior-month rainfall significantly influenced leaf flushing and senescence, while flowering and fruiting were more responsive to drought conditions and lower temperatures. As the study period coincided with a La Niña event, the dataset serves as a valuable baseline for understanding phenological responses under similar ENSO conditions.

These findings highlight the potential impacts of climate-induced phenological shifts on plant–animal interactions, particularly for migratory or specialist species reliant on seasonal cues. Increasing asynchrony between plant phenology and wildlife behavior may ultimately reduce reproductive success and compromise ecosystem resilience. Integrated, long-term phenological monitoring is essential to support adaptive conservation strategies in the face of ongoing climate change.

KEYWORDS:

Climate Change; Limestone Mixed Deciduous Forest; Plant Phenology; Utilization by Wildlife

DNA Barcoding and Molecular-Based Identification of *Capsicum* spp. in Calamba, Misamis Occidental, Philippines

Pearl Mae T. Arbois^{1,*}, Christina A. Barazona-Cuevas^{1,2,3}, Carlo Stephen O. Moneva^{1,2,3}, Mylah Villacorte-Tabelin¹, and Djamae L. Manzanares^{1,2,3}

¹Department of Biological Sciences, College of Science and Mathematics, Mindanao State University-Iligan Institute of Technology, Andres Bonifacio Avenue, Tibanga, 9200, Iligan City, Philippines

²Center for Biodiversity Studies and Conservation, Premier Research Institute of Science and Mathematics, Mindanao State University – Iligan Institute of Technology, Andres Bonifacio Avenue, Tibanga, 9200, Iligan City, Philippines

³Center for Integrative Health, Premier Research Institute of Science and Mathematics, Mindanao State University – Iligan Institute of Technology, Andres Bonifacio Avenue, Tibanga, 9200, Iligan City, Philippines

*Corresponding author, e-mail: pearlmae.arbois@g.msuiit.edu.ph

ABSTRACT:

Species delimitation in the genus *Capsicum* remains a persistent challenge, particularly in the Philippines, where morphological overlaps, inconsistent vernacular naming, and underrepresented germplasm in global reference databases obscure accurate identification. This study used an integrative taxonomic approach by combining morphological characterization with chloroplast DNA barcoding (*rbcl*, *matK*, and *trnH-psbA*) to identify three naturally growing *Capsicum* samples collected from Calamba, Misamis Occidental. Morphologically, the two samples were consistent with *Capsicum frutescens*, exhibiting erect floral orientation, purple anthers, and smooth calyx margins, while the third sample resembled *Capsicum annuum*, characterized by white anthers, variable fruit size and orientation, and occasional calyx constriction. Molecular barcoding, however, revealed 100% sequence identity across all samples, with BLAST matches aligning to multiple species, including *C. annuum*, *C. frutescens*, *C. chinense*, and *C. eximium*. Phylogenetic analysis confirmed placement within the *Capsicum* clade, but minimal sequence divergence and inconsistent placement highlighted the limited discriminatory power of these conserved markers. These findings underscore the limitations of current barcoding protocols and highlight the urgent need for more rigorous genomic tools such as nuclear markers (e.g., ITS), full plastome sequencing, and population-level genomics to enhance species resolution. By addressing these taxonomic bottlenecks, future studies can more effectively uncover *Capsicum* diversity and support conservation and improvement of underutilized Philippine *Capsicum* germplasm—an essential step toward safeguarding genetic resources and enhancing food security through the development of resilient cultivars.

KEYWORDS:

BLAST, *Capsicum*, chloroplast markers, phylogenetic analysis, species identification

Advancing Plant Cytogenomics with Pre-labeled Oligonucleotide Probe for Fluorescence in situ Hybridization to Assess Karyotype Diversity, Cultivar Identity, Chromosome Stability, and Chromosome Painting in Economically Important Plants

Eliazar Alumbro Peniton Jr.¹ and Nomar Espinosa Waminal²

¹Molecular Biology and Biotechnology, Genetics, and Microbiology Division, Institute of Biological Sciences, Central Mindanao University, Musuan, Philippines

²Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), D-06466 Seeland-Gatersleben, Germany

*Corresponding author, e-mail: eliazarpenitonjr7@gmail.com

ABSTRACT:

Plant cytogenomics, integrating cytology and genomics, is crucial for understanding genome organization, evolution, and gene function in plants, providing foundational knowledge for crop improvement and biodiversity conservation. While traditional Fluorescence in situ Hybridization technique (FISH) is valuable, this research leverages the innovative Pre-labeled Oligonucleotide Probe for Fluorescence in situ Hybridization (PLOP-FISH) technique to significantly advance plant cytogenomic analysis. By mining and developing highly abundant, species- and chromosome-specific DNA repeat probes, this study successfully achieved multiple objectives. It accurately determined the karyotypes of tetraploid *Panax ginseng* ($2n=4x=48$), diploid *Aralia elata* ($2n=2x=24$), *Brassica rapa* ($2n=2x=20$), and *Raphanus sativus* ($2n=2x=18$). Specifically, novel *P. ginseng* (Pg167TRa, Pg167TRb, PgDel1, PgDel2) and *A. elata* (AeTR49, AeTR161, AeTR178) repeats, alongside conserved 5S rDNA, 45S rDNA, and telomeric sequences, allowed to effectively discriminate among ten *P. ginseng* cultivars. Also, identified the tetramonosomic TYP1 line, a finding supported by its reduced genome size (3.69 Gbp) compared to Geumsan landrace (4.17 Gbp). Furthermore, probe analysis and a consistent genome size (1.20 Gbp) confirmed the cytogenetic stability of *A. elata* tissue culture regenerants. Impressively, PLOP-FISH also enabled chromosome painting, distinguishing 9 homologous pairs in *B. rapa* and 8 in *R. sativus*, with the exception of chromosome 5 in both. These compelling results demonstrate the immense potential of PLOP-FISH as a versatile and powerful tool for diverse applications in plant genomics, plant breeding advancement, and biodiversity conservation strategies.

KEYWORDS:

Chromosome Painting, Cytogenomics, DNA repeats, Genome size, PLOP-FISH

Zinnia introduced at the flowering stage enhances predator abundance and legume yield

Puntharika Khongruang¹, Kasidit Rison¹, Nipada Ruankaew Disyatat², and Chatchawan Chaisuekul^{2,3,*}

¹Ph.D. Program in Zoology, Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand

²Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand

³Integrative Insect Ecology Research Unit, Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand

*Corresponding author, e-mail: chatchawan.c@chula.ac.th

ABSTRACT:

Incorporating flowering species into crop systems is a promising strategy to enhance biological control by supporting predatory arthropods. However, the timing of floral resource availability relative to crop phenology may critically influence its effectiveness. This study evaluated the effects of intercropping yard-long bean (*Vigna unguiculata* subsp. *Sesquipedalis* L.) with zinnia (*Zinnia* × *hybrida*) introduced at different developmental stages: seedling, vegetative, and flowering stages across two cropping seasons (2019–2020) in Saraburi, central Thailand. Flowering-stage zinnia introduced early in the crop cycle consistently improved dry yield compared to the monoculture plot in both seasons. In contrast, predatory arthropod responses varied by season. Coccinellid beetle abundance was higher in the wet season, whereas syrphid fly abundance increased in the dry season. These findings underscore the importance of synchronizing floral resource provision with seasonal conditions to optimize natural enemy activity and legume productivity, ultimately contributing to more resilient and sustainable agricultural food production systems.

KEYWORDS:

Asteraceae; floral resource; habitat manipulation; leguminous plant

Development of sprinkled rice powder from *Diplazium esculentum*

Leelanun Saksakunwattana¹, Kitima Thaisilpa², Pornchita Nuphet² and Pornpisanu Thammapat²

¹Maharakham University Demonstration School (Secondary), Maharakham University, Maharakham 44150, Thailand

²Program in Food Technology, Faculty of Agricultural Technology, Rajabhat Maharakham University, Maharakham 44000, Thailand

*Corresponding author, e-mail: leelanun04@gmail.com

ABSTRACT:

Diplazium esculentum, commonly known as vegetable fern, is a highly nutritious wild edible plant rich in dietary fiber, antioxidants, and essential micronutrients. Incorporating *Diplazium esculentum* into sprinkled rice powder enhances the nutritional value and introduces functional properties that may help promote health and prevent oxidative stress-related diseases. The aim of this research was the development of sprinkled rice powder from *Diplazium esculentum*. The effects of 2 ingredients, including pork (210-250 g) and *Diplazium esculentum* (280-320 g) mixture, on the organoleptic of sprinkled rice powder were studied. A mixture design was applied to examine the effects of pork and *Diplazium esculentum* on the overall preference of sprinkled rice powder. The results showed that the appropriate ratio for the production of sprinkled rice powder product was the mixture of pork and *Diplazium esculentum* at the rates of 210 and 320 g, respectively. Under the optimum ingredients, the overall preference could be increased by up to 6.66. For the final product, the color of the developed sprinkled rice powder was yellowish with L* a* b* values of 28.73, 6.00, and 20.26, respectively. Protein content, fat, ash, carbohydrate, and fiber were 23.46, 12.73, 7.60, 8.01, 46.34, and 1.86 g/100 g, respectively. While DPPH radical scavenging was 89.38%, higher than dried *Diplazium esculentum* (83.86%).

KEYWORDS:

Diplazium esculentum, Product development, Health food

Putative enhancement effects of ethanolic crude leaf extract of lemongrass (*Cymbopogon citratus* (DC.) Stapf) and lemon basil (*Ocimum x africanum* Lour.) against different pharmacological activities"

Christle Faith L. Orpeza^{1,*}, Christina A. Barazona-Cuevas^{1,2,3}, Djamae L. Manzanares^{1,2,3}, Jeremy Roy Augustus I. Gomez^{1,3}, Adrian Bryan G. Gandecila¹.

¹Department of Biological Sciences, College of Science and Mathematics, Mindanao State University-Iligan Institute of Technology, Andres Bonifacio Avenue, Tibanga, 9200, Iligan City, Philippines

²Center for Biodiversity Studies and Conservation, Premier Research Institute of Science and Mathematics, Mindanao State University – Iligan Institute of Technology, Andres Bonifacio Avenue, Tibanga, 9200, Iligan City, Philippines

³Center for Integrative Health, Premier Research Institute of Science and Mathematics, Mindanao State University – Iligan Institute of Technology, Andres Bonifacio Avenue, Tibanga, 9200, Iligan City, Philippines

*Corresponding author, e-mail: christlefaith.orpeza@g.msuii.edu.ph

ABSTRACT:

Aromatic plants, particularly herbs, are highly valued not only for their culinary uses but also for their ecological significance and functional roles in advancing biodiversity and sustainable food systems. Combining aromatic and functional plants is increasingly explored as a strategy to enhance nutritional value, improve food quality, and support sustainable dietary diversity. This study investigates the potential of ethanolic crude leaf extracts from lemongrass (*Cymbopogon citratus* (DC.) Stapf) and lemon basil (*Ocimum x africanum* Lour.), focusing on their antioxidant and cytotoxic properties as indicators of functional bioactivity. Qualitative phytochemical screening confirmed the presence of flavonoids, phenols, tannins, steroids, terpenoids, and alkaloids, with lemon basil exhibiting the highest concentration of bioactive compounds. The antioxidant capacity of the extracts, measured via DPPH radical scavenging assay, showed that lemon basil extract had the strongest activity ($IC_{50} = 6.0 \pm 0.0 \mu\text{g/mL}$), followed by lemongrass ($IC_{50} = 32.7 \pm 3.1 \mu\text{g/mL}$). The combined extract demonstrated a very strong antioxidant potential ($IC_{50} = 7.3 \mu\text{g/mL}$), indicating synergistic interaction (Combination Index = 0.72). Cytotoxicity, assessed using the Brine Shrimp Lethality Test (BSLT), revealed strong toxicity in lemon basil ($LC_{50} = 6.6 \mu\text{g/mL}$), but moderate toxicity in the combination ($LC_{50} = 739.8 \mu\text{g/mL}$), suggesting an antagonistic interaction (CI = 56.33). These findings support the potential of combining plant extracts to maximize bioefficacy while minimizing harmful effects, offering valuable insights for the sustainable development of functional food ingredients, or health-supportive formulations. The results also highlight the role of underutilized herbs in promoting food and health security, especially in resource-limited or biodiversity-rich communities. Future studies are recommended to conduct quantitative phytochemical screening, antimicrobial assays, trials using varying concentration ratios beyond the 1:1 mixture to optimize synergism, and further research into lemon basil's potential as an anti-cancer agent.

KEYWORDS:

antioxidant, aromatic plants, combination index (CI), cytotoxicity, pharmacological activities, synergistic

Global Distribution Prediction and De Novo Mitogenome Characterization of the Egg Parasitoid *Trissolcus elasmuchae* (Watanabe) (Hymenoptera: Scelionidae)

Rupam Debnath^{1,2}, Keloth Rajmohana^{1,*}, and K. P. Dinesh³

¹Zoological Survey of India, M-Block, New Alipore, Kolkata, West Bengal, 700053, India

²Department of Zoology, University of Calcutta, Kolkata, West Bengal, 700019, India

³Zoological Survey of India, Western Regional Center, Pune, Maharashtra, 411044, India

*Corresponding author, e-mail: mohana.skumar@gmail.com

ABSTRACT:

Members of the genus *Trissolcus* Ashmead (Hymenoptera: Scelionidae) are recognized for their potential as biocontrol agents against agricultural pests. In the past decade, the Asian fauna of this genus has received considerable attention, primarily due to efforts to identify biocontrol agents for managing globally significant invasive stink bug species. *Trissolcus elasmuchae* (Watanabe) is an egg parasitoid of various stink bugs, including *Elasmotethus interstinctus* (Linnaeus), *Elasmucha betulae* (DeGeer), *Elasmucha putonii* Scott (Acanthosomatidae), and *Niphe elongata* (Dallas) (Pentatomidae). This study predicts the current potential global distribution of *T. elasmuchae* using species distribution modelling with maximum entropy, based on occurrence records from countries such as China, France, India, Japan, South Korea, Taiwan, the United Kingdom, and Vietnam, along with global bioclimatic variables (WorldClim). Among 19 variables, seven contributed most significantly to the model. The results indicate that suitable habitats for *T. elasmuchae* exist across all continents except Antarctica. Additionally, this study reports the first de novo sequencing, characterization, and annotation of the complete mitochondrial genome of *T. elasmuchae*. The mitogenome is 15,539 bp in length and comprises 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), two ribosomal RNA genes (rRNAs), and one control region. It exhibits a positive AT skew (+0.05) and a negative GC skew (−0.25), indicating strand-specific nucleotide composition bias. All PCGs initiate with a standard ATN start codon, and most terminate with the typical stop codons TAA or TAG. These results advance our understanding of mitogenomic diversity and offer critical insights for resolving phylogenetic relationships. The implementation of integrated pest management strategies is particularly crucial in the context of predicted habitat suitability for this egg parasitoid. The potential of this species as a biocontrol agent against major pests like *N. elongata* warrants further investigation within the context of sustainable agriculture and food security, aiming to reduce reliance on harmful chemical pesticides.

KEYWORDS:

Biocontrol; mitochondria; platygastroidea; SDM; sustainable agriculture; telenominae.

Genetic Diversity and Insecticide Resistance in the Invasive Fall Armyworm: An Agricultural Management Perspective

Chitsanuphong Phanthian¹, Nontivich Tandavanitj², and Chatchawan Chaisuekul^{1,*}

¹Integrative Insect Ecology Research Unit (IIERU), Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand.

²Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand.

*Corresponding author, e-mail: chatchawan.c@chula.ac.th

ABSTRACT:

Fall armyworm, *Spodoptera frugiperda*, has invaded the Eastern hemisphere since 2016. It now threatens staple crops worldwide, including Thailand since 2018. Although insecticides can be used to control this pest, resistance has been reported and could alter genetic diversity of fall armyworm and subsequent effectiveness of insecticides. This study examines haplotype diversity, in relation to insecticide resistance, and resistance phenotypes in Thai and other Eastern hemisphere populations. Through topical bioassays and molecular analyses of mitochondrial *COI* and nuclear *Tpi* markers, resistances to emamectin benzoate, chlorantraniliprole, and lambda-cyhalothrin, were analyzed alongside the corresponding haplotypes. Results revealed high resistant levels to insecticides, with a distinct association between the emergent nuclear haplotype *TpCa1b* and resistance to multiple insecticides. Despite the presence of specific haplotypes, overall geographic and genetic differentiation was relatively low, suggesting possible loss of intraspecific genetic diversity across regions. This genetic homogenization may induce population adaptation to insecticides, which further accelerate the prevalence of resistance. Increasing resistance can lead to applications of higher dosages in agroecosystem, which may negatively impact beneficial insects and other wildlife. By bridging molecular data with applied entomology and agroecology, our findings highlighted how the loss of genetic diversity from the chemicals control can undermine both ecosystem function and the long-term viability of crop protection strategies. Preserving susceptible haplotypes and monitoring genetic variation in pest populations is not only essential for pest management, but also a critical dimension of biodiversity conservation for global food security.

KEYWORDS:

Pest Adaptation, Genetic Surveillance, Crop Resilience, Invasive Species

From Taxonomy to Food Security: Evaluating *Megachile* Bees as Alternative Pollinators in a Changing Climate

Nontawat Chatthanabun¹, Prapun Traiyasut², Itsarapong Voraphab³, and Natapot Warrit^{1,*}

¹Department of Biology, Faculty of Science, Chulalongkorn University, 254 Phaya Thai road, Wang Mai subdistrict, Pathumwan district, Bangkok, 10330, Thailand

²Program in Biology, Faculty of Science, Ubon Ratchathani Rajabhat University, Nai Mueang subdistrict, Mueang district, 34000, Thailand

³Forest Entomology and Microbiology Group, Forest and Plant Conservation Research Office, Department of National Parks, Wildlife, and Plant Conservation, Bangkok 10900

*Corresponding author, e-mail: Natapot.w@chula.ac.th

ABSTRACT:

Honey bees, extensively employed in agricultural pollination, are currently experiencing significant declines due to various environmental and anthropogenic pressures. This decline necessitates the identification and utilization of alternative pollinators to ensure the sustainability of global food production systems. The genus *Megachile* Latreille, 1802 (Anthophila; Megachilidae), characterized by high species diversity and recognized for its effectiveness in crop pollination, represents a promising candidate. However, taxonomic resolution within Southeast Asian *Megachile* species remains challenging, compounded by issues such as gender misidentification and considerable intraspecific variation in diagnostic morphological characters. This study aims to address these taxonomic ambiguities in Thai *Megachile* taxa using an integrative approach that combines morphological, molecular, and phylogenetic analyses. Morphological assessments were complemented by phylogenetic reconstructions generated through maximum likelihood and Bayesian inference methods based on mitochondrial cytochrome c oxidase subunit I (COI) sequences. Additionally, multiple species delimitation techniques—namely, assemble species by automatic partitioning (ASAP), the general mixed Yule-Coalescent (GMYC) model, and the Poisson tree process (PTP)—were applied to delineate species boundaries more accurately. A total of 556 specimens were examined morphologically, with 140 specimens subjected to molecular analysis. Phylogenetic results revealed that most putative species formed well-supported monophyletic clades, indicating a congruence between morphological characters and molecular data. Among the delimitation methods, ASAP demonstrated higher accuracy and consistency than GMYC and PTP in defining species boundaries within the Thai *Megachile* assemblage. The study also addressed key taxonomic challenges, including clarifying species status, gender associations, and morphological variation. Notably, the widespread presence and abundance of *Megachile disjuncta* (Fabricius, 1781), coupled with its ecological association with legumes (Fabaceae), underscores its potential as an effective alternative pollinator capable of supporting regional food security initiatives.

KEYWORDS:

Dauber bee; leaf-cutting bee; pollinator; Southeast Asia.

Metabarcoding of fish species using environmental DNA (eDNA) in mangrove nursery grounds: A tool for conservation and fish stock assessment

Tricksie Balatero^{1,2,*} and Sharon Rose Tabugo^{1,2}

¹Department of Biological Sciences, College of Science and Mathematics, Mindanao State University-Iligan Institute of Technology, Iligan City, 9200, Philippines

²Molecular Systematics and Conservation Genomics Laboratory, Center for Biodiversity Studies and Conservation (CBSC), Premier Research Institute of Science and Mathematics (PRISM), MSU-Iligan Institute of Technology, Iligan City, 9200 Philippines.

*Corresponding author's email: tricksie.balatero@g.msuiit.edu.ph

ABSTRACT:

Mangrove forests are vital ecosystems that offer crucial services, including acting as nursery grounds for various marine species. Unfortunately, these ecosystems face significant overfishing, habitat destruction, pollution, and climate change threats. This study employs environmental DNA (eDNA) metabarcoding as a non-invasive method to identify fish species within mangrove nursery grounds in Mindanao, Philippines. eDNA metabarcoding enables species detection by analyzing genetic material in environmental samples, providing a cost-effective and highly sensitive approach for fish species identification. Seawater samples were collected from selected mangrove nurseries, and the extracted eDNA was analyzed using high-throughput next-generation sequencing (NGS) techniques. The sampling sites included South Cotabato, Surigao del Norte, Misamis Oriental, and Tawi-Tawi. A total of 29 species from 20 families were identified. Significant species include *Zenarchopterus dunckeri* (Zenarchopteridae), a rare fish in the aquarium trade; *Hippocampus comes* (Syngnathidae), the tiger-tail seahorse, listed as vulnerable by the IUCN; *Sardinops melanostictus* (Clupeidae), a species of high commercial value; *Siganus corallinus* (Siganidae), valued in both the food and aquarium industries; and *Gymnothorax flavimarginatus* (Muraenidae), which plays a key role in the food chain as a natural predator of the invasive lionfish. Tawi-Tawi Island emerged as the most biodiverse site, with species from 11 different families recorded. These results emphasize the vital role of mangrove nurseries in supporting diverse fish populations and demonstrate the effectiveness of eDNA metabarcoding in compiling a comprehensive species inventory. These findings are crucial for guiding conservation efforts and ensuring the sustainable management of these vital ecosystems.

KEYWORDS:

eDNA, mangrove, metabarcoding, NGS

Discovery of a Specific Repetitive Element Marker in the Clariid Catfish Genome: Insights into Genetic Variation and Species Identification

Konekham Soutana^{1,2}, Thitipong Panthum^{1,3}, Narongrit Muangmai^{1,3,4}, Kyudong Han^{1,5,6}, Aingorn Chaiyes^{1,7}, Prateep Duengkae^{1,3}, Darren K. Griffin^{1,8}, Yoichi Matsuda^{1,9}, Worapong Singchat^{1,2,3*}, and Kornorn Srikulnath^{1,2,3,9,10*}

¹Animal Genomics and Bioresource Research Unit (AGB Research Unit), Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

²Interdisciplinary Graduate Program in Bioscience, Faculty of Science, Kasetsart University, 50 Ngamwongwan, Chatuchak, Bangkok 10900, Thailand

³Special Research Unit for Wildlife Genomics (SRUWG), Department of Forest Biology, Faculty of Forestry, Kasetsart University, 50 Ngamwongwan, Chatuchak, Bangkok 10900, Thailand

⁴Department of Fishery Biology, Faculty of Fisheries, Kasetsart University, Bangkok 10900, Thailand

⁵Department of Microbiology, Dankook University, Cheonan 31116, Korea

⁶Bio-Medical Engineering Core Facility Research Center, Dankook University, Cheonan 31116, Korea

⁷The Bachelor of Science Program in Biological Science and Technology, Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

⁸School of Biosciences, University of Kent, Canterbury, United Kingdom

⁹Laboratory of Animal Cytogenetics and Comparative Genomics (ACCG), Department of Genetics, Faculty of Science, Kasetsart University, Chatuchak, Bangkok, 10900, Thailand

¹⁰Biodiversity Center Kasetsart University (BDCKU), Bangkok 10900, Thailand

*Correspondence autor, email: worapong.singc@ku.ac.th; kornorn.s@ku.ac.th

ABSTRACT:

Hybrid catfish production, involving *Clarias gariepinus* (North African catfish) and *Clarias macrocephalus* (bighead catfish), plays an important role in aquaculture across Southeast Asia. However, accurate identification of hybrids and pure parental species remains challenging due to the lack of distinct morphological traits, especially when individuals are of similar size. This study aims to develop a reliable, cost-effective genetic marker system using species-specific repetitive elements to distinguish *C. gariepinus*, *C. macrocephalus*, and their hybrids. Genomic DNA will be extracted using the salting-out method, followed by Illumina sequencing. High-quality reads will be processed and analyzed using RepeatExplorer and TAREAN to identify satellite DNA elements unique to each species. Consensus sequences of the identified elements will serve as templates for primer design. Validation of these markers will be performed through PCR and quantitative PCR (qPCR), with melt curve analysis applied to ensure specificity and to determine copy number variation. In addition, fluorescence in situ hybridization (FISH) mapping will be used to visualize the chromosomal localization of selected repetitive elements, providing cytogenetic confirmation of species specificity. The resulting markers will enable efficient species and hybrid differentiation, supporting accurate bloodstock management, promoting sustainable aquaculture practices, and offering potential applications in genetic monitoring of other teleosts.

KEYWORDS:

Catfish, repetitive element, genetic marker.

Complete Mitochondrial Genome of the Slender Walking Catfish, *Clarias nieuhofii* (Siluriformes, Clariidae) from Phatthalung Province, Thailand: Genome Characterization and Phylogenetic Analysis

Karnjanapond Sornchai^{1,2}, Artem Lisachov¹, Thitipong Panthum¹, Suphada Kiriratnikom³, Narongrit Muangmai^{1,4}, Prateep Duengkae^{1,5}, Worapong Singchat^{1,2,3,6,*} and Kornorn Srikulnath^{1,2,3,6,*}

¹Animal Genomics and Bioresource Research Unit (AGB Research Unit), Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

²Interdisciplinary Graduate Program in Bioscience, Faculty of Science, Kasetsart University, 50 Ngamwongwan, Chatuchak, Bangkok 10900, Thailand

³Modern Agriculture - Fishery, Faculty of Technology and Community Development, Thaksin University, Phatthalung 93210, Thailand

⁴Department of Fishery Biology, Faculty of Fisheries, Kasetsart University, Bangkok 10900, Thailand

⁵Special Research Unit for Wildlife Genomics (SRUWG), Department of Forest Biology, Faculty of Forestry, Kasetsart University, Bangkok 10900, Thailand

⁶Biodiversity Center Kasetsart University (BDCKU), Bangkok 10900, Thailand

*Corresponding author, e-mail: worapong.singc@ku.ac.th; kornorn.s@ku.ac.th

ABSTRACT:

The slender walking catfish (*Clarias nieuhofii*) is a lesser-known species within the Clariidae family, yet it holds ecological and evolutionary significance due to its restricted distribution and unique morphological traits. Mitochondrial genomes (mitogenomes) have been widely used for species identification and phylogenetic research. However, there are limited reports of complete mitogenomes for *Clarias* species, and only a few mitochondrial gene sequences are available in GenBank. In this study, we present detailed annotations of four newly sequenced mitogenomes of *C. nieuhofii* from Phatthalung Province, Thailand, along with a comparative analysis of gene composition, codon usage, and phylogenetic relationships with other *Clarias* species for the first time. We found that the mitogenome of *C. nieuhofii* is 16,502 base pairs in length and contains 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, 2 ribosomal RNA (rRNA) genes, and a control region. The base composition of the 13 PCGs in the *C. nieuhofii* mitogenome is 29.92% A, 28.05% T, 26.79% C, and 15.24% G. Phylogenetic analysis indicated that *C. nieuhofii* forms a distinct lineage, clearly separated from other clariid species. It clusters within the same clade as *C. batrachus*, *C. fuscus*, *C. macrocephalus*, and *C. meladerma*. Overall, the findings of this study establish a genetic foundation for future investigations into *C. nieuhofii* and highlight the unique characteristics of its mitogenome, providing a valuable reference for future research on the phylogenetic evolution of the genus *Clarias*.

KEYWORDS:

Clarias nieuhofii; Mitogenome; Phylogenetics; Evolution; Clariidae

Comparative analysis of Allelic Polymorphism in Interleukin-1Beta2 (*IL-1β2*) and T-cell receptor beta (*TCRβ*) genes in Clariid catfishes Using Amplicon-Based sequencing

Tanaporn Wongsu^{1,2}, Worapong Singchat^{1,3}, Karnjanapond Sornchai^{1,3}, Konekham Soutana^{1,2} and Kornorn Srikulnath^{1,3,*}

¹Animal Genomics and Bioresource Research Unit (AGB Research Unit), Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

²Master of Science Program in Bioscience, Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

³Interdisciplinary Graduate Program in Bioscience, Faculty of Science, Kasetsart University, 50 Ngamwongwan, Chatuchak, Bangkok 10900, Thailand

*Corresponding author, e-mail: kornorn.s@ku.ac.th

ABSTRACT:

The vertebrate immune system comprises both innate and adaptive components that work in concert to protect the host against pathogenic threats. Interleukin-1 beta 2 (*IL-1β2*) is a key pro-inflammatory cytokine in the innate immune response, while the T-cell receptor beta (*TCRβ*) gene plays a central role in adaptive immunity by mediating antigen-specific T-cell activation. In teleost fishes, these genes often undergo duplication and functional divergence, reflecting evolutionary adaptations to pathogen-rich aquatic environments. Clariid catfishes, including *Clarias macrocephalus*, *Clarias gariepinus* and their hybrids, are of considerable aquacultural importance due to their rapid growth, environmental tolerance, and hybrid vigor. Despite their economic relevance, the immunogenetic diversity of these species remains poorly characterized. Investigating allelic polymorphism in *IL-1β2* and *TCRβ* can provide valuable insights into immune function, disease resistance, and hybrid fitness, thereby informing selective breeding strategies. This study aims to characterize the allelic variation of these genes across *Clarias* species and hybrids using amplicon-based sequencing. Analyses of per-exon and gene-wide diversity will help identify regions under purifying or diversifying selection, while comparative analyses with teleost orthologs will place *Clarias* immune gene variation in an evolutionary context and highlight both conserved and lineage-specific immune features.

KEYWORDS:

Clariid catfish; *IL-1β2*; *TCRβ*; allelic polymorphism; immunogenetics; amplicon-based sequencing

Comparative genomics and evolution of growth-, immune- and oxygen-related gene families in Clariid catfish

Rinrapat Nitipatpornpanya¹, Karnjanapond Sornchai¹, Konekham Soutana¹, Kornorn Srikulnath¹, Worapong Singchat^{1,*}

¹Animal Genomics and Bioresource Research Unit (AGB Research Unit), Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

*Corresponding author, e-mail: worapong.singc@ku.ac.th

ABSTRACT:

Clariid catfish is one of the economically important freshwater fish species in Thailand, known for its ability to thrive even under suboptimal environmental conditions. In recent years, increasing genomic resources have become available for catfish species. However, comprehensive comparative analyses focusing on gene families involved in growth, immunity, and oxygen utilization remain limited. Such information is crucial for genetic improvement programs aiming to enhance growth performance and environmental resilience in Clariid catfish aquaculture. This study aims to investigate the evolutionary dynamics of key gene functions in 4 Clariid catfish species (*Clarias gariepinus*, *C. macrocephalus*, *C. batrachus* and *C. nieuhofii*), with a specific focus on three gene families related to growth, immune response, and oxygen utilization. The research will begin by designing gene-specific primers for each target gene, followed by next-generation sequencing (NGS) and bioinformatic analyses to characterize sequence variation, gene evolution, and functional divergence among the four species. Expected outcomes of this study include gene repertoire maps of growth-, immune- and oxygen-related gene families across Clariid catfish, evidence of gene duplication events or lineage-specific expansions, identification of positively selected sites or genes, and evolutionary insights that could support the development of molecular markers for future selective breeding programs. Overall, this research will fill critical gaps in our understanding of gene function and evolution in Clariid catfish and contribute valuable information for improving catfish breeding strategies and sustainable aquaculture practices in Thailand.

KEYWORDS:

Clariid catfish, gene family evolution, growth gene, immune gene, oxygen related gene

Identity of *Apis cerana* Honey from Phayao Province, Thailand, Based on Melissopalynology and Some Chemical Content Analysis

Wasita Samerthung^{1,*}, Kingkarn Chaikan², Tharathip Pavara², and Tipwan Suppasat^{1*}

¹School of Science, University of Phayao, Maeka, Mueang District, Phayao, 56000, Thailand

²Agricultural Technology Promotion Center (Economic Insects), Nong Kwai, Hang Dong District, Chiang Mai, 50230, Thailand

*Corresponding author, e-mail: 64080918@up.ac.th and tipwan.su@up.ac.th

ABSTRACT:

Honey is the major bee product of Asian honeybees (*Apis cerana*), a native species in Asia. Currently, *A. cerana* honey is an important bee product from Phayao province in northern Thailand. Melissopalynology delineates the floral foraging preferences and diversity of honeybees in tropical environments. The unique characteristics of *A. cerana* honey depend on the botanical origins and geographical location of its floral sources. The study aims to identify the pollen family in *A. cerana* honey and to determine the botanical origin of *A. cerana* honey from Phayao province using the Acetolysis method. Additionally, it analyzes some chemical contents such as sugars, total protein, and total phenolic contents. The forty-one samples of *A. cerana* honey were collected from Phayao province between April and June 2024. The botanical origins identification results showed 17 families that belong to Asteraceae, Amaranthaceae, Arceraceae, Bignoniaceae, Brassicaceae, Cannabaceae, Combretaceae, Cucurbitaceae, Dipterocarpaceae, Euphorbiaceae, Fabaceae, Fagaceae, Malpighiaceae, Myrtaceae, Poaceae, Polygonaceae, and Sapindaceae. The *A. cerana* honey in Phayao province found that the dominant pollen family was Asteraceae, followed by the Sapindaceae, Fabaceae, and Poaceae, respectively. The Bradford assay showed that total protein ranged between 0.499 and 0.656 µg/mL with honey samples. The highest average total protein content was mainly pollen of the Asteraceae. Conversely, the honey samples showed the pollen from the Poaceae had the lowest average total protein content. Also, the total phenolic content ranged between 15.279 and 59.097 mg/L using the Folin-Ciocalteu assay. The honey samples with the pollen of the Sapindaceae had the highest total phenolic content, whereas they had the lowest that contained the pollen of the Asteraceae. Especially the total phenolic content that contributes importantly to antioxidant activity in honey. The analysis of total sugar content, which relates to the nutritional benefits of honey, helped a deeper understanding of the honey's compositions. The quality of *A. cerana* honey depends on the harvest and storage processing of honey as well as floral source, seasonal, and environmental factors. This research can be beneficial in demonstrating the geographical uniqueness of *A. cerana* honey products from Phayao Province and can help increase the value of these products.

KEYWORDS:

Apis cerana, Melissopalynology; Botanical origin; Phayao province; Chemical Composition

Diversity and phylogeny of the fluke genus *Prosthogonimus* in domestic chickens (*Gallus gallus*) from upper northern Thailand

Thitichai Arttra^{1,2} and Preeyaporn Butboonchoo^{2,*}

¹PhD's degree Program in Biodiversity and Ethnobiology (International Program), Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai, 50200, Thailand.

²Applied Parasitology Research Laboratory, Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai, 50200, Thailand.

* Corresponding author, e-mail: p.bootboonchoo@gmail.com

ABSTRACT:

The meat of domestic chicken (*Gallus gallus*) is very nutritious, widely regarded as a popular protein source globally, and holds significant economic value. In northern Thailand, approximately 16 million chickens are raised in battery farms or free-range for the food business. Chickens are vulnerable to *Prosthogonimus* trematode infection, which causes inflammation of reproductive organs, hence decreasing egg production. The purpose of this study is to examine the diversity of *Prosthogonimus* species in chickens from upper northern Thailand, as there is a lack of knowledge regarding this trematode in this area. Molecular investigations of the nuclear ribosomal internal transcribed spacer 2 (ITS2), mitochondrial cytochrome c oxidase I (COXI), and nicotinamide adenine dinucleotide dehydrogenase subunit 1 (ND1) sequences were conducted to elucidate the evolutionary relationships among *Prosthogonimus* taxa. Two hundred seventy-five gastrointestinal organs from domestic chickens were purchased from the local market throughout nine provinces: Chiang Mai, Chiang Rai, Mae Hong Son, Lamphun, Lampang, and Phayao. The overall prevalence and intensity of *Prosthogonimus* infection were 4.36% and 3.17 respectively. Two species of *Prosthogonimus* were identified along with their prevalence and intensity: *P. cuneatus* (4% prevalence and 2.64 intensity) and an unspecified *Prosthogonimus* species (2.18% prevalence and 1.5 intensity). Observations under a light microscope revealed morphological differences between the species, including (1) the relative size of the suckers, (2) the shape of the reproductive organs, and (3) the distension of the vitelline glands. The phylogenetic tree constructed from ITS2, COXI, and ND1 sequences revealed that *P. cuneatus* is closely associated with European *P. cuneatus*, while *Prosthogonimus* species is phylogenetically separate from *P. falconis*, suggesting that the worm represents a novel species with distinct morphological characteristics. Consequently, it may be categorized as a potentially novel species. The current infection status of *Prosthogonimus* trematode from this study can be utilized for the prevention and monitoring of healthcare for domestic chickens in outbreak regions. This trematode should continue to be explored through systematics and the advancement of molecular approaches.

KEYWORDS:

Prosthogonimus, *Gallus gallus*, ITS2, COXI, ND1,

Genotypic variability in β -Casein and its association with milk yield performance in crossbred Anglo-Nubian goat population in the Philippines

Catherine A. Buyan¹, Sharon Rose M. Tabugo^{1,2}, Mark Anthony I. Jose^{1,2}, and **Carlo Stephen O. Moneva**^{1,2,*}

¹Department of Biological Sciences, College of Science and Mathematics, Mindanao State University – Iligan Institute of Technology, Iligan City, 9200, Philippines

²Center for Biodiversity Studies and Conservation, Premier Research Institute of Science and Mathematics, Mindanao State University – Iligan Institute of Technology, Iligan City, 9200, Philippines

*Corresponding author, e-mail: carlostephen.moneva@g.msuit.edu.ph

ABSTRACT:

In the evolving field of animal genetic diversity, an increasing number of studies have explored the association between specific genes and economically important traits such as milk yield. The β -casein (*CSN2*) gene, which encodes one of the primary milk proteins, has been recognized as a key candidate gene influencing milk production. This study investigates the genotypic variability of the *CSN2* gene in crossbred Anglo-Nubian dairy goats (n = 101) collected from three different farms in the Philippines. *CSN2* genotypes present in the population is then subjected to association analysis with the milk yield. Hair follicle samples and available milk yield records were used for genetic and phenotypic analyses. Genetic variation in *CSN2* was identified using polymerase chain reaction–restriction fragment length polymorphism (PCR-RFLP). A 360 bp amplicon was amplified and digested with the restriction enzyme *SspI*. Two genotypes were observed in the population: the homozygous X^+X^+ genotype with a frequency of 0.81, and the heterozygous $A1X^+$ genotype with a frequency of 0.19. The homozygous $A1A1$ genotype was absent. The allele frequency for X^+ (0.91) was higher than that of $A1$ (0.09). The population was found to be in Hardy-Weinberg equilibrium ($\chi^2 = 0.46$). To determine the association between genotype and milk yield, a two-way factorial (2×4) randomized complete block design (RCBD) was used. The main factors were genotype and parity, while farm served as the blocking factor. Results revealed a significant association between *CSN2* genotypes and milk yield ($p < 0.05$), with the X^+X^+ genotype yielding significantly higher milk production compared to the $A1X^+$ genotype. These findings suggest the potential of *CSN2* as a marker for milk yield selection in dairy goats. Further studies involving a larger population are recommended to validate these results.

KEYWORDS:

Animal genetic diversity; *CSN2*; PCR-RFLP; restriction enzyme; marker for milk yield

Characterization and association of Bovine Interferon-gamma (BoIFNG) polymorphisms to hematological parameters and anemia scores of Panay native and crossbred Holstein - Jersey cattle in the Philippines

Eissa Matiyn Pandangan¹, Jorge Michael Dominguez^{2,3}, Kimberly I Turaja², Gerard Guadayo⁴, Nannette Hope Sumaya^{1,5}, Sharon Rose Tabugo^{1,5}, Kwan Suk Kim^{3*} and Carlo Stephen Moneva^{1,5}

¹Department of Biological Sciences, College of Science and Mathematics, Mindanao State University–Iligan Institute of Technology, Iligan City 9200, Philippines

²Institute of Animal Science, College of Agriculture and Food Science, University of the Philippines Los Banos, College, Laguna, Philippines

³Department of Animal Science, College of Agriculture, Life and Environment Science, Chungbuk National University, Cheongju City 28644, South Korea

⁴Dairy Training and Research Institute, College of Agriculture and Food Science, University of the Philippines Los Baños, College, Laguna 4031, Philippines

⁵Premier Research Institute of Science and Mathematics, Mindanao State University–Iligan Institute of Technology, Iligan City 9200, Philippines

*Corresponding author, email: kwanskim@chungbuk.ac.kr

ABSTRACT:

Bovine Interferon-gamma (BoIFNG) is a cytokine that plays a major role in immune response and is often investigated as a candidate gene for disease resistance against intracellular pathogens. Variation in IFNG gene expression could influence hematological parameters which are reflections of immune system status. This study aimed to characterize BoIFNG polymorphism in Panay Native (PN) and Crossbred Holstein – Jersey (HxJ) cattle and associate its genotype with eleven blood parameters and three anemia categories using three differing reference intervals. Forty PN and 18 HxJ heifers ages three years below were studied. A total of 936 bp was amplified and analyzed from the Exon 1 to Intron 1 of BoIFNG gene. One microsatellite and eleven single-nucleotide polymorphisms (SNPs) previously reported were identified, of which one is a missense mutation the rest are intronic variants. Nine SNPs associated to cattle breed. Most polymorphism are associated with hematological parameters and are mostly exhibiting overdominance. Four SNPs showed association to absolute and hemolytic anemia, while only two in non-regenerative anemia, commonly recessive inheritance model. These findings highlight the unique genetic characteristics of Panay native cattle. Moreover, this study provides baseline information for improving monitoring and management strategies under tropical conditions.

KEYWORDS:

Hematological parameters, Anemia, Interferon-gamma, Polymorphism, Microsatellite, Bovines

Bacterial diversity in the roots of *Cissampelos pareira*

Ponlawat Thinwongyod¹ and Sirinapa Chungopast^{1,*}

¹Department of Soil Science, Faculty of Agriculture at Kamphaeng Saen, Kasetsart University, Kamphaeng Saen campus, Nakhon Pathom 73140, Thailand

*Correspondence e-mail: agrsrnp@ku.ac.th

ABSTRACT:

Cissampelos pareira (Krueo Ma Noy) is a climbing plant in the *Menispermaceae* family. Its vine and leaves are crushed in water, and subsequently becoming jelly-like due to the presence of pectin. This plant can be used as the food and herbal purposes. The object of this research was to investigate diversity of bacteria in the roots *C. pareira*. Genomic DNA was extracted from plant samples using the PureDirex gDNA Isolation Kit (Taiwan) following the manufacturer's instructions. The 16S rRNA gene (V3–V4 region) was amplified using the primers 341F (5'-CCTAYGGGRBGCASCAG-3') and 806R (5'-GGACTACNNGGTATCTAAT-3'). The amplified products were then subjected to Illumina sequencing and subsequent metagenomic analysis. The most abundant bacteria belonged to five phyla: *Proteobacteria* (87.37%), *Bacteroidetes* (3.25%), *Actinobacteria* (2.86%), *Firmicutes* (2.44%) and *Acidobacteria* (1.17%). The top five families of 253 were *Burkholderiaceae* (2.16%), *Enterobacteriaceae* (1.64%), *Pseudomonadaceae* (1.39%), *Moraxellaceae* (0.52%) and *Sphingobacteriaceae* (0.41%). At the genus level, the most prevalent were *Pseudomonas* (2.18%), *Acinetobacter* (0.81%), *Duganella* (0.73%), *Herbaspirillum* (0.73%) and *Pectobacterium* (0.63%). The Shannon-Weaver diversity index was relatively low at 2.20. Consequently, the roots of Krueo Ma Noy were dominated by bacteria from the phylum *Proteobacteria*, with the family *Burkholderiaceae* and genus *Pseudomonas* showing the highest relative abundance. These bacteria are likely members of plant growth-promoting rhizobacteria (PGPR), which are known to enhance root and shoot fresh weight, confer resistance to heavy metals, and exhibit biocontrol activity.

KEYWORDS:

Cissampelos pareira; bacteria; diversity; roots; microbiome

Isolation, Characterization, and Molecular Identification of stem-associated endophytic bacteria from *Coffea arabica* L. with plant growth-promoting potential

Reignnette Skye Mirasol Ecleo¹, Reggie Y. Dela Cuz¹, Meraluna J. Canunayon¹ and

Emmanuel Pacheco Leaña^{1,*}

¹Molecular Biology and Biotechnology, Genetics and Microbiology Division, Institute of Biological Sciences, Central Mindanao University, University Town, Musuan, Maramag, 8714 Bukidnon, Philippines

*Correspondence e-mail: emmanuelpleano@gmail.com

ABSTRACT:

This study investigated the diverse microbial communities within *Coffea arabica* L., focusing on both beneficial stem-associated endophytic bacteria (EB) and potentially pathogenic leaf-associated bacteria. The objective was to isolate, characterize, and assess the plant growth-promoting (PGP) potential of these bacterial isolates, and to identify them molecularly. Using culture-dependent techniques, nine EB isolates and three potential phytopathogenic bacterial (PPB) isolates were successfully obtained from healthy stems and symptomatic leaves, respectively. Morphological characteristics and Gram staining were performed on all isolates. All EB isolates were screened for key PGP traits, including indole-3-acetic acid (IAA) production and acid phosphatase activity. Among the EB isolates, SEBE50 and SEBN3 exhibited strong IAA production and enzyme activity, while all isolates demonstrated acid phosphatase production. Molecular identification through 16S rRNA gene sequencing revealed that SEBE50 and SEBN3 are closely related to *Enterobacter* species, specifically *E. mori* and *E. quasirogerkampii*, both recognized for their beneficial roles in plant growth. Conversely, the leaf-associated isolate SPME was affiliated with the genus *Buttiauxella* and phylogenetically clustered with *Erwinia*, a genus known for opportunistic and pathogenic behaviors in plants. These findings indicate that *C. arabica* hosts a complex microbiome comprising both beneficial and potentially harmful bacteria. This highlights the critical importance of microbial profiling in developing sustainable strategies to enhance crop health and productivity in coffee cultivation.

KEYWORDS:

Endophytic bacteria, *Coffea arabica*, Plant growth-promoting traits, Indole-3-acetic acid (IAA), acid phosphatase, *Enterobacter*, *Erwinia*, *Buttiauxella*, Sustainable agriculture

Characterization of Pathogenic and Drug-Resistant Bacteria in *Escherichia coli*, *Salmonella* spp., and *Vibrio cholerae* Isolated from Clariid catfish and Water from Phatthalung, Thailand

Nuha Yalaedae^{1,2}, Worapong Singchat^{1,2,3,*}, Saharuetai Jeamsripong⁵, Suphada Kiriratnikom⁶, Narongrit Muangmai^{1,4}, Prateep Duengkae^{1,3} and Kornorn Srikulnath^{1,2,3}

¹Animal Genomics and Bioresource Research Unit, Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

²Interdisciplinary Graduate Program in Bioscience, Faculty of Science, Kasetsart University, 50 Ngamwongwan, Chatuchak, Bangkok 10900, Thailand

³Special Research Unit for Wildlife Genomics (SRUWG), Department of Forest Biology, Faculty of Forestry, Kasetsart University, 50 Ngamwongwan, Chatuchak, Bangkok 10900, Thailand

⁴Department of Fishery Biology, Faculty of Fisheries, Kasetsart University, Bangkok 10900, Thailand

⁵Research Unit in Microbial Food Safety and Antimicrobial Resistance, Department of Veterinary Public Health, Faculty of Veterinary Science, Chulalongkorn University, Bangkok, Thailand

⁶Modern Agriculture - Fishery, Faculty of Technology and Community Development, Thaksin University, Phatthalung 93210, Thailand

*Correspondence Email: worapong.singc@ku.ac.th.

ABSTRACT:

Catfish play an increasingly important role in the economy due to their rising demand in both consumption and aquaculture. Their ease of breeding, fast growth, and low cost make them a popular choice among rural farmers, contributing to local economies through value-added products such as fermented catfish an OTOP product in southern Thailand. However, bacterial infections, particularly from antibiotic-resistant strains, pose a significant challenge. These outbreaks not only reduce productivity but also affect the quality and safety of fermented products. Pathogenic bacteria are of particular concern in food safety. Studying microbial communities in the farming environment and on the fish is essential to detect harmful and drug-resistant organisms. Phenotypic antibiotic resistance was assessed using the disk diffusion method against 7 antibiotic groups: aminoglycosides, tetracyclines, sulfonamides, phenicol, cephalosporins, penicillin and fluoroquinolones. Genotypic characterization was performed using PCR technique to detect virulence and antibiotic resistance genes in *Escherichia coli*, *Salmonella* spp., and *Vibrio cholerae* isolated from farmed catfish in Phatthalung Province. The findings provide essential insights for the rational use of antibiotics and improved disease management strategies to enhance food safety and sustainability in catfish farming.

KEYWORDS:

Clariid Catfish, virulence gene, antibiotic resistance gene

Isolation and Selection of Indigenous Yeasts and Acetic Acid Bacteria from Kombucha for the Development of Specified Starter Cultures

Nanthasak Buakhareem¹, Siriluk Tipana¹, and Wanlapa Lorliam^{1,*}

¹Department of Microbiology, Faculty of Science, Srinakharinwirot University, Bangkok, 10110, Thailand

*Corresponding author, wanlapal@g.swu.ac.th

ABSTRACT:

Kombucha is a widely consumed fermented beverage known for its health-promoting properties, including the presence of organic acids and antioxidants. However, the fermentation process can have variability due to the use of natural starter cultures with inconsistent microbial compositions. This study aimed to isolate and select specific strains of acetic acid bacteria (AAB) and yeast for developing a kombucha beverage by designing a synthetic microbial community (SMC). Microorganisms were isolated from SCOBY (Symbiotic culture of bacteria and yeast) samples obtained from commercial sources in Thailand. A total of 43 AAB and 71 yeast isolates were obtained. The AAB isolates were biochemically characterized according to carbon source utilization, resulting in 18 distinct groups. The isolates were identified using 16S rDNA sequencing and found to belong to the species *Acetobacter tropicalis* (16.27%), *Acetobacter musti* (20.93%), *Komagataeibacter diospyri* (2.30%), and *Komagataeibacter saccharivorans* (60.46%), with isolate NELGN5-1 (*K. saccharivorans*) having the highest total acid at 3.84 g/L. The 71 yeast isolates were grouped biochemically based on carbon fermentation, and species identification through D1/D2 region sequencing revealed that they belong to *Brettanomyces bruxellensis* (70.42%), *Zygosaccharomyces bisporus* (22.53%), and *Saccharomyces cerevisiae* (5.63%). The highest ethanol-producing strains from each group were selected and combined with NELGN5-1 to construct the SMC for fermenting cascara tea, a high-value by-product of the coffee industry rich in bioactive compounds. Fermentation results demonstrated that the designed SMC effectively supported microbial growth and produced a high-quality beverage. The KZ (*K. saccharivorans* and *Z. bisporus*) and formulation exhibited the highest total phenolic content (30.05 mg GAE/mL), while the KS (*K. saccharivorans* and *S. cerevisiae*) formulation received the highest sensory evaluation scores in terms of taste, sweetness, and sourness. These findings suggest that the application of SMC with cascara enhances kombucha quality and provides an effective strategy for utilizing agricultural waste and reducing

KEYWORDS:

Kombucha, Synthetic microbial community (SMC), Cascara, Yeast, Acetic acid bacteria

Enhancing lipid accumulation in a newly isolated oleaginous yeast *Lipomyces mesembrius* SWU-NGP14-6: A biodiversity-driven approach for sustainable oil-food applications

Orawan Dawjang¹, Sirawich Sapsirisuk¹, Chutipra Daosangsawang¹, Wanlapa Lorliam¹ and Pirapan Polburee^{1,*}

¹Department of Microbiology, Faculty of Science, Srinakharinwirot University, Bangkok, 10110, Thailand

*Corresponding author, e-mail: Pirapan@g.swu.ac.th

ABSTRACT:

Microbial biodiversity plays a crucial role in securing sustainable food systems by providing novel bioresources with high nutritional and functional potential. This study focuses on *Lipomyces mesembrius* SWU-NGP 14-6, a newly isolated oleaginous yeast strain from soil in Thailand, which represents an untapped microbial resource capable of accumulating lipids up to 50% of its cell dry weight. To valorize this strain for food and feed applications, a two-stage fermentation strategy was developed to optimize lipid production. Key parameters influencing lipid accumulation were systematically investigated, including (1) carbon source type (glucose, xylose, glycerol, and sucrose), (2) glucose concentration (30–100 g/L), (3) initial pH (4–7), and (4) aeration rate (1 and 3 vvm) in a 5-L stirred-tank bioreactor. In the first stage, yeast cells were cultivated in limited medium (20 g/L glucose and 20 g/L malt extract) for 72 hours. In the second stage, the cells were transferred to a medium containing only a carbon source and incubated for an additional 72 hours. Among the carbon sources tested, glucose yielded the best results, producing 3.50 ± 0.30 g/L biomass, 3.31 ± 0.39 g/L lipid, and a lipid content of 94.57%. The optimal glucose concentration was 60 g/L, resulting in 8.12 ± 0.72 g/L biomass, 6.44 ± 0.40 g/L lipid, and a lipid yield of 0.12 g/g. Varying pH values had no significant effect on lipid production ($p > 0.05$); therefore, pH 5 was selected for further experiments. In the bioreactor trials, 1 vvm aeration supported higher biomass accumulation, while 3 vvm enhanced lipid production. The results highlight the biotechnological potential of *L. mesembrius* SWU-NGP 14-6 as a high-lipid microbial strain derived from local biodiversity. This work underscores the value of microbial diversity in developing sustainable food ingredients and supports the utilization of native yeast strains as alternative lipid sources for future food and feed systems.

KEYWORDS:

Oleaginous yeast, Two-stage fermentation, *Lipomyces mesembrius*, Microbial lipid

Biodiversity of Phylloplane Yeasts from Mangrove Forest and Their Antagonistic Activity Against Post-Harvest Plant Pathogenic Fungi

Pannida Khunnamwong^{1,2,*}, Pajongwan Gungprakhon¹, Nantana Srisuk^{1,2} and Savitree Limtong^{1,2,3}

¹Department of Microbiology, Faculty of Science, Kasetsart University, Bangkok, 10900, Thailand

²Biodiversity Center Kasetsart University (BDCKU), Bangkok, 10900, Thailand.

³Academy of Science, Royal Society of Thailand, Bangkok, 10300, Thailand.

*Corresponding author, e-mail: pannida.kh@ku.th

ABSTRACT:

The phylloplane serves as an important habitat for yeasts. Although research on phylloplane yeasts has been conducted in various environments, only a few studies have focused specifically on yeasts associated with mangrove plants. In recent years, increasing attention has been given to the search for microorganisms with potential applications in agriculture. Among these, yeasts have been reported for their potential in controlling of various post-harvest diseases caused by fungal pathogens. Therefore, this study aimed to investigate the diversity of phylloplane yeasts on mangrove leaves and to evaluate their antagonistic activity against post-harvest plant pathogenic fungi. A total of 40 mangrove leaf samples were collected from the King Rama IX International Mangrove Botanical Garden in Chanthaburi province, Thailand. Yeasts were isolated from the surface of leaves by dilution plating of leaf washings. A total of 242 strains were obtained and identified by sequence analysis of the D1/D2 domain of the large subunit (LSU) rRNA gene. Molecular identification of all strains revealed that both ascomycetous yeasts and basidiomycetous yeasts were detected on mangrove leaf surfaces in both seasons, but with higher number of ascomycetous yeasts. In addition to yeasts, *Aureobasidium melanogenum*, a yeast-like fungus species, was also detected. The most prevalent species detected on mangrove leaves was *A. melanogenum* (82.3%), followed by *Vishniacozyma siamensis* sp. nov. (17.6%). Moreover, eight new yeast species belonging to six genera were discovered and characterized using polyphasic taxonomy. Evaluation of antagonistic activity of all yeast strains against *Penicillium allii* PG1, the causal agent of blue mold disease on shallot and garlic, was carried out by a dual culture method. Thirty-three strains were able to inhibit the mycelial growth of *P. allii* PG1 with 34.8–48.9% of inhibition. The investigation of antagonistic mechanism revealed that all 33 yeast strains were capable of producing cell wall-degrading enzymes (chitinase and glucanase). Additionally, 14 strains were found to produce volatile organic compounds (VOCs) that capable of inhibiting fungal growth. This study suggests that the mangrove environment is a good source of yeasts and a promising source of antagonistic yeasts.

KEYWORDS:

yeasts; mangrove forest; post-harvest pathogenic fungi; garlic; shallot

A Novel Epiphytic Fungal Species in the Genus *Clonostachys* from Mangrove Leaves Exhibiting Promising Mycoparasitic Traits

Ananya Sahathippayakul¹, Vassana Supapongsri¹, Chatree Maknual², Nawin Phormsin², Pradittha Nueakaeo² and Piyangkun Lueangjaroenkit^{1,3,*}

¹Department of Microbiology, Faculty of Science, Kasetsart University, Bangkok, 10900, Thailand

²King Rama IX International Mangrove Botanical Garden, Department of Marine and Coastal Resources (DMCR), 99 Nong Bua Sub-district, Muang District, Chanthaburi 22000, Thailand

³Biodiversity Center Kasetsart University (BDCKU), Bangkok 10900, Thailand

*Corresponding author, e-mail: Piyangkun.lu@ku.th

ABSTRACT:

Two epiphytic fungal strains were isolated from the leaves of *Ceriops tagal* (Perr.) C.B. Rob., collected at the King Rama IX International Mangrove Botanical Garden in Chanthaburi, Thailand. These isolates, designated DMKU-RG2M15 and DMKU-RG2P11, were identified using morphological traits and multilocus sequence analysis of the internal transcribed spacer (ITS), beta-tubulin (*tub2*), and translation elongation factor 1-alpha (*tef-1α*) genes. The fungi produced verticillium-like primary and secondary conidiophores bearing oval to ellipsoidal conidia. Compared to their closest relative, *Clonostachys viticola*, these isolates exhibited shorter conidiophores, smaller conidia, and an inability to grow at 35 °C - a feature distinguishing them from related species. BLASTN results revealed high similarity to *C. viticola*, but with notable nucleotide differences: 9 substitutions (1.80%) in the ITS region, 10 substitutions (3.07%) in *tub2*, and 12 substitutions (2.84%) in *tef-1α*. Phylogenetic analysis based on concatenated ITS, *tub2*, and *tef-1α* sequences confirmed that these isolates formed a distinct and well-supported clade, separate from all previously known species. Based on these morphological and molecular differences, the two isolates are proposed as a novel species in the genus *Clonostachys*. Remarkably, this species also exhibited mycoparasitic activity against *Collectotrichum siamense* DMKU-CG5, underscoring its potential application as a natural biocontrol agent against plant-pathogenic fungi in sustainable agriculture.

KEYWORDS:

Clonostachys; Epiphytic fungi; Leaf surface; Mangrove; Mycoparasitism; Novel fungi

Fungus-Growing Termites in Huay Tak Teak Biosphere Reserve, Ngao, Lampang Province

Chanjira Ayawong¹ and Itsarapong Voraphab^{1,*}

¹Forest Entomology and Microbiology Research Group, Forest and Plant Conservation Research Office, Department of National Parks, Wildlife and Plant Conservation, Bangkok 10900, Thailand

*Corresponding author, e-mail: itsarapong.dnp@gmail.com

ABSTRACT:

The Huay Tak Teak Biosphere Reserve represents a biodiversity conservation area of significant ecological importance, recognized internationally by the United Nations Educational, Scientific and Cultural Organization (UNESCO). Beyond its conservation value, this area serves as a vital resource for surrounding local communities who utilize various forest products for subsistence. Termite mushrooms (*Termitomyces* spp.) constitute one of the most extensively harvested and consumed wild mushroom species in the region, maintaining an obligate symbiotic relationship with fungus-growing termites. This study aimed to investigate the diversity of termite species through direct sampling along established nature trails across four survey sites: Tham Pha Thai National Park, Huay Tak Arboretum, Forest Research and Conservation Center No. 1 (Lampang), and Ban Pong Forest Reserve. The result showed that termite total of 28 species 9 genera across 2 families. Among these, fungus-growing termites comprised 5 genera with 15 species: *Ancistrotermes* (1 species: *A. pakistanicus*); *Hypotermes* (1 species: *H. makhamensis*); *Microtermes* (2 species: *M. obesi* and *Microtermes* sp. 1); *Macrotermes* (3 species: *M. annandalei*, *M. gilvus*, and *Macrotermes* sp. 1); and *Odontotermes* (8 species: *O. feae*, *O. longignathus*, *O. oblongathus*, *O. takensis*, and *Odontotermes* spp. 1-4). These findings provide essential baseline data for sustainable management planning of the biosphere reserve and establish a taxonomic database for future investigations into species-specific termite mushroom cultivation. The documented diversity contributes valuable information toward the development of sustainable resource utilization strategies that balance conservation objectives with community needs for forest-derived resources.

KEYWORDS:

diversity, termite, *Termitomyces* spp., Huay Tak Teak Biosphere Reserve

Identification of *Colletotrichum* spp. causing anthracnose in economic mature fruits using morphological and sequences of *actin* and *chitin synthase* genes data

Maliwan Nakkuntod^{1,*} and Worachayut Muakyod¹

¹Department of Biology, Faculty of Science, Naresuan University, Phitsanulok, 65000, Thailand

*Corresponding author, e-mail: maliwann@nu.ac.th

ABSTRACT:

Anthrachnose is caused by *Colletotrichum* species, which damage many economically important crops. Each *Colletotrichum* species can infect various plants, and each plant species may be attacked by one or more fungal species. The aims of this study were to identify and characterize the morphology of *Colletotrichum* isolates from 3 samples of each banana, dragon and mango fruits, as well as to study their genetic diversity. The results presented at 2, 1, and 7 fungal isolates, respectively. Among these 10 isolates, colonies from banana exhibited white mycelia with orange conidia at the center, while those from dragon fruit had white mycelia. The colonies from mango fruit showed either white mycelia with a yellowish-brown coloration or grayish-black mycelia. Generally, shape of conidia was cylindrical shape. Based on DNA sequencing and phylogenetic analyses of the *actin* (*ACT*) and *chitin synthase* (*CHS-I*) genes, fungal isolates were identified as *C. musae* (2 isolates), *C. fructicola* (1 isolate) and *C. asianum* (7 isolates). This knowledge of the pathogens causing anthracnose in various host plants contributes to the management of the disease both pre- and post-harvest.

KEYWORDS:

anthracnose; *Colletotrichum*; fungi; *actin* gene; *chitin synthase* gene

Selection of microorganisms as feed supplement to improve the growth performance of black soldier fly (*Hermetia illucens* L.)

Suvisit Wiruchkul^{1,*} and Jureemart Wangkeeree¹

¹Department of Agricultural Technology, Faculty of Science and Technology, Thammasat University, Rangsit Campus, Pathum Thani, 12120, Thailand

*Corresponding author, e-mail: suvisit.wiru@dome.tu.ac.th

ABSTRACT:

The black soldier fly (BSF; *Hermetia illucens* L.) larvae contain a high-quality nutrition and it is an alternative protein source for animal feed. This study was aimed to select bacteria and fungi for use in combination with feeding substrates to enhance the growth performance and body composition of BSF larvae. Five isolates of bacteria, including *Rhodococcus* sp., *Lactobacillus buchneri*, *Bacillus subtilis*, *Bacillus licheniformis* and *Lactobacillus plantarum* and five isolates of fungi, including *Aspergillus flavus*, *Aspergillus fumigatus*, *Aspergillus oryzae*, *Aspergillus niger* and *Trichoderma reesei* were tested for their effect on larvae weight, by supplement in standard diet (chicken feed and soy bean residue). Result show that the most effective promote the growth of BSF larvae were *L. buchneri* and *A. oryzae*, which resulted in the highest average larvae weight of 382.58 and 335.02 mg per individual. Subsequently, the effects of *L. buchneri* and *A. oryzae* supplement with agriculture wastes, including soybean residue and palm kernel cake were investigated, compared with a standard diet. Results show that standard diet supplemented with *L. buchneri* and *A. oryzae* had the highest average weights of 271.26 and 252.38 mg per individual, with corresponding highest dry weights of 78.73 and 61.93 mg per individual, respectively. However, microbial supplementation in soybean residue and palm kernel cake did not significantly improve larval weight compared to non-supplemented group. The group of standard diet supplemented with *L. buchneri* showed the shortest larva and prepupa development periods, at 17.75 and 9.29 days, respectively, and exhibited the highest lipid content at 43.82%. However, larva fed with soybean residue supplemented with *L. buchneri* had the highest protein content, at 54.27%. For conclusion, *L. buchneri* is the greater to the other isolates as a feed additive and supplement with standard diet was recommended for BSF larvae. Nevertheless, microbial supplementation in agricultural waste appeared inappropriate in term of growth performance.

KEYWORD:

black soldier fly, *Hermetia illucens*, microbial feed supplement, growth performance

Diatom-based Water Quality Assessment via Morphological and eDNA Approaches in Lake Buluan, Mindanao, Philippines

Claudine Ann Nakila^{1,2*} and Sharon Rose Tabugo^{1,2}

¹Department of Biological Sciences, College of Science and Mathematics, Mindanao State University-Iligan Institute of Technology, Andres Bonifacio Ave., Tibanga, Iligan City, 9200 Lanao del Norte, Philippines

²Molecular Systematics and Conservation Genomics Laboratory, Center for Biodiversity Studies and Conservation (CBSC), Premier Research Institute of Science and Mathematics (PRISM), Mindanao State University-Iligan Institute of Technology, Andres Bonifacio Ave., Tibanga, Iligan City, 9200 Lanao del Norte, Philippines

*Corresponding author's email: claudineann.nakila@g.msuiit.edu.ph

ABSTRACT:

Diatoms play an essential role in freshwater ecosystems, contributing to primary production and serving as sensitive indicators of environmental change. Their adaptability to thrive under various ecological conditions makes them ideal for assessing water quality, especially in aquaculture-impacted habitats. This study examined diatom communities in Lake Buluan, Mindanao, Philippines, using both morphological identification and environmental DNA (eDNA) metabarcoding of the 18S rRNA gene (V4 region), sequenced on the Illumina MiSeq platform. Microscopy revealed *Nitzschia*, *Navicula*, *Synedra*, and *Sellaphora* as the most abundant genera, reflecting nutrient enrichment. eDNA metabarcoding generated five amplicon libraries analyzed with the Parallel-Meta-Suite software, yielding total of 24,686 amplicon sequence variants (ASVs) across 52 families and 84 genera. The molecular data revealed a complementary assemblage dominated by green algae such as *Chlamydomonas reinhardtii*, *Scenedesmus acutus* (an indicator of nutrient-rich conditions), and the colonial alga *Pseudopediastrium boryanum*. Notably, *Nitzschia* was the only diatom genus detected in the eDNA dataset. Several eDNA-detected taxa are known indicators of eutrophication and organic pollution. Higher alpha diversity was observed outside the fish pens, indicating more stable ecological conditions, while samples inside were dominated by smaller, potentially pollution-tolerant taxa. This study highlights the synergistic power of classical and molecular methods to comprehensively characterize phytoplankton assemblages and provides baseline data for ecological monitoring and sustainable aquaculture management.

KEYWORDS:

amplicon sequence variants (ASVs); aquaculture; diatom; eDNA; water monitoring.

Microalgal extract as a biostimulant inducing rice growth and defense against rice blast fungus

Wuthichai Srisuwan^{1,*}, Chatchawan Jantrasuriyarat¹ and Anchalee Sirikhachornkit¹

¹ Department of Genetics, Faculty of Science, Kasetsart University, Bangkok, 10900, Thailand

*Corresponding author, e-mail: anchalee.si@ku.th

ABSTRACT:

Rice blast disease, caused by a rice blast fungus, *Magnaporthe oryzae*, poses a significant threat to global rice production, leading to annual yield losses of 10%–30% and, potentially resulting in total crop failure. The necrotic lesions induced by the disease reduce photosynthetic efficiency, thereby compromising food security worldwide. As concerns over the environmental and health impacts of chemical fungicides continue to grow, farmers are increasingly seeking sustainable alternatives. Among these, algae-based biostimulants have emerged as promising, environmentally friendly options. These biostimulants are rich in bioactive compounds, including polysaccharides, phytohormones, polyunsaturated fatty acids (PUFAs), and amino acids, which not only promote plant growth and yield but also enhance plant defense mechanisms. One of their key modes of action involves the induction of damage-associated molecular patterns (DAMPs), which can trigger systemic acquired resistance (SAR) in plants. In this study, we investigated the potential of the green microalga *Chlamydomonas reinhardtii*, a well-established model organism for photosynthesis, as a biostimulant. This alga is particularly promising due to its high content of polysaccharides and phytohormones, which are known to act as elicitors of DAMPs and phytohormones to induce plant growth. *C. reinhardtii* was cultured in Tris-Acetate-Phosphate (TAP) medium for seven days. Rice leaves were then treated with the algal extract, incubated for one hour, and subsequently inoculated with *M. oryzae* spores (1×10^5) using the punch inoculation method. The inoculated leaves were maintained under dark, humid conditions, and disease symptoms were monitored over five days. Lesion length, width, and area were measured across four treatment groups. Preliminary results revealed significant differences in lesion parameters among treatments, suggesting that *C. reinhardtii* extract may be effective in mitigating the symptoms of rice blast disease. This research aligns with Sustainable Development Goal (SDG) 2: Zero Hunger, particularly Target 2.1, by exploring innovative, sustainable, and non-toxic strategies to protect rice crops. The findings underscore the potential of algae-based solutions to enhance agricultural resilience and support global food security.

KEYWORDS:

algae-biostimulant; *Chlamydomonas reinhardtii*; *Oryza sativa*; *Magnaporthe oryzae*; plant defenses responses.

SESSION 2

BIODIVERSITY AND HEALTH



INVITED SPEAKER 2-1:

Ethnobotany of the Thai flora

Henrik Balslev

Department of Biology, Aarhus University, DK-8000 Aarhus C., Denmark

*Corresponding author, e-mail: henrik.balslev@bio.au.dk



ABSTRACT:

From a beginning ethnobotany was a very narrative and descriptive activity focusing on indigenous peoples' use of plants. Later, ethnobotany was inspired by more analytical approaches, mostly based on research in plant ecology. With this change ethnobotany started using a series of concepts and indices which transformed it into a quantitative science. With the quantitative approach it became possible to make comparative studies, for instance between plant uses among different ethnic groups, or between age groups focusing on the breakdown of traditional knowledge. Finally, in the last decade, ethnobotany has focused on the usefulness of the research, and in this context specifically its contribution to the United Nation's 17 Sustainable Development Goals (SDGs).

Ethnobotany is a very field-oriented kind of research. Data are gathered among the ethnic groups studied by field observations and, in particular, by using interviews with informants. Interview techniques vary from open ended interviews with informants to more strictly planned and structured interviews with pre-defined questions. The questions involve information about the informants (gender, age, occupation, healer/general villager, etc.) and then the questions related to their use of plants. The plants mentioned in the interviews should be vouchered with well-preserved herbarium specimens, which are eventually deposited in a recognized herbarium. The questions related to the plants should involve what they are used for, which part of the plant is used, and how it is prepared for that use. All data should be collected so it is represented as a "use record" which includes information about a particular part of a species which is used by a particular person (informant), at a particular place (village) at a particular time (date of interview). When the data is broken down to this basic unit it can be used to answer almost any question concerning the ethnobotany of a particular group in a particular place, and also for making comparative studies. Such comparative studies can be between ethnic groups, genders, age-classes and much more. Local knowledge about medicinal uses of plants has helped humans to combat disease from time immemorial. Such knowledge can be transmitted from generation to generation, diffused from neighboring villages, or produced *de novo*, for example based on similarity to other already known medicinal plants. Sometimes plant uses are based on the *doctrine of signatures* according to which the shape of a plant part leads people to associate it with the form of human organ and thereby apply it for treatment of that organ. But it is well documented that traditional plant-based medicines often include phytochemical compounds with physiological effects in the treatments. Because many medicinal plants used locally actually have pharmacological efficacy, traditional knowledge of medicinal plants is an invaluable source of information for discovery of plant derived active compounds used in the modern pharmaceutical industry. Pharmaceutical companies around the world constantly develop new medicines derived from plants. However, the process leading to drug discovery requires enormous amounts of time and funding, and a large numbers of laboratory experts and scientists. In this context ethnobotanical knowledge of traditional medicines can lead developers to new discoveries while reducing the costs of doing so.

KEYWORDS:

descriptive, quantitative, comparative, methodology, drug discovery

INVITED SPEAKER 2-2:

Diversity of Plants, Animals and Minerals in Thai Traditional Medical Wisdom

Chayan Picheansoonthon, Ph.D.

Professor of Pharmacy, and Fellow of The Royal Society of Thailand Academy of Science of The Royal Society of Thailand



ABSTRACT:

Thai Traditional Medicine has a well-structured pharmacological system, with a clear framework for formulating remedies by defining the roles of medicinal ingredients as principal drugs, auxiliary drugs, and complementary drugs, each in differing proportions. The Thai ancestors possessed extensive knowledge of diverse materia medica, most of which were derived from local plants and animals, though some came from distant regions. Later, through international trade and cultural exchange, valuable medicinal ingredients from other medical traditions were integrated into Thai traditional medical formulations, enriching and shaping the unique identity of Thai medicine.

A prominent example is found in the “Treatise on the Remedies of King Narai”, a royal compendium of 81 prescriptions prepared by court physicians for the King. This treatise employs more than 300 substances, including botanicals, zoological materials, and mineral substances—though plants formed the majority. These prescriptions illustrate both the remarkable biodiversity of the region and the ancestral wisdom in harnessing it.

The breadth of biodiversity in Thai medical knowledge is also reflected in the classification of materia medica into a so-called “Groups of Drugs” with similar tastes and therapeutic properties, a system that facilitated both the creation and the transmission of Thai traditional formulations. For instance, “The Nine Kesorns” (Keson Thang Kao) consists of flowers and stamens from nine plant species: *Mimusops elengi* L. (pikun), *Mesua ferrea* L. (bunnak), *Magnolia champaca* (L.) Baill. ex Pierre var. *champaca* (champa), *Mammea siamensis* (T.And.) Kosterm. (sarapee), *Jasminum sambac* (mali), (stamens of) *Nelumbo nucifera* Gaertn. (bua laung), *Cananga odorata* (kradang-nga), *Melodorum fruticosum* Lour. (lamduan), and (male inflorescence of) *Pandanus odoratissimus* L.f. (lamchiak). Likewise, “The Nine Shells” (Naowa Hoi) is composed of nine types of shells: *Filopaludina* spp. (hoi khom), *Saccostrea* spp. (hoi e-rom), *Anadara granosa* Linnaeus (hoi kraeng), *Cerithidea obtusa* (Lamarck) (hoi jub-jaeng), *Strombus* spp. (hoi sang), *Turbo* spp. (hoi ta woa), *Physunio* spp. (hoi kab), *Pinctada* spp. (hoi muk), and *Pholas orientalis* Gmelin (hoi pimpagarang).

Mineral substances, too, were widely employed in traditional Thai remedies, such as red orpiment, table salt, cinnabar, and alum. Thus, the study of materia medica used in traditional formulations may serve as a method of **rapid biodiversity appraisal**, offering insight into both the natural resources and the cultural heritage embedded in Thai Traditional Medicine.

KEYWORDS:

Thai Traditional Medicine, The Nine Kesorns, The Nine Shells

ORAL PRESENTATION

SESSION 2



Household case-bearing moths (Lepidoptera: Tineidae, *Phereoeca uterella*) as a possible bioindicator for microplastic pollution

Miss Punyisa Churboonmee^{1,*}, Mr. Chawakorn Tangpraditchai¹, Mr. Latthichai Bupha¹ and Assoc. Prof. Dr. Teang-On Prommi²

¹Kasetsart University Laboratory School Kamphaeng Saen Campus Educational Research and Development Center, Nakhon Pathom, 73140, Thailand

²Department of Biological Sciences and Innovation, Faculty of Arts and Sciences, Kamphaeng Saen Campus, Nakhon Pathom, 73140, Thailand

*Corresponding author, e-mail: punyisapun0012@gmail.com

ABSTRACT:

Microplastics (MPs) have become a major problem in the context of environmental contamination, with a particular emphasis on their prevalence in indoor environments such as residences and university campuses. This study investigates the presence and characteristics of microplastics in a terrestrial insect, *Phereoeca uterella*, that feeds on indoor/outdoor dust from university and residential environments for five months. The initial examination of MPs in insects was physical characterization using stereomicroscopy, with a focus on identifying MPs by shape, size, and color. Several types of MPs, including fibers, fragments, spheres, and rods, were discovered, with blue and violet being the most common colors. The majority of MPs observed were fibers, ranging in size from 100 to 500 μm . House 3 had the highest average of MP items per individual (4.45 ± 5.13), while House 1 had the lowest (1.92 ± 2.31). Subsequent chemical characterization was conducted using FTIR, revealing the presence of 23 different types of MPs, including cellulose acetate, poly(vinyl propionate), poly(vinyl acetate), cellulose propionate, poly(vinylpyrrolidone), and vinyl alcohol/vinyl acetate. These polymers are widely utilized in textiles, furniture, carpeting, packaging, and synthetic fibers. The statistical analysis was carried out with the Statistics 20.0 program. The number of MPs varied significantly throughout the various indoor environments investigated. This research is the first to use terrestrial insects to comprehensively examine MPs in four distinct indoor habitats. Finding and eliminating MP contamination in these places could raise awareness, encourage in-depth research, and make it easier to create well-informed regulations.

KEYWORDS:

Household case-bearing moths; indicators; indoor environment; microplastics.

Assessing marine plankton community assemblages in selected areas of Illana Bay, Celebes Sea, and Sangay-Paril Kalamansig, Philippines

Rande B. Dechavez^{1,*}, Rodelyn M. Dalayap², Ziljih S. Molina² and Sharon Rose M. Tabugo³

¹Faculty of College of Fisheries, Sultan Kudarat State University, Kalamansig, Sultan Kudarat, 9808, Philippines

²Faculty of Biology Department, Sultan Kudarat State University, Tacurong City, 9800, Philippines

³Faculty of Biological Science Department, Mindanao State University-Iligan Institute of Technology, Iligan City, 9200, Philippines

*Corresponding author, e-mail: randedechavez@sksu.edu.ph

ABSTRACT:

Illana Bay, Celebes Sea, and Sangay-Paril, Kalamansig are marine biodiversity hotspots and economically critical marine areas that support fisheries in Mindanao Island. This study was conducted to assess marine plankton, as they play a crucial role in maintaining the health of marine ecosystems. Plankton, including phytoplankton, zooplankton, algae, fungi, and bacteria play a vital role in fisheries, as they are crucial components of marine food chains. eDNA metabarcoding was used to analyze plankton. A total of 67 eDNA plankton species, with 10 genera belonging to Calanoida, Siphonophorae, Oikopleuridae, Diliolida, Harpacticoida, Gynodinium, Micromonas, Galeidinium, Plagiogrammopsis, and Tetrastelmis; and 11 families comprising Copepoda, Mamiellales, Peridiniales, Copelata, Mediophyceae, Chlorodendreales, Bacillariophyceae, Thaliacea, Dinophyceae, Gymnodiniophycidae, and Oligotrichia were recorded. The Parallel-Meta Suite (PMS) pipeline with the reference sequence database SILVA 18S rRNA was used to determine the diversity of plankton. Bacteria were the dominant group across all three sites, constituting a significant proportion of the planktonic community. The Celebes Sea has a more diverse planktonic community. Principal component (PC) analysis of water pH, temperature, salinity, sites, and marine habitat types for plankton revealed distinct clusters of taxa, indicating that certain plankton groups are more closely related based on their habitat types and physicochemical parameters. The phytoplankton *Cylindrotheca closterium* and *Psammodyctyon panduriforme* clustered together, indicating similar physicochemical parameters and habitat types. *Galeidinium rugatum* and *Karlodinium veneficum* were more tolerant to higher temperatures within the range of 32-34°C, indicating that water temperature is an essential factor influencing the distribution of these plankton taxa. These findings offer insights into plankton community assemblages for assessing marine ecosystem health amidst climate change. It is recommended to consider the season for sampling, as it can influence the concentration of eDNA in marine ecosystems.

KEYWORDS:

Diversity; eDNA; genera; marine habitat; physicochemical

***Amblyomma* (bont ticks) of Southeast Asia: an overview on its diversity, host associations, and associated pathogens**

Ace Kevin S. Amarga^{1,2,*} and Ming-Chung Chiu¹

¹Department of Entomology, National Taiwan University, Taipei 106, Taiwan

²International Union for Conservation of Nature Species Survival Commission (IUCN SSC) Parasite Specialist Group

*Corresponding author, e-mail: ace_amarga061@yahoo.com

ABSTRACT:

Hard ticks (Ixodidae) are one of the most important arthropod groups that transmit disease in humans and a wide range of animals. Currently, this family contains more than 700 species, many of which remain understudied and are considered species complexes. The third largest genera of Ixodidae, *Amblyomma* Koch (bont ticks), currently comprise more than 130 extant species distributed across all zoogeographic realms.

This genus exhibits the most elaborate scutal ornamentation ranging from light hues on reticulated lines to iridescent colorations. *Amblyomma* ticks exhibit a wide range of host utilization, and are known as important vectors of zoonotic pathogens including *Borrelia* and *Rickettsia*. Despite its medical and veterinary importance, many Asiatic bont ticks associated with wildlife vertebrates are relatively understudied, especially on several aspects of their natural history. In this paper, we present an overview of the diversity, host associations, and roles of *Amblyomma* species as vectors of tropical zoonotic pathogens on Asiatic wildlife vertebrates. In addition, using field collected specimens and museum preserved materials, we have recent discoveries on the distribution records and host associations of bont ticks across Southeast Asia, including the Philippines, Myanmar, and Thailand. Furthermore, gaps and future works on *Amblyomma* research in Southeast Asia will also be discussed.

KEYWORDS:

Ectoparasites, Ixodidae, Southeast Asia, vector, wildlife.

POSTER PRESENTATION

SESSION 2



GreenRx Platform: Harnessing Biodiversity for Microbiome Driven Allergy Prevention

Parin Duangekanong^{1,*}

¹Ramkhamhaeng Advent International School, Bangkok, 10240, Thailand

*Corresponding author, e-mail: sernparin@gmail.com

ABSTRACT:

Rapid urban expansion in Thailand is strongly correlated with the rising incidence of allergic diseases and chronic inflammatory conditions, particularly among urban populations with diminished access to green spaces. The Biodiversity Hypothesis posits that reduced exposure to environmental microbial diversity impairs the development of the human microbiota, thereby compromising immunoregulatory functions and increasing susceptibility to immune-mediated disorders. A preliminary study conducted in Bangkok revealed that individuals residing within a 3-kilometer radius of urban green spaces exhibited a 25% higher expression of interleukin-10 (IL-10) in peripheral blood mononuclear cells (PBMCs) compared to control groups ($p < 0.05$), indicating enhanced immunoregulatory capacity.

This article proposes a conceptual framework for leveraging environmental biodiversity to enhance immune resilience in urban settings. It introduces the GreenRx Platform—an integrative health innovation that synthesizes microbial data, ecological knowledge, and digital technology to promote equitable and continuous access to nature in daily life.

The GreenRx Platform offers personalized health recommendations by integrating microbiome analysis with real-time environmental data. It employs GPS-based tools to identify nearby green spaces, monitors pollen and air quality indices, and tracks individual health behaviors, thereby supporting the restoration of immune homeostasis through nature-based interventions.

The findings underscore the need to incorporate biodiversity-informed strategies into public health and urban planning policies. The article advocates for further microbiome-immunity research in the Thai context and calls for the continued development of the GreenRx Platform as a scalable digital health solution, reinforced by proactive health communication through community and digital outreach.

KEYWORDS:

Biodiversity; Immunity; Microbiota; Health Platform

Exploring the gut microbiota of *Holothuria atra*: A marine reservoir of bacteria with promising health applications

Mary Grace Ereguero^{1,2,*}, and Sharon Rose Tabugo^{1,2}

¹Department of Biological Sciences, College of Science and Mathematics, Mindanao State University-Iligan Institute of Technology, Iligan City, 9200, Philippines

²Molecular Systematics and Conservation Genomics Laboratory, Center for Biodiversity Studies and Conservation, Premier Research Institute of Science and Mathematics, MSU-Iligan Institute of Technology, Iligan City, 9200, Philippines

*Corresponding author, e-mail: marygrace.ereguero@gmail.com

ABSTRACT:

Sea cucumbers are benthic invertebrates that play an important ecological role in marine environment, such as bioturbation and nutrient recycling. Aside from their ecological importance, they are widely used in Asian cuisines and traditional medicine. Sea cucumbers have a long history of use in Asian medicine, and researchers have isolated a range of pharmacologically active compounds from these species. These species host a diverse and abundant array of microorganisms, and several natural products from these species exhibit structural similarities of those microbial origins, suggesting that microorganisms are possibly the true producers of these marine natural products. Metabarcoding analysis, particularly focusing on the 16S rRNA gene, was performed to assess the bacterial composition of the gut of *Holothuria atra*. The microbiome's functional composition at the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway level were predicted using Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt). Results revealed a bacterial community make up of four phyla, Acidobacteria, Actinobacteria, Firmicutes, and Proteobacteria. Notable genera were recorded, many of which have documented or emerging therapeutic applications. The predicted KEGG functions unveiled a diverse range of pathways such as biosynthesis of secondary metabolites metabolism of cofactors and vitamins, xenobiotic degradation, amino acid and lipid metabolism, and various cellular processes related to replication, repair, and membrane transport. The presence of such functionally versatile bacteria in *H. atra*'s gut underscores its significance not only as marine dietary resource but also as a potential source of beneficial microbes for therapeutic applications. The results of this study highlight the gut microbiome of marine invertebrates as a promising underexplored source of bioactive microbial symbionts. Given the promising therapeutic potential of the microbes associated with sea cucumbers, conservation efforts can be complemented by culturing these beneficial microbes, offering a sustainable alternative to the host species.

KEYWORDS:

Bacteria; gut; *Holothuria atra*; KEGG; microbiota; sea cucumber

Relationships between immunological character and herbicide contamination in rodents living in low land agricultural area in Nan province

Kasidit Rison^{1,*} and Julien Claude^{1,2}

¹Department of Biology Faculty of Science, Chulalongkorn University, Bangkok, 10330, Thailand

²Institut des Sciences de l'Evolution UM/CNRS/IRD/EPHE, Montpellier, 34090, France

*Corresponding author: rkasidit47@gmail.com

ABSTRACT:

Rodents are key reservoirs for zoonotic pathogens in agricultural landscapes, where they are frequently exposed to herbicides applied for crop management. However, the combined implications of such exposure for rodent biodiversity and health remain poorly understood, especially in Thailand. This study aims to investigate species diversity and assess the relationships between herbicide exposure and immune function in agricultural rodents. Field sampling was conducted between May 2024 and May 2025 in Nan Province, where rodents were live-trapped in paddy fields and surrounding corn fields. A total of four species were recorded: *Bandicota indica*, *B. savilei*, *Rattus exulans*, and *R. tanezumi*. Collected specimens were measured and sampled for blood serum and liver tissue for subsequent immunological and toxicological analyses. In addition, soil and water samples were collected from trapping sites to evaluate environmental herbicide contamination. Although laboratory assays are ongoing, this research will assess immunoglobulin concentrations, cholinesterase activity, and herbicide residue levels in both rodents and environmental matrices. The results are expected to contribute to a better understanding of how agricultural chemicals influence rodent community composition and health, with potential implications for disease dynamics and ecosystem management. This study highlights the importance of integrating biodiversity monitoring, ecotoxicology, and wildlife health assessments to inform sustainable agriculture and public health strategies in Thailand.

KEYWORDS:

Ecotoxicology, Herbicide, Immunoglobulin, Paddy fields, Rodents

Effect of Bisphenol-A on Human colon epithelial cells

Nattanicha Sakulpaet^{1,*}, Laksika Petmune¹, Mariam Watthanard¹ and Chittipong Tipbunjong²

¹Hatyaiwittayalai School, Songkhla 90110, Thailand

²Department of Anatomy, Faculty of Science, Prince of Songkla University, Songkhla 90110, Thailand

*Corresponding author: withwnattanicha@gmail.com

ABSTRACT:

Bisphenol-A (BPA) is commonly used in the production of plastic food containers, such as water bottles, infant bottles, and other food packaging. This method has the potential to contaminate food and cause health risks. The objective of this research was to investigate the impact of BPA on human colon epithelial cells, which are essential for absorption of various nutrients. Different concentrations of BPA were introduced into the culture medium of human colon epithelial cells. The MTT assay was used to measure cytotoxicity, while tubulin protein and KI-67 antibody immunostaining and cell counting were used to measure cell proliferation. The production of reactive oxygen species (ROS) was quantified using H2-DCFDA, and nuclear staining was conducted using Hoechst dye.

This study examined the effects of Bisphenol-A (BPA) on human colon epithelial cells by exposing them to 6 concentrations (0, 1.25, 2.5, 5, 7.5, 10 µg/mL) and assessing cell viability, proliferation, and reactive oxygen species (ROS) production. Cytotoxicity was evaluated using the MTT assay after 24, 48, and 72 hours of BPA treatment. Cell proliferation was measured through cell counting and immunofluorescence staining with KI-67 and tubulin markers, while ROS generation was detected using H2-DCFDA staining. Results showed that BPA concentrations up to 5 µg/mL did not significantly affect cell viability, whereas higher concentrations (7.5 and 10 µg/mL) caused dose-dependent cytotoxicity and reduced proliferation. Additionally, ROS levels increased with rising BPA concentrations, indicating oxidative stress. These findings suggest that elevated BPA exposure impairs colon epithelial cell survival and growth through increased oxidative damage.

KEYWORD:

Bisphenol-A; plastic; proliferation; reactive oxygen species; toxicity

Cyanobacterial biodiversity from Thai karstic caves as a potential source for antioxidant bioactive compounds

Wanthanee Khetkorn^{1,*}, Kasinee Kula¹, Kanaporn Sujarit¹, Thanasak Lomthong¹ and Sutthawan Suphan¹

¹Division of Biology, Faculty of Science and Technology, Rajamangala University of Technology Thanyaburi, Pathum Thani 12110, Thailand

*Corresponding author, e-mail: wanthanee_k@rmutt.ac.th

ABSTRACT:

Cyanobacteria are microorganisms that are highly adaptive and capable of surviving in severe environments. They have outstanding biotechnology potential, including the capacity to produce value-added compounds. The karstic caves are extreme environments with low light and nutrient availability, which are interesting areas for exploring cyanobacterial biodiversity as a potential source for antioxidant bioactive compounds. This research aimed to isolate cyanobacteria from the 23 karstic caves in Thailand. All isolates were morphotyped and identified as 86 species and 12 genera, with *Leptolyngbya* as the typically abundant species. The isolated cyanobacteria were cultured in BG11 medium under low light intensity ($10 \mu\text{mol m}^{-2}\text{s}^{-1}$) for three weeks before cells were collected to extract bioactive compounds. The results found that crude extracts from karstic cave cyanobacterial strains contained many bioactive molecules, including chlorophyll *a*, carotenoids, phenolic acids, and flavonoids. The contents were varied based on the species. The 24 strains exhibited effective antioxidant properties regarding DPPH radical scavenging activity. There were seven cyanobacterial species, namely *Chroococcus* sp. SRK01, *Anabaena* sp. SRK02, *Oscillatoria* sp. SW04, *Nostoc* sp. CHK02, *Synechococcus* sp. CHK03, *Leptolyngbya* sp. LP01, and *Leptolyngbya* sp. LKK14 showed 100% DPPH radical scavenging activity at 1.0 mg mL^{-1} of crude extract. The highest antioxidant activity, with an IC_{50} value of $55.6 \mu\text{g mL}^{-1}$, was found in strain *Leptolyngbya* sp. LP01. The LC-MS/MS analysis of crude extract revealed a variety of secondary metabolites with antioxidant properties. Consequently, cyanobacteria are a prospective and alternative candidate for identifying new chemical leads for industrial applications in pharmaceuticals, nutraceuticals, and biomolecules of significance. Furthermore, the predominant presence of antioxidant bioactive compounds in cyanobacteria species may indicate their adaptation strategies against abiotic stresses, essential for their ecological success in habitats.

KEYWORDS:

Cyanobacteria; biodiversity; karstic cave; bioactive compounds; antioxidant

Diversity and Antimicrobial Potential of Actinobacteria Isolated from Mekong River Sediments

Thanida Hemchinakun¹, Thanasak Lomthong¹, Neeraya Pakeetum¹, Nongnapat Insee¹, Sutthawan Suphan¹, Wanthanee Khetkorn¹ and Kanaporn Sujarit^{1,*}

¹Division of Biology, Faculty of Science and Technology, Rajamangala University of Technology Thanyaburi, Pathum Thani 12110, Thailand

*Corresponding author, e-mail: kanaporn_s@rmutt.ac.th

ABSTRACT:

The Mekong River, known for its ecological richness, contains mineral-rich sediments that support diverse microbial life. This study focused on exploring the diversity and antimicrobial properties of actinobacteria isolated from sediments of the Mekong River. A total of 147 actinobacterial isolates were collected. Based on morphological traits, these isolates were grouped into two categories: streptomycetes and non-streptomycetes, which included genera such as *Actinomadura*, *Micromonospora*, *Nocardia*, *Nonomuraea*, and *Brevibacterium*. Representative isolates with similar colony morphology were classified using 16S rRNA gene sequencing, leading to the identification of 17 major groups based on their genetic similarity to established reference strains. Among these, 20 species of *Streptomyces* were identified, with *Streptomyces rhizosphaericus* being the most prevalent. The antimicrobial potential of the isolates was assessed using a disc diffusion assay on culture supernatants. Nineteen isolates demonstrated the ability to inhibit the growth of bacteria, yeasts, and fungi. Notably, the crude extract from isolate 48 M1PS-8 showed the strongest activity against *Candida albicans* ATCC 10231, with a minimum inhibitory concentration (MIC) of 0.50 mg/ml. Meanwhile, the extract from 57 M1PS-17 displayed the most potent inhibition against *Colletotrichum siamense*, with an MIC of 0.25 mg/ml. Both isolates demonstrated the ability to produce amylase and protease enzymes but showed no activity for cellulase or lipase. Phylogenetic analysis identified both 48 M1PS-8 and 57 M1PS-17 as *Streptomyces hygroscopicus*. Further analysis of secondary metabolites in the 57 M1PS-17 extract using liquid chromatography-mass spectrometry (LC-MS/MS) revealed over 31 identifiable compounds. The identified metabolites were categorized into three main groups: antifungal agents (e.g., diethyldithiocarbamate, streptodiketopiperazine A, erucamide), antibacterial compounds (e.g., hygromycin A, cyclo(D)-pro-(D)-phe, xylariolide C, oleamide), and dual-activity compounds (e.g., acetophenone, sporovexin C). This finding highlights the Mekong River sediments as a valuable source of taxonomically diverse actinobacteria with significant antimicrobial potential. The identification of *Streptomyces hygroscopicus* isolates producing multiple bioactive compounds underscores their relevance as promising candidates for pharmaceutical and biotechnological applications.

KEYWORDS:

biodiversity, bioactive compounds, enzyme production, metabolite profiling, *Streptomyces*

Harnessing biodiversity for wound care: antibacterial hydrogels from *Diplazium esculentum* and green-synthesized silver nanoparticles from *Asplenium nidus*

Glenda Z. Doblas^{1,*}, Kenny Anthony M. Alforque¹, Victoria Catherine S. Borrero¹ and Reggie Y. Dela Cruz¹

¹Molecular Biology & Biotechnology, Genetics, & Microbiology Division, Institute of Biological Sciences, Central Mindanao University, Musuan, Maramag, Bukidnon 8714, Philippines.

*Corresponding author, e-mail: gzdoblas@cmu.edu.ph

ABSTRACT:

Biodiversity serves as a vital resource for developing sustainable biomedical solutions, offering natural compounds with therapeutic potential. This study explores the intersection of biodiversity and health by harnessing medicinal fern extracts (*Diplazium esculentum* and *Asplenium nidus*) to develop advanced wound care materials. A biocompatible hydrogel was synthesized from alginate and carboxymethyl cellulose, crosslinked with calcium ions, and infused with *D. esculentum* frond extract to leverage its bioactive properties. The hydrogel demonstrated selective antibacterial activity against *Staphylococcus aureus*, exhibiting a zone of inhibition measuring 19.32 millimeters and a minimum inhibitory concentration of 12.5 milligrams, supporting its role in infection control. In vivo studies using laboratory mice (*Mus musculus*) revealed accelerated wound closure, with healing rates reaching 86.58 percent within four days, underscoring the potential of biodiversity-derived hydrogels in regenerative medicine. Complementing this approach, silver nanoparticles were synthesized through a green, eco-friendly process using *A. nidus* extract, presenting a sustainable alternative to conventional chemical methods. The optimized silver nanoparticles, characterized by a surface plasmon resonance peak at 430 nanometers and particle sizes ranging from 300 to 400 nanometers, exhibited potent broad-spectrum antibacterial effects against *S. aureus* and *Pseudomonas aeruginosa*, with a minimum inhibitory concentration at a dilution of one part in two hundred fifty-six, outperforming conventional agents. Rigorous biosafety measures ensured the eco-friendly synthesis of the materials, aligning with health objectives. Together, these findings highlight how biodiversity from fern-derived polymers to synthesized nanomaterial can address global health challenges such as antimicrobial resistance and chronic wounds. By integrating ecological resources with biomedical innovation, this work advances nature-inspired strategies for therapeutic development, emphasizing the conservation and sustainable utilization of biodiversity for human health.

KEYWORDS:

Hydrogel, nanoparticles, medicinal ferns, wound healing, antibacterial

Acute Oral Toxicity, Antioxidant, and Anti-Inflammatory Activities of *Coix lacryma-jobi* L. Leaf Ethanolic Extract via In Vitro Cyclooxygenase (COX) Inhibition and In Vivo Gene Expression Analysis

Reggie Y. dela Cruz¹, Charlene T. Marcial¹, Princess Lyn B. Taping and Jovsrie T. Gault¹
and Gianina Sophia P. Cordova¹

¹Molecular Biology and Biotechnology, Genetics and Microbiology Division, Institute of Biological Sciences,
Central Mindanao University

*Corresponding author, e-mail: rydelacruz@cmu.edu.ph

ABSTRACT:

Coix lacryma-jobi L. (adlay) is a medicinal plant traditionally recognized for its therapeutic properties, particularly the anti-inflammatory effects of its seed oil. However, limited research has focused on its leaf extract. This study evaluated the acute oral toxicity, antioxidant, and anti-inflammatory activities of *C. lacryma-jobi* leaf ethanolic extract using both in vitro and in vivo approaches. In vitro assessments included cyclooxygenase (COX)-1 and COX-2 enzyme inhibition assays, while in vivo analyses involved carrageenan-induced paw edema in ICR mice and gene expression profiling of COX-2, tumor necrosis factor (TNF)- α , and inducible nitric synthase (iNOS) via quantitative polymerase chain reaction (qPCR). The extract exhibited no signs of acute toxicity in mice and demonstrated notable antioxidant activity. It also showed significant inhibition of COX enzymes, with a higher selectivity toward COX-2. In the paw edema model, the extract effectively reduced inflammation and downregulated pro-inflammatory gene expression compared to untreated controls. These findings support the potential of *C. lacryma-jobi* leaf extract as a natural anti-inflammatory agent and provide a basis for further pharmacological investigation.

KEYWORDS:

Coix lacryma-jobi L.; COX inhibition; antioxidant; paw edema; anti-inflammatory; gene expression.

Screening of Antibacterial Activities of Different Extracts of Marine Macroalgae using Modified Microtiter-plate Resazurin Assay

Kimberly Jane A. Adrias^{1,2,*}, Olive A. Amparado¹, Liza A. Adamat¹ and Sharon Rose M. Tabugo^{1,2}

¹Department of Biological Science, College of Science and Mathematics, Mindanao State University – Iligan Institute of Technology, Iligan City, Lanao del Norte, 9200, Philippines

²Molecular Systematics and Conservation Genetics Laboratory, Center for Biodiversity Studies and Conservation, Premier Research Institute of Science and Mathematics, Mindanao State University-Iligan Institute of Technology, Iligan City, Lanao del Norte, 9200, Philippines

*Corresponding author, e-mail: kimberlyjane.adrias@g.msuiit.edu.ph

ABSTRACT:

The marine environment contains a vast array of organisms with unique biological properties, offering significant potential to address the growing problem of multidrug-resistant pathogens driven by the misuse of antibiotics. As conventional treatments become increasingly ineffective, marine macroalgae have emerged as promising sources of antibacterial agents. This study investigated the antibacterial activity of *Padina japonica* and *Halimeda discoidea* collected from Sacol Island, Zamboanga City, Philippines. Macroalgal samples were extracted using ethanol, hexane, and ethyl acetate solvents. Crude extracts were tested for their antibacterial activity against four bacterial strains – *Escherichia coli* and *Pseudomonas aeruginosa* (Gram-negative bacteria) and *Staphylococcus aureus* and *Bacillus subtilis* (Gram-positive bacteria) – using a modified microtiter plate resazurin assay. Minimum inhibitory concentrations (MICs) were determined and compared to Ciprofloxacin as a positive control. Results displayed varying degrees of antibacterial activities among different extracts against tested bacterial strains, with MIC values ranging 0.16-3.61 mg/mL. Among the extracts, the hexane extract of *P. japonica* exhibited the highest antibacterial activity against *P. aeruginosa* and *B. subtilis* (0.16 mg/mL). Additionally, its ethanol extract showed strong activity against *S. aureus* (0.16 mg/mL). Statistical analyses (One-way ANOVA and Tukey's pairwise test) revealed a comparable antibacterial activity with Ciprofloxacin (p value > 0.05). This study revealed the potential of *P. japonica* and *H. discoidea* extracts as antibacterial agents, supporting further exploration of macroalgae as sustainable sources of alternative antibacterial compounds. Further tests are also necessary to validate these findings.

KEYWORDS:

Antibacterial activity; macroalgae; MIC; Sacol Island

Three new *Penicillium* species from mangrove sediment with notable antibacterial activity against *Staphylococcus aureus*

Vassana Supapongsri¹, Mohit Chand², Natprima Sae-Heng³, Ananya Sahathippayakul¹, Chatree Maknual⁴, Nawin Phormsin⁴, Pradittha Nueakaeo⁴, Wanchat Sirisarn⁵ and Piyangkun Lueangjaroenkit^{1,6,*}

¹Department of Microbiology, Faculty of Science, Kasetsart University, Bangkok, 10900, Thailand

²International Program for Master of Science in Materials and Biological Technology, National Changhua University of Education (NCUE), Changhua, 50007, Taiwan

³Ruamrudee International School, Bangkok, 10510, Thailand

⁴King Rama IX International Mangrove Botanical Garden, Department of Marine and Coastal Resources, 99 Nong Bua Sub-district, Muang District, Chanthaburi 22000, Thailand

⁵Department of Microbiology, Faculty of Medicine, Kasetsart University, Bangkok, 10900, Thailand

⁶Biodiversity Center Kasetsart University (BDCKU), Bangkok 10900, Thailand

*Corresponding author, e-mail: Piyangkun.lu@ku.th

ABSTRACT:

Three novel fungal species belonging to the genus *Penicillium* were isolated from mangrove soil sediments collected at the King Rama IX International Mangrove Botanical Garden, Chanthaburi Province, Thailand. Comprehensive morphological examinations combined with multilocus phylogenetic analyses based on the internal transcribed spacer (ITS) region, β -tubulin (*BenA*), calmodulin (*CaM*), and the second largest subunit of RNA polymerase II (*RPB2*) were employed to delineate their taxonomic positions. Two of the new species were classified within section *Exilicaulis*, series *Erubescens*, while the third species was placed in section *Lanata-Divariata* and represents a newly proposed series within that group. These species exhibited inhibitory activity against *Staphylococcus aureus*, highlighting the potential of mangrove-derived *Penicillium* in antimicrobial research. These findings not only expand our understanding of fungal diversity in mangrove ecosystems but also highlight the rich and underexplored taxonomic complexity within the genus *Penicillium*, along with its promising implications for medical biotechnology.

KEYWORDS:

Antimicrobial activity; Mangrove; Novel fungi; *Penicillium*; soil sediment

The Efficacy of *Zingiber officinale* Roscoe, *Alpinia galanga*, and *Cymbopogon citratus* extracts in inhibiting *Staphylococcus aureus*

Arunnee Saetung¹, Jirawan Bootkam², Numpech Nopakun^{1,*}, Onuma Hongsapol¹
and Wanwisa Anantaphat¹

¹Department of Science and Technology, Satri Si Suriyothai, Bangkok, 10220, Thailand

²Siriraj Neuroimmunology Centre, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, 10700, Thailand

*Corresponding author, e-mail: Numpech@suriyothai.ac.th

ABSTRACT:

The antibacterial efficacy of *Zingiber officinale* Roscoe (ginger), *Alpinia galanga* (galangal), and *Cymbopogon citratus* (lemongrass) extracts against *Staphylococcus aureus*, a common pathogenic bacterium responsible for various infections. Ethanolic extracts of the selected herbs were prepared and tested using the agar well diffusion method to determine their inhibitory activity. The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were also assessed. Ginger and galangal, both from the Zingiberaceae family, are known for their anti-inflammatory, antioxidant, and antimicrobial properties, while lemongrass is valued for its antispasmodic, analgesic, anti-inflammatory, and sedative effects. The results demonstrated that all three extracts exhibited significant antibacterial activity against *Staphylococcus aureus*, with varying degrees of inhibition zones. Among them, *Zingiber officinale* showed the highest antibacterial effect, followed by *Alpinia galanga* and *Cymbopogon citratus*. The study suggests that these herbal extracts possess potent bioactive compounds that can be considered as alternative natural antibacterial agents to combat *S. aureus*-related infections. Further research is recommended to isolate active constituents and evaluate their potential applications in pharmaceutical and food industries.

KEYWORDS:

antibacterial, bioactive, inhibitory activity, inhibition zones, pharmaceutical

Pharmacological Evaluation of *Hornstedtia conoidea* Ridl.: Safety Profile and Antidiabetic Potential of Leaf Extracts

Mary Queen J. Acop¹, Shaina Levie E. Sentones¹, Noe P. Mendez², Reggie Y. Dela Cruz¹ and **Meraluna J. Canunayon^{1,*}**

¹Molecular Biology and Biotechnology, Genetics, and Microbiology Division, Institute of Biological Sciences, College of Arts and Sciences

²Plant Biology Division, Institute of Biological Sciences, College of Arts and Sciences, Central Mindanao University, University Town, Musuan, Bukidnon, Philippines

*Corresponding author, e-mail: f.meraluna.canunayon@cmu.edu.ph

ABSTRACT:

Despite the rich biodiversity of the Philippine endemic ginger, *Hornstedtia conoidea* Ridl. and its traditional use, scientific data on its safety profile and antidiabetic efficacy remain scarce. Existing literature has primarily focused on its phytochemical composition and antioxidant properties, leaving a critical gap in understanding its toxicological effects and mechanism of action in diabetes management. This study addresses these gaps by systematically evaluating the acute oral toxicity, histopathological impact, and alpha-glucosidase inhibitory activity of *H. conoidea* leaf extracts.

Acute oral toxicity assessment in Swiss albino mice using the aqueous leaf extract at varying doses demonstrated no mortality or severe adverse effects at doses up to 500 mg/kg, establishing this as a safe consumption threshold. Higher doses (1,000 and 2,000 mg/kg) induced mild to moderate organ toxicity, evidenced by behavioral changes and histopathological alterations such as inflammation and tubular degeneration in kidney and liver tissues. These findings highlight the importance of adhering to doses at or below 500 mg/kg to avoid potential toxicity.

The antidiabetic potential of *H. conoidea* leaf extracts was confirmed through in vitro and in vivo studies. The ethanolic extract exhibited potent alpha-glucosidase inhibition ($175.8 \pm 23.0\%$ at 150 ppm), outperforming the standard drug acarbose, while the aqueous extract also showed significant inhibition ($91.29 \pm 1.82\%$ at 100 ppm). In alloxan-induced diabetic Swiss albino mice, oral administration of both extracts at 200mg/kg significantly lowered fasting blood glucose levels and improved body weight over 15 days, demonstrating effective glucose regulation at therapeutically relevant doses. These effects were not statistically significant compared to the acarbose-treated group, the positive control.

In conclusion, *Hornstedtia conoidea* leaf extracts possess strong antidiabetic activity and are safe for consumption at doses up to 500 mg/kg. However, doses exceeding this threshold may cause mild organ toxicity, underscoring the need for careful dose management in future therapeutic applications. These findings provide a solid foundation for developing *H. conoidea*-based natural antidiabetic agents with defined safety parameters.

KEYWORDS:

Hornstedtia conoidea, Acute Oral Toxicity, Safe Dose, Histopathology, Alpha-Glucosidase Inhibition, Antidiabetic Activity

Rangoon Creeper Leaf Extract (*Cumbretum indicum* (L.) DeFilipps) Against *Escherichia coli* and *Staphylococcus saprophyticus*

Siony S. Brunio^{1,*} and Clarice B. Catedrilla¹

¹Faculty of Biology Department, College of Arts and Sciences, Sultan Kudarat State University, Tacurong City, Sultan Kudarat, Philippines

*Corresponding author, e-mail: sionybrunio@sksu.edu.ph

ABSTRACT:

As antibiotic-resistant bacteria increasingly threaten public health, the search for effective natural remedies has never been more urgent. The study aims to determine the antibacterial activity of rangoon creeper leaf extract *Cumbretum indicum* (L.) DeFilipps against *Escherichia coli* and *Staphylococcus saprophyticus*. It utilizes randomize block design (CRD) examining multiple concentrations of extract (100%, 75%, 50% and 25%) and amoxicillin as control.

Result reveals that rangoon creeper extract (*C.indicum*) exhibits selective antimicrobial activity against infections diseases caused by *Escherichia coli* and *Staphylococcus saprophyticus*. While *E. coli* demonstrated resistance to the leaf extract, a notably strong antimicrobial effect was observed against *S. saprophyticus*. The full concentration of the extract produced an inhibition zone measuring 28.67 mm, exceeding the 26.7 mm zone generated by amoxicillin. The statistical analyses clearly show significant differences among the treatment groups, underscoring the extract's selective antimicrobial capabilities. These findings propose *Cumbretum indicum* (L.) DeFilipps as a potential natural alternative in antimicrobial therapy, particularly against Gram-positive infections.

KEYWORDS:

Cumbretum indicum (L.) DeFilipps ; Zone of inhibition; *Escherichia coli*; *Staphylococcus saprophyticus*

The efficacy of *Thunbergia laurifolia* and *Plectranthus amboinicus* extracts to reduction of pesticide residues on vegetables

Khruaeawan Klinruen¹, Numpech Nopakun^{1,*}, Phattarasita Phithakworabut¹, Rattanaorn Siripornpiriya¹ and Thanaporn Kanchanakunchorn¹

¹Department of Science and Technology, Satri Si Suriyothai, Bangkok, 10220, Thailand

*Corresponding author, e-mail: Numpech@suriyothai.ac.th

ABSTRACT:

The presence of pesticide residues on vegetables poses significant health risks to consumers and represents a growing public concern. This study investigates the effectiveness of natural plant-based extracts, specifically *Thunbergia laurifolia* (laurel clock vine) and *Plectranthus amboinicus* (Indian borage) in reducing pesticide residues on commonly consumed vegetables. *Thunbergia laurifolia* is commonly used as a detoxifying agent, and *Plectranthus amboinicus* is known for its antimicrobial, wound healing, and respiratory health benefits. The extracts were prepared using aqueous and ethanolic methods and applied to vegetables contaminated with organophosphate and carbamate pesticides. Residue levels were measured using gas chromatography before and after treatment. Results demonstrated that both laurel clock vine and Indian borage leaf extracts significantly reduced pesticide residues, with efficacy depending on the type of extract and pesticide. Notably, a combination of both extracts showed synergistic effects, achieving higher reduction rates compared to individual treatments. These findings suggest that laurel clock vine and Indian borage leaf extracts offer a safe, eco-friendly, and cost-effective alternative for reducing pesticide residues on vegetables, contributing to improved food safety and public health.

KEYWORDS:

antioxidant, carbamate, chromatography, organophosphate, pesticide,

Inventory and Assessment of Medicinal Seed Plants in Mt. Hamiguitan Range Wildlife Sanctuary, Davao Oriental, Philippines

Ken Bien Mar L. Caballes^{1,*}, Lordeth Christelle V. Escobio¹, Bryan C. Perez¹, Honorah Yegevnay A. Cueme¹, Glaiza Mae R. Sindol¹, Aki O. Vicente¹, Caila Mae H. Obogon¹

¹Plant Biology Division, Institute of Biological Sciences, College of Arts and Sciences, Central Mindanao University, University Town, Musuan, Bukidnon, 8714, Philippines

*Corresponding author, e-mail: caballeskenbienmar.crs@cmu.edu.ph

ABSTRACT:

Medicinal plants have been integral to human health since ancient times. In the Philippines, the use of medicinal plants dates back to pre-colonial periods and remains prevalent among both indigenous and non-indigenous communities in Mindanao. This study investigates the medicinal seed plants found in the Mt. Hamiguitan Range Wildlife Sanctuary, highlighting their traditional uses, conservation status, and ecological importance. Through repeated transect walks, field documentations, and semi-structured open-ended interviews, a preliminary inventory documented a total of 35 medicinal seed plant species across 17 families. The most represented families—Fabaceae, Lauraceae, Piperaceae, Pandanaceae, and Rutaceae—each contributed two species. These plants are primarily used to treat ailments such as postpartum conditions (14%), fatigue (14%), and wounds (12%). The most commonly used plant parts were leaves and bark, typically prepared by boiling and drinking, or pounding and applying topically. Furthermore, the majority of the species (71%) are listed as Least Concern on the IUCN Red List, and a significant proportion (81.8%) are native to the Philippines. This study underscores the importance of preserving both traditional knowledge and the biodiversity of medicinal plants, which are vital to local healthcare systems. It also calls for sustained conservation efforts to mitigate threats such as habitat degradation and climate change. The findings provide a baseline for future research and conservation initiatives focused on protecting medicinal plant resources and the cultural heritage linked to their use.

KEYWORDS:

Biodiversity, conservation, ethnobotany, medicinal plants, Philippines

Chitosan-Based Hydrogel Incorporating Thai Medicinal Plant Extracts for Dental Wound Management

Patcharakorn Raksasee¹, **Safira Minham**¹, Kornkanok Ubolchollakhet² and Netnapa Chana^{3,4*}

¹Paphayompittayakom School (SCiUS-Thaksin University), Phatthalung, 93210, Thailand

²Department of Rubber and Polymer, Faculty of Engineering, Thaksin University, Phatthalung campus, Phatthalung, 93210 Thailand

³Department of Biological Science, Faculty of Science and Digital Innovation, Thaksin University, Phatthalung Campus, Phatthalung, 93210, Thailand

⁴Innovative Material Chemistry for Environment Center, Department of Chemistry, Faculty of Science and Digital Innovation, Thaksin University, Phatthalung campus, Phatthalung, 93210, Thailand

*Corresponding author email: netnapa@tsu.ac.th

ABSTRACT:

Post-dental extraction complications, particularly infection and inflammation, remain significant challenges in dental practice. This study developed a chitosan-based hydrogel incorporating bioactive extracts from Thai medicinal plants (*Psidium guajava*, *Piper betle*, *Tridax procumbens*, and *Chromolaena odorata*) with antimicrobial, antioxidant, and anti-inflammatory properties. *P. guajava* water and ethanol extracts, and *P. betle* ethanol exhibited exceptional DPPH antioxidant activity (IC_{50} : 15.04 ± 0.48 , 15.59 ± 0.55 , and $14.46 \mu\text{g/mL}$). In antimicrobial testing, *P. guajava* water extract hydrogel showed the strongest inhibition against *E. coli* ($17.44 \pm 0.13 \text{ mm}$), while effectively inhibiting *S. mutans* ($13.86 \pm 0.09 \text{ mm}$) and *S. aureus* ($13.58 \pm 0.08 \text{ mm}$). *P. guajava* ethanol extract and *P. betle* ethanol extract hydrogels also demonstrated antimicrobial activity. Release compounds studies revealed that *P. guajava* water extract hydrogel released maximum phenolic compounds ($\sim 2.4 \text{ mgGAE/mL}$) at 6 h, decreasing at 24 h, while *P. betle* ethanol extract hydrogel showed minimal initial release but substantial increase at 24 h ($\sim 1.6 \text{ mgGAE/mL}$), correlating with DPPH antioxidant activity. Chemical analysis identified *P. guajava* bioactive compounds including myricetin and quercetin derivatives, which showed strong binding affinity to COX-2 anti-inflammatory targets. The *P. guajava* water extract hydrogel formulation, with its potent antimicrobial activity and optimal compound release profile, offers the most promising solution for dental wound management.

KEYWORDS:

Hydrogel, Medicinal plants, Natural products, *Piper betle*, *Psidium guajava*, wound management.

Antibiotic Resistance-Mediated Isolation and Genome Mining Reveal a Novel *Amycolatopsis* Species Producing Potential Ansamycin Derivatives from Tailed Pepper (*Piper cubeba* L.f.) Endophyte

Darika Kongrit^{1,*}, Wuttichai Mhuanong ² and Wongsakorn Kwandee¹

¹Faculty of Innovative Agriculture, Fisheries and Food, Prince of Songkla University (Surat Thani campus), Surat Thani, A. Muang Surat Thani, Surat Thani, 84000, Thailand

²Enzyme Technology Research Team, National Center of Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), Phaholyothin Rd., Khlong Luang, Pathum Thani, 12120, Thailand

*Corresponding author, e-mail: darika.k@psu.ac.th; darika.kng@gmail.com

ABSTRACT:

The growing challenge of antimicrobial resistance emphasizes the need for discovering novel antibiotics with unique biosynthetic origins. Actinomycetes, particularly the genus *Amycolatopsis*, are recognized for producing clinically significant compounds such as rifampin, yet the potential for novel metabolite production from endophytic strains remains underexplored.

In this study, an antibiotic resistance-mediated isolation approach was applied based on the principle that antibiotic-producing actinomycetes possess self-resistance mechanisms, enabling them to survive in the presence of their own bioactive compounds. Rifampin, a derivative of rifamycin B and member of the ansamycin antibiotic class, was used as a selective agent at a concentration of 20 µg/mL to enrich for endophytic actinomycetes with potential ansamycin biosynthetic capacity. Endophytes were isolated from the medicinal plant *Piper cubeba* L.f., and candidate strains were screened for the *rifK* gene, a gene from the rifamycin biosynthetic cluster encoding 3-amino-5-hydroxybenzoic acid (AHBA) synthase, an essential enzyme involved in forming the ansamycin polyketide backbone, using PCR.

Among the four rifampin-resistant isolates chosen, strain PC701R exhibited clear antimicrobial activity against Gram-positive bacteria and non-filamentous fungi, as demonstrated by disc diffusion assays. The strain was cultured in International *Streptomyces* Project Medium No. 2 (ISP2) broth at 30 °C with shaking at 200 rpm for two days. Genomic DNA was extracted using the GF-1 Bacterial DNA Extraction Kit (Vivantis, Malaysia), and library preparation was performed with the NEBNext Ultra II DNA Library Prep Kit (NEB, USA). Whole-genome sequencing was conducted on the Illumina HiSeq platform using 150 bp paired-end reads. The 16S rRNA gene sequence analysis indicated that strain PC701R belongs to the genus *Amycolatopsis*, sharing approximately 99% sequence similarity with its phylogenetically closest type strains. Whole-genome taxonomic assessment revealed Digital DNA–DNA Hybridization (dDDH) and Average Nucleotide Identity (ANI) values of around 60% and 92%, respectively, which fall below the established species delineation thresholds, supporting the recognition of PC701R as a potential novel species within the genus. Genome mining using antiSMASH version 6.0 and Antibiotic Resistant Target Seeker (ARTS) version 2.0 revealed biosynthetic gene clusters (BGCs) showing 55% similarity to those associated with rifamorpholine biosynthesis, a subclass of ansamycins belonging to the naphthalenic acid family. These results, coupled with observed antimicrobial activity, indicate that PC701R has the potential to produce novel ansamycin derivatives. Ongoing morphological studies, chemotaxonomic characterization, and LC-MS/MS profiling are being conducted to confirm the strain's taxonomy and elucidate the structures of the bioactive compounds produced. This study demonstrates the utility of combining self-resistance-guided isolation with genome mining to uncover endophytic actinomycetes with unexplored biosynthetic capacity, contributing to ongoing efforts to discover novel antibiotics in the fight against antimicrobial resistance.

KEYWORDS: *Amycolatopsis* novel species; ansamycin producers; antibiotic resistance-mediated isolation

Tracking Antibiotic Resistance Genes (ARGs) from the epithelial surface of yellow seahorse (*Hippocampus kuda*) and its implications to human health

Noel John Ian Feben S. Maguate^{1,*} and Sharon Rose M. Tabugo^{1,2}

¹Department of Biological Sciences, Mindanao State University-Iligan Institute of Technology. Iligan City 9200, Philippines

²Molecular Systematics and Conservation Genomics Laboratory, Center for Biodiversity Studies and Conservation, Premier Research Institute of Science and Mathematics, Mindanao State University-Iligan Institute of Technology. Iligan City 9200, Philippines

*Corresponding author, e-mail: noeljohnianfeben.maguete@g.msuiit.edu.ph

ABSTRACT:

In recent years, antimicrobial resistance has emerged as a global health concern. The increasing detection of antibiotic-resistant bacteria and ARGs in the marine environment highlights its potential impact to human health. Minimum inhibitory concentration (MIC) testing, whole genome shotgun sequencing (WGS), and ARG detection using an automated cloud-based pipeline were employed to survey antibiotic resistance genes (ARGs) in bacterial isolates from the epithelial surface of *Hippocampus kuda* collected from Bongo Island, Philippines. Shotgun metagenomics via CZ ID a cloud-based pipeline revealed genes from the two bacterial isolates related to resistance. *Pseudomonas putida* (M1) demonstrated the prevalence of multidrug efflux genes and resistance (β -lactams, aminoglycosides, fluoroquinolone, phenicol, macrolide, diaminopyrimidine, aminocoumarin, peptide, sulfonamide, glycopeptide, oxazolidinone, rifamycin, and tetracycline). On the other hand, *Vibrio alginolyticus* (S2) also demonstrated the prevalence of multidrug efflux genes, and resistance (β -lactams, fluoroquinolone, fusidane, macrolide, and tetracycline), respectively. Overall, findings underscore the need for heightened awareness regarding antibiotic use and the importance of understanding and managing antibiotic resistance dynamics in aquatic ecosystems and the risk of human exposure to contaminated seafood or water sources.

KEYWORDS:

Antimicrobial resistance, Fish, Bacteria, AMR, Antibiotics

An assessment of microplastic contamination in shrimp paste with suggested mitigation strategies

Chanansiri Phutthaphibankun¹, Laongdow Jungrak¹, Charernmee Chamchoy¹, Wiphawan Aunkhongthong¹, Maneerat Sukkeaw¹, Wichin Suebpala¹, Makamas Sutthacheep¹, and Thamasak Yeemin¹

¹Marine Biodiversity Research Group, Department of Biology, Faculty of Science, Ramkhamhaeng University, Huamark, Bangkok, 10240, Thailand

*Corresponding author, e-mail: 6711710001@rumail.ru.ac.th

ABSTRACT:

Shrimp paste is a seafood product used in a variety of dishes, especially in Asian regions such as Thailand, Malaysia, Indonesia, the Philippines, Vietnam, and some areas in China, where it is popularly used in local cuisine. It has a high potential to accumulate microplastics at each stage of the production process, so proper controls and hygiene improvements should be implemented to reduce contamination. This study aimed to examine microplastics contamination in Thailand's shrimp paste products and provide recommendations to reduce microplastics in shrimp paste products. The shrimp paste samples were collected from Rayong, Samut Sakhon, Samut Prakan, Surat Thani, Krabi, Phuket, Trang and Satun Provinces. They were digested with a 30% hydrogen peroxide solution, filtered through filter paper, and examined under a stereomicroscope to observe microplastic characteristic (color, shape, and size). The results showed that the amount of microplastics in shrimp paste from Samut Sakhon was the highest (4.00 ± 2.20 pieces/gram), followed by Phuket (3.20 ± 2.62 pieces/gram) and Samut Prakan (2.80 ± 2.02 pieces/gram), with the lowest amount found in Satun (1.60 ± 1.84 pieces/gram). Most of the microplastics found were fibers and fragments. The results of the study found that shrimp paste products are contaminated with microplastics at concerning levels. Therefore, additional measures should be implemented to control cleanliness and reduce the chances of contamination at every step of the production process, starting with the selection of appropriate fishing gear. The water should be filtered before washing the shrimp paste, measures should be taken to prevent contamination from the air during drying, safe containers that do not deteriorate should be selected, and standardized packaging should be used to control contamination effectively. Implementing these measures will significantly reduce the amount of microplastics in shrimp paste consumed.

KEYWORDS:

Fishing gear; microplastic; seafood; shrimp paste product; Thailand

Taxonomic Account and Ethnomycological survey of Macrofungi in Sultan Kudarat Province, Mindanao Island, Philippines

Steven Jan T. Millendez¹, Rodelyn M. Dalayap², and Ziljih S. Molina^{3,*}

¹Alumnus, Department of Biology, Sultan Kudarat State University, Tacurong City, 9800, Philippines

²Faculty of College of Arts and Sciences, Department of Biology, Sultan Kudarat State University, Tacurong City, 9800, Philippines¹

³Faculty of College of Arts and Sciences, Department of Biology, Sultan Kudarat State University, Tacurong City, 9800, Philippines

*Corresponding author, e-mail: ziljihmolina@sksu.edu.ph

ABSTRACT:

Macrofungal diversity is one of the most critical indicators of terrestrial ecosystems. It is also essential for some local communities, as it serves food and medicine. The present study was conducted to assess the diversity and utilization of wild macrofungi in the province of Sultan Kudarat, Philippines. Samples were collected and photographed for identification using a taxonomic key for macrofungi. A total of sixty-three species of macrofungi have been identified, comprising 38 different genera, and 16 of these have been validated by mycology experts. While an ethnomycological survey revealed that the majority of respondents were unaware of the use of certain macrofungi, some, particularly vendors stated that they used these macrofungi to treat conditions such as breast cancer, diabetes, colds and flu, cancer, and kidney problems. Vendors have suggested that some macrofungi are edible, whereas others are poisonous. These findings could provide valuable information for conservation efforts on macrofungi, potentially leading to biotechnological and medicinal applications.

KEYWORDS:

food; medicine; mushroom; poisonous; survey.

A.I. Based Classification of Thai Horse-shoe Crab Species

Rungphob Lertvilaivithaya¹, **Pabhungkorn Jeamthiranart**², Thanit Yuanlae³

¹International School Bangkok (ISB), Nonthaburi, 11120, Thailand

²Ekamai International School, Bangkok, 10110, Thailand

³Srinakharinwirot University Demonstration School Prasarnmit, Secondary Division, Bangkok, 10110, Thailand

*Corresponding author: ronnie111555@hotmail.com

ABSTRACT:

In Southeast Asia, particularly the coastal regions of Thailand, the consumption of horseshoe crabs represents both a culinary tradition and a public health concern. Two morphologically similar but toxicologically divergent horseshoe crab species, *Carcinoscorpius Rotundicauda* and *Tachypleus Gigas* are present in this area. *C. Rotundicauda*, known as the mangrove horseshoe crab, contains the lethal neurotoxin tetrodotoxin, which is known to cause severe foodborne poisoning and death. While *T. Gigas*, commonly known as the Indo-Pacific horseshoe crab, is safe for human consumption and widely regarded as a delicacy in traditional Thai cuisine, particularly for its roe. Despite subtle phenotypic differences, such as cuticle granulation and coloration, these two taxonomically distinct species, *C. Rotundicauda* and *T. Gigas* exhibit a high degree of morphological convergence, particularly in carapace shape, size, and general appearance. This visual similarity contributes to frequent misclassification in culinary contexts. Consequently, the accidental consumption of *C. Rotundicauda* continues to result in numerous incidences of acute food poisoning and fatalities.

To address this issue, this study investigates the application of artificial intelligence (AI) through deep learning-based image processing to differentiate these morphologically similar species. A dataset was constructed using a combination of 128 publicly available and synthetically generated images. It was preprocessed and organized into training, validation, and test subsets to ensure structured evaluation. Model training used three convolutional neural network (CNN) architectures: VGG16, Xception, and EfficientNetB0. Each model was trained for 30 epochs under consistent hyperparameters. The Xception model achieved the highest performance, with 87.5% test accuracy compared to VGG16 (54.2%) and EfficientNetB0 (50.0%), demonstrating superior generalization in identifying subtle phenotypic cues. Reliability was further confirmed through a confusion matrix, showing strong classification of both species with minimal false results. Accuracy and loss curves indicated stable learning progression over the 30 epochs. Both training and validation accuracy increased steadily, showing generalization, with mild overfitting near the end.

The successful application of AI in this study demonstrates the practical potential of deep learning through image processing in real-world contexts. Accurate classification between two morphologically similar but taxonomically divergent horseshoe crab species highlights feasibility for developing automated tools. These could be used in markets, restaurants, and other outlets to mitigate the risk of misidentifying toxic species. By enabling real-time, portable binary classifications, AI offers a solution to address public health concerns in contexts where misidentification may prove fatal. However, this study also reveals limitations. Though carefully curated, the dataset may not represent the full range of environmental variety, including background noise, occlusion, and lighting changes. Intra-class phenotypic variation also introduced classification challenges, possibly reducing model accuracy. Additionally, the study's small test size ($n = 12$) restricts the generalizability of findings. Further research is warranted with a more diverse dataset and larger test sample to improve robustness and validity.

KEYWORDS:

Horseshoe crab, Image processing, Convolutional Neural Network (CNN), Species identification

First Account of Tadpole Abnormalities on Philippine Megophryids and Additional Records in Taiwan Bufonids

Andrie Bon A. Flores^{1,2 *}, Martin Ouellet³ and Ace Kevin S. Amarga^{1,2}

¹Biodiversity Program, Taiwan International Graduate Program, Biodiversity Research Center, Academia Sinica. No. 128, Academia Road Sec. 2, Taipei 11529, Taiwan.

²School of Life Science, National Taiwan Normal University. No. 88, Tingzhou Road Sec. 4, Taipei 116059, Taiwan.

³Amphibia-Nature, 3380 rang Rochon, Rouyn-Noranda, Québec J0Z 2X0 Canada

*Corresponding author, e-mail: andriebon.flores@g.msuiiit.edu.ph

ABSTRACT:

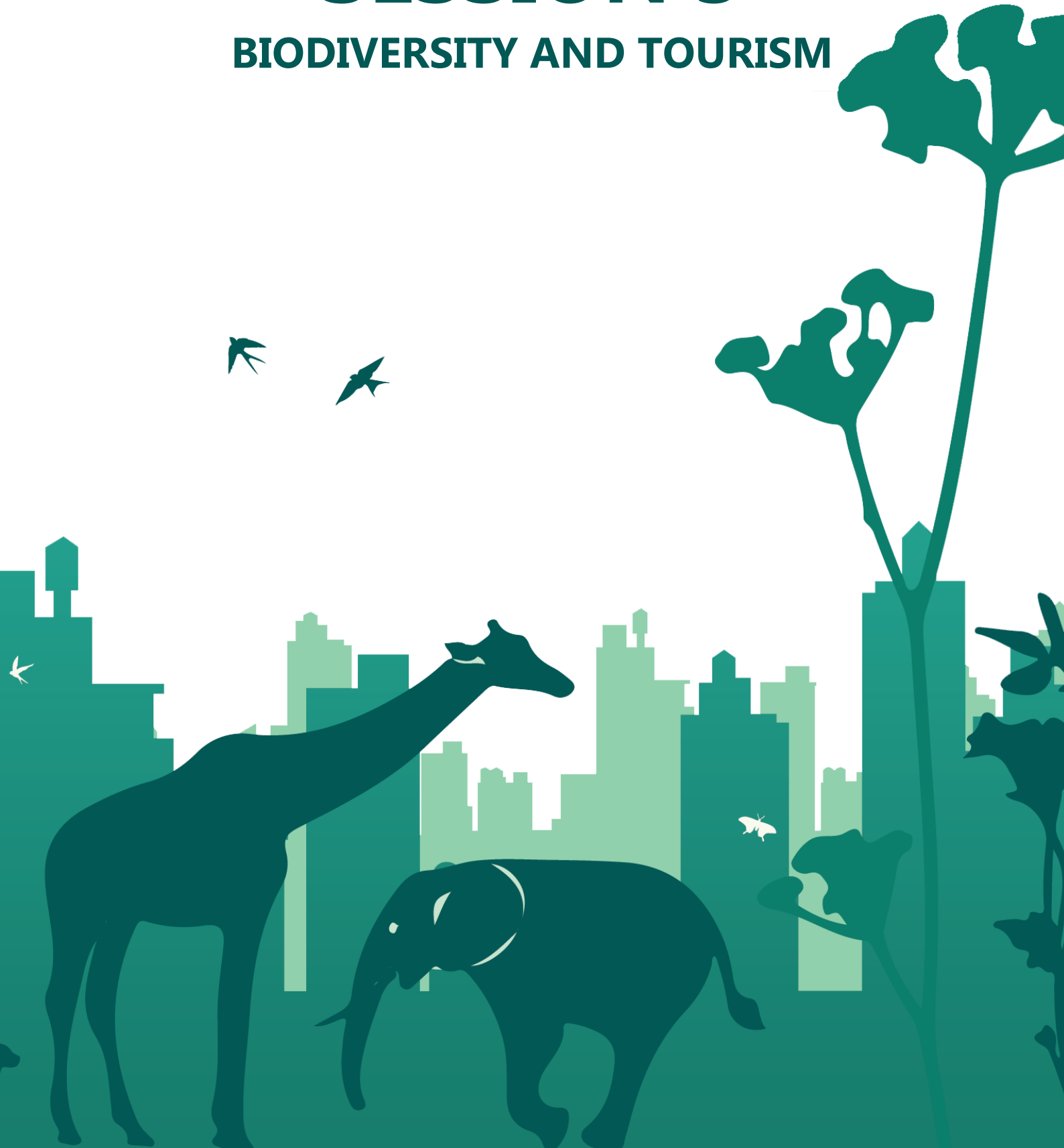
This study presents the first documented occurrences of tadpole abnormalities in Philippine megophryids (*Pelobatrachus stejnegeri* and *Leptobrachium lumadorum*) and additional cases in Taiwan bufonids (*Bufo bankorensis* and *Duttaphrynus melanostictus*). Records of morphological deviations in museum specimens were noted against species-specific baseline. We documented seven different morphological abnormalities, including body asymmetry, kyphosis, tail bifurcation, ectromelia, oral disk deformities, abnormal eye and prolapsed cloaca. Although etiologies for these abnormalities were not investigated in this account, we provide an overview on the causative agents for tadpole abnormalities. This highlights the importance of future research on the potential etiologies of tadpole abnormalities. Furthermore, this study provides the baseline information for accounts of tadpole abnormalities in Taiwan and the Philippines and highlights the role of natural history observations on the study of developmental malformations in anurans.

KEYWORDS:

Abnormalities, Anura, Philippines, tadpole specimens, Taiwan

SESSION 3

BIODIVERSITY AND TOURISM



INVITED SPEAKER 3-1:



Nature Positive Tourism: A Turning Point, Not a Trend

Weerasak Kowsurat

Chairman of Breathe Bangkok Council

98/324 Moo 5 Tambon Bangkuwieng Amphur Bangkruay Nontaburi 11130

*Corresponding author, e-mail: kowsuratwk@gmail.com

ABSTRACT:

This speech introduces Nature Positive Tourism as a transformative approach that goes beyond minimizing harm to actively restoring and regenerating ecosystems. Using vivid examples—the dragonfly as a sign of healthy waters, the mosquito as a misunderstood pollinator, and the coconut as a living ecosystem—the address highlights how tourism can embrace biodiversity as a partner rather than a backdrop. Cultural diversity and indigenous knowledge are positioned as essential allies, while case studies from Thailand and the region show practical models of coral restoration, community forests, butterfly trails, and urban wetlands. The call to action urges tourism stakeholders to design for life, tell better stories, foster participation, and protect both nature and culture, envisioning a future where travel enriches biodiversity and communities alike

KEYWORDS :

Nature Positive Tourism, Biodiversity, Ecosystems, Cultural diversity, Indigenous knowledge, Restoration

ORAL PRESENTATION

SESSION 3



03-01

From Biodiversity to Business Value: A Multidimensional BEQI Approach to Sustainable Coastal Tourism

Panichat Kitisittichai^{1,*}, Ariya Aruninta² and Manop Kaewmoracharoen³

¹Technology Management and Innopreneurship, Graduate School, Chulalongkorn University, Bangkok, 10330, Thailand

²Department of Landscape Architecture, Faculty of Architecture, Chulalongkorn University, Bangkok, 10330, Thailand

³Department of Civil Engineering, Faculty of Engineering, Chulalongkorn University, Bangkok, 10300, Thailand

*Corresponding author, e-mail: 6581019720@student.chula.ac.th

ABSTRACT:

Coastal tourism destinations are increasingly subjected to acute environmental stressors—biodiversity loss, habitat fragmentation, ecosystem degradation, and water pollution—that erode the integrity of marine and littoral systems and diminish the quality of visitor experiences. These pressures imperil both ecological sustainability and the long-term economic resilience of tourism sectors. Effectively mitigating such interconnected threats requires a transformative paradigm that integrates rigorous ecosystem conservation, human well-being, and sustainable economic development.

In response, we advance the Biophilic Environmental Quality Index (BEQI) Framework, an innovative business model firmly rooted in Blue Economy principles. The BEQI Framework systematically operationalizes six interrelated dimensions (1) Environment & Ecosystem dimension: carrying-capacity utilization, coastal green-space density, ecological connectivity, biodiversity richness, blue-water access frequency, and biophilic feature count (2) Well-being dimension (3) Social dimension (4) Experiential dimension (5) Business Value dimension (6) Economic impact dimension.

By quantifying and benchmarking these dimensions, BEQI reveals the synergistic value of ecological integrity and human experience. It underscores how biophilic environments foster physical and psychological health, enrich visitor engagement, strengthen community cohesion and cultural exchange, optimize commercial performance through innovative service design, and generate equitable economic outcomes—such as increased local spending, job creation, and enhanced income equity.

The BEQI Framework is instantiated via a digital platform offering three integrated services:

1. Insights-as-a-Service: Real-time dashboards and GIS-based zoning to delineate ecological thresholds and guide adaptive management of vulnerable habitats.
2. Subscription-Based Analytics: Predictive modeling and tiered reporting to optimize visitation patterns, calibrate green-premium pricing, and monitor return on investment.
3. Certification Services: “BEQI-Certified” accreditation for destinations meeting stringent biophilic criteria, accompanied by performance visualizations and renewal alerts to sustain market differentiation.

By embedding robust ecosystem health metrics into strategic and commercial decision-making, the BEQI Framework advances sustainable coastal tourism practices aligned with Blue Economy objectives. Anticipated benefits include the development of premium, value-added tourism offerings, preservation of ecological integrity, elevated visitor satisfaction, and durable economic viability. Ultimately, this conceptual model furnishes a scalable blueprint for policymakers, destination managers, and private stakeholders to place biophilic environmental quality at the core of strategic planning thereby reconciling ecological stewardship with resilient economic growth in coastal regions.

KEYWORDS:

Biophilic Environmental Quality Index, Environment & Ecosystem, Sustainable Coastal Tourism, Well-being, Business Innovation

03-02

Dragonflies as Narrative Ambassadors: An Interdisciplinary Approach to Promoting Education, Ecotourism and Conservation Engagement in Khao Yai National Park

Tosaphol Saetung Keetapithchayakul^{1,*}, Watchara Chiengkul² and Nachanok Lohsomboon³

¹The Center for Entomology & Parasitology Research, College of Medicine and Pharmacy, Duy Tan University, Da Nang, 550000, Vietnam

²Faculty of Business Administration and Information Technology, Rajamangala University of Technology, Khon Kaen, 40000, Thailand

³Sasipa School, Khlong Sam Wa, Bangkok 10510, Thailand

*Corresponding author: Keetapithchayakul.TS@gmail.com

ABSTRACT:

Khao Yai National Park (KYNP), part of the Dong Phrayayen–Khao Yai Forest Complex and a UNESCO World Heritage Site, is a flagship destination for ecotourism in Thailand, renowned for its rich biodiversity and intact freshwater ecosystems. Dragonflies (Odonata) were selected as the focal taxon in this study due to their dual value—as sensitive bioindicators of aquatic ecosystem health and as visually striking organisms that naturally attract the attention and curiosity of ecotourists. Their life history, habitat specificity, and aesthetic appeal make them ideal ambassadors for communicating ecological concepts to the public.

This interdisciplinary study integrates Odonata diversity, education, and tourism science to (1) develop storytelling content centered on dragonflies in KYNP as a tool for ecotourism communication, and (2) examine the causal relationships among narrative transportation, nature connectedness, and behavioral intentions among ecotourists. The narrative content was designed to combine scientific accuracy with emotional resonance, conveying the ecological importance of dragonflies and their role in maintaining ecosystem balance. A total of 230 individuals interested in ecotourism participated by reading the narrative and completing a questionnaire assessing narrative engagement, nature connectedness, and behavioral intentions (e.g., seeking further knowledge, intention to visit KYNP, and willingness to participate in conservation activities). partial least squares structural equation modeling revealed significant relationships among all variables ($p < .05$): narrative transportation positively influenced nature connectedness, which in turn predicted all dimensions of pro-environmental behavioral intentions. The results highlight the effectiveness of applying natural history knowledge through pedagogically informed storytelling, with dragonflies as a model, to foster ecological awareness and conservation-minded behavior in sustainable tourism contexts.

KEYWORDS:

Dragonflies, environmental education, narrative transportation, ecotourism, Khao Yai National Park

03-03

Enhancing coral reef biodiversity through Novel Restoration Techniques for Nature Positive Tourism in Thailand

Wichin Suebpala^{1,*}, Makamas Sutthacheep¹, Thamasak Yeemin¹, Sittiporn Pengsakun¹, Wanlaya Klinthong¹, Charernmee Chamchoy¹, Nipatpong Chuanchuen², Supawadee Photiyarach³ and Anaphat Nongkoo⁴

¹Marine Biodiversity Research Group, Faculty of Science, Ramkhamhaeng University, Huamark, Bangkok, Thailand

²Asian Ecotourism Network, Bangkok, Thailand

³Thailand Science Research and Innovation, Samsen Nai, Phaya Thai, Bangkok, Thailand

⁴College of Innovation and Management, Suan Sunandha Rajabhat University, Dusit, Bangkok, Thailand

*Corresponding author, e-mail: wichin.s@gmail.com

ABSTRACT:

Degradation of coral reefs have occurred globally due to both natural and human-induced pressures, affecting critical ecosystem functions and services, particularly tourism, one of the cultural services. In this research, we showcase the application of novel coral restoration strategies, coral micro-fragmentation, to rehabilitate damaged reefs and enhance reef biodiversity. This innovative method accelerates coral growth by using small fragments sourced from genetically diverse coral colonies, selected for their resilience to environmental stressors such as temperature fluctuations, salinity changes, and sediment accumulation. In Thailand, the technique was first applied in coral nursery plots at Ko Khang Khao and Ko Lan, Chonburi Province (Upper Gulf of Thailand) and coral restoration with coral fragments in Mu Ko Chumphon (Western Gulf of Thailand), revealing positive outcomes in terms of survival and growth rates across several coral species, including *Diploastrea heliopora*, *Pavona decussata*, *Pavona varians*, *Lithophyllon undulatum*, *Porites lutea*, *Pocillopora acuta*, *Pavona decussata* and *Dipsastraea favus*. These restoration efforts have enhanced biodiversity, attracted marine life, and contributed to nature-positive tourism. The restored sites have been integrated into dive tourism routes, enhancing tourist experiences and diversifying tourism products. Tour operators and local communities have played key roles in coral restoration, nursery maintenance, and reef monitoring. This study demonstrates the strong connection between coral reef restoration and nature-positive tourism, highlighting their synergistic potential for marine conservation and sustainable economic development.

KEYWORDS:

biodiversity, coral restoration, conservation, Gulf of Thailand, nature positive tourism

POSTER PRESENTATION

SESSION 3



Community-based tourism management through participatory processes: A case study of Wang Phang Subdistrict, Wiang Nong Long District, Lamphun Province

Nathitakarn Phayakka^{1,*}, Pattavara Pathomrungsyounggul², Sasitorn Baipong², Panuphan Prapatigul¹
and Chalita Sangwannak¹

¹Faculty of Agriculture, Chiang Mai University, Chiang Mai, 50200, Thailand

²Faculty of Agro-Industry, Chiang Mai University, Chiang Mai, 50200, Thailand

*Corresponding author, e-mail: nathitakarn.p@cmu.ac.th

ABSTRACT:

This research examines the integration of community-based tourism with biodiversity conservation and sustainable natural resource management in Wang Phang Subdistrict, Wiang Nong Long District, Lamphun Province. The study focuses on developing low-impact tourism that preserves local biodiversity while fostering cultural heritage conservation through Lanna traditions, indigenous ecological knowledge, and organic agricultural practices. A qualitative research methodology was employed, with data collected through document analysis, focus group discussions, and in-depth interviews with community leaders, representatives of community enterprises, local entrepreneurs, and local residents. Research instruments included tourism site surveys and semi-structured interview guides, with data analysed using content analysis.

The findings reveal that Wang Phang Subdistrict possesses significant potential for biodiversity-centered community tourism. Key natural attractions include the Nong Pling Sufficiency Economy Agricultural Learning centre, which demonstrates organic farming techniques that support local biodiversity conservation. Cultural sites such as Ku Khao Pagoda and the Elephant and Horse Pillars serve as venues for environmental education, where traditional ecological knowledge is transmitted through hands-on activities including herbal compress making using native medicinal plants, traditional snack preparation from local organic produce, and the "Footsteps of Queen Chamthewi" cultural tour that highlights the historical relationship between Lanna culture and natural resource management.

Community participation emerges as a crucial factor in sustainable tourism development, with local residents actively contributing as ecological educators, organic agriculture practitioners, and conservation volunteers. The participatory planning process has successfully created a structured one-day tourism route that integrates organic agriculture demonstrations, biodiversity observation activities, and cultural heritage experiences. This approach emphasizes environmental impact control through visitor capacity limits, waste reduction strategies, and conservation education programs that raise awareness about local ecosystems and traditional ecological practices.

The research demonstrates that community-based tourism, when managed through participatory approaches that prioritize biodiversity conservation, can effectively bridge cultural heritage preservation with natural resource protection. The integration of organic agriculture showcase, native species conservation activities, and traditional ecological knowledge transmission creates a sustainable tourism model that supports both local economic development and long-term biodiversity conservation. This case study illustrates how community participation in low-impact tourism planning can foster sustainable relationships between visitors, local communities, and natural ecosystems, contributing to broader biodiversity conservation goals while maintaining cultural authenticity and economic viability.

KEYWORDS:

Community-based tourism; Process; Participation

Current Status and Potential for Developing Water Resources in Phu Toei National Park and Surrounding Areas for Water Consumption and Community-Based Tourism

Punnamate Wongwian¹, Watcharotai kaewpanpha¹, Pannawit Kitbowonchai¹, Benjawan Bhutinan¹, Kittipong Changthong¹, Apipum Pliawplod¹, Chakkrit Samphaothong², **Patharawit Tunninkul^{1,*}**

¹Department of Social Studies, Vajiravudh College, Bangkok, 10300, Thailand

²Phu Toei National Park, Suphan Buri, 72180, Thailand

*Corresponding author, e-mail: patharawit.t@vajiravudh.ac.th

ABSTRACT:

Water is essential for all living and plays a crucial role in supporting and shaping biodiversity. Although Dan Chang District is home to Phu Toei National Park, an area characterized by rich forest ecosystems, parts of the district are vulnerable to seasonal drought. The district's varied physical environment contributes to differing water resource challenges across locations, including limited access to drinking water during the dry season and a water shortage for the plantation. Moreover, according to a synthesis of this district's community needs and the quality of life development plan, there is a pressing need to promote community-based tourism as a means to increase the community's income, which is equally distributed to villagers. These challenges underscore the importance of identifying high-quality water sources within the area and developing strategic guidelines for their sustainable utilization, both to support safe water consumption and to serve as a foundation for community-based tourism development. This research had two objectives: 1) To study the current status of water resources in Phu Toei National Park and nearby areas, and 2) To suggest guidelines for promoting water resources in Phu Toei National Park and surrounding areas for consumption and community-based tourism. Data were collected from 11 water sample sources in Phu Toei National Park, Kok Chang Temple, and Wat Kok Chang School, Dan Chang District, Suphan Buri Province. The instruments used for data collection were: 1) Water Transparency Test Kit, 2) pH Paper, 3) Thermometer, 4) Monitor test kit conforms to AWWA Method, 5) Water Hardness Test Kit, 6) Water Quality Measurement Record Form, and 7) Semi-structured interview protocol to survey information about water sources from officials and local scholars. Then, all collected data were analyzed and summarized about the quality of water from various sources, and these data were the basis for synthesizing guidelines to promote water resources for Water Consumption and Community-Based Tourism. The results showed that different water sources had different transparency depending on the surrounding environment. Groundwater sources had lower oxygen solubility than other sources. The pH value of water from all sources was safe for drinking. Most of the water samples were hard, except for rainwater and water from water filters. The water temperature was within the standard range. In addition, from the field survey at the Karen village of Tapernkee, which was named after the Karen word "headwater", which refers to the relationship between the water resource and the local cultures for more than 2 decades. However, the community faces challenges due to limited access to resources, primarily related to laws governing the national park. Furthermore, villagers had limited access to public infrastructure due to the community's rural and remote location. Their primary sources of income are agriculture and tourism. At that village, there were many households that grew bitter beans (*Parkia speciosa* Hassk) for consumption and trade. Those bitter beans were very popular in the local market. Therefore, the guidelines for promoting water resources in Phu Toei National Park and nearby areas to develop for consumption and community tourism can be divided into 4 guidelines: 1) Phu Toei drinking water products, 2) Pickled bitter bean from Tapernkee village in mineral water, 3) Cold water treatment wells, and 4) Natural water study trails.

KEYWORDS:

Phu Toei National Park, Water Resources, Water Consumption, Community-Based Tourism

Exploring the Connection of Tourism and Insect Biodiversity in Mount Tapulao, Zambales, Philippines

Sheryl A. Yap^{1,2}, Thierry Bourgoïn³, Adeline Soulier⁴, Cyrille D'Haese⁴, Tony Robillard³, Olivier Montreuil⁴, Arnaud Faille⁵, Elorde Jr. S. Crispolon^{4,6}, Cristian C. Lucañas², Maxime Le Cesne³, Jade Aster T. Badon⁷, Manon Bucher³, Gerwin T. Alcalde¹, Rio S. Antion¹, Ruby Ana P. Laude¹, Orlando L. Eusebio², Elisabeth Huber⁸, Gernot Kunz⁹, Johanna Gunczy⁹, and Eric Guilbert⁴

¹Institute of Weed Science, Entomology and Plant Pathology, College of Agriculture and Food Science, University of the Philippines Los Baños, Laguna, Philippines

²Museum of Natural History, University of the Philippines Los Baños, Laguna, Philippines

³Institut de Systématique, Evolution, Biodiversité, UMR 7205 MNHN, CNRS, UPMC, EPHE, Sorbonne Universités, Muséum national d'Histoire naturelle, Paris, France

⁴Mécanismes adaptatifs et évolution, UMR MECADEV 7179 CNRS - MNHN, Muséum National d'Histoire Naturelle, Paris, France

⁵State Museum of Natural History Stuttgart, Rosenstein 1-3, 70191 Stuttgart, Germany

⁶Department of Crop Protection, Division of Entomology, College of Agriculture, University of Southern Mindanao, Kabacan, Cotabato, Philippines

⁷Institute of Biological Science, College of Arts and Sciences, University of the Philippines Los Baños, Laguna, Philippines

⁸ÖKOTEAM - Institut für Tierökologie und Naturraumplanung OG, Institute for Animal Ecology and Landscape Planning, Bergmannsgasse, Graz, Austria

⁹Universalmuseum Joanneum Studienzentrum Naturkunde, Weinzöttlstraße, and Department of Biology, Karl Franzens University of Graz, Universitätsplatz 2, Graz, Austria

*Corresponding author, e-mail: sayap3@up.edu.ph

ABSTRACT:

Mount Tapulao, also known as High Peak, is the highest mountain in Zambales, Philippines, reaching 2,037 meters above sea level, with the forest line starting at around 1,875 meters. Recognized as a Key Biodiversity Area (KBA) it boasts high species richness and diverse flora and fauna. Despite its popularity among hikers and nature enthusiasts, scientific studies on its insect biodiversity remain limited. It's been selected for an insect inventory survey due to its accessibility, high level of biodiversity, and diverse ecosystem. This study aims to document insect diversity and assess the ecological impacts of ecotourism in the area. Field surveys were conducted along established and lesser-known trails using sweep netting, light trapping, malaise traps, and pitfall traps. Preliminary results reveal a rich assemblage of insect taxa, which includes morphospecies of Coleoptera, Collembola, Blattodea, Diptera, Hemiptera, Hymenoptera, Lepidoptera, Neuroptera, and Orthoptera—some potentially undescribed or endemic. Insects contribute significantly to ecosystem functions such as pollination, decomposition, and environmental health indicators. The study also evaluated tourism activities and their potential impacts on insect habitats through field observation and interviews with local guides and stakeholders. While tourism contributes to local livelihood and environmental awareness, unmanaged foot traffic, trail widening, and littering pose threats to sensitive microhabitats. The findings underscore the need for an integrated approach that balances ecotourism development with the conservation of biodiversity. Recommendations include implementing low-impact tourism guidelines, establishing insect monitoring programs, and involving local communities in biodiversity education. Mt. Tapulao offers not only scenic landscapes but also a living repository of insect diversity that, if sustainably managed, can enhance its value as both a scientific research site and a model for ecotourism-based conservation in the Philippines.

KEYWORDS:

arthropod, diversity, insect assessment, mossy forest, tropical forest

From Biodiversity to Business Value: A Multidimensional BEQI Approach to Sustainable Coastal Tourism

Panichat Kitisittichai^{1,*}, Ariya Aruninta² and Manop Kaewmoracharoen³

¹Technology Management and Innopreneurship, Graduate School, Chulalongkorn University, Bangkok, 10330, Thailand

²Department of Landscape Architecture, Faculty of Architecture, Chulalongkorn University, Bangkok, 10330, Thailand

³Department of Civil Engineering, Faculty of Engineering, Chulalongkorn University, Bangkok, 10300, Thailand

*Corresponding author, e-mail: 6581019720@student.chula.ac.th

ABSTRACT:

Coastal tourism destinations are increasingly subjected to acute environmental stressors—biodiversity loss, habitat fragmentation, ecosystem degradation, and water pollution—that erode the integrity of marine and littoral systems and diminish the quality of visitor experiences. These pressures imperil both ecological sustainability and the long-term economic resilience of tourism sectors. Effectively mitigating such interconnected threats requires a transformative paradigm that integrates rigorous ecosystem conservation, human well-being, and sustainable economic development.

In response, we advance the Biophilic Environmental Quality Index (BEQI) Framework, an innovative business model firmly rooted in Blue Economy principles. The BEQI Framework systematically operationalizes six interrelated dimensions (1) Environment & Ecosystem dimension: carrying-capacity utilization, coastal green-space density, ecological connectivity, biodiversity richness, blue-water access frequency, and biophilic feature count (2) Well-being dimension (3) Social dimension (4) Experiential dimension (5) Business Value dimension (6) Economic impact dimension.

By quantifying and benchmarking these dimensions, BEQI reveals the synergistic value of ecological integrity and human experience. It underscores how biophilic environments foster physical and psychological health, enrich visitor engagement, strengthen community cohesion and cultural exchange, optimize commercial performance through innovative service design, and generate equitable economic outcomes—such as increased local spending, job creation, and enhanced income equity.

The BEQI Framework is instantiated via a digital platform offering three integrated services:

4. Insights-as-a-Service: Real-time dashboards and GIS-based zoning to delineate ecological thresholds and guide adaptive management of vulnerable habitats.
5. Subscription-Based Analytics: Predictive modeling and tiered reporting to optimize visitation patterns, calibrate green-premium pricing, and monitor return on investment.
6. Certification Services: “BEQI-Certified” accreditation for destinations meeting stringent biophilic criteria, accompanied by performance visualizations and renewal alerts to sustain market differentiation.

By embedding robust ecosystem health metrics into strategic and commercial decision-making, the BEQI Framework advances sustainable coastal tourism practices aligned with Blue Economy objectives. Anticipated benefits include the development of premium, value-added tourism offerings, preservation of ecological integrity, elevated visitor satisfaction, and durable economic viability. Ultimately, this conceptual model furnishes a scalable blueprint for policymakers, destination managers, and private stakeholders to place biophilic environmental quality at the core of strategic planning thereby reconciling ecological stewardship with resilient economic growth in coastal regions.

KEYWORDS:

Biophilic Environmental Quality Index, Environment & Ecosystem, Sustainable Coastal Tourism, Well-being, Business Innovation

Decarbonizing marine tourism in the coral reefs at Mu Ko Chumphon, Gulf of Thailand: Moving Towards Net-Zero Tourism

Makamas Sutthacheep^{1,*}, Charernmee Chamchoy¹, Wichin Subpala¹, Laongdow Jungrak¹, Wanlaya Klinthong and Wiphawan Aunkhongthong¹ and Thamasak Yeemin¹

¹Marine Biodiversity Research Group, Department of Biology, Faculty of Science, Ramkhamhaeng University, Huamark, Bangkok, 10240, Thailand

*Corresponding author, e-mail: smakamas@hotmail.com

ABSTRACT:

Tourism generates around 8% of global carbon dioxide emissions, mainly from transport, energy use, and infrastructure. The rapid growth of marine tourism is placing increasing pressure on coastal ecosystems through pollution and habitat degradation. In Thailand, marine tourism plays a central role in the blue economy and supports economic growth, yet its environmental impacts highlight the need for effective decarbonization and conservation measures. This study evaluates the carbon footprint of a one-day snorkeling trip at Ko Mud Wai Yai, Chumphon Province. A Life Cycle Assessment was conducted to quantify CO₂ emissions from transport, accommodation, food, and waste, aiming to support the transition toward Net-Zero Tourism. The study found that snorkeling activities emitted about 7.24 kg CO₂ eq. per person, mainly from transportation (52.49%), food (31.36%), and waste (16.5%). To address these impacts, the study collaborated with stakeholder consultations to identify feasible low-carbon interventions. The mitigation measures included adopting solar-powered facilities, reducing the use of plastics, and utilizing seasonal fruits, vegetables, and seafood. After applying these strategies, the estimated emissions decreased to 1.74 kg CO₂ equivalent per person mainly food (94.84%), and waste (5.16%). To further offset the remaining emissions, nature-based solutions such as seagrass restoration and mangrove rehabilitation are recommended to enhance carbon sequestration and support ecosystem resilience. The findings were critically examined, leading to practical strategies to reduce greenhouse gas emissions from marine tourism. These measures highlight the importance of sustainable practices and strong environmental commitments among operators, stakeholders, and local communities. Overall, the proposed actions provide a pathway to systematically lower emissions and contribute to the transition toward Net-Zero Tourism.

KEYWORDS:

carbon footprint, coral reef, Gulf of Thailand, marine tourism, net zero tourism

Enhancing coral reef biodiversity through Novel Restoration Techniques for Nature Positive Tourism in Thailand

Wichin Suebpala^{1,*}, Makamas Sutthacheep¹, Thamasak Yeemin¹, Sittiporn Pengsakun¹, Wanlaya Klinthong¹, Charernmee Chamchoy¹, Nipatpong Chuanchuen², Supawadee Photiyarach³ and Anaphat Nongkoo⁴

¹Marine Biodiversity Research Group, Faculty of Science, Ramkhamhaeng University, Huamark, Bangkok, Thailand

²Asian Ecotourism Network, Bangkok, Thailand

³Thailand Science Research and Innovation, Samsen Nai, Phaya Thai, Bangkok, Thailand

⁴College of Innovation and Management, Suan Sunandha Rajabhat University, Dusit, Bangkok, Thailand

*Corresponding author, e-mail: wichin.s@gmail.com

ABSTRACT:

Degradation of coral reefs have occurred globally due to both natural and human-induced pressures, affecting critical ecosystem functions and services, particularly tourism, one of the cultural services. In this research, we showcase the application of novel coral restoration strategies, coral micro-fragmentation, to rehabilitate damaged reefs and enhance reef biodiversity. This innovative method accelerates coral growth by using small fragments sourced from genetically diverse coral colonies, selected for their resilience to environmental stressors such as temperature fluctuations, salinity changes, and sediment accumulation. In Thailand, the technique was first applied in coral nursery plots at Ko Khang Khao and Ko Lan, Chonburi Province (Upper Gulf of Thailand) and coral restoration with coral fragments in Mu Ko Chumphon (Western Gulf of Thailand), revealing positive outcomes in terms of survival and growth rates across several coral species, including *Diploastrea heliopora*, *Pavona decussata*, *Pavona varians*, *Lithophyllon undulatum*, *Porites lutea*, *Pocillopora acuta*, *Pavona decussata* and *Dipsastraea favus*. These restoration efforts have enhanced biodiversity, attracted marine life, and contributed to nature-positive tourism. The restored sites have been integrated into dive tourism routes, enhancing tourist experiences and diversifying tourism products. Tour operators and local communities have played key roles in coral restoration, nursery maintenance, and reef monitoring. This study demonstrates the strong connection between coral reef restoration and nature-positive tourism, highlighting their synergistic potential for marine conservation and sustainable economic development.

KEYWORDS:

biodiversity, coral restoration, conservation, Gulf of Thailand, nature positive tourism

Towards carbon-neutral and nature-positive marine tourism in coral reef ecosystems: A case study of Ko Rangkajiu, the Western Gulf of Thailand on sustainable conservation

Maneerat Sukkeaw^{1,*}, Charernmee Chamchoy¹, Thamasak Yeemin¹, Laongdow Jungrak¹, Wanlaya Klinthong and Wiphawan Aunkhongthong¹, Makamas Sutthacheep¹ and Thamasak Yeemin¹

¹Marine Biodiversity Research Group, Department of Biology, Faculty of Science, Ramkhamhaeng University, Huamark, Bangkok, 10240, Thailand

*Corresponding author, e-mail: maneerut8728@gmail.com

ABSTRACT:

The transition towards carbon-neutral and nature-positive tourism is increasingly vital for addressing climate change and biodiversity loss in vulnerable coral reef regions. Marine tourism not only generates significant greenhouse gas emissions but also contributes to habitat degradation and pollution. Integrated approaches that combine decarbonization with ecological restoration and conservation are essential to sustain the environmental and socio-economic value of coral reef destinations. This study examines pathways to implementing carbon neutral marine tourism in conjunction with coral reef restoration, specifically through the transplantation of stress-tolerant coral fragments onto dome-shaped concrete nurseries, to achieve nature positive outcomes at Ko Rangkajiu in the Western Gulf of Thailand. The research project brings together government agencies, such as the Department of National Parks, Wildlife and Plant Conservation and the Department of Marine and Coastal Resources, along with diving tour operators in Chumphon Province, to collaborate on reducing greenhouse gas emissions and promoting nature-positive tourism by supporting coral biodiversity conservation. This initiative expands marine tourism opportunities, supports local dive businesses, and enhances tourist awareness of the importance of coral reefs and the threats they face. Educational activities and community participation in coral restoration contribute to a deeper understanding of conservation practices and promote sustainable resource management. This project aims not only to restore coral reef ecosystems but also to establish a model for long-term coastal resilience and environmentally sustainable economic development.

KEYWORDS:

Biodiversity; carbon-neutral tourism; coral reef restoration; Gulf of Thailand; nature-positive tourism

Floristic Assessment in Selected Cave Ecosystems in Calubian, Leyte Island, Philippines towards Sustainable Ecotourism Initiatives

Zhereeleen D. Meneses-Adorador^{1,2,*}, Michelle A. San Pascual², Jiro T. Adorador^{1,2}, Analee S. Hadsall^{1,2}, Chabelita A. Aviquivil², Danilo Tandang³, Eugene Lorance R. Logatoc^{1,2}, John Rey Callado⁴, Pastor L. Malabrigo Jr.⁵, Ariel Larona² and Jeff Latayan²

¹Institute of Biological Sciences, CAS, University of the Philippines Los Baños, 4031, Philippines

²Museum of Natural History, University of the Philippines Los Baños, 4031, Philippines

³National Museum of the Philippines, Manila, 1000, Philippines

⁴Forest Products Research and Development Institute, UPLB, Laguna 4031, Philippines

⁵Forest Biological Sciences, CFNR, UPLB, 4031, Philippines

*Corresponding author, e-mail: zdmeneases@up.edu.ph

ABSTRACT:

Baseline floristic assessment in selected cave ecosystems in Calubian, Leyte Island, Philippines was conducted to evaluate the suitability of the sites for ecotourism initiatives. The survey includes six candidate cave sites that were initially chosen by the local government to be included in a proposed ecotourism loop. Species richness ranges from 71 to 149 species across over 123 genera and 60 families. Of these, several species are listed under the country's National Threatened Plant List which includes the following: *Piper retrofractum*, *Canarium ovatum*, *C. luzonicum* and *Syzygium densinervum* (OTS); *Vitex parviflora* (EN); and *Ardisia elliptica*, *A. romanii*, *Wallaceodendron celebicum*, *Diospyros pyrrhocarpa* and *Clerodendrum quadriloculare* (VU) while four (4) are listed in the IUCN Red List (*Swietenia macrophylla* (EN); *Planchonia spectabilis*, *Wallaceodendron celebicum*, and *Albizia acle* (NT). Moreover, a new species of rattan (*Calamus* sp.) was also documented within the environs of Kinubkoban Cave. Although anthropogenic activities are evident in some of the sites, endemic species are still thriving in the area with about 15 documented endemics. Data suggests that despite the fragmented forest in some of the sites, it still holds important flora that can be used as flagship species for sustainable ecotourism activities.

KEYWORDS:

caves, sustainable tourism, flora, endemic

A Report on the Vascular Plants of Mt. Tapulao in Luzon Island, Philippines: Reaffirming its Ecotourism Value

Paul Alfonso C. Ondoy^{1,2}, Michelle Alejado-San Pascual¹, Sami Touafchia¹, Ariel Larona¹, Jhun Carlo T. Traquena², Jarvis N. Tirao^{1,*}, Eugene Lorence R. Logatoc⁴, Sheryl A. Yap^{1,5}, **Jiro T. Adorador^{1,4}**

¹Museum of Natural History, University of the Philippines Los Baños, Philippines

²Graduate School, University of the Philippines Los Baños, Philippines

³Muséum National d'Histoire Naturelle, Paris, France

⁴Institute of Biological Sciences, College of Arts and Sciences, University of the Philippines Los Baños, Philippines

⁵Institute of Weed Science, Entomology, and Plant Pathology College of Agriculture and Food Science, University of the Philippines Los Baños, Philippines*BSc Thesis Student

*Corresponding author, e-mail: jtadorador@up.edu.ph

ABSTRACT:

Mt. Tapulao (2,037 m asl) in Luzon Island, Philippines, classically known for its unique floristic diversity and highly valued mineral ores, is now conserved for its socio-economic benefits through ecotourism. In support of its conservation, a joint Philippine-French biodiversity expedition and assessment was recently conducted across three vegetation types (e.g. lowland, pine, and mossy forest). For the floristic components, the amassed herbarium materials correspond to a total of 367 distinct morpho-species which are distributed in 99 families [83 angiosperms, 3 gymnosperms, and 13 pteridophytes]. The most speciose are Orchidaceae and Poaceae with 48 and 42 species, respectively, then distantly followed by Rubiaceae (17), Asteraceae (11), Melastomataceae (10), Urticaceae and Polypodiaceae (9 each). These taxa mostly inhabit the lowland forests (36%), then mossy forests (34%) and pine forest (20%), while the remaining 10% occurs in the transition zones of these major vegetation types. Habit-wise, the most documented plants are herbs (36%), followed by trees (30%) and epiphytes (17%), while vines and shrubs constitute 7% each. Geographically, of the identified species, 35% are Philippine-endemic, while 60% are native and 5% are considered naturalized. Meanwhile, 24% are new province records, while 6% have been unofficially documented previously, and 7 taxa are highly threatened (based on IUCN 2025-1) namely, VU—*Lithocarpus jordanae*, *Syzygium congestum*; EN—*Microtropis curranii*, *Clerodendrum multibracteatum*, *Syzygium acrophilum*, *Mussaenda pinatubensis*; and CR—*Melicope zambalensis*. Among the collections, there are at least 6 new plant species (in *Heterospathe*, *Berberis*, *Melastoma*, *Haptapleurum*, *Nepenthes* and *Elatostema*) and several taxonomically significant observations were documented. Altogether, these botanical findings reaffirm the mountain's ecological wealth which should be safeguarded through community-led responsible ecotourism.

KEYWORD:

floristic diversity, nature tourism, serpentine, ultramafic, Zambales

Above-ground Biomass and Carbon Stock of Trees in Selected Urban Green Spaces and Schools of Iligan City, Philippines

Djamae L. Manzanares^{1,3,4,*}, Liza A. Adamat^{1,3,4}, Isidro B. Arquisal¹, Lorrenne C. Caburatan¹, Christina A. Barazona-Cuevas^{1,3,4}, Kimverly Hazel Coronel-Dapar^{1,3,4}, Frandel Louis S. Dagoc², Patricia Mae A. Dalagan¹, Israelee Praise T. Eslabon¹, Leonardo A. Estaño^{1,3}, Lady Jane C. Fanuncio^{1,4,5}, Jeremy Roy Augustus I. Gomez^{1,4}, Jaime Q. Guihawan², Mark Anthony I. Jose^{1,4,5}, Carol Socorro Maguinsay¹, Muhmin Michael E. Manting^{1,3,4}, Lady Jane G. Morilla¹, Nanette Hope N. Sumaya^{1,3,4}, Sharon Rose M. Tabugo^{1,3,4}, Wella T. Tatil², Vanessa Mae C. Tumang^{1,4}, and Carlo Stephen O. Moneva^{1,3,4}

¹Department of Biological Sciences, College of Science and Mathematics, Mindanao State University-Iligan Institute of Technology, Andres Bonifacio Avenue, Tibanga, 9200, Iligan City, Philippines

²Department of Environmental Science, School of Interdisciplinary Studies, Mindanao State University-Iligan Institute of Technology, Andres Bonifacio Avenue, Tibanga, 9200, Iligan City, Philippines

³Center for Biodiversity Studies and Conservation, Premier Research Institute of Science and Mathematics, Mindanao State University – Iligan Institute of Technology, Andres Bonifacio Avenue, Tibanga, 9200, Iligan City Philippines

⁴Center for Integrative Health, Premier Research Institute of Science and Mathematics, Mindanao State University – Iligan Institute of Technology, Andres Bonifacio Avenue, Tibanga, 9200, Iligan City Philippines

⁵Center for Microbial Genomics and Proteomics Innovation, Premier Research Institute of Science and Mathematics, Mindanao State University – Iligan Institute of Technology, Andres Bonifacio Avenue, Tibanga, 9200, Iligan City Philippines

*Corresponding author, e-mail: djamae.manzanares@g.msuiit.edu.ph

ABSTRACT:

Rapid urbanization and industrial expansion have significantly increased carbon dioxide emissions, intensifying global warming, accelerating biodiversity loss, and exacerbating the urban heat island effect. Urban green spaces (UGS), including those within school campuses, serve as vital ecological infrastructure that sequesters carbon, conserves biodiversity, and delivers essential ecosystem services. However, baseline data on carbon stock and tree species composition remain limited in many urbanized areas, particularly in Iligan City, Philippines. This study evaluated aboveground biomass (AGB), carbon stock, and tree diversity across five selected UGS and schools in the city: Buhanginan Hills, Centennial Park, Iligan Polytechnic State College, Tambacan Elementary School, and Iligan City East National High School. Trees with a diameter at breast height (DBH) ≥ 5 cm were measured, AGB was estimated using allometric equations, and carbon stock was calculated using a standard carbon fraction constant. A total of 2,526 individual trees representing 63 species were recorded. Invasive species were dominant, with *Swietenia macrophylla* (51%) and *Gmelina arborea* (12%) comprising the majority. Buhanginan Hills exhibited the highest biomass (704.21 Mg/ha) and carbon stock (309.61 Mg/ha), comparable to those of secondary and old-growth forests. The overall mean AGB and carbon stock were 283.80 Mg/ha and 126.25 Mg/ha, respectively. The most represented families included Moraceae, Fabaceae, Meliaceae, and Myrtaceae. While exotic species were prevalent, notable endemics, including *Artocarpus blancoi*, *Canarium ovatum*, and *Ficus odorata*, were identified. Notably, six locally threatened species were identified, including *Vitex parviflora* (Endangered), *Diospyros blancoi*, and *Pterocarpus indicus* (both Vulnerable), underscoring the conservation value of these urban sites. These findings underscore the crucial role of UGS in climate mitigation and biodiversity conservation, providing vital data to inform sustainable urban planning and green space management in Iligan City and other rapidly expanding urban centers.

KEYWORDS:

allometric equations; biodiversity conservation; climate mitigation; invasive species; tree diversity; urbanization

Next Generation Sequencing- Based eDNA Metabarcoding for Detecting Planktonic Communities in Bukidnon Lakes, Mindanao, Philippines

Rasel A. Lacandula^{1,2,3,*} and Sharon Rose M. Tabugo^{1,3,*}

¹Department of Biological Sciences, College of Science and Mathematics, Mindanao State University-Iligan Institute of Technology (MSU-IIT), Andres Bonifacio Avenue, Tibanga, 9200 Iligan City, Philippines

²Institute of Biological Sciences, College of Arts and Sciences, Central Mindanao University, University Town, Musuan, Bukidnon 8710, Philippines

³Molecular Systematics and Conservation Genomics Laboratory, Center for Biodiversity Studies and Conservation, Premier Research Institute of Science and Mathematics (PRISM), MSU-IIT, Andres Bonifacio Avenue, Tibanga, 9200 Iligan City, Philippines

*Corresponding author, e-mail: rasel.lacandula@g.msuiit.edu.ph, sharonrose.tabugo@g.msuiit.edu.ph

ABSTRACT:

Bukidnon is endowed with freshwater ecosystems such as lakes that harbor rich biodiversity which is crucial for maintaining ecological stability and providing essential ecosystem services. Thus, it faces major ecological problems such as climate change, deforestation, and land use change. This study focused on analyzing planktonic community composition using eDNA metabarcoding with Illumina Miseq platform of the V4 region 18S rRNA gene amplicon sequencing. Bioinformatics tools such as FLASH and Parallel Meta Suite (PMS) were used for taxonomic assignment and diversity metrics. Only successful libraries were considered in the study. A total of 55,380 Amplicon Sequence Variants (ASVs) were generated from the high- quality metabarcoding reads obtained from six (6) libraries, comprising 128 families and 203 genera. The results revealed nine (9) dominant taxa that have high abundant ASVs of plankton, categorized into phytoplankton/microalgae (7 species), protozoan/ciliates (1 species), and zooplankton (1 species). Alpha diversity analysis revealed Napalit18 as most diverse, and evenly distributed plankton community but with a fewer estimated species despite high diversity and evenness (Shannon: 2.35; Simpson: 0.86; Chao1: 20) while Napalit13 suggests low diversity, possibly dominated by a few species but with greatest number of estimated species (Shannon:1.19; Simpson:0.44; Chao1:32). Furthermore, *Levicolaps biwae* is known to be endemic in Lake Biwa, Japan and now considered noteworthy species first record in the Philippines. In addition, *Selenastrum capricornutum*, an important indicator species, is used for water quality assessment due to its sensitivity to pollutants and nutrient fluctuations. The presence of this species suggests that adequate nutrient levels and balanced ecological conditions, making it a valuable marker for monitoring freshwater ecosystems. Next generation sequencing (NGS) is critical in reinforcing the detection of species and boost the conservation measures for lake management.

KEYWORDS:

biodiversity, eDNA metabarcoding, Parallel Meta Suite (PMS), 18S rRNA, MiSeq

Species diversity of seaweeds in Mu Ko Similan, with the updated record of the genus *Titanophora* (Nemastomatales, Rhodophyta) from Thailand

Suttikarn Sutti^{1,*}, Ratchaneewan Sumitrakij¹, Sirikanya Chungthanawong¹ and Nattapon Noppornchareonkul¹

¹National Science Museum, 39, Moo 3, Khlong Ha, Khlong Luang, Pathum Thani, 12120 Thailand

*Corresponding author, e-mail: suttikarn@nsm.or.th

ABSTRACT:

The Similan islands or Mu Ko Similan consist of nine islands positioned from north to south in the Andaman Sea on the West Coast of Southern Thailand, Phang-nga Province to be exact. These islands are one of the major marine attractions due to their unique ecosystems with high biodiversity and unmatched livings in Thailand.

This field survey for species diversity of seaweeds in Mu Ko Similan, under the Project "Species diversity and genetic resources assessment of the genus *Caulerpa* (Caulerpaceae, Chlorophyta) in Thailand for the principal conservation and sustainable utilization" was done in 19–26 March 2025. Seaweeds and some seagrasses were collected by scuba diving in the areas of Mu Ko Similan totaling eleven dive sites. Based on solely morphological characters, at least 25 genera from 13 orders of seaweeds were recorded including "jelly weed", the genus *Titanophora*. This is the most updated record of *Titanophora* from Thailand and not present in the book "Seaweeds around Mu Ko Silmilan" in 2003 (in Thai). All seaweeds and seagrasses were prepared as voucher specimens to deposit in the collection of the Thailand Natural History Museum (THNHM), National Science Museum, Thailand (NSM). For better precision of species diversity in these areas, small fraction of voucher specimens, especially the genus *Caulerpa* including the so-called "killer algae" *Caulerpa taxifolia* (M.Vahl) C.Agardh, were sent for DNA extraction and molecular analysis. The molecular results are pending.

KEYWORDS:

Mu Ko Similan; Species diversity; seaweeds; *Titanophora*, *Caulerpa*

Environmental DNA (eDNA) Metabarcoding of Fish in Marine Sanctuaries of Sarangani Bay Protected Seascape, Philippines

Ziljih S. Molina^{1,*} and Sharon Rose M. Tabugo²

¹Biological Science Department, Doctor of Philosophy in Biology Student, Mindanao State University-Iligan Institute of Technology, Iligan City, 9200, Philippines

²Faculty of Biological Science Department, Mindanao State University-Iligan Institute of Technology, Iligan City, 9200

*Corresponding author, e-mail: ziljih.molina@g.msuiit.edu.ph

ABSTRACT:

Monitoring marine sanctuaries is critical for marine ecosystem management. These sanctuaries serve as breeding and feeding grounds for marine species, supporting the food web for commercially valuable species. Sarangani Bay Protected Seascape, located in the southern part of Mindanao, is one of the country's marine protected areas (MPAs) due to its rich biodiversity; however, efforts to catalog fish diversity remain inadequate. Tourism-related items were the most dominant type of macroplastic litter found on the rural and urban beaches of Sarangani Bay, directly impacting SDG 14 (Life Below Water). This study aimed to assess fish species diversity in the marine sanctuaries of Sarangani Bay using eDNA metabarcoding. Seawater samples were collected from marine sanctuaries to extract eDNA, which was analyzed using high-throughput next-generation sequencing (NGS). Fish species diversity and relative abundance were analyzed using the Mifish pipeline version 3.89. The results revealed eight genera and eight species: *Pomacentrus vaiuli*, *Acanthochromis polyacanthus*, *Ctenochaetus striatus*, *Acanthurus japonicus*, *Seriola quinqueradiata*, *Thysanophrys celebica*, *Balistapus undulatus*, and *Canthigaster valentini*. The most abundant genus was *Seriola*, with 47.17% relative abundance. The highest species diversity and richness were observed in the Marine Sanctuary of Batulaki, Glan, with the highest values in Shannon, Simpson, and Chao1 indices: 1.93, 0.73, and 4.00, respectively. Although most fish species are of commercial and minor commercial importance in fisheries, many remain categorized as Least Concern (LC) or Not Evaluated (NE). eDNA metabarcoding has also detected three fish species that pose a threat to humans, as listed in the International Union for Conservation of Nature (IUCN) Red List. These species have been reported to be poisonous when consumed, causing ciguatera poisoning. These findings provide valuable insights for future biodiversity management and conservation efforts in the Sarangani Bay Protected Seascape.

KEYWORDS:

Biodiversity; conservation efforts; fish diversity; relative abundance; tourism.

Abundance, Diversity, And Distribution of Freshwater Mollusks In Lake Sebu, South Cotabato, Philippines

Annabel C. Bornaes^{1,*} and Mary Grace G. Maglantay^{2,*}

¹Student, Sultan Kudarat State University, President Quirino, Sultan Kudarat, 9804, Philippines

²Faculty of Biology, Sultan Kudarat State University, Tacurong City, Sultan Kudarat, 9800, Philippines

*Corresponding author, e-mail: annabelbornales@sksu.edu.ph, marygracemaglantay@sksu.edu.ph

ABSTRACT:

This study investigates the abundance, diversity, and distribution of freshwater mollusks in Lake Sebu, South Cotabato, Philippines a vital aquatic ecosystem known for its rich biodiversity. Field surveys were conducted using quadrat sampling technique and hand picking method across various habitats within the lake. A total of 6 mollusk species were identified, comprising both gastropods and bivalve, with species richness varying significantly across different sampling sites. The Shannon-Wiener diversity index indicated lower diversity in areas with vulnerable aquatic vegetation and unstable water conditions. Abundance was influenced by habitat characteristics; species such as *Pomacea canalicuta* and *Sinondota woodiana* were particularly prevalent in nutrient-rich zones. The distribution patterns revealed that certain species are confined to undisturbed habitats, serving as bioindicators of ecological health. Conversely, areas impacted by human activities, natural causes like “kamahong” (oxygen depletion) which involves a sudden drop in oxygen levels, and anthropogenic influences such as overstocking of fish cages and overfeeding showed reduced mollusk populations and shifts in species composition. This research underscores the importance of freshwater mollusks in assessing the ecological integrity of Lake Sebu and highlights the need for conservation strategies to protect this critical habitat from ongoing environmental pressures.

KEYWORDS:

Abundance, Anthropogenic stressors, Bioindicator, Freshwater Mollusks, Lake Sebu

Elevational Gradient of Insect Diversity and Abundance in Mt. Tapulao, Zambales, Philippines

Rio Antion^{1,*}, Gerwin Alcalde², Adeline Soulier-Perkins³, Maxime Le Cesne⁴, Elorde Jr. Crispolon^{2,3}, Ruby Ana Laude¹, Cristian Lucañas⁵, Orlando Eusebio⁵, Eric Guilbert³ and Sheryl Yap¹

¹Institute of Weed Science, Entomology and Plant Pathology, College of Agriculture and Food Science, University of the Philippines Los Baños, College, Laguna, 4031, Philippines

²Division of Entomology, Department of Crop Protection, College of Agriculture, University of Southern Mindanao, Kabacan, Cotabato, Philippines

³Mécanismes adaptatifs et évolution (MECADEV), Muséum National d'Histoire Naturelle (MNHN), UMR 7179 MNHN-CNRS, CP 50, Entomologie, Paris, France

⁴Institut de Systématique, Évolution, Biodiversité (ISYEB), Muséum National d'Histoire Naturelle (MNHN), UMR 7205 CNRS-UPMC-EPHE, Sorbonne Universités, Paris, France

⁵Museum of Natural History, University of the Philippines Los Baños, College, Laguna, 4031, Philippines

*Corresponding author, e-mail: rsantion@up.edu.ph

ABSTRACT:

Understanding how environmental factors, particularly elevation, influence insect community structure is crucial for biodiversity conservation in tropical mountainous regions like the Philippines. This study investigated the distribution and abundance of various insect orders along the west slope of Mt. Tapulao, Palauig, Zambales. Insect samples were collected through Malaise trapping across nine distinct elevational bands ranging from 880m to 2037 meters above sea level (masl), with individuals identified to the order level and their abundances recorded. A total of 1699 insect individuals belonging to 12 orders were collected. Total insect abundance did not exhibit a linear relationship with elevation but showed a pronounced peak at higher elevations. The highest abundance was recorded at 1680 masl (n=707), followed by 1800 masl (n=186) and 1760 masl (n=173). Total insect counts declined significantly at both the highest elevation (n=62 at 2037 masl) and lowest elevations (n=41 at 1020 masl and n=31 at 880 masl). Diptera was the most abundant order overall, demonstrating remarkable dominance at 1680 masl (n=368). Coleoptera exhibited a broader distribution with a peak at 1050 masl, indicating adaptability across a wider elevational range. Lepidoptera was notably abundant at 1680 masl (n=115) and 1760 masl (n=84). Other orders like Hemiptera and Hymenoptera also showed increased abundances around these high elevational zones, while Neuroptera, Orthoptera, Phasmatodea, Psocoptera, Embioptera, and Blattodea were found in lower numbers and with restricted distributions. The observed peak in insect abundance at higher elevations, driven by Diptera, Coleoptera, and Lepidoptera, suggests that these zones in the mountain may represent optimal habitats offering a favorable combination of climatic conditions and resources. This research provides valuable baseline data on the elevational distribution and abundance of key insect groups in Mt. Tapulao, which is essential for guiding conservation efforts and developing effective management strategies to protect its rich and unique biodiversity.

KEYWORDS:

abundance patterns, altitude, biodiversity, elevational gradient, Mt. Tapulao

Assessment of Population and Lighting Impacts on the Black-bearded Tomb Bat (*Taphozous melanopogon*) in Pha Nang Khoi Cave, Phrae Province, Northern Thailand

Jirapa Thepdech¹, Tongchai Khonbang², Yuwadee Ponpithuk³ and **Supalak Siri^{3,*}**

¹Program in Agroforestry, Maejo University Phrae Campus, Phrae, 54140, Thailand

²Pha Nang Khoi Cave, Phrae Provincial Administrative Organization, Phrae, 54140, Thailand

³Program in Forestry, The Established Project of College of Forestry, Maejo University Phrae Campus, Phrae, 54140, Thailand

*Corresponding author, e-mail: supalak_sr@mju.ac.th

ABSTRACT:

This study aimed to assess the population and roosting sites of the Black-bearded Tomb Bat (*Taphozous melanopogon*) in Pha Nang Khoi Cave, Phrae Province, Thailand. Pha Nang Khoi is a tunnel-shaped limestone cave approximately 150 meters long and 10 meters wide. Seven surveys were conducted in August 2024 to: (1) estimate the bat population in the cave, (2) assess population sizes across 44 identified roosting sites, (3) analyze the relationship between population size and both roosting height and distance from artificial lighting, and (4) examine the effects of artificial light on bat populations. Bat population surveys were conducted using direct observation with the aid of a spotlight. The mean bat population was 593.43 ± 21.77 individuals, with the highest count (700 bats) recorded during the second survey and the lowest (506 bats) during the first. Roosting site heights ranged from 4.95 to 17.08 meters above the cave floor, and distances from light sources ranged from 4.47 to 15.06 meters. The most populated roosting sites were sites 18, 1, and 17, with average populations of 131.85, 63.85, and 59.00 bats, respectively. Bats were absent from 10 roosting sites. A low but statistically significant correlation was found between population size and roost height ($r = 0.21$, $p = 0.00$), while no significant correlation was found with distance from light ($r = 0.08$, $p = 0.15$). A t-test comparing bat populations during periods of light-on and light-off conditions revealed significantly higher populations during the light-off periods ($p = 0.01$), with an average of 647.66 ± 20.34 individuals when lights were off and 243 ± 28.48 when lights were on. These findings suggest that artificial lighting negatively impacts the population of *T. melanopogon* in Pha Nang Khoi Cave. These findings highlight the need for sustainable cave tourism practices. Installing interpretive signage to mark sensitive roosting sites and reducing light and noise pollution within the cave are recommended strategies to balance visitor access and bat conservation.

KEYWORDS:

Black-bearded Tomb Bat; cave; lighting; population; tourism

From the Forest to the City: Threatened Wildlife Kept as Pets in Valencia City, Bukidnon, The Philippines

Khean Harvey S. Acuevas^{1,*}, Adrian C. Aturo¹, and Dave P. Buenavista^{1,*}

¹Institute of Biological Sciences-Animal Biology Division, Central Mindanao University, 8714 Bukidnon, The Philippines

*Corresponding authors, e-mail: kheanharveysacuevas@gmail.com and aturoadrian520@gmail.com

ABSTRACT:

The hunting, trade, and pet ownership of wildlife is a well-known yet understudied field in the Philippines. While significant seizures of poached animals were recorded in the country, many remain undocumented and undetected. This study assessed the pet ownership of wildlife in five locations in Valencia City, Bukidnon, Philippines. A covert research approach was used to elicit information from the owners. A total of 26 pet owners were interviewed, majority are male (n=19, 73%), aged 40-45 years old (n=12, 46%), low-income farmers (n=17, 65%), and with primary education (n=16, 62%). The results revealed 63 individuals from 15 species; 8 species of birds, 4 species of mammals, and 3 species of reptiles. Of which, 12 (80%) species are classified as least concern, two (13%) are endangered, and one is undetermined. Birds are the most frequently recorded group (24 individuals), mainly intended for consumption, while *Macaca fascicularis philippensis* exist across all five barangays because of their behavioral flexibility and presumed human compatibility. Owners' responses indicate that they keep such animals mainly for recreation or hobby (n=15, 25%), which reflects that the affinity of locals to keep wild animals in the city may have been associated with human-wildlife interactions and humans' familiarity with native and endemic animals. Thereof, the study recommends strengthening the enforcement of existing national laws and international provisions through community-based conservation models, local wildlife amnesty programs, and partnerships with government and non-government organizations.

KEYWORDS:

Illegal trade; wildlife management; human-wildlife interactions; conservation; pet trade; hunting.

SESSION 4

BIODIVERSITY AND ENVIRONMENTAL REHABILITATION





The restoration of natural forests and biodiversity based on Miyawaki method for human life

Kazue Fujiwara

Graduate School in Nanobioscience, Yokohama City University, Seto 22-2, Kanazawa-ku, Yokohama, 236-0027 Japan

*Corresponding author, e-mail: Kazue05fujiwara@gmail.com

ABSTRACT:

The restoration of natural forests based on the Miyawaki method has already about 50 years of history. There are about 3000 examples in Japan and worldwide. Recently many volunteer groups have sprung up in the world and are working to restore natural forests. The characteristics of the Miyawaki method are: 1) rapid growth using natural forest species and skipping succession; and 2) rapid restoration of closed groves making rapid support for biodiversity. This method involves: 1) potted saplings of potential natural-forest dominant (climax) species and some late-successional species; 2) soil preparation on the planting sites (good drainage and nutrients) ; 3) dense, random, mixed-species planting (1-3 individuals per square meter); 4) planting by local children, students, handicapped people, old people, families and any other people; 5) mulching with rice straw, weeds or bark chips to reduce evaporation and soil erosion, to add nutrients and foster soil animals, and to save moisture and suppress weeds; and 6) no maintenance after three years from plantation. The dense planting encourages competition, coexistence, and endurance among seedlings, helping early growth of natural species and high accumulation of carbon dioxide by local forests. Such forests also have other functions: habitat for mammals and birds; mitigation of disasters (fire, tsunami, flood, etc.); protection against wind, salt spray, sand, noise, dust, etc., meeting various SDG objectives. Yokohama National University was established on an old golf course. Prior to the integration of all faculties, an environmental conservation forest was established in 1986 using the Miyawaki Method in the name of restoring natural forests; in 1989, a natural forest regeneration project was carried out on campus to commemorate the integration of all faculties. Since then, as the forest has developed, the flora, birds and animals have increased (cf. Kitagawa et al. 1968, Okuda 1994, Tohma et al. 2001; Harada et al. 1998; Fujiwara et al. 2009). In the urban area, many mini-forests were established at factories, schools, shopping malls, power plants, etc. Such mini-forests are effective in urban areas. Shopping malls in urban areas can easily supply birds' nests and living area (Yoshino et al. 2023). Even factory forests by the Miyawaki method increase bird species as the forests grow (Suzuki et al. 2014). The combination of Miyawaki forest and 'Satoyama' (rural land use, such as paddy fields, ponds, streams, grassland, etc.) by Eco Sango, increased the fauna (birds and insects). We can also see good examples in the PTT Metroforest Learning Center, Forestias Project in Bangkok.

KEYWORDS:

Dense; random; mixed-species planting; habitats for biodiversity; disaster mitigation; potted saplings of potential natural-forest dominants; rapid growth using natural forest species and skipping succession; SDG objectives



Adapting Miyawaki forests to tropical and other climates

Elgene O. Box

University of Georgia, Athens (Georgia), USA

ABSTRACT:

The “Miyawaki Method” is a process for creating potentially stable forest environments in open as well as smaller, even densely built-up areas. This generally involves six basic steps: 1) Understanding the local potential natural forest vegetation and its long-term canopy dominant species; 2) Preparing and planting pot-grown saplings of these species, with root systems already well developed; 3) Planting on a prepared, usually slightly raised site, with imported better soil if necessary; 4) Planting mixtures of perhaps 6-15 local canopy tree species, plus a few understorey species; 5) Planting at a high density, which promotes rapid, light-seeking upward growth that creates a shady, humid forest microclimate and minimizes invasion by light-demanding weeds; and 6) Mulching immediately after planting, to hold water and prevent weeds.

The aim is to create stable natural forests quickly, without going through all the usual successional stages (needing 50 years or more). This is done by planting mainly the potential canopy-dominant (“climax”) tree species, which in Japan are trees with dark green (high chlorophyll density), evergreen broad leaves, as from the laurel and oak families. These are the most shade-tolerant and thus the natural end stage of succession. Though more demanding, their saplings will grow well if they have well-developed root systems and the soil is well-prepared. This scheme works well in the benign climate of Japan because the climax species all grow at somewhat similar rates, thus steadily raising an intact canopy and preserving enough shade to keep out faster-growing competitors. Biodiversity increases, both above and below ground, as new species arrive naturally.

The idea of “Miyawaki forests” has suddenly caught on in many parts of the world, where climates may be drier, have cold winters, or have no winter at all. Different climates require adjustments in the methodology, and site preparation depends entirely on the local substrate. Outside Japan, tropical plantations have been established in Brazil, India, Indonesia, Kenya, Malaysia and Thailand; and others in China, Nepal and Southeast Asia, and in some parts of Europe and North America. Most now have at least 8-10 years of growth and a few more than 30 years, old enough to be showing results that may provide insight in other climatic situations. Tropical climates present special challenges, due to poor soils, high evaporation rates, and faster growth of all plants. One of the oldest large-area tropical plantings is on a university campus in Malaysia. We do not have all the answers. As a result, tropical plantings need to be monitored closely, for biodiversity as well as growth, and problems need to be communicated readily to others, in order to improve tropical techniques.

KEYWORDS:

Climax species, intact canopies, natural biodiversity, shade tolerance, tropical climates

ORAL PRESENTATION

SESSION 4



Rebuilding Biodiversity on Tsunami-Devastated Land: A Decade of Miyawaki Forest Creation in Iwanuma and Minamisoma, Japan

Teruko Sano^{1,*}

¹Public Relations and External Affairs, MORINO PROJECT Public Interest Incorporated Foundation, Tokyo, Japan

*Corresponding author, e-mail: sano@morinoproject.com

ABSTRACT:

As a result of the Great East Japan Earthquake in 2011, the coastal areas of Iwanuma City and Minamisoma City were struck by tsunamis that reached maximum heights of 10.5 meters and 22.1 meters, respectively. In Iwanuma, approximately 2,900 hectares—about 48% of the city's area—were inundated, while in Minamisoma, about 4,418 hectares—around 11% of the city—were flooded. On this salt-damaged and devastated land, the MORINO PROJECT created coastal forest belts—"Green Seawalls"—stretching 10 kilometers in each city, 20 kilometers in total, using the Miyawaki Method. More than a decade later, these forests are contributing not only to disaster risk reduction but also to the significant recovery of biodiversity.

In Minamisoma, 21 native tree species were mixed and densely planted based on the theory of potential natural vegetation (PNV). One to two years after planting, skylark nests were observed. Around years two to four, as the forest canopy began to close, soil-dwelling organisms such as isopods, earthworms, and ants became readily visible under the moist leaf litter and undergrowth. In addition, sightings of Japanese tree frogs, Japanese grass lizards, and burrows and individuals of Japanese hares were confirmed. During this same period, however, skylark nests disappeared—likely due to the emergence of predators such as snakes. At a planting site further north, 12 years after planting, trees had reached heights of 6 to 7 meters. Multiple nests of Oriental turtle doves were observed among the trees, indicating changes in wildlife composition as the forest matures.

Adjacent to these planting areas lies the Haramachi Thermal Power Plant, where a 12-hectare Miyawaki forest was created between 1995 and 1997. This forest, consisting of approximately 400,000 native trees, has grown over nearly 30 years into a mature ecosystem with trees reaching about 20 meters in height and supporting a wide range of flora and fauna. Located on elevated ground, it was spared from tsunami-related salt damage. It is believed that a variety of organisms, including insects and small mammals, have migrated from this established forest to the nearby newly planted zones, playing a critical role in ecological recovery. Thus, the 20-kilometer-long Green Seawalls spanning Iwanuma and Minamisoma function as both cradles of biodiversity and ecological corridors. They offer a pioneering, nature-based model for restoring ecosystems and enhancing disaster resilience in coastal areas devastated by tsunamis.

These forest creation efforts have been carried out in collaboration with volunteer tree planters. To date, more than 60,000 people—including children and elderly participants from across Japan—have joined the annual planting activities. These events have served as spaces for mourning the tsunami victims, passing down the lessons of the disaster, and promoting environmental education. All of the seedlings have been funded through donations, and the project continues with strong support from local communities and society at large.

KEYWORDS:

Biodiversity restoration, ecological corridor, Great East Japan Earthquake, Potential natural vegetation (PNV), Tsunami Resilience

Biodiversity Restoration based on the Miyawaki method and Ecosystem benefits in Thailand

Sirin Kawlaierd¹ *, Anong Chanamool ¹, and Santanee Phasuk ²

¹School of Innovative Agriculture, Chitralada Technology Institute, Rayong Province, 21210, Thailand

²Chitralada Technology Institute, Bangkok, 10300, Thailand Chitralada Technology Institute (CDTI), Si Ayutthaya Rd., Dusit, Bangkok 10300, Thailand

*Corresponding author, e-mail: skdrsirin@gmail.com

ABSTRACT:

The “Miyawaki method” is a man-made restoration process to create a native forest within a short time with native species, mixed species, high density, multi-layer, and random planting. In Thailand, the restoration of biodiversity and ecosystems, based on the Miyawaki method, has been carried out since 1991, and at present (2025), there are over 60 restoration sites. The good practices can be categorized into 4 types of biodiversity restorations as follows: 1) Create a natural forest to restore degraded land into a forest ecosystem; 2) Protection strip/ buffer zone as fence to protect and improve the environment; 3) Rehabilitation for well-being, particularly in urban areas; and 4) Establishment of learning centers for biodiversity and environment education.

For a good illustration, Kasetnawat (Innovative Agriculture) Learning Center is a holistic management based on biodiversity restoration and sustainable agriculture at the community scale. There are more than 300 species that have been planted. The center functions not only in agriculture but also ex- situ biodiversity conservation. The Miyawaki forest methodology has been applied to create the protection strip along the fence. Further, a mixed fruit orchard was created by planting native tree species mixed with fruit and herb species.

The benefits of biodiversity and ecosystem restoration are significant. Firstly, native species are being reintroduced to reduce threats to biodiversity loss and maintaining ecological balance. Secondly, the habitats can recover to a more complex ecosystem in terms of food web and biological control. Thirdly, the environment, such as air, water, temperature, CO₂ absorption, dust, Particulate Matter (PM) 2.5, and so on, is enhancing for our society. Finally, local communities are becoming more resilient due to the healthy and sustainable ecosystems providing food, water, medicine, shelter, fabric dye, and other basic necessities for human survival.

The results from the over 30 years of experience on biodiversity restoration can be summarized that the Miyawaki forest methodology promotes not only flora conservation but also increases fauna, which consists of insects, butterflies, birds, etc. Besides, such a high-potential method can be applied for environmental education, sustainable agriculture, and so on. The approaches and practices contribute to nature-based solutions for our society.

KEYWORDS:

Biodiversity restoration, ecosystem benefits, Miyawaki method.

Mangrove Plantation at Abandoned Shrimp Ponds in Nakhon Si Thammarat: Restoring Biodiversity and Countering Climate Change

Shigeru Kato^{1,3,*}, Savettachat Boonming², Suthira Thongkao¹, Seiichi Suzuki³ and Sanit Aksornkoae⁴

¹Walailak University, Nakhon Si Thammarat, Thailand

²Department of National Parks, Wildlife and Plant Protection, Bangkok, Thailand

³Seikei University, Tokyo, Japan

⁴The Sirindhorn International Environmental Park, Phetchaburi, Thailand

*Corresponding author: e-mail address, hirugiman@yahoo.co.jp

ABSTRACT:

Mangrove forests rank among the most biologically productive ecosystems on Earth, spanning approximately 14 million hectares across tropical and subtropical regions. Southeast Asia hosts some of the most extensive mangrove coverage globally. These ecosystems have garnered increasing attention not only for their role in supporting biodiversity and sustaining livelihoods, but also for their exceptional capacity to sequester carbon, estimated to be over five times greater than that of tropical rainforests.

From the 1980s to the 1990s, widespread deforestation of mangroves occurred due to agricultural expansion, firewood harvesting, and industrial development. In southern Thailand's Nakhon Si Thammarat Province, large tracts of mangrove forest were converted into shrimp farms. However, due to economic and environmental challenges, shrimp farming declined, leaving over 4,000 hectares of ponds abandoned.

In response, the "Operation Green Carpet" initiative was launched in 1998 to reforest these degraded areas with mangroves. With strong support from local communities, the project aimed to: (1) Mitigate climate change by restoring carbon sinks through mangrove reforestation; (2) Promote sustainable production of biological resources, including plants and seafood; and (3) Foster environmental awareness and stewardship among residents.

Operation Green Carpet's achievements include: (1) Reforestation of 1,000 hectares of abandoned shrimp ponds over a decade; (2) Significant carbon dioxide absorption and underground carbon storage by mangrove biomass; (3) Return of diverse aquatic species, including fish, crabs, and mollusks; and (4) Enhanced environmental consciousness within local communities.

Initial trophic analyses revealed 7–8 feeding stages among coastal and estuarine fish. Recent studies, however, indicate a complex food web with 24–25 trophic levels, underscoring the ecological richness fostered by restored mangrove habitats. In January 2025, an environmental DNA (eDNA) survey commenced in Pak Phanang Bay to monitor seasonal fish diversity and assess fishery resource potential for future food security.

KEYWORDS:

Mangrove plantation, ecosystem restoration, food web complexity, carbon sequestration, stable isotopes, environmental DNA

Understanding and Mitigating Human-Elephant Conflict in Thailand: An Interdisciplinary and Community-based Ecotourism Approach

Chution Savini^{1,*}, Poldej Kochprapa^{2,3}, Dusit Ngoprasert², Tommaso Savini² and George A. Gale²

¹Department of Hospitality and Tourism Management, International College of Sustainability Studies (SWUIC), Srinakharinwirot University, 114 Sukumvit 23 Bangkok 10110, Thailand

²Conservation Ecology Program, School of Bioresources & Technology, King Mongkut's University of Technology, 49 Soi Tientalay 25, Bangkhuntien-Chaitalay Road, Thakham, Bangkhuntien, Bangkok 10150, Thailand

³WWF Thailand, 9 Pra Dipat 10, Pra Dipat Road, Phaya Thai, Bangkok 10400, Thailand

*Corresponding author, e-mail: chution@g.swu.ac.th

ABSTRACT:

As global demand for food and biofuels continues to increase alongside population growth, widespread agricultural expansion has globally intensified particularly in Southeast Asia and other tropical regions that are also critical biodiversity hotspots. These land-use changes have led to significant habitat loss, a key driver of biodiversity decline, and have increased human-wildlife interactions, often resulting in conflict. Despite Thailand having a well-established protected area system, forest fragmentation persists, making habitats increasingly unsuitable for wide-ranging species such as wild elephants. This has contributed to the growing challenge of Human-Elephant Conflict (HEC), which results in both elephants and human fatalities as well as economic losses. This study aims to investigate the dynamics of HEC in Thailand over the past 30 years, analyse land-use patterns surrounding elephant habitats. It also explores the spatial and temporal movements of elephants, assesses local communities' knowledge, attitudes, and perceptions toward elephants, and promotes sustainable mitigation strategies and community-based ecotourism as tools to reduce conflict, support elephant conservation, and strengthen local livelihoods. The survey from secondary data in the past 30 years indicated an increasing number of elephants and human's deaths caused by HEC, with particularly high conflict intensity in eastern Thailand. The study was conducted in the Kaeng Krachan Forest Complex, specifically in Kaeng Krachan and Kui Buri National Parks. Both ecological and social science approaches were conducted from August 2020 to July 2021, aimed to understand the drivers and spatio-temporal patterns of HEC. Focusing on crop raiding near Kui Buri National Park, we analysed incident locations in relation to environmental variables, crop types, and availability. Results revealed that although pineapple plantations were frequently raided, fruit orchards were elephants' preferred targets due to their high raid frequency in smaller areas. Notably, it showed that no area in Kui Buri was free from elephant raids, exposing the entire community to risk. In parallel, social science research was conducted to understand the perceptions of communities that have experienced persistent HEC since 1992. A mixed-methods approach was used, combining field observations with structured questionnaires administered to park rangers and local communities. In-depth interviews also contributed to the development of a practical guidebook outlining appropriate elephant deterrent techniques for patrol teams. The findings support the development of targeted mitigation strategies, such as conflict-reduction interventions, to foster sustainable coexistence between humans and elephants. Key recommendations include improved coordination among stakeholders, the development of a comprehensive multi-stakeholder action plan, and the empowerment of local communities through ecotourism and tour guide training initiatives.

KEYWORDS:

Biodiversity, Elephant Conservation Human-elephant Conflict, Kaeng Krachan National Park, Kuiburi National Park

Haplotype Diversity of Wild Asian Elephants in Phu Khieo and Khao Ang Rue Nai Wildlife Sanctuaries, Thailand

Supansa Rerkdee^{1,*}, Worapong Singchat^{1,2}, Thitipong Panthum^{1,2}, Trifan Budi², Warong Suksavate¹, Pannita Neepai¹, Aingorn Chaiyes^{2,3}, Thiti Sornsa⁴, Wichanon Saenphala⁵, Boripat Siriaronrat⁶, Kornson Srikulnath^{1,2}, Prateep Duengkae^{1,2,*}

¹Special Research Unit for Wildlife Genomics (SRUWG), Department of Forest Biology, Faculty of Forestry, Kasetsart University, Bangkok 10900, Thailand

²Animal Genomics and Bioresource Research Unit (AGB Research Unit), Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

³The International Undergraduate Program in Bioscience and Technology, Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

⁴Chachoengsao Wildlife Research Station, Department of National Parks, Wildlife and Plant Conservation, Chachoengsao 24160, Thailand

⁵Phu Khieo Wildlife Sanctuary, Department of National Parks, Wildlife and Plant Conservation, Chaiyaphum 36180, Thailand

⁶Faculty of Environment and Resource Studies, Mahidol University, Nakhon Pathom 73170, Thailand

*Corresponding author, e-mail: fforptd@ku.ac.th

ABSTRACT:

Understanding the genetic diversity of wild Asian elephants (*Elephas maximus*) is essential for assessing their adaptability and long-term viability, particularly in fragmented habitats. This study investigates the mitochondrial DNA (mtDNA) D-loop haplotype diversity, a region known for its high variability, to provide insights into the genetic structure of elephants in two protected areas in Thailand: Phu Khieo (PK) and Khao Ang Rue Nai (ARN) Wildlife Sanctuaries. Both PK and ARN are key conservation areas, home to wild elephants and other wildlife, making them ideal for studying elephant genetic diversity. Non-invasive fecal sampling was conducted, with 133 samples collected from PK and 192 from ARN. However, for the analysis, 32 samples from PK and 34 from ARN were successfully used for mtDNA extraction. A total of 14 haplotypes were identified across these individuals. In PK, 9 haplotypes were found, with high haplotype diversity ($h = 0.712$) and low nucleotide diversity ($\pi = 0.020$), suggesting stable genetic structure. In contrast, ARN had 6 haplotypes, with lower haplotype diversity ($h = 0.624$) and higher nucleotide diversity ($\pi = 0.022$), indicating a more dynamic population history. Only one haplotype (TH2) was shared between the two populations, reflecting genetic differentiation. As shown by Analysis of Molecular Variance (AMOVA), 11.65% of the genetic variation occurred between the two elephant populations, suggesting that differences in their genetic makeup may be linked to barriers such as habitat fragmentation. These findings emphasize the importance of preserving movement corridors, especially in fragmented areas like ARN, to maintain genetic diversity, reduce isolation, and ensure long-term population health. Such conservation strategies directly contribute to environmental rehabilitation by restoring connectivity between fragmented habitats, supporting biodiversity, and mitigating the adverse effects of human-induced landscape changes.

KEYWORDS:

Asian elephant; haplotype diversity; mitochondrial DNA; non-invasive sampling

Habitat associations of critically endangered big-headed turtles in Northern Thailand: a study to support grassroots river conservation

Mark R. Herse^{1,2,*}, Wanlop Chutipong², Noppasorn Khuntong³ and George A. Gale²

¹Kasetsart University International College, Kasetsart University, Bangkok

²Conservation Ecology Group, King Mongkut's University of Technology Thonburi, Bangkok

³Independent Researcher, Chiang Mai

*Corresponding author, e-mail: markr.herse@gmail.com

ABSTRACT:

Modern wildlife conservation in many countries such as Thailand relies on state protected areas and laws against hunting and wildlife trade, whereas community-driven conservation initiatives are underrepresented and receive limited scientific support. We investigated habitat associations of critically endangered big-headed turtles (*Platysternon megacephalum*) to assist a grassroots river conservation initiative in Phayao Province, Thailand. The study area was an upper watershed comprising an ambiguous national park boundary, state-owned lands used and cultivated by local villagers, and a state-planned large dam site. We trapped for turtles at 250 river or stream pools (494 total trap-nights) upstream of the planned dam site in 2024–2025 and assessed how species occurrence and body size varied with different pool features.

We captured 24 individual big-headed turtles in 22 widely distributed pools, as close as ~500 meters to the planned dam reservoir. Species occurrence increased with pool width and depth and percent substrate comprising boulders, likely reflecting big-headed turtles' space-use requirements and preferences for pools containing caves and crevices that are suitable for feeding and taking shelter. Body size decreased with water pH and was correspondingly lower in stream pools than river pools, possibly reflecting favorable conditions for nesting and juvenile survival in streams. More data is needed to account for imperfect detection and identify ecological causes of habitat associations. In the meantime, our results could inform potential species-level conservation interventions (e.g. fishing and irrigation guidelines). Importantly, our results also show that the planned dam could destroy, degrade, and/or isolate habitats of turtles, adding to concerns expressed by villagers about risks to the local fishery and community livelihoods. As prevailing economic growth policies call for ever-expanding infrastructure and development projects (e.g. dams), often at the expense of the environment, grassroots initiatives to prevent undesirable projects and improve local conservation are key to protecting threatened species and ecosystems.

KEYWORDS:

Community-based conservation, wildlife ecology, endangered species, dams, Mekong River Basin

Flight altitude of bats and associated collision risk at wind turbines in Central Thailand

Supawan Srilopan¹, Jennifer J. Krauel⁴, Kamonporn Srilopan^{5,6}, and Christian C. Voigt^{2,3} and Sara Brumrungsri^{1,*}

¹Division of Biological Science, Prince of Songkla University, Hat Yai, Songkhla, Thailand

²Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany

³Universität Potsdam, Am Mühlenberg 3, 14476 Potsdam, Germany

⁴Department of Biology and Microbiology, South Dakota State University, Brookings, South Dakota, USA

⁵Division of Physics, Rajamangala University of Technology Thanyaburi, Pathum Thani, Thailand

⁶Smart Materials Research Unit, Rajamangala University of Technology Thanyaburi, Pathum Thani, Thailand

*Corresponding author, e-mail: sara.b@psu.ac.th

ABSTRACT:

Wind energy production can have a negative impact on wildlife if vulnerable species lose habitats or collide with the turbine structure. Studies from the temperate northern hemisphere have shown that many bats may collide with turbine blades, especially species adapted to foraging in open spaces and edge habitats like forest margins. Unfortunately, data on the susceptibility of tropical and subtropical bat species to turbine blade collisions is limited, despite the growing use of wind energy in emerging markets and the need for high environmental standards in turbine operation. Here, we investigated bat acoustic foraging activity at different altitudes above ground (2, 25, 50, 75, and 100 m) in Thailand to assess collision risk for local species. We used automated ultrasonic detectors suspended from a helium-filled balloon kite to monitor bats. We observed the following 6 bat species within the potential rotor-swept zone of local wind turbines: *Mops plicatus*, *Taphozous theobaldi*, *T. melanopogon*, *Scotophilus kuhlii*, *S. heathii*, and *Myotis siligorensis*. These species are primarily open-space foragers, except *M. siligorensis*, which is classified as an edge-space forager. Our results show that the flight altitudes of several bat species in Thailand overlap with the operating range of local wind turbines, which may put them at risk of collisions. This highlights the need for implementing efficient mitigation measures such as restricting the operation of wind turbines at night during critical times and environmental conditions to minimise the collision risk for bats.

KEYWORDS:

Open space bats, balloon-kite, wind energy production

Population Density and Distribution of Great Hornbills (*Buceros bicornis*) During the Breeding Season on Koh Chang Island, Trat Province, Thailand

Peerawut Rincam¹, Nantida Sutummawong^{1,*}, Chattraphas Pongcharoen¹ and Neramit Songsang²

¹Department of Forest Biology, Faculty of Forestry, Kasetsart University, Bangkok, 10900, Thailand

²Mu Ko Chang National Park, Koh Chang Subdistrict, Koh Chang District, Trat Province 23170, Thailand

*Corresponding author, e-mail: fforinis@ku.ac.th

ABSTRACT:

Koh Chang, Thailand's second-largest island, is recognized for its ecological richness and conservation value. Its diverse topography and relatively intact forest ecosystems provide important habitat for the Great Hornbill (*Buceros bicornis*), the largest hornbill species in Thailand, currently listed as Vulnerable with a declining population trend on the IUCN Red List (2025). Despite the island's conservation importance, data on the population density and spatial distribution of Great Hornbills remain limited, posing challenges for effective management. This study aimed to estimate the breeding-season population density and assess the spatial distribution of Great Hornbills on Koh Chang. Line transect surveys were conducted across four national park protection units, covering a total transect length of approximately 25 kilometers. Each transect was surveyed twice during the 2025 breeding season. A total of 36 hornbill detections were recorded, including 27 visual sightings and 9 auditory detections. Population density was estimated using distance sampling via the *unmarked* package in R. When combining both visual and auditory detections, the estimated density was 2.72 ± 0.64 individuals per square kilometer; based solely on visual detections, the estimate was slightly lower at 2.56 ± 0.65 individuals per square kilometer. To assess spatial distribution, data from SMART patrol records and direct field observations were integrated with habitat suitability modelling predicted by MaxEnt. Three key habitat clusters emerged: (1) the central-eastern highlands near Klong Plu and Salak Khok, (2) the southern forested peninsula including the Kai Bae and Bang Bao hills, and (3) the northwestern forest slopes above Klong Son. These areas are characterized by high elevation, mature evergreen forest, and relatively low human disturbance. In contrast, coastal lowlands and developed areas showed little to no hornbill activity. The combined dataset illustrates a fragmented but ecologically coherent distribution, with hornbills concentrated in interior and upland forest zones. This study provides the first robust estimate of Great Hornbill population density on Koh Chang and highlights the island's critical breeding habitats. The findings serve as a baseline for long-term population monitoring and offer valuable insights for habitat protection, nest-site conservation, and ecological corridor planning. These data provide a critical evidence base for assessing the effectiveness of ongoing conservation efforts and guiding adaptive management strategies to ensure the long-term survival of the species on the island.

KEYWORDS:

Evidence-based conservation; Great Hornbill (*Buceros bicornis*); Population density estimation; Habitat suitability modeling; Koh Chang Island

POSTER PRESENTATION

SESSION 4



The influence of ground cover plants on erosion control in sloping areas in irrigated agriculture systems with soil quality improvement through the application of lime treatment and alum treatment

Wasan Sodsri^{1,*}, Prapapan Suesat¹, Chollachai Kamtawai¹, Rungnapa Somnark¹ and Teepakorn Kasikphand¹

¹Research and Development Bureau, Royal Irrigation Department, Ministry of Agriculture and Cooperatives, Nonthaburi, 11120, Thailand

*Corresponding author, e-mail: myhedwig7@gmail.com

ABSTRACT:

The influence of ground cover plants on erosion control in sloping areas in irrigated agriculture systems with soil quality improvement through the application of lime treatment and alum treatment, what soil quality has been amended with hydrated lime and alum solution. The study compares the effectiveness of cover crops combined with lime and alum treatments in mitigating soil erosion caused by dispersive soils under a slope gradient of 1: 1.5 and simulated rainfall intensity of 200 mm/ hr (400 mm/ d).

Soil samples were obtained from km 11+500 of the Pa Sak Jolasid Operation and Maintenance Project. Lime treatment was conducted by incorporating 2.20% hydrated lime by weight or 0.34% alum by weight into the soil, which effectively reduced soil dispersion to within acceptable standards.

A two-way ANOVA was employed to analyze the erosion data based on sediment yield from test plots. The F-test indicated a statistically significant effect of cover crop presence ($F = 15.476$, $p < 0.001$) and soil amendment type ($F = 125.239$, $p < 0.000$), with both p - values falling below the 0.05 threshold. These findings demonstrate that both the implementation of soil amendments and the cultivation of cover crops significantly impact sediment yield at the 0.05 significance level.

Multiple comparison analysis revealed that sediment yields from plots treated with lime and planted with cover crops, those treated with alum and planted with cover crops, and lime - only plots were not significantly different from each other. However, significant differences were observed among dispersive soils, dispersive soils with cover crops, and soils treated with alum, all with p -values less than 0.05. Homogeneous subsets analysis indicated no significant difference in sediment yield between lime-treated plots with cover crops and lime-only plots, which exhibited the lowest sediment yields, followed by alum-treated plots with cover crops. Plots with alum alone, cover crops alone on dispersive soil, and untreated dispersive soil yielded progressively higher sediment levels, with statistically significant differences at the 0.05 level.

The combined use of lime or alum with cover crops effectively reduced erosion on 1:1.5 slopes. Specifically, lime-amended soils with cover crops reduced sediment yield by 7,047.20 g/m² (97.52%), followed by lime-only soils (6,897.14 g/m², 95.44%), alum-treated soils with cover crops (6,537.91 g/m², 90.48%), alum-only soils (5,773.77 g/m², 79.90%), and dispersive soils with cover crops (2,763.13 g/m², 38.23%). Analysis by amendment type confirms that combining cover crops with either lime or alum significantly reduces sediment yield more effectively than using either amendment alone, at the 0.05 significance level.

KEYWORDS:

Alum Treatment; Dispersive Soil; Erosion; Ground Cover Plants; Lime Treatment

Soil fertility evaluation and guidelines for fertilization in an irrigated area of project of Huai Chorakhe Mak Reservoir, Buri Ram Province

Rungnapa Somnark^{1,*}, Prapapan Suesat¹, Teepakorn Kasiphand¹, and Wasan Sodsri¹

¹Office of Research and Development, Royal Irrigation Department, Ministry of Agriculture and Cooperatives, Nonthaburi, 11120, Thailand

*Corresponding author, e-mail: s_rungnapa@kkumail.com

ABSTRACT:

The objective of this study was to investigate soil properties, evaluate soil fertility levels and provide fertilization recommendations for irrigated areas of the Huai Chorakhe Mak Reservoir, Buri Ram Province. A total of 46 soil samples were collected from paddy fields surrounding the study area using a detailed reconnaissance soil survey. The samples were analyzed for their physical and chemical properties, as well as for soil fertility assessment. The results indicated that soil texture ranged from fine to medium. Soil reaction (pH) was moderately acidic. The electrical conductivity (EC) of saturated soil extracts was low, suggesting no salinity hazard to crop growth. Organic matter (OM), available phosphorus (P), and potassium (K) contents were found to be very low, while cation exchange capacity (CEC) and base saturation (BS) values were at medium to high levels. The soil fertility assessment revealed that the soils in the study area exhibited low to medium fertility levels. Based on the soil analysis results from this study, 11 fertilizer application plans were formulated in accordance with the Rice Department guidelines (2009). The findings highlight the area under investigation requires enhancement of soil fertility for agricultural cultivation. This research provides valuable information for guiding fertilizer application based on soil analysis results. Such recommendations aim to enhance fertilizer use efficiency, promote sustainable agricultural practices. This approach helps reduce excessive fertilizer use, which may lead to the accumulation of chemical residues in the soil and runoff into irrigation water sources, potentially promoting algal blooms and leading to eutrophication.

KEYWORDS:

Huai Chorakhe Mak Reservoir; Fertilizer; Soil analysis; Soil fertility.

Carbon Sequestration in The Soil of Mae Moh Mine Reclamation Area

Kawinthida Suvanna^{1,*}, Nipon Mawan², Pimraphat Sricharoenta¹, Thitinan Hutayanon³ and Panida Kachina²

¹Department of Plant and Soil Sciences, Faculty of Agriculture, Chiang Mai University, Chiang Mai, 50200, Thailand

²Department of Highland Agriculture and Natural Resources, Faculty of Agriculture, Chiang Mai University, Chiang Mai, 50200, Thailand

³Mine Reclamation Technique Section, Mine Reclamation Department, Mae Moh Mine, Lampang, 52220, Thailand

*Corresponding author, e-mail: kawinthida_suvanna@cmu.ac.th

ABSTRACT:

Carbon sequestration is a crucial outcome of mine area restoration, contributing to both ecosystem recovery and climate change mitigation. This study aims to investigate carbon sequestration in the forest restoration areas of the Mae Moh mine which started in 2001, 2006, and 2011. Soil samples were collected using both destructive and non-destructive methods at soil depths of 0–10 cm and 10–20 cm. Soil properties, such as bulk density, soil moisture, soil pH, organic matter, and carbon stock were assessed. The results of the study showed that soil carbon sequestration in the forest restoration areas of the Mae Moh mine in 2001, 2006, and 2011 averaged 36.17, 21.94, and 13.97 t C/ha. In comparison, the mixed deciduous forest had an average soil carbon stock of 51.25 t C/ha, these differences were statistically significant ($P < 0.05$). In addition, the Generalized Linear Model (GLM) analysis revealed that the forest age has a significant influence on soil carbon sequestration, while the Principal Component Analysis (PCA) demonstrated a correlation between soil properties and soil carbon storage. Therefore, as the forest ages, its carbon sequestration capacity tends to approach that of natural forests, with increasing stability over time.

KEYWORDS:

Soil Carbon; Mae Moh Mine Reclamation Forest; Mixed Deciduous Forest.

Soil Organic Carbon Storage in Wetlands Under Restoration: A Case Study of Thung Luang Rajapruek

Nattanan Phosiri^{1,*}, Sukritchai Teeraroengrit² and Pornwiwan Pothasin¹

¹Conservation Biology, Mahidol University, Kanchanaburi Campus, Sai Yok, Kanchanaburi 71150, Thailand

²The Rajapruek Institute Foundation, Bang Kapi, Bangkok, 10240, Thailand

*Corresponding author, e-mail: nattanan.phs@gmail.com

ABSTRACT:

Wetlands are critical ecosystems for long-term soil organic carbon (SOC) sequestration due to their saturated and low-oxygen soil conditions, which slow organic matter decomposition. The reforested Thung Luang Rajapruek wetland, dominated by pioneer species such as *Typha angustifolia*, presents potential for both ecological recovery and carbon storage. This study aimed to assess SOC sequestration across different soil depths and seasonal conditions and to explore potential associations with plant diversity and key environmental variables, including bulk density, temperature, pH, and water level.

Vegetation surveys and soil sampling were conducted along four transects using seven randomly selected quadrats. Soil samples were collected using an auger at four points per quadrat, yielding a total of 112 samples. SOC was analyzed using the dry combustion method with a multiEA4000 elemental analyzer. The results revealed significant seasonal variation in SOC ($p < 0.05$), with higher concentrations observed during the dry season and in the upper soil layers (0–15 cm). The maximum recorded SOC was 2,704.5 MgC ha⁻¹. Bulk density averaged 1.22 g cm⁻³ and showed a strong negative correlation with SOC ($r = -0.62$, $p < 0.001$). A significant positive correlation was also found between SOC content and SOC density ($r = 0.72$, $p < 0.001$). While plant diversity was surveyed, its influence on SOC accumulation remains inconclusive and warrants further investigation.

These findings highlight the importance of understanding both ecological and environmental drivers of carbon dynamics in restored wetlands. Such insights are essential for informing adaptive management strategies aimed at enhancing long-term, sustainable carbon sequestration in wetland ecosystems.

KEYWORDS:

Plant diversity; Soil carbon sequestration; Wetland; *Typha angustifolia*

The Study of Tree Diversity and Above ground Carbon Storage in The Area of Kasetsart University Laboratory School Center for Educational Research and Development

Pishamon Tungvijitsakul^{1,*}, Alisa Worawuthangkul, Pimpicha Vichiensan, Krissana Pokpun and Santichai Anuworrachai

¹Kasetsart University Laboratory School Center for Educational Research and Development

*Corresponding author, e-mail: tpishamon@gmail.com

ABSTRACT:

Human activities have significantly increased atmospheric carbon dioxide, which is a major driver of climate change. To mitigate climate change issue, trees play a crucial role by absorb carbon dioxide from the atmosphere through photosynthesis, storing it as biomass in leaves, branches, trunks, and roots. This study aimed to assess tree diversity and above-ground carbon storage within the green spaces of the Kasetsart University Laboratory School (KUS). The objective of this research was to: 1) survey tree diversity at KUS and 2) quantify above-ground biomass and carbon storage of trees within the area. Methodology involved identifying study points, surveying tree species and numbers, and measuring diameter at breast height (DBH) and height. Allometric equations were used to estimate biomass, from which carbon storage was calculated. The survey was conducted in June 2025 which identified 175 large trees with a circumference over 100 cm, belonging to 41 species across 17 families, with Leguminosae being the most diverse at 13 species. The total above-ground biomass was estimated at 87,880.74 kg, with total above-ground carbon storage at 41,303.94 kg. The top three species contributing to biomass and carbon storage were *Albizia saman* (Jacq.) Merr. (15,191.25 kg biomass; 7,139.89 kg carbon), *Ficus maclellandii* King. (10,391.41 kg biomass; 4,883.97 kg carbon), and *Ficus religiosa* L. (3,750 kg biomass; 1,762.79 kg carbon). These findings indicate that the surveyed trees, characterized by their age, tall trunks, and numerous branches, contribute significantly to carbon absorption due to their high biomass. This study emphasizes the importance of urban trees in carbon storage and provides valuable data for effective green space management and tree selection for future planting initiatives.

KEYWORDS:

Tree diversity, Tree carbon storage

Carbon Storage Potential of Residential Green Spaces: A Study of Centro Housing Projects in Bangkok

Suttinee Panjai^{1,*}, Pornwiwan Pothasin¹, Ausanee Suttiwong² and Orawee Thongkua³

¹Conservation Biology Program, Mahidol University Kanchanaburi Campus, Sai Yok, Kanchanaburi, 71150, Thailand

²Faculty of Environment and Resource Studies, Mahidol University Phutthamonthon Sai 4 Rd, Salaya, Phutthamonthon District, Nakhon Pathom 73170

³AP (Thailand) Public Company Limited 170/57, Ocean Tower 1 Building, 18th Floor, Ratchadaphisek Tat Mai Road, Khlong Toei Sub-district, Khlong Toei District, Bangkok 10110

*Corresponding author, e-mail: panjaineena15@gmail.com

ABSTRACT:

As urbanization accelerates, over half of the global population now resides in cities, resulting in increased carbon emissions, air pollution, and ecosystem degradation. Urban green spaces—particularly trees—play a critical role in enhancing urban resilience and contributing to global sustainability targets, including SDG 11 (Sustainable Cities and Communities) and SDG 13 (Climate Action). This study assesses the carbon sequestration potential of urban trees in two residential projects: Centro Bangna and Centro Onnut–Suvarnabhumi, located within Bangkok’s expanding metropolitan region. Tree height and diameter at breast height (DBH) were recorded, and carbon storage was estimated using established allometric equations. Results revealed that Centro Bangna, with 485 trees across 13 species and 9 families, stored approximately 106.7 tCO₂e, while Centro Onnut–Suvarnabhumi, with 522 trees across 14 species and 7 families, sequestered 192 tCO₂e. The native species *Dolichandrone serrulate* (Kae-na) exhibited the highest carbon uptake at both sites. Additionally, the project developed an urban-friendly plant identification guide, which received positive feedback for its visual appeal, clarity, and educational value. Suggestions included increasing font size and incorporating more information on ecosystem services. These results emphasize the significant but often overlooked role of urban trees in climate change mitigation and biodiversity conservation. The study also presents practical tools to support sustainable urban planning and foster public engagement in green infrastructure development.

KEYWORDS:

Carbon sequestration; Plant identification guide; Urban green space

Seedling Survival Rate and Assessing the Carbon Sequestration Potential of a Reforestation Project

Jariyaporn Kaewviset^{1,*}, Sukritchai Teeraroengrit², and Pornwiwan Pothasin¹

¹Conservation Biology Program, Mahidol University Kanchanaburi Campus, Sai Yok, Kanchanaburi, 71150, Thailand

²The Rajapruek Institute Foundation, Bang Kapi, Bangkok, 10240, Thailand

*Corresponding author, e-mail: Jariyaporn.kaewviset@gmail.com

ABSTRACT:

Climate change driven by anthropogenic greenhouse gas emissions remains a critical global challenge. Forest restoration is widely recognized as a nature-based solution for enhancing long-term carbon sequestration and ecosystem resilience. This study evaluates the carbon sequestration potential of a reforestation project which involves planting native tree species selected for their ability to accelerate canopy closure and facilitate ecological succession. We assessed seven restoration sites established by the Rajapruek Institute Foundation across northern and central Thailand. Tree height and root collar diameter were measured to evaluate seedling survival, growth, biomass, and carbon storage. The highest survival rate occurred at Wat Phra Phutthabat Phra Ruea (Chiang Rai) 85.28%, followed by Mon Jam (Chiang Mai) 71.43%, dominated by *Psydrax umbellata* and *Gmelina arborea*. Ban Phu Yang (Ratchaburi), affected by wildfire, had the lowest survival 4.02% but still showed carbon storage potential through resilient hardwoods like *Pterocarpus macrocarpus*. On Nut recorded 27.18% survival but the highest carbon accumulation 14.3 kgC, mainly from *Senna siamea*. This study reinforces the importance of selecting species suited to local environmental conditions and adopting adaptive, site-specific restoration strategies. While the Framework Species Method offers a promising approach, restoration outcomes can vary significantly across sites. Tailored, ecologically informed practices are essential for restoring resilient, diverse, and carbon-rich forest ecosystems.

KEYWORDS:

Carbon sequestration; climate change; reforestation; seedling survival

Soil microbial groups and quantity in the reclamation areas of Mae Moh mine, Lampang Province

Pimrapat Sricharoenta^{1,*}, Yupa Chromkaew¹, Toungporn Uttarotai², Kawinthida Suvanna¹, Thitinan Hutayanon³ and Panida Kachina²

¹Department of Plant and Soil Sciences, Faculty of Agriculture, Chiang Mai University, Chiang Mai, 50200, Thailand

²Department of Highland Agriculture and Natural Resources, Faculty of Agriculture, Chiang Mai University, Chiang Mai, 50200, Thailand

³Mine Reclamation Technique Section, Mine Reclamation Department, Mae Moh Mine, Lampang 52220, Thailand

Corresponding author, e-mail: Pimrapat.sricharoenta@gmail.com

ABSTRACT:

Soil improvement is an important part of restoring environments affected by mining activities. The microorganisms in soil can reflect the completeness and potential of the ecosystem through their biological characteristics. This study aimed to investigate the amount and groups of microorganisms in the soil of the forest restoration area at Mae Moh Mine, Lampang Province, by collecting soil samples from restoration areas that started in 2001, 2006, and 2011. The soil samples were collected at the topsoil (0-5 cm) and subsoil (5-10 cm). The abundance of microorganisms including fungi, bacteria, actinomycetes, and cellulose-degrading microorganisms was analyzed by the dilution factor method, and the microorganisms were grown on nutrient agar (NA) plates using the spread plate technique. The results of the analysis linear mixed-effects model showed that the abundance of fungi and degraded cellulose microorganisms were not significantly different by the age of the restored forest, the depth of the soil, and the interaction between these factors. While the abundance of bacteria was affected by soil depth but forest age and the interaction between age and soil depth were not significantly affected. The amount of actinomycetes was significantly affected by soil depth which was higher in topsoil than in the subsoil. The results of this study indicate that the age of the restored forest and soil depth may play a role in the abundance and composition of some microbial communities, which can be used as basic information to promote sustainable soil ecosystem restoration planning and management in impacted mining areas.

KEYWORDS:

Soil microorganisms, Forest age, Restored Forest

Environmental Gradients Shape Soil Microbial Communities Revealed by Metabarcoding in a Lowland Dry Evergreen Forest in Thailand

Siwapohn Hamsart¹, Wongsatorn Phumphuang², Sathid Thinkampheang², Warong Suksavate², Dokrak Marod², Prateep Duengkae² and Anchalee Sirikhachornkit^{1,*}

¹Department of Genetics, Faculty of Science, Kasetsart University, Bangkok, 10900, Thailand

²Department of Forest Biology, Faculty of Forestry, Kasetsart University, Bangkok, 10900, Thailand

*Corresponding author, e-mail: anchalee.si@ku.th

ABSTRACT:

Soil microbial communities play a vital role in ecosystem processes such as nutrient cycling, organic matter decomposition, and maintaining belowground biodiversity. In a lowland dry evergreen forest (DEF) in eastern Thailand, previous research has shown that tree species distributions are shaped by environmental gradients, particularly elevation, slope, and soil bulk density, leading to distinct communities on ridges versus flat streamside terrain. Building on these insights, this study investigates whether soil microbial communities exhibit similar spatial structuring using a metabarcoding approach. Soil samples were collected from six 30 × 30 m plots—three located on flat terrain (P1, P3, P7) and three on ridges (P24, P28, P30)—within a 3-hectare permanent plot at the Wang Nam Khiao Forestry Research and Training Station. Genomic DNA was extracted and sequenced, targeting the 16S rRNA V4 region for prokaryotes and the 18S rRNA V4 region for eukaryotes. The aim is to assess how microbial composition varies along environmental gradients and whether belowground communities mirror the ecological patterns observed in plant assemblages. The findings will enhance understanding of environmental filtering and inform integrative forest restoration strategies that account for both microbial and plant diversity.

KEYWORDS:

Soil microbiome; metabarcoding analysis; lowland tropical forest; environmental gradients; forest restoration

Efficiency of keratinase – producing bacteria for keratin waste degradation

Phichayathida Suwanchana¹, Koonlapat Durongtam^{2,*}, Paranan Sukulthanasorn³, Chommanart Kerdkong⁴ and Rattiya Padungpol¹

¹Kasetsart University Laboratory School Kamphaeng Saen Campus Educational Research and Development Center, Nakhon Pathom, 73140, Thailand

²Central Laboratory and Greenhouse Complex, Faculty of Agriculture at Kamphaeng, Kasetsart University Kamphaeng saen campus, Nakhon Pathom, 73140, Thailand

*Corresponding author, e-mail: koonlapat.d@ku.th

ABSTRACT:

The accumulation of keratin waste in the environment is continuously increasing every year. Keratin waste management by physical and chemical processes affects environmental pollution and is harmful to the ecosystem. Therefore, the biodegradation of keratin waste is an interesting alternative because it is highly efficient and environmentally friendly. This study aims to isolate keratinase-producing bacteria from soil and poultry litter samples and select bacteria with the highest keratinase production to test the degradation efficiency of chicken feathers. 153 isolates of keratin-degrading bacteria were isolated from four soil and poultry litter samples. Six isolated bacterial strains which were identified as *Bacillus velezensis* P2-20, *B. velezensis* N1-64, *Bacillus cereus* P3-3, *B. velezensis* N1-5, *Bacillus stercoris* N1-33, and *B. cereus* P3-5 showed high keratinase production efficiency indices on skim milk agar (SMA), with values... of 2.2, 2.1, 1.9, 1.8, 1.7 and 1.6, respectively. After that, six strains of bacteria were tested on the primary chicken feather degradation by adding 1 piece of chicken feather to minimal broth (MB) for 14 days and observing the characteristics of chicken feather by eye. The results found are that N1-33 and P3-5 exhibited significant degradation of the feather structure compared to the control. Subsequently, N1-33 and P3-5 were tested for chicken feathers degradation in MB medium adding 3 g of hydrolyzed chicken feathers incubated at 37°C with shaking at 200 rpm for 7 days. N1-33 and P3-5 were effective in degradation efficiency with $36.7 \pm 0.2\%$ and $21.1 \pm 3.0\%$, respectively. The keratinase activity of N1-33 and P3-5 has a maximum enzyme production on day 5 of the experiment with 172.32 units/ml and 139.70 units/ml, respectively. The results suggest that *Bacillus stercoris* N1-33 was highly effective in feather degradation, which can be developed to enhance keratin degradation efficiency. Including, study the optimal conditions for keratinase production and using the enzyme to develop in various industries could lead to maximizing the utilization of biological resources.

KEYWORDS:

Keratinase; keratinase-producing bacteria; chicken feather; keratin waste degradation.

Exploring the Biodiversity of Bioplastic-Degrading Bacteria in the Lower Mekong Basin for Sustainable Waste Management

Sutthawan Suphan¹, **Chayanon Thimyaingam**¹, Napat Kunkhantod¹, Wanthanee Khetkorn¹, Kanaporn Sujarit¹, Ausawadee Phonlamai¹, Chatsuda Sakdapetsiri², Vichien Kitpreechavanich³ and Thanasak Lomthong^{1,*}

¹Division of Biology, Faculty of Science and Technology, Rajamangala University of Technology Thanyaburi, Pathum Thani 12110, Thailand

²Department of Plant Pathology, Faculty of Agriculture at Kamphaengsaen, Kasetsart University Kamphaengsaen Campus, Thailand

³Department of Microbiology, Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

*Corresponding author, e-mail: thanasak_l@rmutt.ac.th

ABSTRACT:

The Lower Mekong basin exhibits a high level of bacterial biodiversity and serves as a source of bioplastic-degrading bacteria with the ability to degrade polylactide (PLA) and polybutylene succinate (PBS) polymers. This study explored the diversity of bacteria in soil samples collected from shoreline areas of the Lower Mekong Basin in Thailand using 16S amplicon metagenomic sequencing. Sampling sites included Kang Ka Bao (Mukdahan Province), Downtown Quayside (Nakhon Phanom Province), the Songkhram River tributary (Nakhon Phanom Province), and Phon Phisai (Nong Khai Province). A total of 1,505 genera were identified across the samples. The overlap analysis revealed 617 genera shared between samples. Proteobacteria predominated in the samples collected from Kang Ka Bao (KB), Downtown Quayside (NP), and Songkhram River tributary (SK). By contrast, Actinobacteriota predominated the sample collected from Phon Phisai Quayside (PS). Six isolates of PLA and 13 isolates of PBS-degrading bacteria were obtained from the sample's isolation. All PLA and PBS-degrading bacteria showed the degrading ability to degrade PLA polymer film and PBS powder, as confirmed by weight reduction and physical change by scanning electron microscope (SEM). The molecular taxonomy of 16S rRNA gene sequences revealed nineteen isolates from four genera and five species, including *Streptomyces thermovulgaris*, *Actinomadura keratinilytica*, *Paenibacillus cisolokensis*, *Brevibacillus thermoruber* and *B. gelatini*. The lower Mekong basin was promised as a reservoir of bioplastics degrading bacteria, which can further be utilized for waste management to reduce global environmental issues.

KEYWORDS:

Mekong basin; bioplastic-degrading bacteria; bioplastics; enzyme · bacterial community

Effects of Green-Synthesized ZnO Nanoparticles from Various Plant Sources on Growth and Pigment Production in *Chlamydomonas*

Sukanya Buakaew^{1,*}, Siwapohn Hamsart¹, Nattanun T. Thianprasert² and Anchalee Sirikhachornkit¹

¹Department of Genetics, Faculty of Science, Kasetsart University, Bangkok, 10900, Thailand

²Department of Biochemistry, Faculty of Science, Kasetsart University, Bangkok, 10900, Thailand

*Corresponding author, e-mail: Sukanyabuakaew404@gmail.com

ABSTRACT:

Zinc oxide nanoparticles (ZnO NPs) have been widely applied across various industries and agriculture. However, the release of these nanoparticles into the environment may pose risks to aquatic ecosystems and organisms, particularly algae, which serve as model organisms in aquatic ecosystems. Additionally, different concentrations of ZnO NPs can have varied effects on plant growth. Studies on various plant species have shown that low concentrations of ZnO NPs can enhance plant yield and quality, such as increasing the number of grains and zinc content in rice seeds, whereas excessively high concentrations may inhibit growth. This study focuses on the green microalga *Chlamydomonas*, a unicellular organism that plays an essential role in aquatic ecosystems. *Chlamydomonas* possesses photosynthetic ability and can rapidly respond to external stimuli, making it a widely used model organism in biological and environmental studies, including investigations on the impact of nanomaterials. The objective of this research is to investigate the effects of ZnO nanoparticles synthesized from natural materials such as mangosteen peel (ZnO-GM), water hyacinth (ZnO-Ec), banana peel, and *Xanthium strumarium* on the growth and pigment production of *Chlamydomonas*. The ZnO nanoparticles are synthesized using environmentally friendly methods, where phytochemicals from each plant source may influence the chemical and physical properties of the ZnO nanoparticles and affect the algae's cellular response differently. This study compares the impact of ZnO nanoparticles derived from each plant source on *Chlamydomonas* to analyze the mechanisms of response to biologically composed nanoparticles. These effects may include both stimulation and inhibition of growth, as well as alterations in pigment production such as chlorophyll. The results are expected to enhance understanding of the interactions between nanoparticles and biological systems and promote the development of safe and effective naturally sourced nanoparticles for applications in biotechnology and environmental technology.

KEYWORDS:

ZnO nanoparticles; *Chlamydomonas*; Photosynthetic pigments, Green synthesis

Shifts in ectomycorrhizal community structure across a seedling-sapling age gradient in restored dipterocarp forests in Thailand

Natarus Kurtkid¹, Nipada Ruankaew Disyatat², Marut Fuangarworn³ and Chatchawan Chaisuekul^{3,*}

¹Program in Zoology, Department of Biology, Faculty of Science, Chulalongkorn University, 254 Phayathai Road, Pathumwan, Bangkok, 10330, Thailand

²Department of Biology, Faculty of Science, Chulalongkorn University, 254 Phayathai Road, Pathumwan, Bangkok, 10330, Thailand

³Integrative Insect Ecology Research Unit, Department of Biology, Faculty of Science, Chulalongkorn University, 254 Phayathai Road, Pathumwan, Bangkok, 10330, Thailand

*Corresponding author, e-mail: Chatchawan.c@chula.ac.th

ABSTRACT:

Seedling-sapling age plays a critical role in shaping the structure and function of ectomycorrhizal (ECM) fungal communities, which are essential for nutrient uptake, plant growth, and forest ecosystem stability. This study investigates the influence of seedling-sapling age on ECM diversity and abundance in dipterocarp-dominated forest restoration sites. A chronosequence approach was employed to compare ECM communities across two seedling-sapling age ranges: young (<5 years), intermediate (5–15 years), and secondary forests (15–26 years), representing different stages of natural succession and restoration in Saraburi and Nan provinces, Thailand. Soil samples were collected and analyzed using next-generation Illumina MiSeq sequencing of the fungal ITS region. Results showed that ECM species richness patterns varied by location. In Saraburi, richness was lowest in young plots (8.33 ± 2.08 OTUs), increased in intermediate plots (19.33 ± 2.08 OTUs), and remained relatively high in secondary forests (17.33 ± 3.06 OTUs). In contrast, in Nan, richness was highest in secondary forests (41.33 ± 9.87 OTUs), lower in young plots (27.33 ± 7.23 OTUs), and lowest in intermediate plots (18.00 ± 2.65 OTUs). Low community similarity was observed within each age range. The Bray-Curtis similarity index values in Saraburi were 0.010 (young plots vs. intermediate plots), 0.000 (young plots vs. secondary forest), and 0.003 (intermediate plots vs. secondary forest). In Nan, values were slightly higher: 0.116, 0.123, and 0.299 for the same comparisons, respectively. Dominant ECM genera also varied between locations. In Saraburi, *Tomentella* spp. (13,421 reads), *Sebacina* spp. (31,589 reads), and *Russula* spp. (25,088 reads) were dominant in the young plots, intermediate plots, and secondary forest plots, respectively. In Nan, *Russula* spp. dominated across all age range plots with 20,927, 39,293, and 47,122 reads in the young, intermediate, and secondary forest plots, respectively. These findings indicate that ECM communities alter as forests grow, with distinct patterns observed between locations. Understanding these patterns can inform strategies to enhance soil biodiversity and ecosystem functionality in forest restoration programs.

KEYWORDS:

Dipterocarp forest; Ectomycorrhizal fungi; ITS region; Soil fungal diversity

Elucidation of the role of strigolactone GR24 on the establishment of the ectomycorrhizal fungus, *Rhizopogon roseolus*

Mutiara Nur Pratiwi¹, Tadanori Aimi² and Norihiro Shimomura^{2,*}

¹The United Graduate School of Agricultural Sciences, Tottori University, 4-101 Koyama-cho Minami, Tottori 680- 8553, Japan

²Faculty of Agriculture, Tottori University, 4-101 Koyama-cho Minami, Tottori 680-8553, Japan

*Corresponding author, e-mail: nshimo@tottori-u.ac.jp

ABSTRACT:

Ectomycorrhiza (ECM), a symbiotic association between certain fungi and trees, contributes to environmental rehabilitation by promoting plant growth and resilience, restoring soil function, and supporting biodiversity in degraded areas. Understanding the interaction between ectomycorrhizal fungi and their host plants is essential for optimizing reforestation strategies and managing microbial biodiversity. Plant hormone strigolactone is well-known for its crucial role in regulating plant interactions with soil organism. However, the effect of strigolactone on ectomycorrhizal fungi (ECM) remain unclear. This study aims to investigate the effect of strigolactone on ECM fungi and elucidate the mechanism of its recognition. Synthetic strigolactone GR24 is used in this study because it is widely recognized as a standard model compound in studying strigolactone biosynthesis and perception across various organism. The effect of GR24 was observed on fungal growth and hyphal branching. MitoTracker Red and Nitroblue tetrazolium staining were used to analysed mitochondrial activity and reactive oxygen species (ROS) accumulation, respectively. Our current findings suggested that strigolactone GR24 application leads to increase in hyphal growth and branching in certain ECM strains. This stimulatory effect was associated with increase in mitochondrial activity and ROS accumulation at the hyphal tips. The response to GR24 was observed only in specific ECM strains with concentration dependent manner. Treatment with a mitochondrial inhibitor significantly decreased the effects of GR24 on ROS accumulation, highlight the essential role of mitochondria in GR24 perception in ECM fungi. Notably, this study is the first report of positive effect of strigolactones in ECM fungi as well as elucidating its perception. The findings will contribute to advance the understanding of symbiotic dynamic relevant to biodiversity and their prospect in forest restoration.

KEYWORDS:

Forest restoration; hyphal branching; mushroom; mycorrhiza; root compound

Increasing Arbuscular Mycorrhizal Fungal diversity through the Miyawaki Method

Ming-Yi Yen^{1,*}, Pi-Han Wang² and Ren-Cheng Liu²

¹Forest and Friends Co., Ltd. (Social Enterprise for Miyawaki Forest Promotion), Tainan, 704024, Taiwan

²Department of Life Science, Tunghai University, Taichung, 407224, Taiwan

*Corresponding author, e-mail: mingyiyen@gmail.com

ABSTRACT:

The Miyawaki afforestation method is recognized globally as an effective and rapid strategy for environmental rehabilitation. Plant and soil microbial communities are key drivers in the recovery of degraded environments. In this study, the Miyawaki method was applied to a 200 m² abandoned agricultural site in Tainan City, Taiwan, where 427 seedlings representing 42 native tree species were planted. We monitored plant growth and analysed changes in arbuscular mycorrhizal fungi (AMF) diversity before and nine months after planting using Illumina sequencing. Preliminary results showed that only five AMF virtual taxa (VT) were detected before planting, while 18 VT were identified post-planting. Four VT were shared between the two time points, and 14 were newly detected after planting. These findings indicate that Miyawaki reforestation on abandoned land can significantly enhance AMF diversity in a short period. Long-term monitoring of tree growth and AMF dynamics is necessary for assessing the effectiveness of this method in habitat restoration.

KEYWORDS:

Arbuscular mycorrhizal fungi; Miyawaki method; Long-term monitoring; Diversity; tree

Responses of hyphal cells of the ectomycorrhizal fungus *Rhizopogon roseolus* to salinity stress induced by seawater

Septyani Amini¹, Tadanori Aimi² and Norihiro Shimomura^{2,*}

¹The United Graduate School of Agricultural Sciences, Tottori University, 4-101 Koyama-cho Minami, Tottori 680- 8553, Japan

²Faculty of Agriculture, Tottori University, 4-101 Koyama-cho Minami, Tottori 680-8553, Japan

*Corresponding author, e-mail: nshimo@tottori-u.ac.jp

ABSTRACT:

Ectomycorrhizal (ECM) fungi have been recognized for enhancing the viability and stress tolerance of their host plants, making them promising agents for the restoration of saline soils particularly in coastal regions. In response to salt stress, fungal cells undergo morphological, physiological, and genetic changes. However, the mechanisms underlying salt resistance in ectomycorrhizal hyphae remain poorly understood. In this study, we compared two hybrid strains of *Rhizopogon roseolus*, salt-tolerant (TUFC102052) and salt-sensitive (TUFC102053), under salinity stress induced by artificial seawater. Vacuolar changes in terminal and subterminal cells were observed using a phase contrast light microscope. The salt-tolerant strain exhibited greater mycelial growth after submersion in 50% seawater compared to that in distilled water. Both strains showed vacuolar changes in subterminal cells, with salt-tolerant strain maintaining vacuolar integrity longer than the salt-sensitive strain. In the terminal cells, both strains displayed signs of osmotic adjustment by changing the vacuole and reduced cytoplasmic movement. These morphological changes in *R. roseolus* provide new insights into its ability to tolerate salt stress, deepening our understanding of its ecological adaptability and potential for use in the restoration of saline-affected environments.

KEYWORDS:

Rhizopogon roseolus; salinity; salt-tolerant; seawater; vacuole

Harnessing the power of *Astraeus* mushrooms and the microbial web: A metabarcoding approach for conservation and ecological insight from Mekong to Ganga corridor

Vineet Vishal^{1,2,*}, Nuttika Suwannasai³, Cherdchai Phosri⁴, Geetanjali Singh² and Shalini Lal²

¹Department of Botany, Dr Shyama Prasad Mukherjee University, Ranchi-834008, Jharkhand, India

²Department of Botany, Bangabasi Evening College, Kolkata-700009, West Bengal, India

³Department of Microbiology, Faculty of Science, Srinakharinwirot University, Bangkok- 10110, Thailand

⁴Department of Biology, Faculty of Science, Nakhon Phanom University, Nakhon Phanom- 48000, Thailand

*Corresponding author, e-mail: vineet.vishal73@gmail.com

ABSTRACT:

Beneath the forest floor lies an intricate network of soil fungi and microbial communities that regulate nutrient cycling, enhance soil health, and sustain plant ecosystems. Among these, *Astraeus*, a rare genus of star-shaped ectomycorrhizal fungi, is ecologically significant. Unlike their inedible counterparts in North America and Europe, *Astraeus* species found in tropical and subtropical dipterocarps forests of ASEAN countries are widely consumed as edible mushrooms. This study investigates *Astraeus* biodiversity and microbial interactions across dry deciduous forests from the Mekong to the Ganga, employing integrative taxonomy, nutritional profiling, axenic culture studies, metagenomics, and ecological assessments. Metabarcoding analysis confirms the southeastern origin of *Astraeus* species, including *A. asiaticus*, *A. odoratus*, *A. sirindhorniae*, and Indian *Astraeus* sp., while *A. hygrometricus* type specimens were notably absent. The first successful isolation of pure cultures of Indian *Astraeus* species was achieved on four solid media (potato dextrose agar (PDA), modified Melin–Norkrans (MMN), modified Norklan's C (MNC), and Yeast media (YM). Nutritional analysis reveals that *Astraeus* provides 421.1–415.4 kcal of dietary energy and is rich in potassium and iron, with moderate levels of phosphorus, calcium, magnesium, vitamins B1, B12, and C, but lower concentrations of zinc and vitamin D. Amplicon-based metagenomic profiling of the hypervariable V3–V4 region of the 16S rDNA identifies methanotrophic *Gammaproteobacteria* and *Pseudomonadaceae* as dominant microbial taxa within the mycorrhizosphere, influencing phosphorus and iron mobilization, polycyclic aromatic hydrocarbon (PAH) degradation, mineral weathering, and host plant nutrient dynamics. A decade-long mycoobservations into *Astraeus* fungi across diverse dry deciduous forests suggests their putatively strong ectomycorrhizal association with dipterocarp trees. These findings highlight the potential of *Astraeus* in mycoforestry, sustainable protein production, and biotechnological applications, offering new avenues for harnessing fungal resources along the Mekong–Ganga corridor.

KEYWORDS:

Biodiversity; Earthstar-fungi; Ganga; Mekong; Mycorrhizosphere

Environmental DNA Assessment of Diatom species in Marine sanctuaries of Lanao del Norte using High-throughput Sequencing

Grazzette Anne N. Dablo^{1,*} and Sharon Rose M. Tabugo²

¹Department of Biological Sciences, College of Science and Mathematics Mindanao State University- Iligan Institute of Technology, Iligan City, Philippines

²Molecular Systematics and Conservation Genomics Laboratory, Center for Biodiversity Studies and Conservation (CBSC), Premier Research Institute of Science and Mathematics (PRISM), Mindanao State University- Iligan Institute of Technology, Iligan City, Philippines

*Corresponding author, e-mail: grazzetteanne.dablo@g.msuiit.edu.ph

ABSTRACT:

Phytoplankton such as diatoms are known to adapt to various ecological niches and contribute to 20% of global primary production. Moreover, they are essential for assessing changes in aquatic environments due to their sensitivity to fluctuations in water quality. Their sensitivity makes them valuable indicators for monitoring the ecological status of various aquatic ecosystems. This research aimed to analyze and understand the diatom species in two marine sanctuaries in Iligan City. The analysis was carried out using metabarcoding of the V4 region of the 18S rRNA gene, which was amplified and sequenced on the Illumina MiSeq platform. Three amplicon libraries were created to represent the diatom composition of the study sites. Data processing was conducted with the Parallel-Meta-Suite software. After rigorous quality control and processing, a total of 16,337 amplicon sequence variants (ASVs) were identified, encompassing 80 families and 121 genera. The most abundant ASVs were identified as species belonging to genera *Chaetoceros*, *Melosira*, *Thalassiosira*, *Minidiscus*, *Psuedo-nitzschia*, *Meuniera*, *Navicula*, and *Amphora*. The assessment of diatom alpha diversity evaluated using the Shannon, Simpson, and Chao1 indices, revealed higher species diversity at Site 1 -D1 (Dalipuga, Iligan City), with values of 1.67, 0.62, and 25, respectively. At Site 1 (D1), the most abundant genus was *Thalassiosira*, while at Sites 2 (K1) and 3 (K2) (Kauswagan, Lanao del Norte), the dominant genera were *Chaetoceros* and *Melosira*, respectively. The presence of these genera raises concerns, as *Thalassiosira* and *Chaetoceros* are associated with harmful algal blooms, while *Melosira* thrives in polluted environments, serving as indicators of water quality. This variation in species composition underscores the ecological differences between the sites and highlights the importance of site-specific assessments in understanding diatom diversity. This study provides baseline information for diatom assessments in marine sanctuaries through environmental DNA (eDNA) metabarcoding and next-generation sequencing (NGS).

KEYWORDS:

eDNA, diatom, amplicon, Next generation sequencing

Assessing diversity and abundance of juvenile coral assemblages on underwater pinnacles in the Gulf of Thailand

Laongdow Jungrak^{1,*}, Makamas Sutthacheep¹, Chareernmee Chamchoy¹, Wiphawan Aunkhongthong¹, Wichin Suebpala¹ and Thamasak Yeemin¹

¹Marine Biodiversity Research Group, Department of Biology, Faculty of Science, Ramkhamhaeng University, Huamark, Bangkok, 10240, Thailand

*Corresponding author, e-mail: Laongdow8853@gmail.com

ABSTRACT:

Understanding the patterns, sources, and temporal variability of juvenile coral supply is essential for elucidating the processes that shape coral community structure, biodiversity, and reef resilience. Juvenile corals represent a critical life-history stage that underpins successful recruitment, population connectivity, and the capacity of coral reefs to recover from acute disturbances such as bleaching events and anthropogenic impacts. The study aims to compare the diversity and abundance of juvenile corals on natural substrates in the Eastern and Western Gulf of Thailand. At each study site, quadrats (16x16 cm²) were randomly placed on available substrates using SCUBA diving. The number of juvenile corals (≤ 5 cm in diameter) was counted and identified to genus or species. The results showed that the highest density of juvenile coral was found at Hin Phut (2.39 ± 0.80 recruits/m²), Chanthaburi Province, the Eastern Gulf of Thailand, while the lowest density was at Hin Wong (1.46 ± 0.59 recruits/m²) Surat Thani Province, the Western Gulf of Thailand. The diversity of juvenile corals varied notably among sites, with Hin Phut showing the highest diversity and Hin Wong the lowest. Juvenile corals of *Pocillopora*, *Leptastrea*, *Goniopora*, *Oulastrea crispata*, and *Pseudosiderastrea tayami* were found only in the Eastern Gulf of Thailand, while *Acropora* and *Fungia* were found only in the Western Gulf of Thailand. Species composition of coral recruits was significantly different between the Eastern Gulf and Western Gulf of Thailand. These findings underscore the spatial heterogeneity in juvenile coral assemblages across the Gulf of Thailand and highlight the importance of site-specific recruitment patterns in shaping future reef trajectories.

KEYWORDS:

Abundance, biodiversity, Gulf of Thailand, juvenile coral, recruitment, resilience

Underwater pinnacles as natural refuges supporting juvenile coral communities in the Andaman Sea

Wanlaya Klinthong^{1,*}, Sittiporn Pengsakun¹, Laongdow Jungrak¹, Charernmee Chamchoy¹, Wiphawan Aunkhongthong¹, Wichin Suebpala¹, Makamas Sutthacheep¹ and Thamasak Yeemin¹

¹Marine Biodiversity Research Group, Department of Biology, Faculty of Science, Ramkhamhaeng University, Bangkok 10240, Thailand

*Corresponding author, e-mail: klinthong_fai@hotmail.com

ABSTRACT:

Underwater pinnacles serve as crucial refuges and settlement areas that foster the recruitment and growth of juvenile corals. These pinnacles increase settlement success and promote early survival by creating ideal microhabitats for larval retention due to their intricate structures and remote positions. Their characteristics are vital in supporting reef recovery and resilience over time. This study investigates the composition and density of juvenile corals on three underwater pinnacles in the Andaman Sea. The quadrats (16x16 cm²) were randomly placed on available substrates at each study site using SCUBA diving. Juvenile corals (≤ 5 cm in diameter) were counted and identified to species or genus level within the quadrats. The results indicated that the highest density of juvenile corals was observed at Hin Samphaochom in Trang Province (5.56 ± 1.34 recruits/m²), followed by Hin Nok in Trang Province (4.86 ± 1.09 recruits/m²), and the lowest density was found at Hin Khaw in Satun Province (2.46 ± 0.96 recruits/m²). Statistical analysis revealed significant differences in juvenile coral densities across the study sites ($p < 0.05$). The dominant species of juvenile corals identified were *Turbinaria*, *Oulastrea crispata*, *Leptastrea*, *Porites*, *Pseudosiderastrea tayamai*, *Pocillopora*, and *Tubastraea*. The findings highlight the importance of underwater pinnacles as natural refuges for coral recruitment. Protecting these habitats is critical for the development of effective conservation strategies, which will support the long-term recovery and resilience of coral reef ecosystems in the Andaman Sea. Recognizing the importance of these pinnacles allows us to focus conservation actions on preserving key coral habitats and ensuring the sustainability of marine ecosystems.

KEYWORDS:

Andaman Sea; conservation; juvenile coral; marine ecosystem; underwater pinnacle

Striking a Balance: Sustainable Mining and Coral Reef Conservation in Hinatuan Island, Philippines

Sharon Rose Tabugo^{1,2,*}, Janece Jean Manubag⁴, Nanette Hope Sumaya^{1,2}, Claudine Ann Nakila^{1,2}, Tricksie Balatero^{1,2}, Mark Voltaire Tabugo⁵, Ayoub El Bounaoui⁶ and Jusua Dela Peña³

¹Department of Biological Sciences, College of Science and Mathematics, Mindanao State University-Iligan Institute of Technology (MSU-IIT), Tibanga, Iligan City, Philippines

²Molecular Systematics and Conservation Genomics Laboratory, Center for Biodiversity Studies and Conservation, Premier Research Institute of Science and Mathematics, MSU-IIT, Tibanga, Iligan City, Philippines

³Hinatuan Mining Corporation, Hinatuan Island, Philippines

⁴JCI Iligan Maria Cristina, Iligan City, Philippines

⁵LGU Iligan-City Health Office, Iligan City, Philippines

⁶University Hassan II, Casablanca, Morocco

*Corresponding author, e-mail: sharonrose0297@gmail.com

ABSTRACT:

Hinatuan Island, located in Mindanao, has gained recognition over time, with its surrounding marine areas representing unique ecosystems. This study aimed to document coral species in selected areas around Hinatuan Island, including those near the Hinatuan Mining Corporation (HMC) site. For coral reef assessment, the photoquadrat method (PQ) was utilized, capturing still images along 50-meter transect lines marked every one meter. A total of 300 photographs were analyzed using CPCe software, revealing 20 families and 41 genera of corals. Notably, 20 genera were identified as EDGE (Evolutionarily Distinct and Globally Endangered) corals. Among the species are: *Turbinaria mesenterina*, *Catalaphyllia jardinei*, *Pachyseris rugosa*, *Heliofungia actiniformis*, *Galaxea astreata*, *Porites cumulatus*, *Porites napopora*, *Pocillopora danae*, *Favia rosaria*, *Galaxea astreata*, *Monstatraea multipunctata*, *Acropora aspera*, *Alveopora excelsa*, *Fungia curvata*, *Leptoseris incrustans*, *Acanthastrea regularis*, *Lobophyllia serratus*, *Lobophyllia dentatus* and *Plerogyra discus*. The artificial coral reef established by the HMC demonstrated successful colonization by various coral groups. Although stressors such as physical, environmental, and natural factors may affect the coral reef community, certain coral adaptations enable resilience over time. Coral reef succession becomes also evident after typhoon devastation. Results suggest responsible and sustainable mining practices adhering to international and local standards. The future of mining hinges on embracing good practices to preserve the environment and fulfilling social responsibilities, contributing to community well-being and the environment.

KEYWORDS:

Corals, EDGE, island, health, reef

Effective Coral Reef Ecosystem Monitoring through Citizen Science in Trat Province, Thailand

Wiphawan Aunkhongthong^{1,*}, Sittiporn Pengsakun¹, Laongdow Jungrak¹, Wanlaya Klinthong¹, Charernmee Chamchoy¹, Chanansiri Phutthaphibankun¹, Wichin Suebpala¹, Makamas Sutthacheep¹, and Thamasak Yeemin¹

¹Marine Biodiversity Research Group, Department of Biology, Faculty of Science, Ramkhamhaeng University, Bangkok 10240, Thailand

*Corresponding author, e-mail: toeytoeywiphawan@gmail.com

ABSTRACT:

Coral reefs are vital ecosystems that support tourism, fisheries, and other essential services. Their complex structures provide habitats, food, and nursery grounds for diverse marine life, making them highly biodiverse and valuable resources. However, they face growing threats from climate change, pollution, and human activities, disrupting their ecological balance. Therefore, ongoing monitoring is essential to understand both natural processes and the impacts of human activity on reef health. This study aimed to monitor coral reef ecosystems in Trat Province through a citizen science approach that promotes collaboration among local communities, researchers, and volunteers. The research focused on evaluating the condition of coral reefs, developing suitable monitoring methods, establishing a citizen science network, and advancing coral reef biology research. The results showed that live coral cover ranged from 10.12% to 73.44% with *Porites lutea* being the most dominant species. The Shannon diversity index ranged from 1.8845 to 2.5725, indicating a healthy ecosystem condition. Coral recruits were found at an average density of 1.32–6.82 colonies per square meter, with 11 genera identified. The most prominent were *Porites* spp. and *Oulastrea crispata*, reflecting the natural recovery potential of the reefs. For benthic macroinvertebrates, the total density ranged from 0.46 to 6.97 individuals/m². Dominant species included the long-spined sea urchin (*Diadema setosum*) and the coral-boring bivalve (*Bequina semiorbiculata*). As for reef fish, *Neopomacentrus anabatoides* (a species of damselfish) was the most abundant, with the highest density recorded at Ao Salad (1,071.33 individuals per 100 m²). The use of accessible technologies such as underwater cameras and mobile applications supported systematic data collection through citizen science. The insights gained from this participatory process deepened the understanding of coral reef ecosystem dynamics and changes. This information is critical for managing and conserving coral reefs effectively at the community and policy levels, thereby contributing to sustainable and balanced long-term development.

KEYWORDS:

Citizen science, coral reef ecosystem, Gulf of Thailand, monitoring, sustainable development

Mass culture of Harpacticoid copepods for increasing capacity of coral grouper (*Epinephelus corallicola* Valenciennes, 1828) larviculture in Thailand

Supawadee Chullasom¹, Kriengsak Phadetphair², Supaporn Tangsithiwat², Pradchek Klangsin¹ and Wichin Suebpala^{1,*}

¹Department of Biology, Faculty of Science, Ramkhamhaeng University, Bangkok 10240, Thailand

²Trat Coastal Fisheries Research and Development Center, Trat Province 23000, Thailand

*Corresponding author, e-mail: wichin.s@gmail.com

ABSTRACT:

The aims of this study were to improve mass culture of Harpacticoid copepods, to select the most suitable species of copepod and to increase capacity of feeding, growth and survival of early-stage coral grouper *Epinephelus corallicola* larvae. Throughout the experiments, five species of harpacticoid copepods, i.e. *Tigriopus sindhoma*, *T. thailandensis*, *T. japonicus*, *Paramphiascella choui* and *Nitokra karanovici* were fed with microalgae *Tetraselmis*. The biological data, e.g. total length of adult males and females, development time from NI to CVI, number of eggs in egg sac, number of nauplii produced throughout female copepod life span, of these five species of copepods were studied. The results showed that *T. sirindhornae* was the most suitable species for mass culture. Total length of *T. sirindhornae* was shorter than that of other copepods, i.e. the total length of adult males was 867.8 µm, while that of adult females was 955.9 µm. Egg size length was 85.9 µm, fecundity was 25.1, number of egg hatching to NI was 24.5, life span was 53.9 days, and number of nauplii produced in life span of a female copepod was 134.5 days. Vitamin B Complex was selected as the most effective food supplement for increasing copepod production. *T. sirindhornae* was fed with Vitamin B Complex and *Tetraselmis* supplement in various sizes and shapes of tanks. Production of copepods was highest in round tanks with 50 and 100 liters of sea water after 20 days. In addition, baker yeast was added to the Vitamin B Complex and *Tetraselmis* supplement, in order to increase amino acids for improving survival and growth rates of larval fish. The experiment to culture 3-day fish larvae stocked in a 4-ton tank at an initial density of 4,000 ind./ tank was successfully conducted. *Tigriopus sirindhornae* naupli + *Brachionus* + *Tetraselmis* were fed to 3 crops of fish larvae for 15 days. Survival rates of fish larvae were 23.62%, 3.50% and 36.50% respectively.

KEYWORDS:

Coral Grouper, Harpacticoid copepods, Microalgae, Rotifers

Coral reef restoration through citizen science using micro-fragmentation and colony fusion techniques in Trat Province, Thailand

Sittiporn Pengsakun^{1,*}, Laongdow Jungrak¹, Wanlaya Klinthong¹, Charernmee Chamchoy¹, Wiphawan Aunkhongthong¹, Chanansiri Phutthaphibankun¹, Wichin Suebpala¹, Makamas Sutthacheep¹ and Thamasak Yeemin¹

¹Marine Biodiversity Research Group, Department of Biology, Faculty of Science, Ramkhamhaeng University, Bangkok 10240, Thailand

*Corresponding author, e-mail: Marine_ru@hotmail.com

ABSTRACT:

Coral reefs are among the most important ecosystems in terms of both biodiversity and economic value. They serve as vital sources of food, coastal protection, and tourism, directly supporting the livelihoods and security of coastal communities around the world. However, many coral reefs are facing severe degradation due to human activities and the impacts of climate change. This highlights the urgent need to develop effective and practical restoration techniques, particularly low-cost technologies that can be applied at the community level. One promising method is coral micro-fragmentation, which accelerates coral growth by cutting colonies into small fragments. When combined with coral colony fusion, these fragments can rapidly grow into large colonies with early reproductive capacity. The objective of this study is to develop efficient coral restoration techniques in Trat Province using micro-fragmentation and colony fusion, aiming to enhance coral growth rates and reproductive potential. Additionally, the study focuses on transferring knowledge and technology to local communities through training programs for citizen science volunteers. These volunteers play a key role in coral restoration, long-term monitoring, and strengthening local marine conservation networks. The study identified suitable nursery and restoration sites, including Koh Phi (22.36% live coral cover), Koh Rad (18.45%), and Ao Salad (25.41%) in Trat Province. Broodstock colonies from five coral species, including *Porites lutea*, *Galaxea fascicularis*, *Cyphastrea serailia*, *Montipora aequituberculata*, and *Hydnophora microconos*, were selected for the production of micro-fragments and the implementation of colony fusion at designated restoration sites. This project emphasizes collaboration among researchers, local communities, and volunteers through citizen science. It demonstrates an effective model for sustainable marine resource conservation at the local level and provides a valuable foundation for national-level policy development in long-term marine ecosystem management.

KEYWORDS:

Citizen science; coral colony fusion; micro-fragmentation; restoration; Trat Province

Meiofaunal community structure and biodiversity associated with artificial reefs at Ko Saket, Rayong Province, Thailand

Phatthira Karnpakob^{1,*}, Sittiporn Pengsakun¹, Laongdow Jungrak¹, Wanlaya Klinthong¹, Charernmee Chamchoy¹, Wiphawan Aunkhongthong¹, Chanansiri Phutthaphibankun¹, Wichin Suebpala¹, Makamas Sutthacheep¹ and Thamasak Yeemin¹

¹Marine Biodiversity Research Group, Department of Biology, Faculty of Science, Ramkhamhaeng University, Bangkok 10240, Thailand

*Corresponding author, e-mail: 6611710001@rumail.ru.ac.th

ABSTRACT:

Artificial reefs play a crucial role in marine ecosystem restoration by providing habitats and spawning grounds for marine organisms, thereby enhancing biodiversity. Their three-dimensional structures increase surface area for coral settlement and the attachment of other organisms, reduce pressure on natural coral reefs, and help mitigate coastal erosion. Additionally, artificial reefs promote ecotourism and support small-scale fisheries, contributing to local income generation. They also serve as platforms for learning, research, and public participation in the conservation of marine and coastal resources. This study aimed to examine the diversity and density of meiofauna associated with 3D ceramic printing coral settlement units at Ko Saket, Ban Phe Subdistrict, Rayong Province, Thailand. Sediment samples were collected by SCUBA divers using a corer, penetrating 10 centimeters into the sediment layer, at two intervals following the deployment of artificial reefs, 6 months and 9 months. The results revealed a significant increase in meiofauna density after 9 months (120.61 individuals/10 cm²) compared to 6 months (79.07 individuals/10 cm²) ($p < 0.05$). At 9 months, 16 meiofauna groups were identified, with the dominant groups being Foraminifera (66.42 individuals/10 cm²), Nematoda (9.61 individuals/10 cm²), and Harpacticoida (6.80 individuals/10 cm²). The Shannon diversity index (H') was 0.8417, indicating a moderate level of biodiversity. In contrast, at 6 months, 17 meiofauna groups were identified, with Foraminifera remaining the most dominant (75.82 individuals/10 cm²), followed by Harpacticoida (1.66 individuals/10 cm²) and Nematoda (0.61 individuals/10 cm²). The diversity index at this stage was lower, with $H' = 0.2431$. These findings suggest that the 3D ceramic printing coral settlement units have the potential to enhance meiofauna abundance and biodiversity, particularly with long-term deployment, which supports greater diversity in benthic communities.

KEYWORDS:

Artificial reef; benthic community; foraminifera; meiofauna; settlement

Ecologically and biologically significant locally managed marine protected areas in the Zamboanga Peninsula, Philippines

Yunalyn L. Villantes^{1,2,*}, Russel P. Galindo¹, Karl Maxel O. Lao³, Mark Anthony Manapsal², Hanira B. Abubacar², Jobert Labor², Robelyn Jane Tabil¹ and Charity D. Alvarez¹

¹Misamis University Research Center, Misamis University, Ozamiz City, 7200, Philippines

²Department of Natural Sciences, College of Arts and Sciences, Misamis University, Ozamiz City, 7200, Philippines

³College of Medical Technology, Misamis University, Ozamiz City, 7200, Philippines

*Corresponding author, e-mail: yunalynvillantes@gmail.com

ABSTRACT:

Marine protected areas (MPAs) are the most extensively implemented fisheries management and conservation tools not only in the Philippines but worldwide. It is necessary to determine the state of the MPAs to identify interventions that can further enhance their effective management and conservation. This study determined the ecological and biological status of five locally managed MPAs in Zamboanga Peninsula using the standard methods. Results revealed that the temperature and dissolved oxygen (DO) of the surface water samples from the five marine protected areas were within normal limits. Levels of nitrate (NO_3^-), ammonium (NH_4^+), fluoride (F^-), copper (Cu^{2+}), and lead (Pb^{2+}) were above the permissible limits. In terms of fish, the Sibutad Marine Protected Area is notable for having the highest number of species (31) among the five MPAs, with a total of 413 individuals. The PALS-MISSTA in Tukuran is notable for having the highest number of mangrove species, with seven species and a large population of 1,742 individuals. Tandu Balasan has a 10–100% seagrass cover, suggesting a rich environment for the habitats of marine species. The total number of phytoplankton species varies per site, but Sibutad MPA has the highest diversity. Kaeyoy Sanctuary, with 43 species, has the largest total population of any site, comprising 1,528 individuals. Data can be used to further validate good management and governance among locally managed MPAs in the Zamboanga Peninsula.

KEYWORDS:

Dissolved oxygen; diversity; fish; phytoplankton

Management effectiveness of the locally managed marine protected areas of Zamboanga Peninsula, Philippines

Russel P. Galindo^{1,*}, Yunalyn L. Villantes¹, Robelyn Jane D. Tabil¹ and Teresita I. Taberdo¹

¹Misamis University Research Center, Misamis University, H. T. Feliciano St., Aguada, Ozamiz City, 7200, Philippines

*Corresponding author, e-mail: russelpabriga@gmail.com

ABSTRACT:

Given its prime importance in conserving the country's marine biodiversity, it is necessary to assess the state of Marine Protected Areas to identify interventions that could be recommended to further enhance their effective management. This study empirically assessed the management effectiveness of locally managed MPAs in the Zamboanga Peninsula. It was conducted among the five (5) locally managed MPAs chosen based on size, particularly those with the biggest core area, and those established at the earliest. The management efficacy was assessed using the Management Effectiveness Tracking Tool (METT) version 4. It was implemented through 5 focused group discussions with 7-10 implementers and stakeholders per MPA. Three MPAs have achieved management effectiveness percentages exceeding 50%, with Sibutad MPA having the highest (59.65%), followed by Kaeyoy Sanctuary (59.26%) and PALS-MISSTA MPA (50.83%). On the other hand, Tandu Balasan MPA has the lowest effectiveness percentage (32.26). The management effectiveness of these locally managed MPAs can be attributed to several factors, particularly the specific attributes such as size, number of designated staff, available budget, and physical demarcation. One essential part of the management effectiveness assessments is the outcomes, which examine the condition of key species and habitats protected under the MPAs. It consolidated the actual impact of the MPA establishment on the marine ecosystem across the period. The MPA with the highest management effectiveness score in terms of outcomes may have well-implemented management strategies that enhanced the protection and preservation of its marine ecosystem. Many staff members with a relatively small MPA core area are considered to be on the edge of the most effectively managed MPA compared to their counterparts.

KEYWORDS:

Marine biodiversity, marine ecosystem, management outcomes, marine preservation, METT version 4

Level of access and benefit sharing on the protected coastal and marine resources covered by the MPAs

Haydee D. Villanueva^{1,*}, Virgilio H. Onganiza², Russel P. Galindo³, Yunalyn L. Villantes³ and Robelyn Jane D. Tabil³

¹Department of English, College of Arts and Sciences, Misamis University, Ozamiz City, 7200, Philippines

²Department of Social Sciences, College of Arts and Sciences, Misamis University, Ozamiz City, 7200, Philippines

³Research Center, Misamis University, Ozamiz City, 7200, Philippines

*Corresponding author, e-mail: dumpor1978@gmail.com

ABSTRACT:

Marine Protected Areas (MPAs) offer ecological and economic benefits, making the stakeholders' involvement essential to their implementation and sustainability. The study was conducted in five locally managed marine protected areas in the Zamboanga Peninsula. The descriptive design was used in the study. The respondents were 455 randomly selected household heads in the barangays where the MPAs are situated. A 20-item instrument developed by Wynberg and Hauck (2014) was used to determine the level of access and benefit-sharing resulting from the establishment of the MPAs. Access to MPAs was measured in terms of resource utilization, while benefit sharing was assessed in terms of the economic benefits of marine ecosystems and economic measures of incentives. To ensure the respondents' understanding of the research instrument, the questionnaire was translated into Visayan, the local language in the areas included in the study. Frequency, means, medians, and standard deviations were used as statistical tools in analyzing the data gathered. Results revealed that the level of access and benefit sharing on the protected coastal and marine resources covered by the MPAs was highest in Sibutad MPA, followed by PALS-MISSTA. Tandu Balasan MPA yielded the lowest level of access and benefit sharing. It was concluded that despite adherence to regulations and restrictions involving MPAs, the fisherfolk did not perceive themselves as being deprived of the bounty that marine resources could offer.

KEYWORDS:

Economic benefit; involvement; marine ecosystem; resource utilization; Zamboanga Peninsula

Diversity and distribution of intertidal mollusks in Sindangan Bay, Sindangan, Zamboanga del Norte

James Anderson Ramilo¹, Chelmarie Joy Clavano^{1,2}, Rohanie Abdul² and **Warren Caneos**^{1,2,3,4,*}

¹College of Fisheries and Aquatic Sciences, Mindanao State University – Marawi Campus Sindangan Extension, 7112 Sindangan, Zamboanga del Norte, Philippines

²College of Fisheries and Aquatic Sciences, Mindanao State University – Main Campus, 9700 Marawi City, Philippines

³Mindanao State University – Iligan Institute of Technology, College of Science and Mathematics, Department of Biological Sciences, 9200 Iligan City, Philippines

⁴Molecular Systematics and Conservation Genomics Laboratory, Center for Biodiversity Studies and Conservation (CBSC), Premier Research Institute of Science and Mathematics (PRISM), MSU-Iligan Institute of Technology, 9200 Iligan City, Philippines

*Corresponding author, e-mail: warren.caneos@msumain.edu.ph

ABSTRACT:

Intertidal mollusks play vital ecological roles in coastal ecosystems, contributing to nutrient cycling, substrate stabilization, and food web dynamics. Despite their importance, species diversity and distribution in Sindangan Bay, Zamboanga del Norte remain poorly documented. This study assessed the species composition, relative abundance, and environmental influences on mollusk distribution across three intertidal stations representing rocky, sandy, and mangrove-dominated habitats. A total of 21 mollusk species were identified, with the highest diversity (Shannon-Weiner Index: 2.87) observed in rocky zones and the lowest (1.34) in mangrove areas. The most abundant species across all stations were *Neritina rubricata* (48.98%), *Perumytilus purpuratus* (16.83%), and *Terebralia sulcata* (14.68%). Non-metric multidimensional scaling (nMDS) revealed distinct groupings among the three stations, with low overall similarity (40%) and five major clusters. Cluster analysis showed strong similarity among replicates within Station 1 (58%), moderate in Station 2 (46%), and low in Station 3 (18%), suggesting increasing variability in species composition across habitats. SIMPER analysis indicated that Station 1 had the highest within-group similarity (59.78%), mainly influenced by *Terebralia sulcata*, *Perumytilus purpuratus*, and *Aplus scaber*. Station 2 showed 39.25% similarity, with *Aplus scaber* contributing most, while Station 3 had the lowest (33.96%), dominated by *Neritina rubricata*. Dissimilarity between stations was high: Station 1 vs. 2 (82.65%), Station 1 vs. 3 (93.57%), and Station 2 vs. 3 (94.38%), driven by key differentiating species such as *Neritina rubricata*, *Perumytilus purpuratus*, and *Nerita planospira*. Canonical Correspondence Analysis (CCA) highlighted temperature, salinity, and pH as key environmental drivers, with salinity showing a strong positive correlation with gastropod abundance. These findings emphasize the role of habitat structure in shaping molluscan assemblages and the ecological importance of preserving intertidal biodiversity. Localized conservation and long-term monitoring are recommended to address anthropogenic and climate-related impacts on mollusk populations.

KEYWORDS:

Intertidal mollusks, biodiversity, species distribution, habitat structure, environmental parameters

Biodiversity of land snails and community knowledge, attitudes, and practices toward *Pararyssota maxima* in the Naga-Kabasalan Protected Landscape, Zamboanga Sibugay, Philippines

Keana Aubrey Valdehueza¹, Harold Lipae², Muhmin Michael Manting³, Wella Tatil¹, Marlon Elvira⁴ and Carlo Stephen Moneva^{2,5,*}

¹Department of Environmental Science, School of Interdisciplinary Sciences, Mindanao State University–Iligan Institute of Technology, Iligan City 9200, Philippines

²Department of Biology, College of Arts and Sciences, University of the Philippines Manila, Manila City, Philippines

³Department of Biological Sciences, College of Science and Mathematics, Mindanao State University–Iligan Institute of Technology, Iligan City 9200, Philippines

⁴Department of Environmental Science, College of Forestry and Environmental Science, Caraga State University, Ampayon, Butuan City, 8600, Philippines

⁵Premier Research Institute of Science and Mathematics, Mindanao State University–Iligan Institute of Technology, Iligan City 9200, Philippines

*Corresponding author, email: carlostephen.moneva@g.msuiit.edu.ph

ABSTRACT:

Land snails are vital components of terrestrial ecosystems, functioning as decomposers, bioindicator and serve as food sources for various animals. Recognizing their ecological value, this study explores the seasonal variation in land snail diversity and examines the knowledge, attitudes, and practices (KAP) of residents toward the endemic species *Pararyssota maxima* (*P. maxima*) in Barangay Sandayong, located within the Naga-Kabasalan Protected Landscape in Zamboanga Sibugay, Philippines. This study includes biodiversity sampling for two season (wet and dry) and social interview using the structure KAP survey. The result showed dominance of the family Cyclophoridae with 6 recorded species. The most abundant species recorded was *Allopeas gracile*, followed by the invasive *Achatina fulica*, indicating ecological imbalance and potential threats to native snail populations. The KAP survey also showed that while there is general awareness of the ecological importance of *P. maxima*, conservation practices remain limited. Socio-demographic factors such as education, occupation, and income significantly influenced conservation-related behaviors, with individuals of higher education and more stable employment more likely to engage in protective efforts. This suggests that knowledge alone is not sufficient to drive conservation action. This study recommends implementing targeted environmental education and community engagement programs to bridge the gap between awareness and action. Strengthening local participation and fostering a sense of responsibility are essential to the long-term conservation of *P. maxima* and the broader ecological health of the protected area.

KEYWORDS:

Bioindicator, Biodiversity, KAP, Seasonal variation, Endemic

Morphological and Genetic Characteristics of *Halodule* sp. from the Eastern Coastal Region of Thailand

Supajet Mueanart¹, Thita Nachan¹, Achiraya Luanrit¹, Anan Surawan², Kedsaraporn Motakul³, Jittra Teeramaethee⁴ and Jariyavadee Suriyaphan^{1,*}

¹Department of Aquatic Science, Faculty of Science, Burapha University, Chonburi, 20131, Thailand

²Naval Special Warfare Command, Royal Thai Fleet, Chonburi, 20180, Thailand

³Thai Island and Sea Natural History Museum, Chonburi, 20180, Thailand

⁴Institute of Marine Science, Burapha University, Chonburi, 20131, Thailand

*Corresponding author, e-mail: jariyavadee@go.buu.ac.th

ABSTRACT:

Halodule sp. is a dominant species distributed along the eastern coast of Thailand, typically found at depths ranging from 0.5 to 1 meter. There are two species in Thailand that were similar: *Halodule uninervis* (Forsskål) Ascherson and *Halodule pinifolia* (Miki) Hartog. The primary considerations for the classification of these two varieties of seagrass are the height of the shoots and the tips of the leaves, which can lead to confusion. This study focused on examining the morphological and genetic characteristics of *Halodule* sp. The samples were collected along the coastal zones of Chonburi, Rayong, and Chanthaburi provinces during May to June 2024. Leaf length, leaf width, leaf sheath, erect stem, rhizome, and root were all assessed as morphological characteristics. Three DNA barcode markers were used to conduct genetic analysis: ITS2, matK, and trnH-psbA. Two varieties of seagrass were identified in the morphological study : *H. uninervis* (Forsskål) Ascherson and *H. pinifolia* (Miki) Hartog. While the lateral teeth on the leaf ends were identical, the tips of *H. pinifolia* leaves are reduced. In addition, it was found that the shoot height of *H. uninervis* contains two distinct varieties of mature plants: 2.46 ± 1.16 and 9.75 ± 3.36 centimeters, both of which were found in the same location. The average shoot height of *H. pinifolia* was 6.31 ± 8.36 centimeters. Although genetic analysis can distinguish between *H. uninervis* and *H. pinifolia* showing well-separated clades. This study determined that two sizes of *H. uninervis* were identified and could be categorized according to genetic characteristics by utilizing the ITS2, matK, and trnH-psbA genes for classification.

KEYWORDS:

Seagrass; *Halodule*; Morphology; DNA barcoding

Morphological and Genetic Characteristics of *Halophila* sp. in Samaesarn island, Sattahip District, Chonburi Province

Thita Nachan¹, Supajet Mueanart¹, Achiraya Luanrit¹, Anan Surawan², Kedsaraporn Motakul³, Jittra Teeramaethee⁴ and Jariyavadee Suriyaphan^{1,*}

¹Department of Aquatic Science and Technology, Faculty of Science, Burapha University, Chonburi, 20131, Thailand

²Naval Special Warfare Command, Royal Thai Fleet, Chonburi, 20180, Thailand

³Thai Island and Sea Natural History Museum, Chonburi, 20180, Thailand

⁴Institute of Marine Science, Burapha University, Chonburi, 20131, Thailand

*Corresponding author, e-mail: jariyavadee@go.buu.ac.th

ABSTRACT:

Seagrass morphology varies due to its adaptation to sediment deposition, depth, and water currents. *Halophila* is a genus of seagrasses that is widespread along islands and coastlines. It is difficult to identify the leaves due to their various shapes, including lanceolate, elliptic, and ovate. Therefore, this study aims to use the morphological data of *Halophila* sp. combined with DNA barcoding for more accurate species identification. Collect seagrass samples (*Halophila* sp.) from the coastline and islands of Sattahip District, ChonBuri Province, during January and November 2024. Leaf length, width, root length, and number of leaf veins were all measured. Species classification via a stereo microscope, followed by an examination of leaf structure using a scanning electron microscope (SEM). Finally, use the TIS, MatK, and trnH-psbA genes to identify the species of seagrass. The study found two types of seagrass: *Halophila ovalis* (R.Brown) J.D.Hooker, 1858 and *Halophila decipiens* Ostenfeld, 1902, *H. ovalis* has leaves that are oval-shaped and elliptic, while *H. decipiens* has a stem that grows from a rhizome, with serrated leaf edges and leaves covered in hairs. The morphological characteristics of *H. ovalis* had a leaf width (0.19 ± 0.04 - 0.34 ± 0.15 cm) and leaf length (0.39 ± 0.11 - 0.65 ± 0.21 cm) less than *H. decipiens* (0.34 ± 0.10 - 0.45 ± 0.13 cm and 0.70 ± 0.11 - 0.75 ± 0.23 cm.). Otherwise, the root length of *H. ovalis* is 0.60 ± 0.41 - 0.87 ± 0.51 cm. This value was higher than the root length of *H. decipiens*, which ranges from 0.39 ± 0.29 - 0.61 ± 0.42 cm. Genetic analysis clearly distinguished the two species, with phylogenetic trees revealing distinct clades for *H. ovalis* and *H. decipiens*. This information will be employed to categorize seagrasses of the *Halophila* genus for the purpose of verifying the diversity of this seagrass genus in the area.

KEYWORD:

Halophila, Morphological, Genetic Characteristics

Enhancing Ex-Situ Conservation via Spore Culture and Propagation Techniques for the Protection of Select Rare, Threatened and Endemic Pteridophytes in the Philippines

Cathyrine C. Pajo^{1,*}, Hannah P. Lumista², Maria Melanie M. Guiang^{1,2}, Fulgent P. Coritico^{1,2} and Victor B. Amoroso^{1,2}

¹Plant Biology Division, Institute of Biological Sciences, College of Arts and Sciences, Central Mindanao University, 8714, Philippines

²Center for Biodiversity Research and Extension in Mindanao, 8714, Philippines

*Corresponding author, e-mail: cathyrinecpajo@gmail.com

ABSTRACT:

Pteridophytes, with their intricate microscopic development, represent approximately 16% of the threatened Philippine flora and urgently require conservation efforts. Despite the availability of various conservation strategies, many are not well-suited for spore-bearing plants. This study implemented ex-situ conservation methods—including spore storage, spore culture, wildling propagation, and the collection of gametophytes and sporophytes—for nine fern species (*Davallia solida*, *Angiopteris evecta*, *Helminthostachys zeylanica*, *Christensenia aesculifolia*, *Lecanopteris deparioides*, *L. sinuosa*, *Aglaomorpha heraclea*, *A. splendens*, *Tectaria psomiocarpa*) and three lycophytes (*Phlegmariurus phlegmaria*, *P. salvinoides*, *Selaginella magnifica*). After two years, spore viability and morphology assessments under cold-dry storage conditions (4–8°C, 20–22°C, and 26–32°C) revealed that spores stored at 4–8°C achieved 100% germination. Seven fern species—excluding *H. zeylanica* and *C. aesculifolia*—were successfully mass-propagated via spore culture using indigenous media. Early developmental stages were documented, and large collections of gametophytes and juvenile sporophytes were maintained under controlled laboratory conditions (20–22°C; 40–45% RH; 40 watts light intensity). All species also demonstrated successful propagation via wildlings in a greenhouse, with lycophytes showing the highest survival rates. To support public awareness, several CEPA (Communication, Education, and Public Awareness) materials were developed, including propagation protocols, a poster featuring threatened species, and detailed life cycle diagrams. The results underscore that cold-dry storage best preserves spore viability over extended periods. Spore culture using locally available media is an effective conservation strategy for ferns, while wildling propagation is most suitable for lycophytes. Overall, spore culture presents a practical and efficient method to bridge the gaps in the complex developmental biology of spore-bearing plants.

KEYWORDS:

Gametophyte and sporophyte development; indigenous culture media; life cycle; spore viability

Diversity, Assessment, and Ecology of Ferns and Lycophytes Across Vegetation Types in Mt. Balatukan, Gingoog City, Misamis Oriental, Southern Philippines

Gretl Rae P. Pescuela^{1,*}, Maria Melanie M. Guiang¹, Victor B. Amoroso¹ and Fulgent P. Coritico¹

¹Plant Biology Division, Institute of Biological Sciences, Central Mindanao University, University Town, Musuan, Maramag, Bukidnon

*Corresponding author, e-mail: catheriniansk@gmail.com

ABSTRACT:

Diversity, assessment, and ecology of ferns and lycophytes were conducted in three vegetation types of Mt. Balatukan, Gingoog City, Misamis Oriental. A (4) 20 x 20-meter plot was established, and opportunistic sampling was employed. The results of the study revealed a total of 135 species of ferns and lycophytes belonging to 73 genera and 25 families. Of these, 120 species are ferns and 15 are lycophytes. The overall diversity value had an average of $H=1.32$. *Nephrolepis hirsutula* (G. Forst.) C. Presl had the highest species importance values (SIV) across vegetation types. The Tropical Upper Montane Forest obtained the highest number of species, and most of the species of ferns and lycophytes recorded are epiphytes. The Agroforest and Tropical Lower Montane Forest have highly similar species composition, which obtained the highest percentage of 44.40%. The Conservation status revealed a total of 20 threatened species; of these, 9 are endangered, 6 are vulnerable, 3 are other wildlife species, and 2 are other threatened species. Meanwhile, ecological status shows 15 endemic species in the Philippines, and 1 species is narrowly distributed in Mindanao. Physico-chemical analysis revealed that the Agroforest obtained the highest temperature at 25.37°C, and the Tropical Lower Montane Forest had the highest average relative humidity at 90.90%. Ecology of ferns and lycophytes revealed that the Tropical Upper Montane Forest had the highest species richness of ferns and lycophytes. Biodiversity floristic assessment is recommended to guard, preserve, and manage the flora and fauna of the remaining resources in Mt. Balatukan.

KEYWORDS:

Conservation; endemic; inventory; microclimate; monilophytes

The survey of Araceae diversity from western to northern Thailand

Oraphan Sungkajanttranon^{1,*}, Dokrak Marod², Duangchai Sookchaloem², Sarawood Sungkaew², Yongyut Trisurat² and Sahanat Petchsri¹

¹Department of Science and Bioinnovation, Faculty of Liberal Arts and Science, Kasetsart University, Kamphaeng Saen, Nakhon Pathom, 73140, Thailand

²Department of Forest Biology, Faculty of Forestry, Kasetsart University, Bangkok, 10900, Thailand

*Corresponding author, e-mail: oraphan.s@ku.th

ABSTRACT:

The diversity, distribution, and phenology of Araceae along the nine nature trails of four national parks in Kanchanaburi Province, Chaleamrattanakosin, Erawan, Lamklongngu, and Saiyok National Park, western Thailand were studied between 2008 and 2012. Additionally, 22 nature trails of seven national parks in northern Thailand were studied from 2014 to 2021. These parks included Doi Inthanon, Doi Suthep-Pui, and Mae Takhrai in Chiang Mai Province, Khlong Lan and Khlong Wang Chao in Kamphaeng Petch Province, Tham Pla-Namtok Pha Sue, and Namtok Mae Surin National Park in Mae Hong Son Province. Araceae species in each study were recorded along a transect that was 10 meters wide on each nature trail. A total of 58 species in 19 genera were documented: 20 species of *Amorphophallus*, six species of *Arisaema*, four species each in *Colocasia* and *Rhaphidophora*, three species each in *Hapaline* and *Pothos*, two species each in *Alocasia*, *Remusatia*, *Sauromatum*, *Steudnera*, and *Typhonium*, along with one species each from *Aglaonema*, *Englerarum*, *Homalomena*, *Lasia*, *Lemna*, *Leucocasia*, *Schismatoglottis*, and *Scindapsus*. Twenty-three species in eight genera: *Aglaonema*, *Amorphophallus*, *Arisaema*, *Colocasia*, *Hapaline*, *Lasia*, *Leucosacia* and *Rhaphidophora* found in western, while 44 species in most 19 genera found in northern with the same and different of species. Among these species, 17 species in 10 genera were identified as evergreen (E), while 41 species from 10 genera were deciduous (D). Most species thrive during the rainy season, with many entering a dormancy phase during the winter and summer. The study included a revision and identification of the species, along with an analysis of utilization, and compared the findings with data from Thailand's neighbors.

KEYWORDS:

Aroid, distribution, national park, seasonal change, utilization

Protective effect against copper-induced disorder of membrane permeability in *Pinus thunbergii* roots by the ectomycorrhizal fungus *Rhizopogon roseolus*

Erwin Afrendi¹, Tadanori Aimi² and Norihiro Shimomura^{2,*}

¹The United Graduate School of Agricultural Sciences, Tottori University, 4-101 Koyama-cho Minami, Tottori 680-8553, Japan

²Faculty of Agriculture, Tottori University, 4-101 Koyama-cho Minami, Tottori 680-8553, Japan

*Corresponding author, e-mail: nshimo@tottori-u.ac.jp

ABSTRACT:

Rhizopogon roseolus, an ectomycorrhizal fungus commonly associated with *Pinus thunbergii*, was evaluated for its response to copper (CuSO₄) stress, given the role of ectomycorrhizal fungi in forest rehabilitation. A comparative analysis was conducted between two strains: the wild-type strain TUFC10010 and the EMS-induced hybrid strain TUFC102053. Stress responses were assessed under axenic and symbiotic conditions by examining mycelial growth, accumulation of reactive oxygen species (ROS) detected by NBT or H₂DCFDA staining, and membrane permeability using electrolyte leakage assay. Under axenic conditions, CuSO₄ exposure inhibited mycelial growth and increased ROS accumulation in both strains, with the TUFC10010 strain exhibiting greater inhibition in mycelial growth. NBT staining revealed that exposure to CuSO₄ increased the percentage of hyphal tips with ROS accumulation, rising from 12% to 56% in the TUFC10010 strain and from 13% to 45% in the TUFC102053 strain. Besides, H₂DCFDA fluorescence staining confirmed higher ROS accumulation in the TUFC10010 strain, whereas no significant increase was observed in the TUFC102053 strain. Electrolyte leakage assay showed a markedly higher leakage in the TUFC10010 strain (from 8.2% to 19.8%) compared to the TUFC102053 strain (from 9.9% to 15.0%) following CuSO₄ exposure, suggesting that the TUFC102053 strain exhibited resilience against copper stress. However, the responses observed in axenic conditions were diminished under symbiotic conditions. In planta, the TUFC10010 strain exhibited high colonization on root of *P. thunbergii*, likely contributing to enhanced protection against copper stress. In contrast, the TUFC102053 strain exhibited limited colonization capacity, potentially reducing its protective effectiveness. Notably, copper-stressed non-mycorrhizal seedlings showed electrolyte leakage of 21.4%, compared to 8.6% and 11.2% in seedlings colonized by TUFC10010 and TUFC102053, respectively. These findings highlight strain-specific responses of *R. roseolus* to copper stress and may contribute to the potential application of *R. roseolus* strains in forest restoration under heavy metal-contaminated conditions.

KEYWORDS:

Copper; electrolyte leakage; *Pinus thunbergii*; reactive oxygen species; *Rhizopogon roseolus*.

Morphology and DNA Barcoding of *Sonneratia alba* Sm. in Tañon Strait Protected Seascape, Cebu, Philippines

Airon Dulay^{1,*}, Paul John Geraldino¹ and Janice Leriorato¹

¹Cell and Molecular Biology Laboratory, Department of Biology, University of San Carlos, Cebu City 6000, Philippines

*Corresponding author, e-mail: airondulay@gmail.com

ABSTRACT:

Morphological and genetic data are essential for accurately identifying mangrove species and understanding their phenotypic variation. This study used morphometric traits and molecular markers to assess *Sonneratia alba* populations in the Tañon Strait Protected Seascape, Cebu, Philippines. *Sonneratia alba* is a mangrove species recognized for its crucial role in coastal stabilization and locale establishment, which exhibits considerable phenotypic plasticity that challenges traditional morphology-based taxonomic methods. Specimens were collected from three geographically distinct sites. Key morphometric parameters, including leaf length, leaf width, tree height, and diameter at breast height (DBH), were systematically recorded to assess environmental influences on growth patterns. Genomic DNA was extracted from leaf tissues and amplified using the *rbcL* and *rpL9* markers. Sequence analyses confirmed species identity with greater than 99.98% similarity compared to reference sequences in GenBank. Phylogenetic construction via the Neighbor-Joining method demonstrated that Cebu samples clustered with other Asian populations, although *rbcL* yielded limited resolution compared to *rpL9*. While DBH remained consistent across regions, significant regional differences in leaf dimensions and tree height emphasized the role of local environmental conditions in shaping phenotypic expression. These findings highlight the value of an integrative approach that combines molecular markers with detailed morphometric measurements to achieve accurate species identification. The data generated herein provide a robust baseline that will inform future conservation and management strategies for mangrove ecosystems in the face of ongoing environmental changes.

KEYWORDS:

Sonneratia alba, Mangrove Ecosystems, Morphological Analysis, Molecular Markers, Phylogenetic Analysis

The Ecological Value of *Ficus* Species: Pollination Success and Frugivory Support in the PTT Metro Forest

Aon Arnon^{1,*}, Nattatida Sittilikit² and Pornwiwan Pothasin¹

¹Conservation Biology Program, Mahidol University Kanchanaburi Campus, Sai Yok, Kanchanaburi, 71150, Thailand

²PTT Metro Forest Learning Center

*Corresponding author, e-mail: arnonaon4@gmail.com

ABSTRACT:

Ficus is one of the most diverse and ecologically significant plant genera, forming an obligate mutualism with fig wasps that is essential for successful pollination and forest regeneration. However, this interaction is increasingly threatened by habitat fragmentation and pollinator decline. In urban forests such as the PTT Metro Forest in Thailand, various *Ficus* species have been planted to enhance biodiversity, yet their pollination success and ecological function remain underexplored. This study assessed pollination success and frugivore use of five native *Ficus* species (*F. religiosa*, *F. benjamina*, *F. superba*, *F. microcarpa*, and *F. racemosa*) in the PTT Metro Forest. Phenological monitoring and fig wasp surveys were conducted from September 2024 to February 2025. The presence of foundress and offspring wasps at the D-phase (wasp-releasing stage) was used as an indicator of successful pollination. Wildlife interactions were recorded using motion-activated camera traps. Results revealed asynchronous and irregular fruiting across species. Only *F. religiosa*, *F. microcarpa*, and *F. racemosa* reached the D-phase. Among these, *F. religiosa* exhibited the highest pollination success (92.26%), while *F. racemosa* had the lowest (32.81%). *F. benjamina* and *F. superba* failed to progress beyond the B-phase, indicating a probable absence of suitable pollinators. Wildlife visitation was most frequent on *F. racemosa* and *F. religiosa*, both of which had extended fruiting periods. This study highlights the role of *Ficus* in promoting urban biodiversity. However, the limited presence of fig wasps constrains fig development and, consequently, food availability for urban wildlife. Conservation efforts should therefore integrate the protection of fig wasp populations to support the ecological role of *Ficus* in urban landscapes.

KEYWORDS:

Ficus; Fig wasp; Phenology; Pollination success; Urban Biodiversity

Pollinator resilience maintaining regional biodiversity in Doi Inthanon National Park

Teeradate Srimaneeyanon¹, Kanpat Akkaratejathanan¹, Chawatat Thanoosing¹, Aylssa B. Stewart² and Natapot Warrit^{1,*}

¹Department of Biology, Faculty of Science, Chulalongkorn University, Wang Mai, Pathum Wan, Bangkok, 10330, Thailand

²Department of Plant Science, Faculty of Science, Mahidol University, Thung, Phaya Thai, Ratchathewi, Bangkok, 10400, Thailand

*Corresponding author, e-mail: Natapot.w@chula.ac.th

ABSTRACT:

Bees are crucial pollinators that support biodiversity and ecosystem stability in terrestrial habitats, including mountainous areas. However, bee diversity and functional traits in the highland terrain of Thailand remain largely understudied. Thus, this study aims to investigate the functional diversity of bee pollinator sizes along elevation gradients in Doi Inthanon National Park (DINP). Bee pollinators were observed and collected within 2 x 2 m plots (n = 273 plots) during morning and afternoon periods throughout 5 elevation-based vegetation types (8 study stations). Fieldwork was conducted five times between 2019 and 2021. Collected bees were measured for intertegular distance (ITD) and body length (BL) under a stereoscopic microscope in the laboratory. A total of 1,323 bee individuals belonging to 30 genera from 4 families in DINP were identified and measured, including Apidae (1,058 individuals from 14 genera), Halictidae (192 individuals from 7 genera), Megachilidae (71 individuals from 7 genera) and Colletidae (2 individuals from 2 genera). Results indicated that functional dispersion (FDis), Rao's quadratic entropy (RaoQ), community weighted mean (CWM) and averages of bee pollinator sizes (ITD and BL) differed among elevation-based vegetation types, with an increasing trend at higher elevations. All indices in montane forests (976–2,565 m) were higher than in lower forests (300–975 m) in DINP. These patterns may suggest that functional trait variability enhances the resilience of pollinator communities to environmental changes along elevation gradients. The findings emphasize the importance of conserving diverse habitats to maintain pollinator resilience and sustain regional biodiversity in DINP and other tropical montane ecosystems in Thailand and Southeast Asia.

KEYWORDS:

Functional trait; montane ecosystem; pollination ecology; species composition; vegetation type

Mangrove Rehabilitation in the waters of Sitio Fuentes, Barangay Maria Cristina, Iligan City

Annielyn D. Tampus¹, Jaime Guihawan², Emilie Don¹ and Lor Jireh Jusain¹

¹Department of Marine Science, College of Science and Mathematics, MSU-Iligan Institute of Technology

²Department of Environmental Science, School of Interdisciplinary Studies, MSU-Iligan Institute of Technology

*Corresponding author, e-mail: annielyn.tampus@g.msuiit.edu.ph

ABSTRACT:

Mangrove is a valuable resource for the environment, economy and society. Apart from being used as a raw material to produce charcoal and firewood, mangrove is also useful for the ecology and the environment since it serves as a food source and nursery for young fauna, and a source of oxygen, as well as a barrier against storms and waves, preventing coastal erosion. The main objective of the project is to restore the mangrove ecosystem, support their biodiversity and to designate environmental conservation awareness to the local community living in the coastal areas. Mangrove planting was done for 5 consecutive days during lowest low tide and the project ran for one year to continue monitoring the seedlings that was planted in the waters of Sitio Fuentes, Barangay Maria Cristina, Iligan City. The result of one-way ANOVA ($p = 1$, $p > 0.05$) showed there were no significant differences between the growth of the seedlings every month in the mangrove area. Canonical correspondence analysis (CCA) indicated that environmental factors like dissolved oxygen, salinity, pH, and temperature influenced mangrove growth in the study area.

KEYWORDS:

Mangrove; Rehabilitation; Dissolved Oxygen; Salinity; pH

Assessment and Monitoring of the Mangrove Rehabilitation Program in the waters of Sitio Fuentes, Barangay Maria Cristina, Iligan City

Annielyn D. Tampus^{1,*}, Emilie L. Don¹, Jaime Q. Guihawan² and Maria Lourdes Dorothy G. Lacuna¹

¹Department of Marine Science, Mindanao State University – Iligan Institute of Technology, Iligan City, 9200, Philippines

²Department of Environmental Science, Mindanao State University – Iligan Institute of Technology, Iligan City, 9200, Philippines

*Corresponding author, e-mail: annielyn.tampus@g.msuiit.edu.ph

ABSTRACT:

Mangroves play a crucial role in reducing the risks and impacts of natural disasters such as typhoons, storm surges, and tsunamis. They also provide numerous ecological, economic, and social benefits by protecting coastal zones, supporting biodiversity, and sequestering atmospheric carbon dioxide. This study aimed to assess and monitor the mangrove species planted in Sitio Fuentes, Barangay Maria Cristina. Mangrove saplings were counted and recorded, while mature trees were measured for height and diameter at breast height (DBH). Monthly field assessments were conducted during spring low tides from March to December 2023 using a 50-meter transect line. Two mangrove species were identified in the area: *Rhizophora mucronata* and *Rhizophora apiculata*, with a total of 218 individuals recorded. Findings suggest that the site exhibits low mangrove biodiversity, as only two species were present. To improve the health and ecological function of the plantation, continued monitoring is recommended, along with the introduction of additional native mangrove species as part of a broader rehabilitation strategy.

KEYWORDS:

Assessment; mangroves; monitoring; rehabilitation

Variation in tree distributions across abiotic factors at a local scale in a dry evergreen forest, northeastern Thailand

Wongsatorn Phumphuang^{1,*}, Dokrak Marod¹, Sarawood Sungkaew¹ and Surachit Waengsothorn²

¹Department of Forest Biology, Faculty of Forestry, Kasetsart University, Bangkok 10900, Thailand

²Sakaerat Environmental Research Station, Nakhon Ratchasima 30370, Thailand

*Corresponding author, e-mail: fforwop@ku.ac.th

ABSTRACT:

Plant communities in tropical forests are influenced by multiple environmental variables. For trees, soil and topographic characteristics are key factors that impact the establishment of many species. In this study, the impacts of soil properties and topography on forest structure, species composition, and tree species distribution across size classes were investigated in a dry evergreen forest (DEF) in the Sakaerat Biosphere Reserve, northeastern Thailand. Within a 16 ha permanent plot, all trees with a diameter at breast height (DBH) ≥ 1 cm were recorded. Canonical correspondence analyses were used to identify relationship between tree distribution and their environments. The results showed that the DEF portion of the SBR host a high tree species diversity. In total, 81,728 trees, representing 204 species from 153 genera and 60 families, were found. Tree species distributions mostly respected gradients of plot elevation and soil nutrient, including available P; these variables were strongly associated for most size classes. Despite these environmental gradients, only four species, *Hydnocarpus ilicifolia*, *Walsura pinnata*, *Murraya paniculata*, and *Rothmannia sootepensis*, were retained as generalists, being widely distributed throughout the plot. These findings highlight the significant role of topographic and edaphic factors in shaping the structure and composition of the DEF. This study also provides insight into how environmental heterogeneity contributes to ecological niche differentiation in tropical forests.

KEYWORDS:

Canonical correspondence analysis; forest structure; Man and biosphere programme; permanent plot; tree distribution.

A Study of Botanical diversity and Environmental Factors Influencing the Formation of the Only Two-Needle Pine Forest in Central Region of Thailand: A Case Study in Phu Toei National Park

Nantaphat Sae-tia¹, Pokpong Limsuwan¹, Parlot Chakshuraksha¹, Pitibhum Pathak¹, Natthaphat Lakul¹, Netkamon Hongchan¹, Nichira Chatikul¹, Watsaphon Khamieam¹, Chakkrit Samphaothong², Wassana Silaket^{1,*}

¹Department of Social Studies, Vajiravudh College, Bangkok, 10300, Thailand

²Phu Toei National Park, Suphan Buri, 72180, Thailand

*Corresponding author, e-mail: patharawit.t@vajiravudh.ac.th

ABSTRACT:

This research aims to 1) survey and classify the types of natural vegetation in Phu Toei National Park and 2) analyze the factors that cause the formation of two-leaf pine forests in the central region of Thailand. The study involved collecting data on vegetation types and environmental factors that contribute to biodiversity in the national park. Tools used for data collection included vegetation recording forms and interview protocols with park officials and local experts. The researcher classified forest types in Phu Toei National Park based on altitude above mean sea level. The types of forests identified are as follows. The first type was mixed deciduous forest, where four types of bamboo were found: *Dendrocalamus strictus*, *Thyrsostachys siamensis* Gamble, *Gigantochloa hasskarliana*, and *Bambusa bambos*. Those bamboos had relative abundances of 33.14%. Whereas *Dipterocarpus alatus* Roxb. ex G.Don. and *Kydia calycina* Roxb had relative abundances of 27.19% and 24.53% of the forests' area. The second type was dry dipterocarp forest, where species such as *Stephania venosa*, *Croton oblongifolius* Roxb, and *Lagerstroemia floribunda* were found, with relative abundances of 21.412%, 11.70 %, and 9.80%, respectively. The survey of plant biodiversity in Phu Toei National Park suggests that altitude significantly affects soil properties, including soil color, which in turn is related to the mineral composition of the soil. These changes contribute to the diversity of forest types found at different elevations. Moreover, at an altitude of 670 meters above sea level in this national park, the only two-needle pine forest (*Pinus merkusii*) was found - this is the only pine forest of its kind in the central region of Thailand. The height of this forest is not significantly greater than other forests in the central region, despite similar topographic features. The formation of the two-needle pine forest at elevations of 670 meters and above may be influenced by several environmental factors: the surrounding area is mountainous, and wind directions channel cool air into the pine forest valley. This results in lower temperatures within the pine forest compared to surrounding mountainous forests. Therefore, temperature appears to be one key environmental factor contributing to the formation of the two-needle pine forest in Phu Toei National Park. From the findings of this research, forest conservation in Phu Toei National Park was a sustainable collaboration between communities, government agencies, and civil society organizations. The use of appropriate technology and laws would help conservation to be effective so Phu Toei forest remains fertile and abundant natural resource for the country.

KEYWORDS:

Phu Toei National Park, Natural Vegetation, Botanical Diversity

Sustainable Biocontrol in Coffee Agroforestry: Restoring Ecosystems and Managing Pests in Thailand

Chettida Srisuksam¹, Somruetai Jaiyen¹, Varangkana Junda¹, Siwarin Sriket¹ and Alongkorn Amnuaykanjanasin^{1,*}

¹National Center of Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), Phaholyothin Rd., Khlong Luang, Pathum Thani, 12120, Thailand

*Corresponding author, e-mail: alongkorn@biotec.or.th

ABSTRACT:

Agroforestry coffee cultivation is expanding in Thailand, holding significant promise for forest restoration and offering profound ecological benefits through the adoption of biological control agents (BCAs) and integrated pest management (IPM). This study evaluated the efficacy of these strategies in two coffee test plots (Muser and Huay Lueang) in Tak province. Field applications demonstrated that *Trichoderma asperellum* TBRC 4734 was as effective as, or even superior to, chemical treatments in controlling and reducing the severity of coffee fungal diseases, particularly Sooty Mold (*Capnodium sp.*) and Coffee Leaf Rust (*Hemileia vastatrix*). In the Muser plot, Sooty Mold incidence dropped by 70% and disappeared after three months of continuous spraying, a significant improvement over the 50% incidence observed in conventionally treated plots. Similarly, in the Huay Lueang plot, Coffee Leaf Rust incidence decreased by 51% with biocontrol application, while conventional plots showed 95% incidence. Biocontrol also significantly reduced Anthracnose (*Collectotrichum siamense*) spread, with only 30% incidence in biocontrol plots. For insect pest control, *Beauveria bassiana* BCC2660 and *Metarhizium anisopliae* BCC4849 (as BCAs) proved most effective against key coffee pests such as coffee berry borers, green scale, brown scale, aphids, mealybugs, and leafhoppers. In the Huay Lueang plot, bioproducts combined with borer traps significantly reduced initial coffee berry borer damage (from 7.02% to 0.8% in four months), a statistically significant improvement over conventional method (starting at 1.04%). The presence of entomopathogenic fungi on insect carcasses indicated their good persistence in the coffee environment. Furthermore, biocontrol-treated plots showed a statistically significant increase in natural enemy insect populations compared to chemical-treated plots, highlighting bioproducts' positive impact on agroecosystem biodiversity.

KEYWORDS:

Biocontrol; Agroforestry; forest restoration; Coffee; Sustainable Agriculture

Entomofaunal Diversity in Urban Green Spaces: Insights from Miyawaki Forests and Beyond

Jain Therattil^{1,*}

¹Department of Zoology St.Aloysius College, Elthuruth,Thrissur , Kerala, India

*Corresponding author, e-mail: jaintherattil@stalloysiuselt.edu.in

ABSTRACT:

Urbanization profoundly alters insect communities, threatening ecosystem functions like pollination, decomposition, and natural pest control. In this context, the Miyawaki afforestation method—which emphasizes dense, multi-layered native vegetation—offers a promising model for urban biodiversity restoration. However, scientific evaluations of its effectiveness in supporting entomofaunal diversity, especially in South India, remain scarce. This study presents a comparative assessment of entomofaunal diversity in Miyawaki forests across urban sites in Kerala and Tamil Nadu, against two contrasting baselines: adjacent natural forest remnants and conventional urban green spaces (e.g., ornamental parks). Insects were sampled using standardized methods including pitfall traps, sweep netting, and light traps across pre-monsoon and post-monsoon periods. Diversity metrics (Shannon-Wiener, Simpson's index), functional group classification, and multivariate analyses were employed to evaluate community structure and habitat associations. Results reveal that Miyawaki forests support significantly higher species richness, functional diversity, and abundance of key taxa (e.g., Hymenoptera, Coleoptera, Diptera) than conventional green spaces. Though natural forests exhibited the greatest overall diversity, Miyawaki plots demonstrated rapid ecological convergence within 3–5 years, particularly in terms of pollinator and predator assemblages. Habitat complexity, native floral composition, and microclimatic buffering emerged as key drivers of this pattern. The findings highlight the ecological value of Miyawaki forests as emerging insect biodiversity hotspots in urban areas of south India, reinforcing their potential role in climate-resilient urban planning. The study recommends integrating native forest microhabitats into city landscapes and emphasizes the need for longitudinal monitoring of insect-mediated ecosystem services.

KEYWORDS:

Entomofaunal Diversity; Miyawaki Forest; Urban Ecology; Comparative Biodiversity Study; Native Afforestation

Aquatic Insects as Bioindicators for Water Quality Assessment in Wastewater Treatment Ponds of Chiang Rai Municipality

Nutthakit Taphianthong^{1,*}

¹Faculty of Science, Mahidol University

*Corresponding author, e-mail: sitian.nxxthxxit.2549@gmail.com

ABSTRACT:

This study focuses on using aquatic insects to check the water quality in wastewater treatment ponds in Chiang Rai Municipality. The research was done over three months from November 2024 to January 2025. We studied four ponds that have different conditions. Water samples were tested for pH, water temperature, and dissolved oxygen (DO). At the same time, we collected aquatic insects and identified them to find out the diversity using the Shannon-Wiener Diversity Index. The results showed clear differences among the ponds. Pond 1 had the lowest DO of 3.68 mg/L and diversity index (H') of 1.5777. Pond 2 had DO 5.02 mg/L and H' 1.5347. Pond 3 had DO 5.04 mg/L and H' 1.8334. Pond 4 had the highest DO at 5.48 mg/L and H' 1.96. We found a moderate positive correlation ($r = 0.6388$) between DO and insect diversity, which means that as oxygen in the water increases, the number of different insects also tends to increase. This shows that aquatic insects are good indicators of water quality because they respond to changes in oxygen levels. Ponds with better oxygen levels have more insect species, meaning the water is healthier. Using both biological monitoring and water testing gives a clearer picture of water quality. Our findings can help Chiang Rai Municipality better manage wastewater treatment and protect the environment. This study supports sustainable water management to keep the water clean and safe for living things in the future. This study helped the local government to better understand the diversity index of aquatic insects in the wastewater treatment ponds, which can improve the management of water quality.

KEYWORDS:

Aquatic insects; Bioindicator; Water quality; Wastewater treatment; Biodiversity monitoring

Baselines for Biodiversity Rehabilitation: Insect Monitoring and Conservation for the Southeast Asian Tropics

Akihiro Nakamura^{1,2,*}, Ekgachai Jeratthitikul^{2,3}, Alyssa Stewart^{2,4}, Natapot Warrit^{2,5}, Montarika Promchaisri², Sontaya Promchaisri², Pattraporn Chaikong², Hassanai Kaewyod², Manus Leunkaew², Nareethip Nuankaew² and Yves Basset⁶

¹Yunnan Key Laboratory of Forest Ecosystem Stability and Global Change Response, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Mengla, Yunnan 666303, China

²Cooperation in Insect Biodiversity Research and Conservation, Personnel Training and Academic Exchange, Khao Chong Botanic Garden, Na Yong, Trang 92170, Thailand

³Department of Biology, Faculty of Science, Mahidol University, Ratchathewi, Bangkok 10400, Thailand

⁴Department of Plant Science, Faculty of Science, Mahidol University, Ratchathewi, Bangkok 10400, Thailand

⁵Department of Biology, Faculty of Science, Chulalongkorn University, Pathumwan, Bangkok 10330, Thailand

⁶ForestGEO, Smithsonian Tropical Research Institute, Ancon 0533, Panama

*Corresponding author, e-mail: a.nakamura@xtbg.ac.cn

ABSTRACT:

Insects, as a major component of eukaryotic biodiversity, play indispensable roles in maintaining and restoring forest ecosystems. Their ecosystem services shape community dynamics across multiple trophic levels—from plants to vertebrates, including humans. Despite growing global concern over the decline of insect populations, insect diversity in tropical regions, particularly Southeast Asia, remains poorly studied. Establishing robust baseline data is urgently needed, as it forms the foundation for effective biodiversity restoration and ecological rehabilitation. To address this critical gap, we aim to develop a long-term, cross-regional monitoring platform to track the dynamic changes in tropical forest insect communities under climate change and anthropogenic disturbances. Our approach integrates taxonomic, phylogenetic, and functional perspectives, combining efforts from Southwest China, Thailand, and Laos. Here, I present our ongoing efforts to document the spatiotemporal dynamics of key insect groups, including ants, moths, beetles, and hymenopterans, in southern Thailand. Preliminary findings emphasize the importance of standardized monitoring protocols for accurately assessing population and community shifts. However, traditional survey methods remain labor-intensive and inefficient. To overcome this limitation, we are incorporating DNA metabarcoding and automated monitoring tools powered by machine learning, including camera and acoustic detection systems. Advancing our understanding of insect taxonomy, biogeography, and ecological roles is essential not only for biodiversity conservation but also for informing effective restoration strategies. Establishing long-term reference datasets through innovative and scalable monitoring approaches will be key to managing and rehabilitating megadiverse insect communities in tropical forest ecosystems.

KEYWORDS:

Insect, Biodiversity restoration, Baseline data, Tropical Forest, Automated monitoring, DNA metabarcoding, Spatiotemporal dynamics

Diversity of Protected insect in North Protected Area of Thailand

Phattanian Chotmetaphon^{1,*}, Itsaraphong Voraphab¹, Sasiwimon Manasin¹

¹Department of National Parks, Wildlife and Plant Conservation, Bangkok, Thailand, 10900

*Corresponding author, e-mail: 99chey@gmail.com

ABSTRACT:

Studies on diversity of Protected insect in 10 conservation areas in the north of Thailand, namely Khun Pha Wo National Park, Taksin Maharat National Park, Huai Nam Dang National Park, Doi Inthanon National Park, Doi Pha Hom Pok National Park, Sri Lanna National Park, Phu Hin Rong Kla National Park, Thung Salaeng Luang National Park, Nam Nao National Park and Samoeng Wildlife Sanctuary. Able to identify 12 protected insect species in total. There were 3 diurnal moths: 2 *Teinopalpus imperialis*, 1 *Meandrusa sciron*, 1 *Troides helena*, 4 moths, 8 *Actias maenas*, 7 *Actias rhodopneuma*, 4 *Actias sinensis*, 10 *Actias selene*, and 5 beetles. One specimen of *Cheirotonus* sp.1, one specimen of *Cheirotonus* sp.2, two specimens of *Mouhotia batesi*, and two specimens of *Prosopocoilus giraffa*, as well as 30 specimens of *Cheirotonus gestroi*, are being considered to be declared protected insects under the Wildlife Preservation and Protection Act. Many protected insects live in high altitude areas. and in the fertile forest. In this study also the presence of *Teinopalpus imperialis*, which had not been present for several years.

KEYWORDS:

Diversity; Protected insect; Protected Area; North of Thailand

Biodiversity Underfoot: Showcasing Millipedes for Ecotourism in Thailand

Natdanai Likhitrakarn^{1,*}, Parin Jirapatrasilp², Somsak Panha^{2,3} and Chirasak Sutcharit²

¹Program of Agriculture, Faculty of Agricultural Production, Maejo University, Chiang Mai, 50290, Thailand

²Animal Systematics Research Unit, Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok, 10330, Thailand

³Academy of Science, The Royal Society of Thailand, Bangkok 10300, Thailand

*Corresponding author, e-mail: kongerrrr@hotmail.com

ABSTRACT:

Millipedes are often overlooked and misunderstood organisms, yet they play crucial roles in forest ecosystems as decomposers of organic matter and as indicators of soil health. In Thailand, public perception of millipedes has significantly shifted due to continuous taxonomic research and public outreach activities. A pivotal turning point began with the "Millipede and Earthworm Project," initiated by Prof. Dr. Somsak Panha from Chulalongkorn University in 2010, which aimed to enhance the capacity of local researchers in invertebrate taxonomy. Significant discoveries of new millipede species in Thailand, such as the shocking pink dragon millipede, *Desmoxytes purpuresea* Enghoff, Sutcharit, & Panha, 2007, which was selected as one of the world's top 10 new species in 2007, garnered international attention. This discovery played a vital role in elevating Hup Pa Tat, a collapsed limestone cave which is the site of the discovery in Uthai Thani Province, central Thailand into a significant ecotourism destination and environmental learning centre. Furthermore, 180 other new millipede species have been discovered in Thailand, including the pill millipedes *Zephronia lannaensis* Likhitrakarn & Golovatch, 2021 and *Z. phrain* Likhitrakarn & Golovatch, 2021. These discoveries led to the establishment of the "Pill millipede trail" as a living natural learning hub at Queen Sirikit Botanic Garden in Chiang Mai Province, northern Thailand, making it the first millipede learning centre in Asia. Concurrently, the discovery of various other endemic and beautifully colourful species, such as the zebra millipede, *Enghoffosoma zebra* Likhitrakarn, Golovatch & Panha, 2014, the turquoise pill millipede, *Sphaerobelum turcosa* Srisonchai & Pimvichai, 2023, and the Dragon Ball pill millipede, *Hyleoglomeris dracosphaera* Likhitrakarn, Sutcharit & Panha, 2024, has revealed additional natural sites with high potential for ecotourism development. This body of research demonstrates that the discovery of new species is not merely an academic endeavour but a catalyst for local ecotourism that fosters awareness, conservation, and sustainable development. Thus, millipedes serve as representatives of Thailand's hidden, vast, and valuable biodiversity, which still awaits further discovery while underscoring the urgent need for conservation of natural habitats.

KEYWORDS:

Biodiversity; conservation; ecotourism; millipede; new species

Integrative Taxonomy Reveals Endemic Bemmeridae Spider Diversity, Supporting Biodiversity Conservation and Ecological Rehabilitation in Thailand

Chawakorn Kunsete¹, Varat Sivayyapram², Chawatat Thanoosing¹, Prapun Traiyasut³ and Natapot Warrit^{1,*}

¹Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok, 10330, Thailand

²Faculty of Biology, Hubei University, Road 368, Wuchang District, Wuhan City, Hubei, China

³Department of Biology, Faculty of Science, Ubon Ratchathani Rajabhat University, Ubon Ratchathani, 34000, Thailand

*Corresponding author, e-mail: Natapot.w@chula.ac.th

ABSTRACT:

Atmetochilus Simon, 1887, and *Damarchus* Thorell, 1891, are genera within the family Bemmeridae, comprising mygalomorph spiders distributed across Asia. Most described species have been recorded solely from their type localities and are considered endemic, underscoring their contribution to regional biodiversity. In Thailand, four species have been previously documented; however, extensive sampling conducted since 2015 across 71 sites has revealed numerous additional populations that remain formally undescribed at the species level. The high morphological similarity among these taxa presents challenges to accurate species delimitation, highlighting the need for refined taxonomic approaches. This study employs an integrative taxonomic framework to delineate species boundaries and assess the biodiversity of Bemmeridae spiders in Thailand, thereby supporting ecological research and habitat restoration efforts. By combining morphological assessments, phylogenetic reconstructions utilizing maximum likelihood and Bayesian inference, and multiple species delimitation methods—including ABGD, ASAP, GMYC, and bPTP—we identified approximately 18 distinct species. Of these, four correspond to previously documented taxa (including three *Atmetochilus* and one *Damarchus*), whereas 14 are newly described, with three new species of *Atmetochilus* and eleven of *Damarchus*. Each species was found to be restricted to a single type locality, suggesting patterns of endemism aligned with conservation priorities for preserving regional biodiversity. These findings exemplify the efficacy of integrative taxonomy in resolving complex taxonomic challenges in understudied groups and emphasize Thailand's rich yet vulnerable spider diversity. Recognizing and documenting this biodiversity provides critical baseline data for targeted conservation initiatives and ecological rehabilitation efforts aimed at maintaining and restoring the integrity of native habitats and conserving biological resources essential for environmental resilience.

KEYWORDS:

Classification; New record; Wishbone spider

Assessing scorpion biodiversity for environmental rehabilitation: molecular and morphological insights into *Heterometrus* species in Thailand

Wasin Nawaneti Wong^{1,*}, Natapot Warrit¹, Chawatat Thanooosing¹ and Prapun Traiyasut²

¹Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok, 10150, Thailand

²Program in Biology, Faculty of Science, Ubon Ratchathani Rajabhat University, Ubon Ratchathani, 34000, Thailand

*Corresponding author, e-mail: wasin.nwntw@gmail.com

ABSTRACT:

The genus *Heterometrus* Ehrenberg, 1828, within the family Scorpionidae Latreille, 1802 (class Arachnida; order Scorpiones), comprises large-bodied scorpions that hold significant ecological, economic, and cultural importance. Several species within this genus contribute to biodiversity and local livelihoods as sources of food, pets, and components of traditional medicine. These scorpions typically inhabit underground burrows and are distributed throughout Southeast Asia. In Thailand, at least three species have been documented: *H. laoticus* Couzijn, 1981; *H. laevigatus* (Thorell, 1876); and *H. silenus* (Simon, 1884), primarily occupying northern, southern, and eastern regions, respectively. However, ongoing habitat loss driven by human activities such as agriculture, urbanization, infrastructure development, and land-use change pose a significant threat to populations, emphasizing the importance of conservation efforts rooted in accurate species identification. Current taxonomic classifications of *Heterometrus* rely predominantly on morphological traits, which can be highly variable within and between species, potentially leading to misidentification and misinformed conservation priorities. To enhance taxonomic resolution and support biodiversity conservation, this study combines detailed morphological assessments with molecular techniques, including DNA barcoding of the cytochrome *c* oxidase subunit I (COI) gene. Twelve Thai specimens were collected and analyzed, alongside 35 COI sequences obtained from GenBank, to generate a comprehensive genetic data matrix. Phylogenetic relationships were inferred using Maximum Parsimony, Maximum Likelihood, and Bayesian inference methods. The results revealed discrepancies between traditional morphology-based classifications and molecular phylogenies, particularly demonstrating that the granulation pattern on the carapace, previously used as a diagnostic trait to differentiate *H. laoticus* and *H. silenus*, is unreliable. This trait exhibited variability within populations of *H. laoticus*, indicating it is insufficient for accurate species delimitation. These findings underscore the importance of integrating molecular data into taxonomic frameworks to improve species identification accuracy, which is crucial for biodiversity monitoring, conservation planning, and environmental rehabilitation efforts aimed at preserving native scorpion diversity and their ecological functions.

KEYWORDS:

Arachnida; giant forest scorpion; taxonomy; Southeast Asia; Thailand.

Species Diversity of Trichoptera from Springs and their Streams, Surat Thani Province

Pimpajee Kaewwong^{1,*}, Kanda Kamchoo¹, Sarote Rouangsuwan², Masaki Takenaka³, Hans Malicky⁴, and Pongsak Laudee¹

¹Faculty of Innovative Agriculture Fisheries and Food, Prince of Songkla University, Surat Thani Campus, Muang District, Surat Thani Province, Thailand 84100

²Faculty of Science and Industrial Technology, Prince of Songkla University, Surat Thani Campus, Muang District, Surat Thani Province, Thailand 84100

³Faculty of Life and Environmental Sciences, University of Tsukuba, 1-1-1 Tennodai, Tsukuba, Ibaraki 305-8577 Japan

⁴Sonnengasse 13, A-3293 Lunz am See, Austria

*Corresponding author, e-mail: baitong.pimpajee@gmail.com

ABSTRACT:

A study of Trichoptera diversity was conducted at Surat Thani Province during the rainy and summer season of 2024 - 2025. Samples were collected from four stations including, Hua Khong Waterfall, Bang Sawan Nam Phut, Ban Nam Rad, and Khlong Nam Sai springs using a pond net and hand picking whereas those of the adults were collected using an ultraviolet light trap. During the rainy season (November - December 2024), a total of 157 larval and 1,170 adult males were collected. These specimens represented 27 species belonging to 16 genera and 6 families of caddisflies. Among the sampling sites, Khlong Nam Sai showed the highest species diversity with 22 species, followed by Nam Phut Bang Sawan (11 species), Ban Nam Rad (9 species), and Hua Khong Waterfall (8 species). In summer (March - May 2025), 217 larvae and 3,472 adult males were collected. These specimens represented 27 species belonging to 15 genera and 6 families of caddisflies. Among the sampling sites, Khlong Nam Sai showed the highest species diversity of 16 species, followed by Ban Nam Rad (14 species), Hua Khong Waterfall (14 species) and Nam Phut Bang Sawan (11 species). The family Leptoceridae exhibited the highest diversity (16), and *Leptocerus dirghachuka* was the most abundant species and was found at all sampling sites.

KEYWORDS:

Caddisflies; morphology; southern Thailand; springs

The Dragonflies and Damselflies (Insecta: Odonata) of Misamis Oriental, Philippines: Baseline Composition, Endemism, and Implications for Conservation

John Lloyd V. Manangan^{1,2,*}, Olga M. Nuñez^{1,2}, & Reagan Joseph T. Villanueva³

¹Department of Biological Sciences, College of Science and Mathematics, Mindanao State University-Iligan Institute of Technology, Andres Bonifacio Ave., Tibanga, 9200 Iligan City, Philippines

²Terrestrial and Freshwater Biodiversity Laboratory, Premier Research Institute of Science and Mathematics, Mindanao State University-Iligan Institute of Technology, Andres Bonifacio Ave., Tibanga, 9200 Iligan City, Philippines

³D3C Gahol Apartment, Lopez Jaena St., 8000 Davao City, Philippines

*Corresponding author, e-mail: jlmanangan21@gmail.com

ABSTRACT:

The Philippines is renowned for its rich biodiversity, boasting over 300 species of odonates, with about 60% being endemic to the archipelago. Among the major islands, Mindanao—the second largest island—hosts around 130 of these species. However, as the country faces growing challenges as a biodiversity hotspot, many of these species are under threat and remain undocumented. This study assessed the rich composition of dragonfly and damselfly species in the province of Misamis Oriental, Northern Mindanao, Philippines, with emphasis on their endemism and conservation status for species and habitat conservation initiatives. Odonate species were documented using opportunistic sampling across four (4) study sites in Misamis Oriental. A total of 64 species were recorded, comprising 31 dragonflies and 33 damselflies from 12 families and 41 genera, with 50% identified as endemic. Among these, eleven (11) species are red-listed on the IUCN and DAO 2019-09, including the Endangered (EN) *Drepanosticta clados* and *Risiocnemis moroensis*; Vulnerable (VU) *Coeliccia exoleta*, *Devadatta basilanensis*, *Euphaea cora*, and *Pseudagrion buenafei*; and Near Threatened (NT) *Cyrano angustior*, *Drepanosticta krios*, *Igneocnemis fuligifrons*, *Rhinocypha sanguinolenta*, and *Sangabasis dentifer*. Alarmingly, 21 species are noted by the IUCN as having a decreasing population trend. The findings highlight the richness and diversity of Odonata species in the locality, along the documentation of a number of endemic and threatened species. Their identification and record in the area underscore the need to strengthen the conservation efforts, including habitat protection and possible environmental restoration at both local and regional scales.

KEYWORDS:

Conservation; Diversity; Endemism; Odonata; Threatened

The dragonfly (Odonata) community structure at Sukamade resort, Meru Betiri National Park, Indonesia

Abdu Rohman^{1,3,*}, Dwi Artika Amalia¹, Wachju Subchan¹, and Naila Faradisa²

¹Biology Education, Faculty of Teacher Training and Education, University of Jember, Jember, East Java, 68121, Indonesia

²Indonesia Ministry of Social, Salemba Raya Street, Central Jakarta, Indonesia

³FloraFauna Nusantara, Jember, East Java, 68121, Indonesia.

*Corresponding author, e-mail: abdu.fkip@unej.ac.id

ABSTRACT:

Sukamade Resort, located within Meru Betiri National Park, is a conservation management area. Dragonflies have significant diversity and extensive spread. The presence of dragonflies in conservation areas is intricately linked to the availability of ecological resources. Conservation areas with robust vegetation surrounding aquatic habitats influence the presence of dragonflies. This study seeks to ascertain the composition of the dragonfly community in Sukamade Resort, Meru Betiri National Park, particularly as foundational data for conservation area management. The study utilized four locations as sampling sites. Seventeen species of dragonflies were recognized. *Orthetrum sabina* and *Pseudagrion microcephalum* are the species with the greatest population density across all locales. The diversity index indicated a moderate level, the Margalef index demonstrated low requirements, the dominance index was low, and evenness was strong. The significant value index indicates that *Neurothemis ramburii*, *Orthetrum sabina*, and *Libellago lineata* possess the essential value index (IVI 0.38). Canonical correspondence analysis indicates that the taxa *Pseudagrion microcephalum*, *Zyxomma obtusum*, *Ischnura senegalensis*, *Diplacodes trivialis*, and *Trithemis festiva* are associated with air humidity characteristics at the Great Estuary location. Therefore, it can be concluded that the presence of dragonflies is influenced by habitat factors such as aquatic substrate composition, abiotic parameters (light, temperature, humidity), and riparian vegetation. Protecting riparian habitats and maintaining good water quality are crucial for the conservation of dragonflies, which reflect healthy ecological conditions and support the sustainability of aquatic ecosystems.

KEYWORDS:

Abundance; conservation; dragonfly; diversity; forest; national park

Systematics of selected Pygmy Grasshoppers (Orthoptera: Tetrigidae) in selected sites in Mindanao Island, Philippines

Romeo R. Patano Jr.^{1,*}, Victor B. Amoroso², Fulgent P. Coritico², Maria Melanie M. Guiang², Sheryl A. Yap³ and Alma B. Mohagan¹

¹Animal Biology Division Institute of Biological Sciences College of Arts and Sciences, Central Mindanao University, Musuan, 8710, Mindanao, Philippines

²Plant Biology Division, Institute of Biological Sciences College of Arts and Sciences, Central Mindanao University, Musuan, 8710, Mindanao, Philippines

³Institute of Weed Science, Entomology and Plant Pathology, College of Agriculture and Food Science, University of the Philippines Los Baños, College, Laguna, 4031, Philippines.

*Corresponding author, e-mail: romeonjrpatano@gmail.com

ABSTRACT:

No published studies have been conducted to determine diversity and conservation status assessment, ecological and molecular identification, and thorough geographic ranges of Mindanao pygmy grasshopper species. Thus, this study was conducted to a) provide information on the species composition, richness, and endemism of pygmy grasshoppers; b) assess the conservation status of the species; c) construct a taxonomic key; d) compute the diversity values and provide relationships with their microhabitat preferences; and e) provide diagnostic morphological descriptions and DNA barcodes of selected pygmy grasshoppers in selected sites in Mindanao. Belt transects coupled and opportunistic sampling were done across sites to collect tetrigid samples. For molecular studies, hindlegs were preserved in absolute ethyl alcohol for DNA extraction and sequencing. Species composition revealed 22 species referable to 4 subfamilies and 15 genera with 413 individuals. Mount Natampod had the highest species richness with 19, followed by Mount Balatukan with 15, Mount Apo with 8, and lastly, Mount Musuan with only 5 species. Species diversity across sites revealed that Mount Natampod had the highest index value ($H' = 1.052$), followed by Mount Balatukan ($H' = 2.472$), Mount Apo ($H' = 1.945$), and Mount Musuan with the lowest ($H' = 1.494$). Diversity across vegetation types revealed that the lower montane forest had the highest diversity index ($H' = 2.254$), followed by the upper montane forest ($H' = 2.099$), and the agroforest had the lowest ($H' = 1.728$). The conservation status assessment revealed 12 threatened species and 86.36% are endemic species of which 6 are notably site endemics. Ecological studies revealed that species prefer varieties of microhabitats across sites and vegetation types. Seven detailed descriptions and diagnoses of newly discovered taxa were provided including the 5 DNA barcodes of tetrigid species confirming their identifications and systematic relationships. It is highly recommended that related research be done on the Visayas and Luzon tetrigid species. In addition, a more detailed molecular study with collaborative efforts must be further conducted to provide an exhaustive phylogenetic analysis of pygmy grasshoppers in the Philippines.

KEYWORDS:

Biodiversity; insects; new species; Mindanao; tetrigids; Philippines

Taxonomy and Conservation Assessment of the Mining Bee Genus *Habropoda* in Thailand, Incorporating with Ecological Niches Modeling of *Bombus* species.

Pakorn Nalinrachatakan^{1,*}, Prapun Traiyasut², Teeradate Srimaneeyanon¹, Chawatat Thanooosing¹ and Natapot Warrit¹

¹Bee and Spider Research Unit, Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok, 10500, Thailand

²Program in Biology, Faculty of Science, Ubon Ratchathani Rajabhat University, Ubon Ratchathani, 34000, Thailand

*Corresponding author, e-mail: pakorn.nlr@gmail.com

ABSTRACT:

The digger bees genus *Habropoda* Smith, 1854 (Apidae: Anthophorinae: Anthophorini) consists of medium-sized robust bees. *Habropoda* species are solitary and construct their nests under the ground. Due to the limited fundamental knowledge available, developing an alternative framework to rush conservation assessment is crucially needed. Here, 58 (20♀, 38♂) specimens of *Habropoda* from Chulalongkorn University Natural History Museum were examined and compared with literature and type specimens. The results revealed at least 5 species of Thai *Habropoda*, including one new record and three new species. Subsequently, we altered assessment criteria based on IUCN Red List Guideline and Ascher et al. (2022) framework. We then incorporated ecological niche modeling of *Bombus* species in Thailand using MaxEnt algorithm via R programming, and then evaluated the habitat suitability of both current and climate change situations. In summary, this study proposed an alternative framework for assessing the conservation status of arthropods, and revealed the hidden diversity of pollinators across Thailand.

KEYWORDS:

Biodiversity; insect pollinator; species distribution; species occurrences

The Ecological Restoration for Giant Honeybee (*Apis dorsata* Fabricius, 1793) Populations at The Forestias Project

Parnchanok Nimthapthim^{1,2,*}, Surin Warachun¹, Anong Chanamool¹, Sirin Kaewlaierd¹

¹ The Magnolia Quality Development Corporation Limited, Bangkok, Thailand.

² Biodiversity Research & Innovation Greenery of the Forestias Project.

*Corresponding author, e-mail: Parnchanok_ni@dtgo.com

ABSTRACT:

The Forestias is a novel urban development initiative that integrates advanced real estate technology with a strong commitment to environmental conservation. Employing the Miyawaki reforestation method, the project aims to establish a natural forest and various green spaces across an area spanning over 398 rai, utilizing more than 300 indigenous plant species. Presently, the Miyawaki forest, aged between 4 to 5 years, has induced environmental transformations within its project, such as cooler temperatures, reductions in carbon contamination, PM 2.5 air pollutants and not using chemical insecticides. This has attracted various animals and insects seeking habitation and sustenance, including bees being among them. In the world, bee population is constantly decreasing, a continuous decline in their population attributed to factors like global warming, agricultural chemical usage, and encroachment on their habitats. Interestingly, within The Forestias project, four Giant Honeybee hives have been discovered in areas near Ceylon oak, Copper pod, Chan khao (Edible zone), *Xanthophyllum lanceatum* (Miq.) J.J.Sm.(non-Common name), Chan Khao (Fragrant zone), Yellow mallow tree and *Mallotus nudiflorus* (L.) Kulju & Welzen (non-Common name), with respective trunk diameters of 17, 4.8, 21, 15.2, 18.06, 8.39 and 10.53 inches and nest heights ranging from 4.08, 3.58, 4.5, 2.3, 4.81, 4.59 and 8.54 meter. During the same observation period, three hives were found in the area. Survey before starting the area's development, surveys conducted in 2017 using the Line Transect method reported no bee sightings. The influx and proliferation of the bee population within The Forestias project area suggest its suitability as a habitat. The availability of year-round food sources such as Florida fiddlewood, Peacock flower, Golden penda, and other, coupled with the absence of chemical usage (air pollution), contribute to an environment conducive to sustenance and population growth. The Forestias project is currently open to visitors, with regular exhibitions drawing an average of 7,000 monthly visitors and 1,500 daily visitors during exhibition periods. Habitat Study involves observation and drawing sessions to underscore the significance of bees to humans, with a focus on upper elementary school students.

KEYWORDS:

Miyawaki Forest; Bee Tree; Giant Honeybee

Biodiversity of Predatory ants (Hymenoptera: Formicidae) in Western Forest Complex, Thailand

Netnapa Phosrithong^{1,*}, Sasiwimon Manasin¹, Inthiphon Khamdi¹, Chutima Praingam¹, Kaewpawika Jitthamma Ignatius¹ and Weeyawat Jaitrong²

¹Forest and Plant Conservation Research Office, Department of National Parks, Wildlife and Plant Conservation, Chatuchak, Bangkok, 10900, Thailand

²Office of Natural Science Research, National Science Museum, Technopolis, Khlong 5, Khlong Luang, Pathumthani, 12120, Thailand

*Corresponding author, e-mail: netnapaphosrithong@gmail.com

ABSTRACT:

Ants play a vital role in ecosystems, particularly as natural predators that help regulate soil-dwelling invertebrate populations. This study aimed to examine the diversity of ant species within the western forest complex, the largest conservation forest in Thailand and the most extensive protected area in Southeast Asia. Ant samples were collected from 15 survey sites, yielding 134 species, 45 genera and seven subfamilies. The subfamily Myrmicinae exhibited the highest species richness, accounting for approximately 42.22% of all recorded genera and species. This was followed by Formicinae, Ponerinae, Dorylinae, Dolichoderinae, Ectatomminae, and Pseudomyrmecinae. The most species-rich genera were *Leptogenys* (12 species), *Pheidole* (11 species), *Technomyrmex* (9 species), *Polyrhachis* (8 species), *Tetramorium* (8 species), and *Aenictus* (6 species). Additionally, ten alien ant species were identified. The results of this study provide essential baseline data for long-term monitoring of ant communities in forest ecosystems, particularly regarding potential invasions by alien ant species in protected areas.

KEYWORDS:

Ant; western forest complex; predator; biodiversity

Diversity and status of butterflies (Lepidoptera: Rhopalocera) in selected areas of Misamis Oriental, Philippines

Christine Hope Q. Dela Cruz^{1,*} and Olga M. Nuñez¹

¹Mindanao State University-Iligan Institute of Technology Iligan City, 9200 Philippines

*Corresponding author, e-mail: Christinehope.delacruz@g.msuiit.edu.ph

ABSTRACT:

Butterflies are important bioindicators of an ecosystem. However, studies on their diversity in the Philippines are still limited. Only a few reserves have been explored in Mindanao, leaving significant gaps in our understanding of their diversity and conservation status. This study aimed to assess the species diversity of butterflies across three selected areas of Mount Balatukan, Misamis Oriental: the Mimbilisan Protected Landscape, Kalagonoy, and the Jamboree Site. An opportunistic sampling was conducted, and the collected specimens were identified to species level. Biodiversity indices, including the Shannon-Wiener Index and Simpson's Index, were computed using the PAST (Paleontological Statistics Software Package). A total of 271 individuals, belonging to 67 species of butterflies identified morphologically, were recorded across all sites. The highest diversity level was observed in the Jamboree Site ($H' = 3.931$), despite having the lowest number of individuals ($n = 74$), followed by the Mimbilisan Protected Landscape ($H' = 3.877$), and Kalagonoy ($H' = 3.807$), respectively. Of the 67 species recorded, 22 species (32.84%) were endemic, and only the *Parantica danna* was categorized by the IUCN (International Union for Conservation of Nature) conservation status as Vulnerable. These findings indicate that Mount Balatukan hosts a rich and diverse butterfly fauna, highlighting its ecological significance and potential for biodiversity conservation.

KEYWORDS:

Biodiversity; species; lepidoptera; protected area

Butterfly Species Diversity Of Selected Urban Parks In Metro Manila, Philippines

Micael Gabriel A. Itliong^{1,2,3,*}, Nikki Heherson A. Dagamac^{1,2,4} and Jade Aster T. Badon⁵

¹The Graduate School, University of Santo Tomas, España Blvd, Sampaloc, Manila, 1008 Philippines.

²Initiatives for Conservation, Landscape Ecology, Bioprospecting, and Biomodeling (iCOLABB), Research Center for the Natural and Applied Sciences, University of Santo Tomas, España Blvd, Sampaloc, Manila, 1008 Philippines.

³Department of Biology, Polytechnic University of the Philippines, Sta. Mesa, 1016 Manila, Philippines

⁴Department of Biological Sciences, College of Science, University of Santo Tomas, España Blvd, Sampaloc, Manila, Philippines 1008

⁵Animal Biology Division, Institute of Biol. Sciences, Univ. of the Philippines Los Baños, Laguna, Philippines 4031

*Corresponding author, e-mail: imicaelgabriel@gmail.com

ABSTRACT:

Urban parks can host biodiversity, but research on urban insect diversity remains limited, hindering effective conservation assessment and management. Butterflies are recognized as crucial bioindicators, yet many urban parks in Metro Manila lack comprehensive data on butterfly diversity. This study aims to establish baseline data on butterfly diversity in Arroceros Forest Park (AFP), La Mesa Ecopark (LME), Las Piñas-Parañaque Wetland Park (LPPWP), and Ninoy Aquino Parks and Wildlife Center (NAPWC). Using transect walks and bait traps, we identified 44 butterfly morphospecies from 5 families and 30 genera, with a total of 816 individuals observed during both the dry season (April–May) and the wet season (June–July). Nymphalidae emerged as the dominant butterfly family, contributing the highest species richness. Notably, LME exhibited the highest species richness, abundance, and functional diversity. Euclidean cluster analysis confirmed LME as the most distinct site, while AFP and LPPWP clustered together. Canonical Correspondence Analysis revealed that temperature and vegetation density significantly influence butterfly communities in these urban parks. Ultimately, the functional diversity of butterfly communities in urban parks can provide valuable insights into ecosystem resilience; however, the absence of quantitative data may limit the depth of functional diversity analysis.

KEYWORDS:

α -Diversity; Butterfly Conservation; Metro Manila; Urban Green Spaces; Urban Fauna

Moth Community Structure (Lepidoptera: Geometroidea) and Potential Diversity of Host Plants at Ranu Darungan Resort, Bromo Tengger Semeru National Park, Indonesia

Abdu Rohman^{1,3,*}, Faqihul Birbik Hamdani¹, Wachju Subchan¹ and Doni Catur Saputra²

¹Biology Education, Faculty of Teacher Training and Education, University of Jember, Jember, East Java, 68121, Indonesia

²Bromo Tengger Semeru National Park, Malang City, East Java, 65126, Indonesia

³FloraFauna Nusantara, Jember, East Java, 68121, Indonesia.

*Corresponding author, e-mail: abdu.fkip@unej.ac.id

ABSTRACT:

Ranu Darungan Resort is a designated conservation area inside the Bromo Tengger Semeru National Park (BTSNP). Moths are insect that inhabit the region. Moths are found in various habitats, including primary, secondary, and utilization forests. The phenomena of Mount Semeru's eruption and anthropogenic activities can pose a threat, causing damage to primary and secondary forests, which leads to a reduction in vegetation cover and host plants. This research aims to analyze the structure of the moth community and identify potential host plants at the Ranu Darungan Resort. We documented ten moth species and thirty-eight plant species. Research has documented the wide host range of *Conogethes punctiferalis* (wilderness zone) and *Duponchelia* sp. (utilization zone), which encompasses various agricultural and forestry plants. The Shannon-Wiener index (2.332) exceeds the utilization zone (2.244). The evenness value of the jungle zone is 1.03; on the other hand, the evenness index of the utilization zone is 1.05. The dominance index exhibited a low value. The similarity index (Iss) exhibited a high value in both ecosystems. A vegetation plot analysis identified thirty-eight plant species. *Ageratina riparia*, an invasive plant that spreads rapidly, dominates both habitats and can easily dominate new ones. Canonical Correspondence Analysis (CCA) showed that *Asota heliconia*, *Plodia* sp., *Conogethes punctiferalis*, and *Eacles* sp. significantly correlate with soil moisture, light intensity, wind speed, and air humidity in the jungle habitat. Principal Component Analysis (PCA) revealed a strong correlation between *Clidema hirta*, *Cryptococcum patens*, and *Ageratina riparia* in the same habitat. Our findings demonstrate that moth presence directly depends on the availability of potential host plants, highlighting the importance of plant diversity in sustaining moth species richness.

KEYWORDS:

Biodiversity, Insect, National Parks, Vegetation, Wilderness

Habitat heterogeneity and biodiversity: A comparative analysis of avian and butterfly diversity of two solid waste dumping sites in India

Supratick Seal^{1,*} and Sandip Pal¹

¹Department of Zoology, Barrackpore Rastraguru Surendranath College, Barrackpore, Kolkata- 700120, West Bengal, India

*Corresponding author, e-mail: supratickseal@gmail.com

ABSTRACT:

Rapid increase in human population has led to urbanization mediated modifications to the natural ecosystems and biodiversity. Solid waste dumping sites with an increment in disposals, change the resource availability along with the generation of habitat heterogeneity for different species. Kolkata Metropolitan Area (KMA), under the state of West Bengal, India, had been a historically significant zone from socio-economic, cultural and political perspectives, leading to sharp increase in the human population and relatedly solid waste volume. Under KMA, four urban local bodies- Khardah, Titagarh, Barrackpore and North Barrackpore generate approximately 2,31,000 kg. of solid waste per day, dumping to the Titagarh Municipality dumping site, whereas Kamarhati municipality disposing about 1,55,000 kg. every day to the Agarpara garbage dumping site, in which biodegradables are about 60%. This study attempts for a comparative analysis of the avian and butterfly diversity around the two dumping sites- the relatively unexplored habitats. Diversity indices significantly showed the importance of natural ecosystem components like waterbody, native greeneries etc. in perseverance of species diversity both with the avian and butterfly models. Availability of the biodegradable disposals are resources contributing in the dominance and commonness of particular bird species. Initiatives of environmental rehabilitation seems to be challenging with an additional potential risk of emergence of parasitism. However, implementation of proper solid waste management strategies may aid in the restoration of the local diversity.

KEYWORDS:

Avian diversity; butterfly diversity; habitat heterogeneity; solid waste dumping sites.

Herpetofauna of Trankini, Lake Sebu, South Cotabato, Philippines

Allyza Mae D. Paburian^{1,*} and Annie D. Francisco, MS²

¹Bachelor of Science in Biology student, Sultan Kudarat State University- Tacurong Campus, Tacurong City, Sultan Kudarat, 9800

²Department of Biology Faculty, Sultan Kudarat State University- Tacurong Campus, Tacurong City, Sultan Kudarat, 9800

*Corresponding author, e-mail: allyzamaepaburian@sksu.edu.ph

ABSTRACT:

The study of "Herpetofauna of Trankini, Barangay Lamlahak, Lake Sebu, South Cotabato, Philippines" was conducted to identify, classify, and determine the conservation status of amphibians and reptiles in the area. Using opportunistic sampling methods, the survey was carried out from June to August 2024 across four distinct habitat types: riparian vegetation, agricultural areas, community settlements, and terrestrial zones. These varied environments provided a broad ecological scope for species detection. A total of 14 species were recorded, consisting of 5 amphibians and 9 reptiles. The amphibian species identified include *Rhinella marina*, *Hoplobatrachus chinensis*, *Polypedates leucomystax*, *Platymantis dorsalis*, and *Kaloula pulchr*. The reptile species recorded were *Gekko gecko*, *Tropidophorus misaminius*, *Lamprolepis smaragdina*, *Bronchocela jubata*, *Sphenomorphus fasciatus*, *Bronchocela sp.*, *Hemidactylus platyurus*, *Draco volans*, and *Pelodiscus sinensis*. Based on the IUCN Red List, 86% of the species are classified as Least Concern, 7% as Vulnerable (*Pelodiscus sinensis*), and 7% as Near Threatened (*Tropidophorus misaminius*). The presence of Vulnerable and Near Threatened species highlights the need for conservation efforts to protect at risk wildlife species in Trankini, Lake Sebu, South Cotabato. Furthermore, 64% of the species were found to be widespread, while the remaining 36% were endemic to the Philippines, including four reptiles *Bronchocela jubata*, *Pelodiscus sinensis*, *Sphenomorphus fasciatus*, and *Tropidophorus misaminius* and one amphibian (*Platymantis dorsalis*). Endemic species are found only in a specific geographic area and are highly vulnerable to extinction due to their limited range. Therefore, their conservation is crucial not only to protect the unique biodiversity of a region but also to maintain ecological balance and support the health of natural ecosystems. The findings of this study emphasize the ecological importance of Trankini, Lake Sebu, South Cotabato as a refuge for diverse herpetofauna, including endemic and conservation-priority species. The presence of species with varying conservation statuses across different habitats highlights the need for habitat protection, sustainable land use, and targeted conservation efforts. This baseline data supports local biodiversity conservation strategies, ecological research, and sustainable initiatives in biologically rich areas like Lake Sebu.

KEYWORDS:

Conservation; Ecological Status; Herpetofauna; species, status

Too Young to Understand: Current knowledge and research gaps of tadpole research in Taiwan and the Philippines

Andrie Bon A. Flores^{1,2 *}, Ace Kevin S. Amarga^{1,2} and Si-Min Lin^{1,2}

¹Biodiversity Program, Taiwan International Graduate Program, Biodiversity Research Center, Academia Sinica. No. 128, Academia Road Sec. 2, Taipei 11529, Taiwan.

²School of Life Science, National Taiwan Normal University. No. 88, Tingzhou Road Sec. 4, Taipei 116059, Taiwan.

*Corresponding author, e-mail: andriebon.flores@g.msuiit.edu.ph

ABSTRACT:

Tadpoles play a vital role in freshwater ecosystem being a sensitive bioindicator of ecological change. Despite their importance, tadpole research remains globally underrepresented particularly in East and Southeast Asia. This study presents a systematic review of tadpole-related research in Taiwan and the Philippines, one of the amphibian biodiversity hotspots in Asia. Through qualitative synthesis of 100 peer-reviewed studies (1955–2025), we examined geographic trends, methodological approaches, thematic focus, and taxonomic coverage. Results reveal a significant disparity on tadpole research in these two countries: Taiwan demonstrates consistent research growth, dominated by experimental focused studies concerning breeding and behavior-focused studies, particularly in *Kurixalus eiffingeri*, and has documented all known native tadpole species. In contrast, the Philippines shows slower progress, with studies largely descriptive and concentrated in Mindanao, covering only 39 of over 130 described anuran species. Research themes are narrower, with strong bias toward breeding ecology and morphology. These findings highlight critical gaps in the Philippines, particularly in species representation, methodological diversity, and regional research equity. We recommend integrative and standardized approaches to elevate tadpole research across both countries and promote comprehensive amphibian conservation.

KEYWORDS:

Anurans; Philippines; synthesis; tadpoles; Taiwan

Integrated Genomic and AI-Based Approaches for Monitoring and Managing Invasive Hybrid Catfish in Thailand

Worapong Singchat^{1,2,*}, Thitipong Punthum^{1,2}, Narongrit Muangmai^{1,3}, Prateep Duengkae^{1,2}, Kriengsak Treeprapin⁴, Suchin Trirongjitmoah⁵, Jiraboon Prasanpan⁶ and Kornorn Srikulnath^{1,2}

¹Animal Genomics and Bioresource Research Unit, Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

²Special Research Unit for Wildlife Genomics (SRUWG), Faculty of Forestry, Kasetsart University, Bangkok 10900, Thailand

³Department of Fishery Biology, Faculty of Fisheries, Kasetsart University, Bangkok 10900, Thailand

⁴Department of Mathematics Statistics and Computer, Faculty of Science, Ubon Ratchathani University, Ubon Ratchathani 34190, Thailand

⁵Department of Electrical and Electronics Engineering, Faculty of Engineering, Ubon Ratchathani University, Ubon Ratchathani 34190, Thailand

⁶Kalasin Fish Hatchery Farm (Betagro Public Company Limited), Buaban, Yangtalad district, Kalasin 46120, Thailand

*Corresponding author, e-mail: worapong.singc@ku.ac.th

ABSTRACT:

The North African catfish (*Clarias gariepinus*), introduced to Thailand in 1987 for aquaculture, has become a highly invasive species due to farm escapes and intentional religious releases. The release of hybrids between *C. gariepinus* and native bighead catfish (*C. macrocephalus*) has further exacerbated the invasion, posing serious threats to freshwater biodiversity. Hybrid contamination, resulting from unregulated stocking and merit-making practices, has led to ecological disruptions and socio-economic consequences, particularly in the Chao Phraya and Tha Chin river basins. To assess and mitigate these impacts, a combination of molecular genetics and artificial intelligence techniques was employed. Genotyping, mitochondrial d-loop analysis, and SNP/repetitive DNA marker development were utilized to accurately identify pure species and F₁ hybrids in natural populations. Additionally, a deep learning framework was developed using cranial morphology, YOLOv11 segmentation, and ResNet18 classification, achieving 99.5% accuracy in distinguishing *C. gariepinus*, *C. macrocephalus*, and their hybrids. These tools offer scalable and efficient solutions for hybrid detection and species monitoring. A chromosome-scale, haplotype-resolved genome assembly of an F₁ hybrid was also generated, enabling reconstruction of two complete haploid parental genomes. This high-quality reference supports future applications in conservation genomics, selective breeding, and molecular diagnostics. The findings highlight the urgent need to manage invasive hybrids to protect native biodiversity. A Spatial Decision Support System (SDSS) integrating genetic, ecological, and socio-cultural data is proposed to guide evidence-based policy and intervention. Recommended actions include regulation of hybrid fish releases, culturally sensitive awareness campaigns on religious release practices, and implementation of diagnostic tools across aquaculture and fisheries sectors. This integrated approach contributes to environmental rehabilitation, sustainable aquaculture, and One Health goals in Thailand.

KEYWORDS:

Invasive species; Hybrid catfish; DNA barcoding; deep learning; Biodiversity management

Population Assessment of the Dog-faced Water Snake (*Cerberus schneiderii*) to Support Biodiversity Conservation in the Urban Phra Chedi Klang Nam Mangrove Forest at Rayong Province, Thailand

Supavadee Sriwattanachai¹, Nantida Sutummawong^{1,*} and Chattrapas Pongcharoen¹

¹Department of Forest Biology, Faculty of Forestry, Kasetsart University, Bangkok, 10900, Thailand

*Corresponding author, e-mail: ffornis@ku.ac.th

ABSTRACT:

Mangrove forests constitute critical habitats for diverse brackish-water fauna, including the Dog-faced Water Snake (*Cerberus schneiderii*), a key predator contributing to the regulation of prey populations and the maintenance of ecosystem equilibrium. Despite its ecological importance, current data on the distribution and population dynamics of *C. schneiderii* remain scarce, particularly within Thailand. Notably, its conservation status has not been reassessed by the IUCN following its taxonomic separation from *Cerberus rynchops* in 2012. The Phra Chedi Klang Nam Mangrove Forest, an urban green space recognized for its recreational, health, and educational values, provides a significant habitat for this species. Investigating the population trends of *C. schneiderii* in this context is imperative to elucidate the link between biodiversity conservation and urban quality of life, thereby informing sustainable management of urban ecosystems. This study conducted bi-monthly field surveys from June 2024 to August 2025 employing a capture-mark-recapture methodology with microchip implantation for individual identification. Population parameters were estimated using the Cormack-Jolly-Seber (CJS) model for open populations. Results indicate a population size of 809.1 ± 206.2 individuals, with a mean density of 38.5 ± 9.8 individuals per hectare (95% CI: 19.3–57.7 individuals/ha). Temporal variation was observed, with peak captures in March 2025 (70 individuals) and lowest captures in December 2024 (6 individuals), likely influenced by hydrological conditions affecting detectability. Comparatively, the population density at this site is lower than documented in other regional studies. These findings underscore the critical importance of the Phra Chedi Klang Nam Mangrove Forest as a vital urban green space that supports biodiversity, provides ecosystem services, and enhances community wellbeing. Sustained long-term monitoring of *C. schneiderii* populations is essential to accurately assess population trends and inform adaptive management strategies. Effective conservation and management of this mangrove habitat should prioritize habitat protection, pollution control, and community engagement to maintain ecological integrity and promote resilience in the face of urban development pressures. Moreover, a deeper understanding of *C. schneiderii* population dynamics will help fill key knowledge gaps regarding its ecological role and the broader trophic interactions within the mangrove ecosystem, thereby supporting evidence-based conservation planning.

KEYWORDS:

Capture-mark-recapture; *Cerberus schneiderii*; Mangrove conservation; Population dynamic; Urban biodiversity

Integrative Genomic Strategies for the Conservation of Purebred Siamese Crocodiles

Thitipong Panthum^{1,*}, Worapong Singchat¹, Narongrit Muangmai¹, Prateep Duengkae¹, Yusuke Fukuda², Sam Banks³, Yosapong Temsiripong⁴, Tariq Ezaz⁵ and Kornorn Srikulnath¹

¹Animal Genomics and Bioresource Research Unit (AGB Research Unit), Faculty of Science, Kasetsart University, 50 Ngamwongwan, Chatuchak, Bangkok 10900, Thailand.

²Department of Environment, Parks and Water Security, Northern Territory Government, Darwin, Northern Territory, Australia.

³Research Institute for the Environment and Livelihoods, College of Engineering, IT and the Environment, Charles Darwin University, Darwin, Northern Territory, Australia.

⁴R&D Center, Sriracha Moda Co., Ltd., Sriracha, Chonburi 20230, Thailand.

⁵Centre for Conservation Ecology and Genomics, Institute for Applied Ecology, Faculty of Science and Technology, University of Canberra, Canberra, ACT 2617, Australia.

*Corresponding author, e-mail: thitipong.pa@ku.th

ABSTRACT:

Hybrids between the critically endangered Siamese crocodile (*Crocodylus siamensis*) and the saltwater crocodile (*C. porosus*), listed as Least Concern by the IUCN, pose a major challenge to conservation and reintroduction efforts for *C. siamensis*. This study highlights the importance of employing alternative genetic markers and analyzing diverse populations to accurately identify and exclude hybrids from reintroduction programs. To address this, DArT sequencing was utilized to detect genome-wide single nucleotide polymorphisms (SNPs) in both species, allowing for the confirmation of genetic profiles in purebred and hybrid individuals. A reference population of Australian saltwater crocodiles was included to aid in the identification of species-specific diagnostic SNPs. Multiple analytical approaches were employed to evaluate hybridization levels, with particular attention given to three individuals showing signs of potential backcrossing. To validate the diagnostic SNP loci, a PCR-based method was developed, and primers were designed for 20 selected SNPs. Of these, three loci effectively distinguished between purebred individuals and various hybrid classes. By integrating mitochondrial and nuclear genetic data—including microsatellite markers and species-specific SNPs—this study presents a novel, comprehensive approach to overcoming the limitations of individual methods. This strategy enhances conservation efforts by ensuring the genetic purity of reintroduced individuals, ultimately supporting the long-term survival of *C. siamensis* through informed management and reintroduction programs.

KEYWORDS:

Biodiversity conservation; Genome-wide SNPs; Siamese crocodile; Hybridization

Understanding foraging guilds and niche dynamics of avifauna in an Indian seasonal wetland for sustainable biodiversity management

Sandip Pal^{1,*} and Rupam Debnath²

¹Department of Zoology, Barrackpore Rastraguru Surendranath College, Barrackpore, West Bengal, 700120, India

²Department of Zoology, West Bengal State University, Barasat, West Bengal, 700126, India

*Corresponding author, e-mail: sandipzoologybrsc@gmail.com

ABSTRACT:

Integrating community-driven ecological knowledge into biodiversity management strategies is crucial for sustaining avian diversity and enhancing ecosystem resilience. The present study is the first of its kind to investigate the foraging guild structure and niche characteristics of avifauna in a seasonal wetland of West Bengal, India, a habitat known for its fluctuating environmental conditions and rich assemblage of migratory, local, and seasonal bird species. Understanding species interactions and resource use is crucial for biodiversity management, especially in ecologically dynamic habitats. Observational data were collected across three ecological dimensions: food type, foraging substrate, and foraging technique. Guilds were identified through cluster analysis, and niche breadth and overlap were calculated using Levin's and Pianka's indices. The results reveal that House Crow exhibits the highest niche breadth in terms of food type and foraging technique, while Black Drongo has the widest niche breadth for foraging substrate. Others like the Chestnut-tailed Starling, Asian Openbill, and Wood Sandpiper demonstrate high specialization in resource use. Niche overlap is higher within guilds than between them, indicating potential intra-guild competition, particularly among specialists. Despite some overlap in resource dimensions, distinct partitioning is evident among certain species, suggesting adaptive strategies to minimize competition. This pattern underscores the vulnerability of specialist species to habitat and resource fluctuations, a pressing concern in the context of global biodiversity decline.

KEYWORDS:

Birds; biodiversity; conservation; competition; niche overlap

Locally sourced habitat enhancements promote bird visitation in the early stage of dipterocarp restoration plots

Paleerat Nuchpho¹, Chatchawan Chaisuekul^{2,3,*}, and Nipada Ruankaew Disyatat³

¹Ph.D. Program in Zoology, Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand

²Integrative Insect Ecology Research Unit, Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand

³Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand

*Corresponding author, e-mail: chatchawan.c@chula.ac.th

ABSTRACT:

Birds contribute significantly to biodiversity and environmental rehabilitation by providing essential ecosystem services, including insect pest control, seed dispersal, and nutrient cycling. Supporting avian communities through targeted habitat enhancements can accelerate ecological recovery in degraded landscapes. This study investigated the role of simple, locally sourced structures, namely artificial perches and puddles, in attracting birds to early-stage reforestation plots in deciduous dipterocarp forest in Nan Province, northern Thailand. Prior to installing the enhancement structures, a 48-hour point count survey recorded five bird species inhabiting within the plots and 28 species along the edges. Following installation, a total of 34 bird species were observed using the enhancements, with 19 species at perches and 31 at puddles. Insectivorous and carnivorous birds used the perches for foraging, and excretory events were noted beneath them, suggesting potential nutrient input. The puddles attracted a wider range of species, particularly arboreal insectivore-frugivores such as Bulbuls (*Pycnonotus* spp.), primarily for drinking and bathing. These findings demonstrate that low-cost, nature-based enhancements can effectively increase bird visitation, promote species diversity, and support ecosystem functioning in regenerating forests. Incorporating such measures into restoration practices can improve biodiversity outcomes and advance the rehabilitation of forest ecosystems.

KEYWORDS:

Additional resources; bird diversity; habitat enhancement; restoration; video surveillance

Initiative towards active genetic management and viable cell biobanking in avian ex-situ conservation in Thailand

Suparat Chaipipat¹, Tucksorn Bhummakasikorn⁴, Kornkanok Sritabtim¹, Yanika Piyasanti¹, Juthathip Jurutha¹, Rungthiwa Sinsiri¹, Sukumal Prukudom^{1,2}, Bencharong Sangkharak⁵, Chatkamon Bunnam⁶, Chayanid Prasanwong⁶, Prach Kongthong⁶, Sornchai Sungkalerd⁶, Chananya Kanchanasaka⁶, and Kannika Siripattarapavat^{1,3*}

¹Kasetsart University Veterinary Diagnostic Laboratory, Faculty of Veterinary Medicine, Kasetsart University, Bangkok, 10900, Thailand

²Department of Anatomy, Faculty of Veterinary Medicine, Kasetsart University, Bangkok, 10900, Thailand

³Department of Pathology, Faculty of Veterinary Medicine, Kasetsart University, Bangkok, 10900, Thailand

⁴Wildlife Research Division, Conservation Office, Department of National Parks, Wildlife and Plant Conservation, Thailand

⁵Wildlife Law Enforcement Division, Conservation Office, Department of National Parks, Wildlife and Plant Conservation, Thailand

⁶Wildlife Breeding Division, Wildlife, Conservation Office, Department of National Parks, Wildlife and Plant Conservation, Thailand

*Corresponding author, e-mail: kannika.si@ku.th

ABSTRACT:

Thailand is home to a thousand of bird species and alarmingly up to 171 species are being threatened. Currently, only 61 species are maintained in 23 wildlife breeding centers managed by the Department of National Parks, Wildlife and Plant Conservation. Not all captive breeding programs, however, are successful in producing offspring. The integrative management of captive parental stocks, i.e., monitoring of genetic diversity and preserving germplasm, is not implemented as an operating procedure. Therefore, it greatly hampers the efforts of ex-situ conservation to mitigate the declining biodiversity. Here, we aimed to execute a practical strategy for mating pair rearrangement by relying on DNA fingerprinting of parental stocks, and in parallel, banking of their viable cells. As an initiative model, nine species were selected across four breeding facilities. The priority of target species was determined and categorized from the extent of breeding populations and the expertise of facilities specific to species endemic to the geographical region. Genetic diversity of each species was assessed by using mitochondrial genes including cytochrome oxidase subunit I, cytochrome B, and control region. Haplotype analysis based on pairwise distances was used to generate a cage management guideline regarding maximum avoidance of inbreeding. Cryopreservation of primordial germ cells and/or adult fibroblasts was chosen as a suitable means to secure avian germplasm that are compatible with advanced reproductive technology. Animal with low fertility or absence of breeding pairs precluded the isolation of primordial germ cells. The at-risk group consisted of 6 species with very few adults or breeding pairs, and as expected, low haplotype diversities were revealed in a group of lesser adjutant (n=10), greater adjutant (n=3), white-shouldered ibis (n=3), rhinoceros hornbill (n=4), white-crowned hornbill (n=1), and Malayan peacock-pheasant (n=4). An intervention of active breeding management is urgently required in this group to increase genetic diversity. Cryopreserved fibroblast collection was established with high efficiency for these species but the rhinoceros hornbill and white-crowned hornbill, which cultures had emerged but failed to expand. For selected birds that have adequate breeding populations and moderate-to-high haplotype diversities including Bornean crested fireback (n=73), white-winged duck (n=31), and great argus (n=20), a guideline for breeding pair/flock selection has been implemented as a routine operating procedure. Both adult fibroblasts and primordial germ cells were derived and cryopreserved with high efficiency in all three species. We demonstrated that gaining genetic insights and establishing novel collection of avian germplasms can be achieved by a strategy involving routine animal procedures and cost-effective, practical laboratory techniques. This model can be adopted and fine-tuned in additional breeding facilities, building a comprehensive and sustainable ex-situ conservation strategy.

KEYWORDS: Biodiversity; captive-endangered bird; cell banking; germplasms; maximum avoidance of inbreeding; wildlife sanctuary.

Movement and detection probability of *Cyornis banyumas* (Horsfield, 1821) (Hill Blue Flycatcher) in lower montane evergreen forest at Mae Sa-Kog Ma Biosphere reserve, Chiang Mai Province

Yuwadee Ponpithuk^{1,*}, Dokrak Marod², Prateep Duangkae², Paanwaris Paansri³ and Supalak Siri¹

¹Department of Forestry, Maejo University, Phrae Campus, Phrae 54140, Thailand

²Department of Forest Biology, Faculty of Forestry, Kasetsart University, Bangkok, 10900, Thailand

³Department of Fish and Wildlife Conservation, Virginia Polytechnic Institute and State University, VA, United States.

*Corresponding author, e-mail: supalak_sr@mju.ac.th

ABSTRACT:

Forest gap dynamics play a critical role in shaping biodiversity and ecosystem processes, particularly in lower montane forests. This study examines the influence of gap age on the movement patterns and detection probabilities of understory bird species, using *Cyornis banyumas* (Horsfield, 1821), or Hill Blue Flycatcher, as a focal species. Fieldwork was conducted over a five-year period in the lower montane evergreen forest of the Mae Sa-Kog Ma Biosphere Reserve, Chiang Mai Province, Thailand. Birds were sampled using mist-netting at 12 forest gap sites, resulting in a total of 234 individuals banded—147 in closed-canopy areas and 87 in forest gaps—with 66 recaptures. The higher occurrence in closed-canopy habitats suggests that such environments may play a more vital role in sustaining Hill Blue Flycatcher populations. These findings highlight the importance of maintaining intact forest structures while also supporting natural gap regeneration, thereby contributing to more effective conservation strategies in montane forest ecosystems

KEYWORDS:

Movement; detection probability; Hill Blue Flycatcher; forest gap; close canopy

Monitoring Changes in Barking Deer (*Muntiacus muntjak*) Density Following Restoration through Intensive Protected Area Enforcement in Thung Yai Naresuan East Wildlife Sanctuary, Thailand

Krittaphat Lueachang^{1,2}, Pornkamol Jornburom², Piyapong Suebsen³, Warong Suksavate¹, Anak Pattanavibul⁴ and Prateep Duengkae^{1,5}

¹Special Research Unit for Wildlife Genomics (SRUWG), Department of Forest Biology, Faculty of Forestry, Kasetsart University, Bangkok, 10900, Thailand

²Wildlife Conservation Society, Thailand Program, 55/297 Muangthong Thani 5, Chaengwattana Road, Pakkred, Nonthaburi 10210, Thailand

³Department of National Parks, Wildlife and Plant Conservation, Paholyotin Road, Chatuchak, Bangkok 10110, Thailand

⁴Department of Conservation, Faculty of Forestry, Kasetsart University, Bangkok, 10900, Thailand

⁵Animal Genomics and Bioresource Research Unit (AGB Research Unit), Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

*Corresponding author, e-mail: prateepd@hotmail.com

ABSTRACT:

Monitoring prey population trends is essential for evaluating the effectiveness of wildlife protection and restoration efforts. This study investigates changes in the density of Barking Deer (*Muntiacus muntjak*) following the implementation of intensive protected area enforcement in Thung Yai Naresuan East Wildlife Sanctuary (TYE), a core area within Thailand's Western Forest Complex. Historically, TYE experienced widespread habitat encroachment and illegal hunting pressure following the arrival of hill-tribe settlers, in the 1950s. As a result, wildlife populations were severely diminished. In response, a resettlement program was implemented between 1987 and 1994 to relocate local communities outside the sanctuary boundaries. Subsequently, in 2008, an intensive patrolling system was introduced, marking a new era of protection and monitoring. That same year, the first systematic line transect surveys were conducted to assess wildlife populations. In this study, line transect distance sampling was conducted during the dry season from November 2023 to May 2024, covering 15 transects with 150 replicates over a total of 480 km in survey effort. The estimated density of muntjac in 2024 was 3.6 ± 0.58 individuals/km², based on 111 observations, compared to 3.39 ± 0.66 individuals/km² from 90 observations in 2008. This modest increase, coupled with a lower coefficient of variation (16.15% in 2024 vs. 19.43% in 2008), suggests greater population stability and improved detectability. The findings indicate a positive response of Barking Deer populations to sustained protection measures. This research highlights the value of long-term monitoring and intensive enforcement in supporting the recovery of ungulate prey species, which are vital to maintaining ecosystem balance and supporting apex predators such as tigers.

KEYWORDS:

Distance sampling; Large ungulate density; Line transect; Poaching; Species recovery

Non-invasive assessment of Philippine Tarsier (*Carlito syrichta* Linnaeus, 1758) in Barangay Ugoban, Tagbina, Surigao del Sur, Philippines

Cristine Mae F. Luga¹, Kimverly Hazel C. Dapar¹, Leonardo A. Estaño¹, Vanessa Mae C. Tumang^{1,*} and Rafael Ryno G. Sanchez²

¹Department of Biological Sciences, College of Science and Mathematics, MSU-IIT, Iligan City, 9200, Philippines

²University of the Philippines- Los Baños, Pedro R. Sandoval Ave, Los Baños, Laguna, 4031, Philippines

*Corresponding author, e-mail: vanessamae.tumang@g.msuiit.edu.ph

ABSTRACT:

The Philippine tarsier, *Carlito syrichta*, a Near Threatened primate endemic to the Philippines, faces significant threats from habitat loss, human activities, and misconceptions about its ecology. This study aimed to assess the species' presence, distribution, and habitat preferences in Ugoban, Tagbina, Surigao del Sur, while evaluating local community knowledge and attitudes to inform conservation strategies. A non-invasive approach was performed, using camera traps, patch sampling (seven 1,430 m² plots surveyed over seven days), and ethnobiological surveys (50 interviews with locals aged ≥40 years). Habitat assessments documented vegetation, anthropogenic disturbances, and tarsier occurrences. Population density was estimated using detection probability and spatial distribution, whilst community perceptions were analyzed through structured questionnaires. Tarsiers were detected in four of seven sampled sites, with an estimated density of 41.27 individuals/km². Habitat analysis revealed preferences for secondary forests with minimal disturbance. Key threats included illegal logging, agricultural expansion, and natural disasters like typhoons and landslides. Ethnobiological surveys showed moderate local awareness (74% acknowledged tarsier presence), but misconceptions persisted (only 12% correctly identified their insectivorous diet). Despite this, 88% supported conservation efforts, with 98% advocating for protected areas. This study highlights the ecological vulnerability of Philippine tarsiers in Ugoban, Tagbina, Surigao del Sur. It emphasizes the importance of integrating habitat protection and conservation with community awareness. To strengthen the species' conservation, it is recommended to extend camera-trap monitoring, habitat restoration, and implement educational programs to address knowledge gaps. These findings contribute to the primates' conservation efforts and promote sustainable human and biodiversity coexistence.

KEYWORDS:

Carlito syrichta; non-invasive monitoring; primate conservation; local awareness; Surigao del Sur

Diversity and Abundance of wildlife in the Natural World Heritage site, Huai Kha Khaeng Wildlife Sanctuary by using wildlife camera traps

Praewa Mahaphol¹, Warong Suksavate¹, Permsak Kanishthajata², and Prateep Duengkae^{1,*}

¹Department of Forest Biology, Faculty of Forestry, Kasetsart University, Bangkok, 10900, Thailand

²Department of National Parks, Wildlife and Plant Conservation, Paholyotin Road, Chatuchak, Bangkok 10900, Thailand

*Corresponding author, e-mail: prateep.du@ku.ac.th

ABSTRACT:

Huai Kha Khaeng Wildlife Sanctuary is one of the largest and most important forest areas in Thailand. It has been designated as a Natural World Heritage site due to its rich ecosystems and biodiversity. The importance of this area led to the initiation of this study on wildlife diversity and abundance was conducted in the Natural World Heritage site, Huai Kha Khaeng Wildlife Sanctuary, during the period from November 2024 to April 2025. A total of 50 camera traps were deployed with total of 7,931 trap nights and producing 30,792 wildlife images. The results of the study recorded 43 wildlife species, 39 genera, 27 families, and 16 orders. Fifteen wildlife species (34.88%) are classified as threatened. These included: 2 species are Critically Endangered (CR), namely the Banteng (*Bos javanicus*) and the Malayan Tapir (*Tapirus indicus*). 7 species are Endangered (EN), including the Asian Elephant (*Elephas maximus*), Asiatic Black Bear (*Ursus thibetanus*), Sun Bear (*Helarctos malayanus*), Gaur (*Bos gaurus*), Leopard (*Panthera pardus*), Tiger (*Panthera tigris*), and Green Peafowl (*Pavo muticus*). 6 species are Vulnerable (VU), namely the Dhole (*Cuon alpinus*), Golden Jackal (*Canis aureus*), Sambar (*Rusa unicolor*), Sumatran Serow (*Capricornis sumatraensis*), Phayre's Leaf Monkey (*Trachypithecus phayrei*), and Common Palm Civet (*Paradoxurus hermaphroditus*). The calculated Shannon diversity index was 2.11, indicating a relatively high level of species diversity. The abundance of wildlife species, ranked in the top five most abundant categories, were Sambar (*Rusa unicolor*) (35.29), Northern Red Muntjac (*Muntiacus vaginalis*) (21.42), Wild Boar (*Sus scrofa*) (18.99), Banteng (*Bos javanicus*) (16.04), and Asian Elephant (*Elephas maximus*) (4.51). These findings highlight the remarkable biodiversity of this natural World Heritage site, where one-third of the species are classified as threatened. This area reflects the success of current management and conservation strategies. Camera trapping has shown to be an excellent method for wildlife monitoring, providing long-term, diverse, and non-invasive data.

KEYWORDS:

Abundance; Camera trap; Diversity; Wildlife Sanctuary; World Heritage

A Study of Wildlife Biodiversity in Phu Toei National Park

Nutdhavaj Dejakaisaya¹, Pachara Prayong¹, Techit Trakulthongchai¹, Tin Yimtraiporn¹, Nantiya Jaikengdee¹, Pattama Jujiea¹, Piengruethai Nontanaruksa¹, Chakkrit Samphaothong² and Khomkit Sopanate^{1,*}

¹Department of Social Studies, Vajiravudh College, Bangkok, 10300, Thailand

²Phu Toei National Park, Suphan Buri, 72180, Thailand

*Corresponding author, e-mail: patharawit.t@vajiravudh.ac.th

ABSTRACT:

This research aimed to: 1) survey wildlife in Phu Toei National Park, and 2) classify the types of wildlife species found within the park, located in Dan Chang District, Suphan Buri Province. The tools used for data collection included: 1) a wildlife data recording form specific to Phu Toei National Park, 2) geographic information system software (Google Earth), and 3) a semi-structured interview protocols used to gather information about wildlife from park officials and local experts. The study areas were divided according to forest types: mixed deciduous forest, dry dipterocarp forest, and pine forest. After data collection, the information was analyzed to summarize the biodiversity of wildlife across different forest areas in Phu Toei National Park, and the species were classified to examine levels of biodiversity. The findings revealed that the most diverse group of wildlife species in Phu Toei National Park was mammals, such as *Sus scrofa*, *Muntiacus muntjak*, *Talpa micruca*, and *Bos javanicus*. These were mostly found in mixed deciduous forests and bamboo forests. The second most diverse group was birds, particularly *Lophura leucomelanos*, which was mainly observed in mixed deciduous forest areas. The data of both groups were collected through field surveys, interviews with national park officers, and official records of the national park. The study was conducted over a period of two days. The results suggest that wildlife biodiversity in Phu Toei National Park is closely related to forest types, topography, climate conditions, and the availability of natural food sources within the park. From those findings species surveys and classification of animals found in national parks are of great importance for systematic planning for biodiversity conservation.

KEYWORDS:

Phu Toei National Park; Wildlife Biodiversity

Drought Area Assessment in The Thap Salao Buffer Zone Area for Wildlife Management

Kanlayanee Juakwoen¹, Andaman Chankhao^{1, 2}, Warong Suksavate¹ and Prateep Duengkae^{1,*}

¹Department Forest Biology, Faculty of Forestry, Kasetsart University, Bangkok 10900, Thailand

²Faculty of Environment and Resource Studies, Mahidol University, Nakhon Pathom 73170, Thailand

*Corresponding author, e-mail: prateepd@hotmail.com

ABSTRACT:

The Tap Salao buffer zone surrounds the Huai Kha Khaeng Wildlife Sanctuary and Tap Salao Reservoir. It is a conservation area rich in biodiversity and serves as a habitat for various wildlife species, such as banteng and wild elephants. This study aims to assess periods of drought within the buffer zone to provide supporting data for the planning and management of water resources for wildlife in the area. The analysis was conducted using remote sensing technology through the Google Earth Engine (GEE) platform, employing Sentinel-2 satellite imagery and the Normalized Difference Water Index (NDWI) as an indicator of surface moisture conditions. The study retrospectively analyzed NDWI values over a four-year period, from 2020 to 2023. The results revealed that the lowest average NDWI values—indicating reduced moisture or drought—consistently occurred in February, March, and April. Notably, in 2020, these values were particularly low, with NDWI readings of -0.097 in February, -0.133 in March, and -0.126 in April, significantly lower than those in other years. These findings indicate a recurring pattern of seasonal drought and offer valuable insight for identifying priority areas in water resource management for wildlife. Such information can support efforts to mitigate the impacts of climate change and reduce the risk of wildlife migrating beyond the buffer zone during critical dry periods.

KEYWORDS:

Google Earth Engine; Drought; NDWI; Sentinel-2; Management

Sustainable reforestation with Silva: innovations from the Miyawaki Method

Toshiko Kawashita^{1,*}

¹Non-Profit Corporation Silva, Japan

*Corresponding author, e-mail: kawashita.toshiko@silva.or.jp

ABSTRACT:

Silva is a non-profit organisation that carries out reforestation and greening activities using the native plants of the land, based on the philosophy of "sustainable green restoration for the next generation", succeeding and developing the Miyawaki Method, which was proposed and practised by Dr Miyawaki 50 years ago and recognised both in Japan and abroad.

[Advantages and trend of the Miyawaki Method]

Advantages: (i) in addition to functioning as a disaster prevention forest, it improves biodiversity and demonstrates field sustainability. (ii) Reduced running costs as the trees become self-sustaining and maintenance-free within 2-3 years of planting.

Trends: (i) Many cases of application in urban areas and reclaimed land, while mounding is required in mountainous areas due to the lack of soil. (ii) Mounding has been carried out in some cases due to misinterpretation, resulting in the following adverse effects.

- * Loss of diversity due to resetting of the existing landscape.
- * Incineration of large quantities of plant remains.
- * Ecological disturbance due to the delivery of mountain sand from far away.
- * Dichotomisation of vegetation due to the removal of steeply sloping degraded areas.
- * Massive carbon dioxide emissions before the tree-planting festival.
- * Antipathy of local people and misunderstanding of the "Miyawaki Method".

[Silva's challenge to solve the problem: "Ecosystem Function Restoration Vegetation Restoration"]

To overcome these challenges, Silva focused on "soil organisms" based on the Miyawaki Method and added natural materials to the existing soil to create a habitable environment for soil animals. This method is named "Ecosystem Function Restoration Type Vegetation Restoration".

Features: i) Reduced impact on existing landscapes and organisms. (ii) Improved stability and sustainability of biodiversity. (iii) Cost-cutting.

Benefits: i) Enables greening even in harsh mountain environments. (ii) Maintenance work time until self-support is achieved is reduced by half on average. (iii) Avoidance of incineration reduces CO₂ emissions by approximately 150 tons per year. (iv) Construction and maintenance costs are reduced by 30-70%. (v) Enables the acceptance of environmental experiences from land restoration all year round.

[Win-win relationship with local communities]

Silva's reforestation also contributes to stimulating the local economy and solving social problems.

Contribution to local communities: i) Support for farmers and people with disabilities through local production for local consumption. (ii) Avoidance of incineration through the reuse of cut branches and cut grass by local landscapers. (iii) Providing opportunities for public participation in environmental education.

KEYWORDS:

Reforestation, Miyawaki Method

Restoring Biodiversity based on Miyawaki Method for well-being: The Forestias Project, Samut Prakarn, Thailand

Nares Washirapantsaku^{1,2}, Surin Warachun¹, Nuda Boonchoo¹, Sirin Kaewlaierd¹ and Anong Chanamool¹

¹The Magnolia Quality Development Corporation Limited, Bangkok, Thailand

²Vice President of the Forestias Project

*Corresponding author, e-mail: nuda_bo@dtgo.com

ABSTRACT:

The Forestias Project is a town plan for the Enchanted Community District in the Forest. Ultimately, people can live with nature for their well-being. The project has an area of 63.68 ha on flat, saline clay soil. The pre-survey showed existing vegetation dominated by *Typha angustifolia*, plus other weeds and grasses. Since 2020, The Forest has applied the Miyawaki Method for increasing biodiversity and ecological rehabilitation. The results can be summarized as follows: The project planted 271,901 individual seedlings and an estimated 300 species (including native, ornamental, and fruit species) on an area of 77,360 sq. m. The growth rate was measured only once, in June 2025. The average total height was 10.97 m, and the average DBH was 15.86 cm. Animal biodiversity increased from 83 species at the pre-survey to 171 species at present. Particulate matter with a diameter less than 2.5 microns (PM 2.5) averaged 52 µg/m³, as opposed to 62 µg/m³ outside the project (the standard is 50 µg/m³). Approximately 150,342 persons visited the site during August 2020-December 2024. Conclusion and Suggestions Project experiences are as follows: The growth rate and development of planted trees were satisfactory. Some species provided fruits for birds, leading to increased biodiversity. Forests and green areas can reduce PM 2.5 particulate matter, regulate temperature, increase soil organisms, etc. The project also provided environmental education, which can be modified for people and land development businesses, etc.

KEYWORDS:

Restoring Biodiversity; Miyawaki Method; Well-being

Nature Literacy on Unwanted Animals from Miyawaki Forest: A Case Study of The Forestias Bangna Project, Thailand

Thanakorn Yodthongdee^{1,*}

¹MQDC Corporation, Thailand

*Corresponding author, e-mail: thanakorn_yo@dtgo.com

ABSTRACT:

The Forestias Bangna is a mixed-use development project covering 398 rai, featuring a 30-rai Miyawaki forest that serves as a green core connecting various residential areas under the concept "For All Well-Being." The use of the Miyawaki method in selecting and planting native tree species has led to the rapid establishment of a thriving ecosystem, including both plant and animal communities. Various animal species—mammals, birds, fish, amphibians, reptiles, arthropods, and insects—have settled in the area due to the abundance of vegetation, food sources, tranquil environment, and a sense of safety aligned with the project's core philosophy. A biodiversity survey conducted during the construction phase (2024–2025) by experts specializing in six animal groups—mammals, birds, fish, reptiles & amphibians, arthropods & insects, and ground-dwelling fauna—was carried out across all three seasons to ensure year-round coverage. The study recorded a total of 171 species. Among these, 72.5% were species with no major concerns for humans, 24.6% were categorized as unwanted animals, and 2.9% as dangerous species. "Unwanted animals" refers to species that tend to cause discomfort or concern among residents; however, through education about their ecological roles, residents can develop a better understanding and appreciation of their presence. In contrast, "dangerous animals" are species that may pose a threat to human safety and require specialized handling beyond interpretive approaches—such as relocation by trained personnel.

In this shared space between human and animal communities, environmental interpretation plays a key role in fostering understanding among residents and neighboring communities. It emphasizes the value of coexistence and helps people comprehend the natural behaviors of various species. The project highlights the ecological importance of so-called unwanted animals, which not only contribute to forest balance but also offer other ecosystem services. This knowledge is disseminated through three main interpretive activities:

1. **Nature interpretation for visitors** – Conducted by ecologists who educate guests on Miyawaki forest development, plant care, and wildlife diversity management.
2. **Training courses on snake handling** – Led by reptile specialists to equip interested individuals and green space personnel with safe and humane snake management skills.
3. **Environmental education activities in forest-based learning stations** – Designed by ecologists to utilize the Miyawaki forest as a living classroom, nurturing young minds with nature-based perspectives and conservation values.

These activities aim to cultivate positive attitudes through ecological knowledge, helping participants understand the rights of all living beings to inhabit and thrive in natural spaces. Ultimately, the Miyawaki forest becomes a platform for biodiversity and a bridge connecting people to nature. The researchers envision not only the physical growth of trees in the Miyawaki forest but also the germination of conservation-minded values in people's hearts—spreading throughout society to build a global culture that respects green spaces and all living creatures.

KEYWORDS:

Miyawaki Forest, The Forestias Bangna

Species Diversity Assessment along the Tenasserim Corridor in Western Thailand

Premchat Chuatrakun^{1,*}, Warissara Srisenphila¹, On-iriya Fugthaworn¹ and Warut Chaleekarn¹

¹World Wide Fund for Nature International: WWF, Phayathai, Bangkok 10400

*Corresponding author, e-mail: Pluempremchat@gmail.com

ABSTRACT:

The Tenasserim Corridor represents a critical ecological linkage in the Indo-Burma biodiversity hotspot, facilitating wildlife movement and genetic exchange across fragmented landscapes. This study focused on terrestrial vertebrate species diversity across three targeted areas within the Tenasserim Corridor: the Khao Krachome Royal Project Area (KKC), the Proposed Kaeng Som Maew Non-Hunting area (KSM), and the Phu Nam Ron border crossing (PNR). We used camera traps to evaluate species richness and species diversity index (H'), totaling 47 stations, 5,067 trap nights. The results indicate different levels of diversity among the three areas. KKC recorded the highest species richness (44 species and $H' = 3.03$, reflecting relatively entire habitat conditions and effective conservation management. KSM has species richness = 38 and $H' = 2.90$, likely due to its large forest cover and connectivity with adjacent protected areas, despite lacking formal protected status. In contrast, PNR an area influenced by human activities and cross-border development, showed the lowest species richness (20 species), and $H' = 2.00$. These findings highlight the importance of strengthening conservation measures in transitional areas such as PNR and formalizing protection status for key habitats like KSM to maintain ecological connectivity. Maintaining biodiversity in the Tenasserim corridor is crucial not only for national conservation goals but also for regional landscape-scale ecosystem resilience.

KEYWORDS:

Camera trap; Habitat connectivity; Species diversity; Tenasserim corridor; wildlife conservation

Bryological Diversity Assessment Along Man-Made Limestone Waterfall of Bunawan, Iligan city, Philippines

Villaflores, Maye^{1,*}

¹Department of Biological Sciences, College of Science and Mathematics, Mindanao State University-Iligan Institute of Technology, Andres Bonifacio Ave, Iligan City, 9200 Lanao del Norte, Philippines

*Corresponding author, e-mail: maye.villaflores@g.msuiit.edu.ph

ABSTRACT:

This study investigates the bryophyte communities found within Poldo Falls, Bunawan, Iligan City, Philippines. Poldo Falls is a man-made limestone waterfall which is also a tributary stream to Mandulog River and a water source of Barangay Bunawan. Bryophytes play crucial roles in these areas as they help in soil stabilization and water retention to prevent floods and soil erosion. A transect walk was employed along three established strata as bryophytes were collected along 600 meters of the study area. A total of 20 bryophyte species were recorded, namely 12 mosses and 8 liverworts. DNA barcoding and phylogeny has also been leveraged to aid in species identification of 6 species with the use of *rbcl*, a conserved chloroplast region. The contribution of various bryophyte species is significant for such environments for the long-term preservation of smaller habitats with multiple uses. This inference of new data for DNA sequencing and phylogenetic history would also greatly contribute to the scientific community. Moreover, the sequences obtained from this research is a new addition to public repositories for DNA sequences.

KEYWORDS:

Bryophytes; DNA barcoding; headwater; limestone; man-made; Poldo Falls

Halting the 6th Extinction in Thailand; Case Example on OECMs and Iconic Species

Chavalit Vidthayanon^{1,*}

¹SeubNakhasathien Foundation 140 Tiwanon Rd., Tambon Bang Krasor, Muang District, Nontaburi, 11000.

*Corresponding author, e-mail: chavaliv@hotmail.com

ABSTRACT:

Biodiversity loss is far beyond Planetary Boundary both in global and Thai contexts. The 30x30 target: is committing for effectively management for halting the 6th Extinction of species and ecosystems by 2030. The OECMs/Other Effective Area-based Conservation Measures are strongly mobilized for all ecosystems, which can be indicated by the occurrences of Iconic Species. These species both fauna and flora serve as ecosystem health indicators and play a significant role in community livelihoods, food security, eco-tourism, and recreation. Iconic species are selected by several criteria including IUCN and Thai Red List of threatened species, flagship species which drive conservation awareness and efforts, those vital for local ecosystem services, economic or cultural significance, bio-indicators including important migratory and endemic species. Recent study, at least 10 threatened ecosystems from 120 sites nationwide are OECMs potential and hosting over 200 Iconic species, of 173 fauna and 29 flora; including; 58 Endangered-Critically Endangered species, xxxx economic important, 29 endemic fauna and 17 endemic plants and 22 migratory species. Within, this ecosystem list, Freshwater wetlands are the most critical threatened, following by Sandy shore vegetations and Karst-limestone habitats. Two proposed pilot sites are: Tha Rua-Pak Pli floodplain ecosystem, Nakhonayok Province, where host nearly 100 fishes and only remained population of the 1 of 100 Most Critical Endangered Species: Sompong's rasbora *Trigonostigma sompongsi*. And Chana coastal ecosystems, Songkhla, where support local economic with over 100 economic marine species and critical habitats of Red listed species; i.e. Green sea turtle, Whale shark, Indo-Pacific humpback dolphin etc. All iconic species were enlisted for OECMs self-Evaluation form and published inr handbook with details of 20 important species and checklist, by UNDP-GBF-EAS and ONEP.

KEYWORDS:

OECMs, Iconic species, ecosystem extinction, Planetary Boundary, Thailand

Assessment of the carrying capacity for large herbivores in cultivated ruzi grassland of Kui Buri National Park, Thailand

Jedsada Noowong^{1,*}, Warong Suksavate¹, Visanuwit Thong-on², Nopporn Akkamanee³, Attapong Pao-on³, Kornorn Srikulnath^{1,4} and Prateep Duengkae^{1,4,*}

¹Special Research Unit for Wildlife Genomics (SRUWG), Department of Forest Biology, Faculty of Forestry, Kasetsart University. 50 Phahonyothin Road, Chatuchak District, Bangkok 10900, Thailand.

²World Wide Fund for Nature International-Thailand (WWF-Thailand), 9 Phisit Building, Pradiphat Road, Phayathai District, Bangkok 10400, Thailand.

³Department of National Parks, Wildlife and Plants Conservation. 61 Phaholyothin Road, Chatuchak District, Bangkok 10900, Thailand.

⁴Animal Genomics and Bioresource Research Unit (AGB Research Unit), Faculty of Science, Kasetsart University. 50 Phahonyothin Road, Chatuchak District, Bangkok 10900, Thailand.

*Corresponding author, e-mail: fforptd@ku.ac.th

ABSTRACT:

The cultivated ruzi grassland (*Brachiaria ruziziensis*) in Kui Buri National Park, Thailand, were established based on the premise that limited availability of natural forage within forested areas contributes to crop raiding by elephants and other large herbivores. Assessing the carrying capacity of this grassland is therefore crucial for effective wildlife management. This study evaluated the carrying capacity for large herbivores by quantifying above-ground biomass (AGB) in 188 plots (3,024 sub-plots) surveyed between September 2023 and October 2024. Results show that grassland productivity peaked from August to November ($>100 \text{ g/m}^2$), with the highest average biomass recorded in September ($114.29 \pm 3.61 \text{ SE g/m}^2$). In contrast, the lowest productivity was observed from January to May ($<40 \text{ g/m}^2$), reaching a minimum in April ($10.63 \pm 0.62 \text{ SE g/m}^2$). Carrying capacity analysis revealed that the grassland could support the largest populations in September with estimated at 73–164 elephants and 143–325 gaurs and the smallest in April, with only 6–13 elephants and 13–32 gaurs. These findings indicate that the grassland can support large herbivores during the late wet season but have limited capacity in the dry season. To mitigate crop raiding, we recommend developing strategies to maintain grassland productivity during the dry season and attract wildlife to the grassland year-round.

KEYWORDS:

Biomass, Carrying capacity, Cultivated, Grassland, Ruzi grass

The Role of Forest Communities as Other Effective Area-Based Conservation Measures (OECMs): Khoanoijomsawan Community Forest Case study, in Wihan Daeng District, Saraburi Province

Chayanee Raknim¹, Warong Suksavate¹, Chattrapas Pongcharoen¹, Kornson Srikulnath², Yuwadee Ponpituk³, Ronnakorn Triraganon⁴ and Prateep Duengkae^{1,2,*}

¹Department of Forest Biology, Faculty of Forestry, Kasetsart University, 50 Ngamwongwan, Chatuchak, Bangkok 10900, Thailand

²Animal Genomics and Bioresource Research Unit (AGB Research Unit), Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

³Department of Forestry, Maejo University – Phrae Campus, Chalermphrakiat, Phrae 54140, Thailand

⁴RECOFTC – The Center for People and Forests, Kasetsart University, 50 Ngamwongwan, Chatuchak, Bangkok 10900, Thailand

*Corresponding author, e-mail: prateepd@hotmail.com

ABSTRACT:

Khoanoijomsawan Community Forest, located in Wihan Daeng District, Saraburi Province, covers an area of 8.8 hectares and is characterized by limestone hills. A vegetation survey of 2,000 trees with a diameter at breast height (DBH) of at least 10 centimetres recorded 19 families, 46 genera, and 50 species. The Shannon–Wiener diversity index (H') for the vegetation was calculated to be 2.47. Among the recorded tree species, one was classified as Critically Endangered (CR), two as Endangered (EN), and one as Near Threatened (NT). A wildlife diversity survey identified a total of 159 species: 12 mammals, 112 birds, 20 reptiles, and 15 amphibians. The Shannon–Wiener diversity indices (H') for each group were 1.78, 3.82, 2.08, and 2.20, respectively. Among these wildlife species, one was classified as Endangered (EN), two as Vulnerable (VU), and four as Near Threatened (NT), based on IUCN criteria. These findings highlight the ecological richness and conservation significance of the area, providing a valuable baseline for future biodiversity monitoring and community-based forest management, particularly in areas located outside formally designated protected areas. Moreover, it can effectively complement existing protected area networks. This aligns with the concept of Other Effective Conservation Measures (OECMs), which emphasize the value of areas that, although not officially designated as protected under legal frameworks, still maintain essential ecological functions, biodiversity values, and sustainable uses. Khoanoijomsawan Community Forest therefore represents a small-scale area with strong potential for recognition as an OECMs site and can meaningfully contribute to both national and global conservation targets in the long term.

KEYWORDS:

Community Forest, OECMs; Species Diversity; Conservation, Saraburi Province

Miyawaki Forests Empower Youth to Reverse Climate Change

Neelam Patil^{1,*}

¹Science Department, Science Teacher, August Schilling Elementary School, San Francisco Bay Area, California, United States.

*Corresponding author, e-mail: neelam.patil@iahv.org

ABSTRACT:

In the battle against climate change, one of the most potent weapons we have is not just a scientific breakthrough or a policy change but the passion and dedication of our youth. In this crucible of rising temperatures, Miyawaki forests have emerged as a beacon of hope, not only for their environmental benefits but also as a tangible way for our youth to take hands-on action to stop climate change.

"My name is Aviva, and I am in fifth grade. I think Miyawaki Forests are special because they help the environment. Climate change is a big problem, and the more Miyawaki Forests we plant, the better," shares Aviva, a young environmentalist who helped plant the youngest Miyawaki forest in Berkeley at Berkeley TEchnology Academy.

Hannah Lee, another fifth-grader, passionately declares, "Climate change is a huge problem in America, and Miyawaki forests change that. They make the air quality better and peace out!" Hannah's words reflect the determination of young activists who believe in the transformative power of Miyawaki forests to combat climate change and create a brighter future.

In November, 2021, Ms. Neelam Patil and her students planted four schoolyard Miyawaki forests in Berkeley, California. In the process, she empowered thousands of children to participate in a hands-on climate change solution. Four years later, what was historically a barren water guzzling lawn is now a lush, thriving ecosystem with high leaf density, soil moisture levels, all while using a fraction of the water! Learn more about this weapon against climate change and how it is quickly transforming the lives of many and the landscape around

KEYWORDS:

Youth empowerment, leadership development, biodiversity, urban planning

TheOtherForest: a nature-based tool for ecological and social regeneration

Adib Dada^{1,*}, Zouhair Challah¹ and Mohammad Kabakibi¹

¹Forests Department, theOtherDada, Beirut, Lebanon

*Corresponding author, e-mail: adib@theotherdada.com

ABSTRACT:

Urban degradation, biodiversity loss, and climate vulnerability are pressing, interconnected challenges across the Middle East and North Africa. theOtherForest, a nature-based initiative rooted in regenerative design and biomimicry, addresses these challenges by restoring biodiversity through native afforestation, ecological literacy, and participatory community models. Our work focuses on transforming degraded urban landscapes into dense, biodiverse forests using the Miyawaki method, a proven approach for accelerating ecosystem recovery. Since 2019, we have planted over 7,000 native trees spanning 3400 m² along Beirut River's sewage-filled, concrete riverbanks, with a survival rate of 74%, while actively engaging over 1,600 community members. Following the 2020 Beirut port explosion, we launched the "Back to Play" initiative, converting damaged schoolyards into living forests co-created with students, teachers, and staff. These interventions demonstrate the power of integrating ecological restoration with social healing and education. By reclaiming urban dead zones through afforestation and replacing high-maintenance landscapes with native habitats, we are restoring ecological function, improving soil health, and fostering biodiversity resilience. Our model exemplifies how grassroots action, biomimicry, and policy-aligned urban regeneration can work in concert to rehabilitate ecosystems and empower communities in the face of environmental crises, and giving hope in times of war.

KEYWORDS:

Afforestation, Biodiversity, Community engagement, Ecological literacy, Ecosystem restoration

Quantifying the quality: Measuring what matters, when restoring the lost natural environment through forests. A biodiversity & people centric approach, including humans

Shubhendu Sharma^{1,*}

¹Afforestt Institute, Founder, Kashipur, 244713, India

*Corresponding author, e-mail: shubz@afforestt.com

ABSTRACT:

What Gets Measured, Gets Improved. Globally, focus on atmospheric carbon sequestration has resulted in green yet degraded environments that lack biodiversity. Presenting a new, biodiversity centric approach, that is focused on upgraded quality of the environment, thus quality of life, for all the living beings. Proposing a paradigm shift in measuring success of any afforestation/environmental rehabilitation project. The approach of balancing the human impact on environment by capturing atmospheric carbon has created vast expanses of green covers with little or no environmental value. The approach of balancing the human impact on environment by capturing atmospheric carbon has created vast expanses of green covers with little or no environmental value. While the urban pollution levels increase, compensatory afforestation and landscaping efforts to balance this degrading, are mostly focused on carbon-sequestration of atmospheric carbon and beautification. New types of pollutants like, noise, light and other electro magnetic frequencies keeps adding to the already concentrated flux of overly industrialised and concretised urban human habitat. While the urban pollution levels increase, compensatory afforestation and landscaping efforts to balance this degrading, are mostly focused on carbon-sequestration of atmospheric carbon and beautification. New types of pollutants like, noise, light and other electro magnetic frequencies keeps adding to the already concentrated flux of overly industrialised and concretised urban human habitat. Environmental factors contributing to liveability of the impacted environment are often ignored. This carbon focused approach has resulted in continuous degradation of urban environment and quality-of-life in cities. At Afforestt, we have been measuring the qualitative impact of the forests planted in city-centres using the Miyawaki Method. Moving beyond conventional metrics such as the total carbon sequestered and the number of trees planted, our research focuses on a comprehensive evaluation of the ecological and physiological benefits of these forests. Impact on increase in bio-diversity, soil microbiology, air quality index, noise levels, EMF radiation levels, moisture levels are measured. We introduce a comprehensive set of Key Performance Indicators (KPIs) designed to assess the effectiveness of urban afforestation projects from a life-centric perspective, including flora, fauna and humans. The focus is on urban dwellers directly affected by these forests, this includes birds, bees, butterflies, insects and micro-organisms. Prioritising health and quality of life in KPIs selection. Demanding a paradigm shift in what's considered a successful afforestation project.

KEYWORDS:

Soil microbiology; Air Quality Index; EMF radiation levels; Key Performance Indicators (KPIs)

Monitoring Terrestrial Fauna to Assess Ecological Restoration Progress across a Degraded Forest in Nueva Ecija, Philippines

Neil Jun S. Lobite^{1,*}, Nelson M. Pampolina¹, Ramil S. Rodriguez², Romnick L. Pascua², Jomar C. Guzman¹ and Marlo D. Mendoza³

¹Department of Forest Biological Sciences, College of Forestry and Natural Resources, University of the Philippines Los Baños, Laguna, Philippines

²College of Forestry, Environmental and Resource Management, Nueva Vizcaya State University, Bayombong 3700, Nueva Vizcaya, Philippines

³Department of Social Forestry and Forest Governance, College of Forestry and Natural Resources, University of the Philippines Los Baños, Laguna, Philippines

*Corresponding author, e-mail: nslobite@up.edu.ph

ABSTRACT:

Monitoring terrestrial fauna provides valuable insights into the progress of ecological restoration in degraded forest ecosystems. This study presents the results of terrestrial faunal monitoring conducted in the 930-hectare Lucio Tan Legacy Forest in Carranglan, Nueva Ecija, Philippines—an area previously degraded and undergoing forest restoration. The 2023 assessment recorded 56 species of terrestrial vertebrates, comprising 37 bird species, 11 herpetofauna (7 reptiles and 4 amphibians), and 8 mammals (2 volant and 6 non-volant), representing a substantial increase from the 14 species documented during the baseline survey in 2017. Several endemic species of notable conservation importance were recorded, including the Philippine Serpent Eagle (*Spilornis holospilus*), Tarictic Hornbill (*Penelopides manillae*), and the Greater musky fruit bat (*Ptenochirus jagori*), suggesting improved habitat conditions. The increase in species richness—including newly recorded birds, herpetofauna, and mammals—along with the presence of forest-dependent and ecologically significant taxa, highlights measurable progress in biodiversity recovery. These outcomes are likely driven by enhanced habitat structure, increased vegetation complexity, and sustained ecological rehabilitation efforts implemented across the site. Overall, the results reinforce the essential role of long-term faunal monitoring in evaluating restoration success and informing adaptive management in tropical forest ecosystems. These findings provide a scientific basis for prioritizing habitat enhancement, protection measures, and sustained biodiversity monitoring as part of an integrated forest management strategy.

KEYWORDS:

Biodiversity monitoring, Ecological Restoration, Faunal monitoring, Forest Recovery, Reforestation monitoring

Changing the tea industry by putting biodiversity in focus

Alexey Reshchikov^{1,*}, Anders Engvall² and Kenneth Rimdahl²

¹ Insect Biodiversity and Biogeography Laboratory, The University of Hong Kong, Hong Kong SAR

² Monsoon Tea, Chiang Mai 50000, Thailand

*Corresponding author, e-mail: alexeyre@hku.hk

ABSTRACT:

Biodiversity is essential for human being, and we should combine efforts to understand and slow down its decline. The loss driven by agricultural expansion throughout recent years is unprecedented. Notwithstanding, biodiversity is actively encouraged in past and nowadays through some farming practices. The Monsoon Tea is a Thai company introduced Forest Friendly Tea concept. After years of collaboration on biodiversity research with the Tea Fauna Project (funded by the first author), the Monsoon Tea developed a technological system for standardised biodiversity measurement to optimize the forest farming of tea in the mountains of Northern Thailand. The biodiversity data obtained with the help from the tea growing communities allows to measure and distribute generated income from tea sales that sustains these communities and funds our biodiversity studies. Thus, this business method serves for conservation and environmental rehabilitation. The company developed a traceability system for the biodiversity impact from the forest tea farming. This system uses modern technologies including the GIS and the AI to revive traditional forest farming. Bio-acoustic sensors are installed to collect sound profiles from the forest where the tea is grown. After soundscape analysis and species identification, biodiversity scores are assigned to each land plot. That further is used to reward farmers for the biodiversity services they provide and for informing consumers about the positive impact of their tea purchasing. We produce accurate geolocated planting plans for biodiverse afforestation for Forest Friendly Farming for farmers that wish to stop to use conventional agriculture methods. Forest Friendly Farming is exactly what it sounds like. Agricultural products grown and harvested with a sustainable method while protecting the forest. Except methods mentioned above we conduct biodiversity surveys with different sampling techniques e.g. Malaise trapping, pan trapping, Winkler method, to study arthropod communities associated with tea plants, from forest environments to conventional tea plantations. The sampling that already done is including material from 13 Malaise traps deployed at 10 localities in China and Thailand for eight years. The resulting samples are a great resource of data for entomologists and ecologists around the World. The core of the material obtained is the Darwin Wasps (Hymenoptera, Ichneumonidae) collection. These insects belong to very unstudied, superdiverse family. There are 20.000 species of the global fauna known to date, with real diversity estimated as 100.000 species. Being parasitoids, the Darwin Wasps are associated virtually with most of insects that makes them important bioindicators. We believe that further studies of the Darwin Wasps and other groups of organisms around the tea environments will allow us better understanding conservation and rehabilitation aspects of Forest Friendly Farming.

KEYWORDS:

Biodiversity; Darwin wasps; Hymenoptera; forest friendly tea; sustainable agriculture

Biophilic Imperative: A Paradigm Shift Towards Harmonizing Our Environment and Fostering Biodiversity

Ariya Aruninta^{1,*}

¹Department of Landscape Architecture, Chulalongkorn University, Healthy Landscape and Biophilic Planning Research Unit (HeaL-Bip RU), Bangkok, 10900, Thailand

*Corresponding author, e-mail: aariya@chula.ac.th

ABSTRACT:

In an age characterized by extensive Anthropogenic challenges, Biophilic development presents a powerful framework for creating sustainable and harmonious environments. This presentation delves into this paradigm shift, emphasizing the integration of natural elements to enhance both ecological integrity and human well-being. We will explore the ontological dimensions of biophilia hypothesis, illustrating how reconnecting people with nature fosters a profound understanding of our interconnectedness with ecosystems, thereby nurturing biodiversity. The role of Nature-Based Solutions (NbS) as essential strategies within biophilic development, it is not only addressing environmental issues such as climate resilience and biodiversity loss but also contribute to social equity by promoting inclusive communities. We investigate how biophilic development and NbS can serve as catalysts for transformative change, guiding us toward a sustainable future for both humanity and the Earth. Final takeaways include the need for a paradigm shift towards biophilic development, a deeper understanding of urban ontological landscapes, and innovative approaches in landscape planning and design.

KEYWORDS:

Landscape Architecture; Biophilia hypothesis; Biophilic development; Paradigm shift; Nature-Based Solution

Heterogeneity of Lagtaw River, Columbio Sultan Kudarat, Philippines

Norjana A. Macalintangui^{1,*} and Annie D. Francisco^{2,*}

¹Student of Bachelor of Science in Biology, Sultan Kudarat State University-Tacurong City, Sultan Kudarat, 9800 Philippines.

²Faculty of Department of Biology, Sultan Kudarat State University-Tacurong City, Sultan Kudarat, 9800 Philippines.

*Corresponding author, e-mail: norjanamacalintangui@sksu.edu.ph; anniefrancisco@sksu.edu.ph

ABSTRACT:

Rivers are dynamic ecosystems that play a crucial role in biodiversity conservation, nutrient cycling, and ecosystem services. Despite their ecological importance, many rivers remain understudied, particularly in terms of their spatial heterogeneity and its influence on macrofauna diversity. This study investigates the heterogeneity of the Lagtaw River in Barangay Datalblao, Columbio, Sultan Kudarat, Philippines, focusing on its physicochemical parameters and macrofauna diversity across three distinct physical features: riffles, runs, and pools. The research addresses critical gap in understanding the ecological dynamics of the Lagtaw River, vital for effective conservation and sustainable management practices. Key findings reveal significant spatial heterogeneity in physicochemical attributes and diverse macrofauna communities across riffles, runs, and pools. Riffles were characterized by coarse substrates, fast water velocities, shallow depth, low turbidity to slightly murky and favorable temperature and pH levels, supporting 14 different species, where *Pycnopsyche sp.* dominates the area; runs have moderate water velocities, moderate water depth, and low turbidity to slightly murky, optimal pH level and temperature and a substrate composed of gravels and sand inhabited by 19 species and *Rhagovelia sp.* has the greatest number.; pools featured substrate with a mixture of gravels and sand, low turbidity to slightly murky, slower water velocities, deeper depths, and stable pH and temperature conditions, hosting 17 species, *Aquarius remigis* is the most dominant. There are total of 19 different species found in the area of the study, *Hydropsychidae sp.* has the most number among them. These results underscore the importance of physical diversity in fostering varied habitats and sustaining biodiversity. The findings highlight the need for targeted conservation strategies to mitigate human impacts on the Lagtaw River.

KEYWORDS:

Heterogeneity, Riffles, Runs, Pools, River

Landscape Architecture Design for Biodiversity

Tawatchai Kobkaikit^{1,*} and Angsana Boonyobhas¹

¹TK STUDIO, Phaholyothin Rd., Phayathai, Bangkok, 10400, Thailand

*Corresponding author, e-mail: passaporn.s@tkstudio.co.th

ABSTRACT:

Biodiversity is essential to human well-being, as our survival depends on the complex web of life that exists within ecosystems. The greater the complexity of this network, the more sustainable it becomes. As landscape architects, we engage with nature in a unique manner, striving to minimize disruption while addressing the practical needs of safety and accessibility for users. However, even with careful consideration, site grading and infrastructure installation inevitably alter the existing landscape to some degree. Following this, planting strategies are implemented to restore and reintroduce elements of nature to the site.

The approach to planting design, however, varies among landscape architects, influenced by a range of factors. While it is standard practice to incorporate plantings along circulation paths and hardscapes, the creation of biodiversity within landscape design is less commonly emphasized. To successfully integrate biodiversity, it must be considered from the early stages of design. While a diverse array of plants within a similar community may offer some ecological benefits, a truly sustainable landscape requires a variety of plant communities. These varied plant communities are influenced by microclimates—distinct localized conditions of humidity, sunlight, and airflow—that support different plant species.

Landscape features such as softscapes, hardscapes, and water elements are typically included for aesthetic or infrastructural reasons, yet they also present valuable opportunities to create diverse microclimates that enhance biodiversity. By leveraging these features effectively, landscape architects can design environments that not only foster ecological richness but also provide varied atmospheres conducive to human well-being. These microclimates encourage individuals to engage with their surroundings in ways that promote healthy, enjoyable living.

At TK Studio, a small landscape architecture firm, we are deeply committed to the idea that sustainability in landscape projects is as important as aesthetics and infrastructure. We actively seek to incorporate microclimates and diverse plant communities into our designs wherever possible. Each of our projects serves as an experimental platform, guiding our understanding of how landscape architecture can foster harmony with nature and contribute to the creation of sustainable, biodiverse environments.

KEYWORDS:

Biodiversity; Landscape Architecture Design; Micro Climate; Sustainable Design

The Harmony in Diversity (HiD) Effect: A Long-term Sustainable Solution for Ecosystem Restoration in Mining Operations

Ma. Donna Del Moro^{1,*}, Nericel Daulayan¹, Alexis Lapresca¹, Sheila Bimmoy¹ and Paul Cuadra²

¹Environment and Social Responsibility Department, OceanaGold (Philippines) Inc., Didipio, Kasibu, Nueva Vizcaya, 3703

²Forest Ecosystem Research Division, Ecosystems Research and Development Bureau, College Laguna, Philippines

*Corresponding author, e-mail: madonna.delmoro@oceanagold.com

ABSTRACT:

This paper examines the new ecosystem approach implemented at the OceanaGold (Philippines) Inc., Didipio Operations, with a specific focus on mine rehabilitation method enhancement. Spanning 975 hectares, the Didipio Mine is currently operating in a compacted design of its Partial Declaration of Mining Feasibility (PDMF). Ecosystem restoration in the mining industry is now a significant challenge. In previous years, the company has conducted mine rehabilitation in a conventional manner, such as grassing and planting of trees. However, considering the goal of bringing back the land to its original form, the method does not suffice in restoring the ecosystem. Our research employs a combination of four (4) restoration methods across different countries. Utilizing the new Finger 9 mine rehabilitation area with strategically placed 1.5m² plots to establish a new ecosystem restoration approach considering components of potential natural vegetation, abundance planting, water retention pits, and microorganisms. Initial results underscore the rapid growth among the planted species of Philippine Native Trees pioneering species, canopy species, and understorey species through inspection chart mapping and remote sensing. The new ecosystem restoration stands out for the prevalence of its symbiotic relationship among different plants, insects, and microorganisms. Hence, the Harmony in Diversity (HiD Effect). Notably, more than 95% of the trial area in the Finger 9 new mine rehabilitation area has high vegetative cover wherein some of the identified species are not planted or introduced in the area. To bolster ecosystem restoration efforts, we introduce a geodatabase and interactive map storing essential baseline data accessible through ArcGIS software, and enhanced monitoring of plant health through 3D modelling and remote sensing. This research endeavours to contribute significantly to establishing proper mine rehabilitation with respect to ecosystem restoration of the mining industry in the Philippines and provide valuable insights into sustainable management and conservation practices.

KEYWORDS:

Mine Rehabilitation; Ecosystem Restoration; Potential Natural Vegetation; Aerial Monitoring; Inspection Chart Mapping.

BiodeVRestorer: Immersive VR experience for biodiversity restoration

Panyavut Aumpuchin^{1,*}, Usawadee Chaiprom¹, Anuttara Nathalang¹, Sissades Tongsim¹, Nitcha Chamroensaksri¹, Ruetai Chongsrid², Supanee Sitthipairojsakul², Kanogpun Selar², Namchai Chewawiwat², Rakchat Wetiwutajarn², Kulpong Onmanee² and Varunyu Fuvattanasilp³

¹National Center of Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), Phaholyothin Rd., Khlong Luang, Pathum Thani, 12120, Thailand

²Central Office (CO), National Science and Technology Development Agency (NSTDA), Phaholyothin Rd., Khlong Luang, Pathum Thani, 12120, Thailand

³National Electronics and Computer Technology Center (NECTEC), National Science and Technology Development Agency (NSTDA), Phaholyothin Rd., Khlong Luang, Pathum Thani, 12120, Thailand

*Corresponding author, e-mail: Panyavut.aum@biotec.or.th

ABSTRACT:

BiodeVRestorer is an environmental education curriculum that integrated traditional lectures with augmented reality (AR) and virtual reality (VR) technologies to provide an immersive learning experience and raise awareness on the environmental issues. The curriculum targets high school students and focuses on biodiversity loss and forest restoration related contents. All teaching materials are created based on scientific data to ensure accuracy and reliability in the information conveyed to students. The AR component used the Zappar platform to simulate the Rapid Site Assessment (RSA) method, which assesses forest quality before restoration. Students explore forests and collect seeds in the VR section, which was created with Unity and the GAMA platform. This program allows students to understand the environmental consequences of their actions and push towards restoration goals. Following implementation with 13 schools and 104 students, the surveys indicated that students showed an increasing understanding of biodiversity issues and long-term memory of the content. Teachers also noted increased classroom attention and involvement. This curriculum is a prototype for AR and VR-integrated curriculum design, with the possibility for future expansion to include a wider range of educational content.

KEYWORDS:

Biodiversity loss; Forest restoration; Virtual reality; Augmented reality; Curriculum design

A Study on the Efficiency of Sodium Alginate-Based Hydrogel using Coffee Grounds activated carbon and *Terminalia catappa* Leaf Extract for Reducing Microplastics in Water

Phatthranit Kanyakulwararat¹, Schananchida Thananapattanapongs^{1,*} and Sarisa Srisakuna¹

¹Kasetsart University Laboratory School Center for Educational Research and Development.

*Corresponding author, e-mail: plubplueng2009@gmail.com

ABSTRACT:

Microplastics in water sources are a form of environmental pollution that urgently needs to be addressed due to their harmful effects on ecosystems and human health. However, environmentally friendly methods for removing microplastics remain a challenge. This study aimed to formulate and evaluate the efficiency of sodium alginate-based hydrogel, which is commonly used in food products, for removing microplastics from water sources at Kasetsart University. The hydrogel was prepared using coffee grounds, activated carbon, and *Terminalia catappa* leaf extract in different ratios: Formula 1 with a ratio of 1:1:1, Formula 2 with a ratio of 2:1:1, and Formula 3 with a ratio of 1:2:1. In contrast, the hydrogel without any additives served as the control. These hydrogels were then immersed in water samples collected from the school's water sources and analyzed using FT-IR spectroscopy to identify the types of microplastics and assess the hydrogel's adsorption efficiency. The results showed that the predominant microplastics found in the water sources were Polypropylene (PP), Acrylonitrile Butadiene Styrene (ABS), Polybutylene Terephthalate (PBT), and Polyurethane (PU). Among the various hydrogel formulations, formula 3 demonstrated the highest efficiency in reducing microplastics, achieving a 43.75% reduction. This was followed by formula 1 at 34.38% and formula 2 at 31.25%. Meanwhile, the control group exhibited a removal efficiency of 28.12%. The research result indicates that sodium alginate hydrogel modified with natural materials can effectively enhance microplastic adsorption efficiency and represents a strong potential for developing innovative solutions to address water pollution. While the hydrogel effectively removes microplastics, considering the full life cycle of both the hydrogel and the captured particles is essential for true sustainability. In the future, disposal methods such as incineration, microbial degradation, or secured landfilling will be considered.

KEYWORDS:

Microplastics; Sodium Alginate Hydrogel; Coffee Grounds; Activated Carbon; *Terminalia catappa* Leaf

Removal of Antibiotics and Ionic Dyes Using Magnetic CuFe-LDH/CuFe-LDO-Activated Carbon Composites

Krongkhawun Chaipayat¹, Pruettiphong Phiromrak¹ and Sonchai Intachai^{2,*}

¹Paphayompittayakom School (SCiUS-Thaksin University), Phatthalung, 93210, Thailand

²Innovative Material Chemistry for Environment Center, Department of Chemistry, Faculty of Science and Digital Innovation, Thaksin University, Phatthalung campus, Phatthalung, 93210, Thailand

*Corresponding author email: sonchai.i@tsu.ac.th

ABSTRACT:

Water pollution is a serious issue worldwide, exacerbated by human actions, especially the illegal discharge of chemically polluted wastewater from industries like textile dyeing, hospitals, agriculture, and livestock farms. Although numerous technologies exist for effectively treating polluted water, the practical elimination of both cationic and anionic contaminants along with easy water reuse remains challenging. This study focused on creating efficient magnetic composites by combining CuFe-layered double hydroxide (CuFe-LDH) or CuFe-layered double oxide (CuFe-LDO) with activated carbon (AC) derived from djerkol bean fruit (*Archidendron jiringa*), sala langka (*Couroupita guianensis* Abul.), and blue rush fiber (*Lepironia articulata* (Retz.) Domin) using an eco-friendly solid-solid reaction. The composite materials were characterized using XRD, FT-IR, SEM, EDX, zeta potential, VSM, and BET methods, revealing that CuFe-LDH (or CuFe-LDO) exhibited CuO, FeOOH, and Fe₂O₃ deposition, and that AC combined well via electrostatic and magnetic forces, yielding a significant surface area with both positively (from LDH or LDO) and negatively charged (from AC) active sites. Utilizing 0.02 g of the composite adsorbents showed high efficiency in removing malachite green (52-75%), methylene blue (62-82%), aniline blue (67-80%), bieberich scarlet (59-73%), amoxicillin (47-65%), and norfloxacin (53-71%) from water (100 ppm, 100 mL), following a pseudo-second order reaction with monolayer adsorption. After reaching equilibrium, 0.005 g of the composite photocatalysts was able to degrade organic matter in water under visible light over 240 minutes, including organic dyes such as methylene blue and aniline blue. The photocatalytic activity was driven by d-d electronic transitions (from CuFe-LDH) and semiconductor particles of CuO, FeOOH, and Fe₂O₃. These composites remained reusable for up to five cycles via simple magnetic separation, preserving their structural and magnetic integrity. This study offers a potential versatile solution for adsorbing and photocatalyzing the removal of both cationic and anionic dyes and zwitterionic antibiotics from water.

KEYWORDS:

Activated carbon, Adsorption, Antibiotic, CuFe-layer double hydroxide, Dyes, Photocatalysis

SESSION 5

BIODIVERSITY AND CULTURAL CONSERVATION





How can the Flora of Thailand contribute to Nature Conservation?

Peter C. van Welzen^{1,*}

¹Research Group Tropical Botany, Naturalis Biodiversity Center, P.O. Box 9517, 2300 RA Leiden, The Netherlands

*Corresponding author, e-mail: peter.vanwelzen@naturalis.nl

ABSTRACT:

The Flora of Thailand project is an international project that aims to describe all 12,000 indigenous Thai plant species (all with vessels). Many editions, treating one to several families, have been published and the project aims to finish in 2026. In the beginning of the project, start in 1967, mainly foreign scientists contributed, nowadays, it are mainly Thai researchers and students. The Flora is the best instrument to identify Thai plants. However, it is too scientific for most users. A start has been made to popularize the flora by creating an online tool. The end product might be telephone apps that can identify the plant after a photograph has been taken, similar to or using apps like Pl@ntNet and iNaturalist. Why is this important? Due to land use and a changing climate already 363 species are vulnerable, 142 endangered, and one extinct in the wild. It becomes more and more apparent that a monitor system should be initiated. In the Netherlands, a group of enthusiastic amateurs is yearly making inventories of plants, in 5 by 5 km squares but, for targeted species, also 1 by 1 km squares. The apps help to identify the plants. With this monitor grid it becomes easier to see changes in species presences and to find explanations for the changes. The results can and should be used on national political levels to preserve the Thai biodiversity.

KEYWORDS:

Distribution changes; flora; identification; identification apps; monitoring; plant descriptions.



Bees & Biodiversity: A Symbiotic Relationship for Sustainable Futures

Chen Lihong^{1,*}, Siriwat Wongsiri², and Superbear³

¹Asian Apicultural Association No.12, South Street of Zhongguancun, Haidian District, Beijing, 100081, China

²Phayathai Road, Pathumwan, Bangkok 10330 Thailand

³The University of British Columbia, Vancouver, Canada

*Corresponding author, email: clhb@hotmail.com

ABSTRACT:

Bees, as paramount pollinators, are indispensable keystone species within most terrestrial ecosystems. Their activity is fundamentally linked to the maintenance and promotion of biological diversity. There are more than 20,000 different species of wild bees exist in the world. Bees play a critically underappreciated role in maintaining global biodiversity and ensuring the stability of ecosystems. As paramount pollinators, they facilitate the sexual reproduction of a vast majority of flowering plants, including numerous crops vital for human consumption. There are over 75% of the world's leading food crops rely to pollination, and the bees being the primary contributors. This ecosystem service is indispensable for genetic diversity within plant communities, which in turn supports a wide array of fauna. However, the decline of bee populations, driven by habitat loss, pesticide use, pathogens, and climate change, poses a severe threat not only to agricultural productivity but also to the structure and resilience of natural habitats. This paper examines the integral link between bee pollination and biodiversity, arguing that the conservation of bee species is not merely an agricultural concern but a fundamental prerequisite for the preservation of global biological diversity and the health of ecosystems worldwide.

KEYWORDS:

Pollination, Biodiversity, Ecosystem, Conservation, Keystone Species, Food Security

ORAL PRESENTATION

SESSION 5



Biodiversity through a Child's Eyes: Learning with Culture, Environment, and Curiosity

Ruetai Chongsrid^{1,*} and Kanogpun Selar¹

¹National Science and Technology Development Agency (NSTDA), 111 Thailand Science Park, Phahonyothin Rd., Khlong Nueng, Khlong Luang, Pathum Thani, 12120, Thailand

*Corresponding author, e-mail: reutai@nstda.or.th

ABSTRACT:

Biodiversity can be experienced through the lens of a child's natural curiosity and everyday life. In Thailand's "Biodiversity in My Community" program, an initiative under The Little Scientists House Project, over 200 schools empowered students to observe their surroundings, ask meaningful questions, and engage with local knowledge through inquiry-based and project-based learning. Forty outstanding student-led projects illustrate how biodiversity becomes not only scientific content, but also lived culture, environment, and story.

Rooted in constructivist and place-based learning, these projects begin with simple observations and unfold into powerful journeys of discovery. A second-grade girl in Chiang Rai asked why her grandmother's Kaeng Khae soup had so many different greens. Her research revealed over 20 local plant species, linking biodiversity to nutrition and cultural heritage. In Kanchanaburi, a child's fascination with puffball mushrooms led to a hands-on ecological survey after the first monsoon. In Phetchaburi, students turned stained shirts into scientific inquiry, experimenting with natural dyes from the toddy palm.

In Uthai Thani, students raised caterpillars and tested which leaves they preferred, combining biology, documentation, and self-reflection. In Ubon Ratchathani, children explored bamboo biodiversity alongside traditional weavers, bridging generations through knowledge. In Chonburi, students mapped fiddler crab burrows and hosted a coastal conservation festival. And in Satun, young learners followed mangrove roots to discover how nature adapts to protect shorelines. Children worked alongside elders, artisans, and community members. They mapped habitats, tested hypotheses, and shared results through creative formats like eco-festivals, posters, and textile art. Beyond scientific understanding, they gained empathy, environmental awareness, and confidence as local change-makers.

These stories reflect the power of seeing biodiversity through a child's eyes, where culture, nature, and curiosity meet. When learning begins with wonder, science becomes personal and purposeful. This approach offers a hopeful, replicable model for developing young global citizens grounded in their local ecosystems.

KEYWORDS:

Biodiversity education; inquiry-based learning; project-based learning; early childhood; local wisdom

Geospatial Artificial Intelligence (GeoAI) for Estimating tree covered area and number of trees in Historical Sites: A Case of The Old Moat of Nakhonratchasima Municipality City, Thailand

Yaowaret Jantakat^{1,*}, Pongpun Juntakut² and Chomphak Jantakat³

¹Faculty of Sciences and Liberal Arts, Rajamangala University of Technology Isan, Nakhon Ratchasima, 30000 Thailand

²Security Science Institute, National Defense College, National Defense Studies Institute, Royal Thai Armed Forces Headquarters, Bangkok, 10400 Thailand

³Department of Business Administration, Vongchavalitkul University, Nakhonratchasima 30000, Thailand

*Corresponding author, e-mail: yaowaret.ja@rmuti.ac.th

ABSTRACT:

Biodiversity and cultural conservation are connected by biodiversity provides the foundation for many cultural practices, traditions, and spiritual beliefs, making its conservation essential for cultural sustainability. In Nakhon Ratchasima province of Thailand, the old moat of Nakhonratchasima Municipality City (NCM) is urban historical sites where include Thao Suranaree (Ya Mo) Monument and 7 old temples: Wat Phayap, Wat Sa Kao, Wat Bun, Wat Bueng (Phra Aram Luang), Wat Isan, Wat Pha Narai Maha Rat and Wat Sa Kao. In such historical sites, tree data is still lacking or not seriously surveyed in context of urban tropical environment and typically do not provide coverage of private land. However, individual tree inventory in true ground is still takes much time and expensive due to data collection challenges in the dynamic urban landscape. Therefore, the objective of this study is to propose a comprehensive framework of Geospatial Artificial Intelligence (GeoAI) for estimating tree covered area and number of trees over the old moat of NCM. GeoAI is a powerful technique that can enable the development of tree monitoring systems by applying machine learning models to high-resolution image data. This study proposes a deep learning neural network model applied to high resolution collected from the latest Google Earth images, to generate segmented tree crowns and the number of individual trees over the old moat of NCM, encompassing a total studied area of 3.40 km².

As results, the implemented GeoAI approach in the old moat of NCM can detect tree canopy cover about 0.85 km² and then can estimate amount 1,987 trees. Moreover, the results are regressed against coarser resolution tree cover maps to predict the area covered by tree crowns at a provincial level. The accuracy of the tree cover created by this study is compared to those of existing tree cover in true field. This work lays the foundation for establishing a tree-level inventory for the historical sites in Nakhon Ratchasima province using remotely sensed data. Consequently, the implemented GeoAI approach provides important insights to urban planners and government to monitor urban trees with the enhanced Individual Tree Inventory and strategies mitigation plan to reduce the impact of climate change and global warming.

KEYWORDS:

Historical site, Tree segmentation, Tree crown cover, Remote sensing, Geospatial Artificial Intelligence

Investigating the urgency of regulating digital sequence information (DSI) to protect traditional knowledge of indigenous people from digital biopiracy

Sri Oktavia^{1,*} and Nia Rahma Dini²

¹Department of International Law, Faculty of Law, Universitas Andalas, Indonesia

²Centre for International Law and Sustainability, Faculty of Law, Universitas Andalas, Indonesia

*Corresponding author, e-mail: srioktavia@law.unand.ac.id

ABSTRACT:

The phenomenon of genetic resource and traditional knowledge theft, known as *biopiracy*, has evolved into a digital form alongside advancements in synthetic biology and the open accessibility of genetic resource information through public databases. This new trend is referred as *digital biopiracy*. The emergence of **digital biopiracy** is closely linked to **Digital Sequence Information (DSI)**, which was originally intended for academic and research purposes, is now being utilized in the development of commercial products through genetic engineering, often without proper acknowledgment or benefit-sharing with the country or Indigenous communities. In the light of these challenges, this research aims to investigate the urgency of regulating DSI as the digital form of genetic resources to protect Indigenous People from digital biopiracy and ensure indigenous people rights from fair and equitable sharing. This research is normative juridical research, focusing on legal norms, principles, treaties and doctrine to evaluate the adequacy of existing regulations. The research employs statute approaches and **comparative study as its research approaches. Literature review** of academic texts, policy papers, and legal commentaries is combined with **web-based sourcing** to identify the latest update of DSI status in international discussion. It also concerns with the emerging practices, relevant case studies, and the latest positions from international bodies such as World Intellectual Property Organization (WIPO) and the Convention on Biological Diversity (CBD). The findings reveal that in several cases, patents that made use of DSI, such as the Ebola monoclonal antibody (REGN-EB3) and genetically modified (GM) potatoes, failed to engage in benefit-sharing and even caused harm to Indigenous People. These instances serve as examples of digital biopiracy. A major contributing factor is the open-access nature of genetic resource information in public databases, which is not accompanied by specific agreements or benefit-sharing mechanisms. Currently, DSI is not explicitly regulated under key international treaties such as the CBD and the Nagoya Protocol. Although both instruments have facilitated numerous discussions and international conferences addressing the status and implications of DSI in relation to fair and equitable benefit sharing (ABS), there is still no clear and binding interpretation of whether DSI is considered as genetic resources or the utilization of genetic resources. These difference interpretations have led to inconsistencies in the application of ABS principles. Furthermore, the newly adopted WIPO Treaty on Intellectual Property, Genetic Resources, and Associated Traditional Knowledge, which aims to safeguard the rights of Indigenous People within the intellectual property regime, does not classify DSI as part of genetic resources nor as a subject of fair and equitable benefit sharing. Although there is a growing consensus that DSI should be included in benefit-sharing schemes, its current implementation under the Cali Fund a multilateral benefit-sharing mechanism established by the CBD and the Nagoya Protocol lacks legal enforceability. This study also finds that the Cali Fund, introduced through Decision 16/2 of the CBD Conference of the Parties (COP), does not impose legally binding obligations on CBD and Nagoya Protocol parties. Moreover, there is no enforcement mechanism in place to ensure compliance by DSI users, leaving significant gaps in accountability. In the absence of a unified international standard, the regulation and interpretation of DSI status have been left to domestic legal systems. This research finds that the primary challenge in regulating DSI lies in the divergent views among countries regarding its legal status. Some states do not recognize DSI as a genetic resource and therefore do not apply the ABS principles, while others view

DSI as a derivative of genetic resource utilization and believe it should be subject to fair and equitable benefit sharing. Another major challenge is the difficulty in tracing the origin and users of DSI, which complicates the enforcement of ABS mechanisms. Many countries also suffer from weak domestic legal frameworks, making it difficult to uphold benefit-sharing obligations or hold violators accountable. This research proposes the urgent need for binding international regulations and equitable benefit-sharing systems to ensure the protection of indigenous rights in the digital era of genetic resource utilization.

KEYWORDS:

Convention on Biological Diversity, digital biopiracy, Digital Sequence Information, Genetic Resources, traditional knowledge.

POSTER PRESENTATION

SESSION 5



Empowering Local Communities Through Biodiversity Education in Southern Thailand

Montarika Promchaisri¹, Sontaya Promchaisri¹, Pattraporn Chaikong¹, Hassanai Kaewyod¹, Manus Leunkaew¹, Nareethip Nuankaew¹, Ekgachai Jeratthitikul^{1,2}, Alyssa Stewart^{1,3}, Natapot Warrit^{1,4}, Yves Basset⁵ and Akihiro Nakamura^{1,6,*}

¹Cooperation in Insect Biodiversity Research and Conservation, Personnel Training and Academic Exchange, Khao Chong Botanic Garden, Na Yong, Trang 92170, Thailand

²Department of Biology, Faculty of Science, Mahidol University, Ratchathewi, Bangkok 10400, Thailand

³Department of Plant Science, Faculty of Science, Mahidol University, Ratchathewi, Bangkok 10400, Thailand

⁴Department of Biology, Faculty of Science, Chulalongkorn University, Pathumwan, Bangkok 10330, Thailand

⁵ForestGEO, Smithsonian Tropical Research Institute, Ancon 0533, Panama

⁶Yunnan Key Laboratory of Forest Ecosystem Stability and Global Change Response, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Mengla, Yunnan 666303, China

*Corresponding author, e-mail: a.nakamura@xtbg.ac.cn

ABSTRACT:

Insects provide vital ecological services—such as pollination, decomposition, disease regulation, and water cycling—that are fundamental to ecosystem function and human well-being. Yet, despite growing global concern over insect declines, their ecological importance remains largely unrecognized at the community level, particularly due to a lack of accessible education and outreach. In Khao Chong, Trang Province, southern Thailand, researchers have conducted over 15 years of insect monitoring to establish a long-term, cross-regional platform for tracking changes in tropical forest insect communities in response to climate change and other human pressures.

Drawing from the data, specimens, and insights gained through this initiative, we have developed biodiversity education programs for local schools, with a focus on showcasing the rich insect diversity found in the region. The Khao Chong Insect Laboratory houses one of the largest single-locality collections in Thailand, comprising 11 cabinets, 220 drawers, and approximately 37,000 specimens across more than 2,500 focal species—all collected from the Khao Chong tropical forest. These resources are used to tell engaging stories about insect ecology, their essential roles in sustaining life, and their fascinating natural history, fostering curiosity and appreciation among students.

By connecting education to local biodiversity, our programs aim to raise awareness of the ecological and cultural value of insects. In doing so, we aim to empower local communities—especially young people—to recognize biodiversity as a vital part of their natural heritage, deserving of protection and stewardship for generations to come.

KEYWORDS:

Insect biodiversity, Environmental education, Community engagement, Tropical forest, Ecological services, Climate change, Conservation awareness.

Biocultural Heritage at Risk: Conserving Local Zingiberaceae Species through the Tak Bat Dokmai Festival in Saraburi, Central Thailand

Thawatphong Boonma^{1,*}, Surapon Saensouk² and Piyaporn Saensouk³

¹Diversity of Family Zingiberaceae and Vascular Plant for Its Applications, Walai Rukhavej Botanical Research Institute, Mahasarakham University, Maha Sarakham, 44150, Thailand

²Diversity of Family Zingiberaceae and Vascular Plant for Its Applications, Department of Biology, Faculty of Science, Mahasarakham University, Maha Sarakham, 44150, Thailand

*Corresponding author, e-mail: boonma.thawat@gmail.com

ABSTRACT:

The Tak Bat Dokmai Festival, held annually at Phra Phutthabat Temple in Saraburi, Thailand, is a significant cultural and religious event during which flowers are offered to monks on Buddhist Lent Day. The primary species used, *Curcuma supraneeana* (W.J. Kress & K. Larsen) Škorničk., and various *Globba* species, are native members of the Zingiberaceae family whose flowering coincides with the timing of the festival. This study documented the diversity and sources of these plants during the 2024 celebration through field observations and interviews with local vendors and participants. Findings revealed that plant materials were obtained through a combination of wild harvesting, local cultivation, and commercial sourcing. Rare and endemic species, such as *Curcuma saraburiensis* Boonma & Saensouk, were infrequently observed, raising concerns about overharvesting and diminishing local populations. In response, this study proposes a conservation strategy grounded in the principles of Other Effective area-based Conservation Measures (OECMs). By recognizing community-managed areas surrounding the temple as culturally significant conservation zones, traditional harvesting practices can be maintained while safeguarding biodiversity. Encouraging local cultivation and promoting awareness of sustainable use within the community are key to this approach. Integrating conservation efforts with cultural traditions offers a holistic path to preserving both the ecological and spiritual significance of the Tak Bat Dokmai Festival amid modernization and environmental change.

KEYWORDS:

Buddhist; Conservation; Cultural; Local Species; Zingiberaceae

First successful isolation and propagation of Primordial Germ Cells in a reptile: a conservation breakthrough for endangered Softshell Turtles

Yanika Piyasanti¹, Sukumal Prukudom^{1,2}, Suparat Chaipipat¹, Kornkanok Sritabtim¹, Juthathip Jurutha¹, Rungthiwa Sinsiri¹ and Kannika Siripattaraprat^{1,3,*}

¹Kasetsart University Veterinary Diagnostic Laboratory, Faculty of Veterinary Medicine, Kasetsart University, Bangkok, 10900, Thailand

²Department of Anatomy, Faculty of Veterinary Medicine, Kasetsart University, Bangkok, 10900, Thailand

³Department of Pathology, Faculty of Veterinary Medicine, Kasetsart University, Bangkok, 10900, Thailand

*Corresponding author, e-mail: kannika.si@ku.th

ABSTRACT:

Six species of softshell turtle endemic to Thailand are facing population decline and extinction threats. Their risks include habitat encroachment, human consumption, commercial carapace utilization, and the use as substantial formula in traditional Chinese medicine. Currently, no proactive strategy has been implemented to preserve either their existence or genetic diversity. Primordial Germ Cells (PGCs), precursors to germ cells, have been proposed as a potential means for reptilian biodiversity conservation; however, there is no publication on the cultivation of reptile PGCs. In a comparable oviparous animal, however, avian PGCs have been extensively investigated for their remarkable capacity, indefinite proliferation, and their utility in germline chimera production. To translate these technologies to endangered reptile species, we investigated the proposed potential by utilizing the closely related Chinese softshell turtle as a model. The availability of abundant fertilized eggs from commercial farms allowed for extensive exploration. We specifically aimed to investigate isolations of pre-gonadal PGCs at specific embryonic developmental stages. We also proposed to specify protocols of isolation, cultivation, and characterization of turtle PGCs from embryonic tissues. Fertilized eggs were raised in a temperature and humidity-controlled incubator. The embryonic stages were examined daily. Upon reaching specific embryonic stages, embryonic tissues were collected and processed. A total of 80% (12/15) of samples yielded successful PGC isolation. The turtle PGCs possessed distinct PGC characteristics upon microscopic examination including large nuclei, numerous cytoplasmic spikes, and intracytoplasmic vacuoles. A total of 73.33% (11/15) of isolated PGCs were successfully sub-passaged. The proliferation rate of PGCs varied among isolates of different developmental stages. All PGC isolates revealed expression of specific germ cell markers, including DAZL and VASA, by immunofluorescent assay. Taken together, our findings represent the first successful isolation and *in vitro* propagation of PGCs from a reptile species, the Chinese softshell turtle. This finding lays an essential foundation for advancing reproductive technologies in chelonian species. Utilizing PGCs to generate chimeric animals presents a promising path for the sustainable conservation of softshell turtles and other endangered reptile species worldwide.

KEYWORDS:

Wildlife conservation; Softshell Turtles; *Pelodiscus sinensis*; Pregonadal PGCs; Tissue PGC.

DNA Barcoding Diversity of *Apis cerana* Fabricius, 1758 in Breeding Area at Phayao Province, Thailand

Tanapol Boonjittham^{1,*} and Tipwan Suppasat¹

¹School of Science, University of Phayao, Maeka, Muang, Phayao, 56000 Thailand

*Corresponding authors, email: 64081605@up.ac.th

ABSTRACT:

Asian honeybees, *Apis cerana* Fabricius, 1758, are native to Asia and are distributed throughout Thailand. Currently, the *A. cerana* are cultured in the hive and produce bee products, such as honey, pollen, wax, and bee bread etc., in Thailand. In 2018, the southern population of *A. cerana* was relocated to a breeding area in Chun District, Phayao Province, where twelve colonies were maintained alongside the northern population. Then, five years later, *A. cerana* was sampled from 66 colonies (n = 66) in the breeding area and the nearby district in Phayao. The genetic diversity of *A. cerana* populations collected within Phayao Province was investigated using the mitochondrial DNA (COI) gene as a barcoding marker. There were *A. cerana* samples from other provinces in Thailand, including Chantaburi (n = 2), Petchaburi (n = 13), and Chumphon (n = 6), as well as from China (n = 3). Moreover, there were nine samples of the outgroup, whereas *A. dorsata* (n = 1), *A. florea* (n = 3), and *A. mellifera* (n = 5). All samples were amplified using the LepF and LepR primers, which aligned sequences of 720 bp, including gaps. The results of DNA sequence polymorphism analysis of *A. cerana* samples, generated using the DNAsp program, showed that the number of haplotypes (h) was 33, haplotype diversity (hd) was 0.9212, and nucleotide diversity (pi) was 0.00387. Moreover, the phylogenetic relationships, as reconstructed using the NJ and ML methods, were analyzed with the Kimura-2 parameter and the MP method by Mega program. The phylogenetic tree clustered the *A. cerana* clade from the outgroup (*A. dorsata*, *A. florea*, and *A. mellifera*). Focusing on the *A. cerana* clade suggests that it may be clustered into four groups, the first of which includes the northern population, comprising *A. cerana cerana* from China. The second group consisted of the northern population, which comprised *A. cerana* from Phayao, as well as the breeding and nearby areas. The third group consisted of the northern population of *A. cerana* from Phayao and other provinces in Thailand, and the last was the southern population from Chumphon, located on the Malay Peninsula of Thailand. The mitochondrial DNA (COI) gene, as a barcoding marker for *A. cerana* in breeding in Phayao province, may suggest a diagnostic molecular marker for *A. cerana* hybrid populations in apicultural breeding. This research may support resolving the genetic change of the *A. cerana* breeding development program in the beekeeping area of Thailand.

KEYWORDS:

Apis cerana; Diversity; phylogenetic; COI gene

Biodiversity of the Neuropterida (Insecta: Neuroptera, Megaloptera, and Raphidioptera) in Thailand

Kanyakorn Piraonapicha^{1,*}

¹Queen Sirikit Botanic Garden, The Botanical Garden Organization, Chiang Mai 50180, Thailand.

*Corresponding author, e-mail: kanyakorn.qsbg@yahoo.com

ABSTRACT:

The Neuropterida are a multiordinal clade of holometabolous insects that encompasses the extant orders Megaloptera, Neuroptera, and Raphidioptera. Approximately 6,600 extant species were reported, except in Antarctica and near-polar latitudes. Recently, material examined for taxonomic studies on Neuropterida in Thailand has been primarily focused on the order Megaloptera. Currently, eight genera and twenty-three species of Megaloptera are known from Thailand. The megalopterans not only play a significant role in ecological processes but have also formed a part of the human diet. Larvae of corydalids are traditionally edible insects by hill tribes, Pwo Karen, Shan in Mae Hong Son Province and Lua in Nan Province in Northern Thailand. They usually cooked to many dishes such as cooks with curry, steams with fish, and deep fried. To date, around thirty Neuroptera and four Raphidioptera species have been reported in Thailand. Unfortunately, Raphidioptera remain poorly studied in Thailand. As a result, knowledge of their species richness, taxonomy, and biogeography is limited and fragmented. Most of the available studies have been conducted over the past two decades and have primarily focused on specimens from northern Thailand. Consequently, the overall diversity, systematic relationships, and distribution patterns of Thai Raphidioptera remain unclear. This evident knowledge gap highlights the need for more comprehensive and targeted research on this group within the country.

KEYWORDS:

Megaloptera, Neuroptera, Raphidioptera

Why do birds suddenly disappear? An ethno-ornithological study of bird hunting and consumption in Bukidnon, Mindanao Island, Philippines

Cristine Joy C. Paderog¹, Betty La Pia J. Quiñones¹, Chryss Niño J. Arisgado^{1,*} and Dave P. Buenavista²

¹Institute of Biological Sciences, Master of Science Students, Central Mindanao University, Philippines

²Faculty of the Institute of Biological Sciences, Animal Division, Central Mindanao University, Philippines

*Corresponding author, e-mail: chryssninoa@gmail.com

ABSTRACT:

Through the years, interactions with wild animals have profoundly influenced the development of humans as a species. These connections are intricately woven into the fabric of human life, shaping not just physical survival but also cultural expressions, spiritual understanding, and relationships with the natural world. For countless generations, from early hominins like *Homo habilis* to modern *Homo sapiens*, humans coexisted closely with wildlife, depending on it for nourishment, materials, healing, and a sense of identity. Among these creatures, birds have occupied a particularly significant role, aside from being a food source, are also admired and respected for beauty, symbolic meanings, and medicinal properties. This study investigates the patterns, motivations, and implications of wild bird consumption in Dagumbaan Village, Bukidnon, Mindanao Island, Philippines. Through semi-structured interviews and thematic analysis of 15 respondents, the study reveals that avian hunting is deeply rooted in local culture, shaped by necessity, tradition, and economic utility. Eleven bird species belonging to eight families including endemic and vulnerable species like *Anas luzonica* are consumed, primarily sourced through traditional methods such as netting and manual hunting. Despite high awareness (93.3%) of wildlife protection laws, 80% of respondents admitted to occasional bird consumption, reflecting gaps in enforcement and reliance on birds as an accessible protein source. Cultural beliefs further influence which species are hunted or avoided, with some birds symbolizing omens or sacred meanings. The community recognizes a decline in bird populations (60%) and supports conservation (100%), yet 80% still favor continued consumption. Factors such as agricultural expansion, perceived pest behavior of birds, and erosion of traditional practices also affect hunting behaviors.

KEYWORDS:

Ethnozoology; conservation; food culture; biodiversity; ornithology

In Vitro Propagation and Cryopreservation of Green Peafowl (*Pavo muticus*) Primordial Germ Cells for Conservation

Kornkanok Sritabtim¹, Yanika Piyasanti¹, Suparat Chaipipat¹, Juthathip Jurutha¹, Rungthiwa Sinsiri¹, Sukumal Prukudom^{1,2}, Pantaporn Supakankul⁴, Wandia Apithanaphong⁴ and Kannika Siripattarapavat^{1,3,*}

¹Kasetsart University Veterinary Diagnostic Laboratory, Faculty of Veterinary Medicine, Kasetsart University, Bangkok, 10900, Thailand

²Department of Anatomy, Faculty of Veterinary Medicine, Kasetsart University, Bangkok, 10900, Thailand

³Department of Pathology, Faculty of Veterinary Medicine, Kasetsart University, Bangkok, 10900, Thailand

⁴School of Agriculture and Natural Resources, Muang Phayao 56000, Thailand

*Corresponding author, e-mail: kannika.si@ku.th

ABSTRACT:

The Green peafowl (*Pavo muticus*), a striking pheasant from Southeast Asian tropical forests, is classified as endangered species by the IUCN. Their progressive population decline stems from habitat encroachment (mainly for agriculture), illegal hunting, and most critically, genetic contamination through interbreeding with invasive alien species—Indian (blue) peafowls. This hybridization significantly reduces purebred individuals, increases both inbreeding and genetic diversity loss, as well as accelerates introgression. Current conservation efforts focus on raising public awareness and landscape protection, to eliminate possibility of blue peafowl presented in the green peafowl territory. In addition, captive breeding program has been implemented to re-introduce the purebred offsprings, although it constantly faces multiple challenges especially poor breeding soundness. Cryopreservation of germplasms offers a practical solution to maintain the genetic variety of endangered avian species through the long-term storage of living specimens. In this study, we aimed to *in vitro* propagate and cryopreserve primordial germ cells (PGCs), precursor cells to both sperm and oocytes, of green peafowl. By subtle modification of an existing protocol that had been accomplished in chicken and quails, we focused on isolation of PGCs from 3 distinct tissue sources: blood (circulating PGCs - cPGCs), embryonic tissues (tissue PGCs - tPGCs), and extraembryonic tissues (xPGCs). Fertilized eggs of green peafowl were obtained from a commercial farm in Phayao. The eggs were raised in an automatic turner egg incubator until reaching specific developmental stages. Since no publication found on early embryonic staging in peafowl, staging of embryos was done in comparison to Hamburger-Hamilton staging system of chicken. Isolation successes were noticed when embryo stage 12-14 were used. The percentages for isolation and cultivation success of specify isolated types were as following; cPGCs (100%, 80%), tPGCs (100%, 100%), and xPGCs (100%, 100%). Isolated PGCs from all tissue sources expressed germ cell-specific markers (DAZL and CVH proteins). When these PGCs were injected to chicken embryonic recipients, they demonstrated the ability to colonize embryonic gonads, which further confirmed functional characteristics of PGCs. This study successfully demonstrates a refined protocol that can be effectively used for the isolation and cultivation of PGCs from embryonic tissues of green peafowl. These peafowl PGCs fully retain germ cell characteristics and can be long-term cryopreserved. PGC banking should be implemented as a parallel procedure for green peafowl conservation, providing a means to preserve its genetic diversity for future generations through germline chimera biotechnology.

KEYWORDS:

Green peafowl (*Pavo muticus*); endangered; Primordial germ cell (PGCs); tissues PGCs (tPGCs); extraembryonic tissues PGCs (xPGCs); circulating PGCs (cPGCs).

Living with carnivores: Attitudes, Conflicts and Cultural Values in Central Hills of Sri Lanka

Ashan Thudugala^{1,2,*}, Harsha Dissanayake²

¹Southeast Asia Biodiversity Research Institute, Chinese Academy of Sciences & Center for Integrative Conservation, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Mengla, Yunnan, 666303, China

²Small Cat Advocacy and Research, Kandy, Sri Lanka

*Corresponding author, e-mail: ashan@scar.lk

ABSTRACT:

Human-wildlife conflict threatens both human and biodiversity wellbeing, especially when large carnivores and herbivores overlap with the human settlements. However, human dimension towards these species relatively understudied beyond few charismatic species like leopards and elephants. To address this gap, we conducted a semi-structured interview for 303 households bordering to the protected areas in Kandy /Central Hills of Sri Lanka. we investigate how, residents' knowledge, attitude, social economic factors, and cultural values shaping the human carnivore co-existence in these Human dominated landscapes. As results, we observed many residents lack knowledge in species identification while this ability was significantly influenced by distance to forest, gender and education level. 42% of residents show positive attitudes towards certain carnivores like leopards and members of wild cat family while majority show negative attitude towards Civets. These attitudes were significantly influenced by level of urbanization and education of the residents. We observed that negative attitude forms due to disturbance, crop damage, livestock depilation, yet some carnivores like leopards hold complex cultural symbolism, eliciting fear alongside respect. Carnivores related conflicts were reported by 33% of respondents yet 68% believed conflicts have decreased over last two decade of time indicating biodiversity loss alongside with the development. Although 73% respondents had no clear idea about conflict mitigation or co-existence, 17% advocated for relocating the problematic carnivores, despite such interventions often fail and risk further ecological implications. Our study underscores the importance of having locally tailored, holistic, interdisciplinary approach that integrate social, cultural, economic and ecological dimensions to promote effective conservation and co-existence.

KEYWORDS:

Carnivores; Human wildlife conflict; Attitude; Co-existence.

Cryopreservation of Somatic Cells from Banteng (*Bos javanicus*) for Biobanking and Conservation

Juthathip Jurutha¹, Yanika Piyasanthi¹, Kornkanok Sritabtim¹, Suparat Chaipipat¹, Rungthiwa Sinsiri¹, Sukumal Prukudom^{1,2}, Nikorn Thongtip⁴, Supaphen Sripiboon⁴, and Kannika Siripattrarapravat^{1,3,*}

¹Center for Veterinary Diagnostic Laboratory - Bangkhen, Faculty of Veterinary Medicine, Kasetsart University, Bangkok 10900, Thailand

²Department of Anatomy, Faculty of Veterinary Medicine, Kasetsart University, Bangkok 10900, Thailand

³Department of Pathology, Faculty of Veterinary Medicine, Kasetsart University, Bangkok 10900, Thailand

⁴Department of Large Animal and Wildlife Clinical Science, Faculty of Veterinary Medicine, Kasetsart University, Kampong Saen, Nakhon Pathom Province 73140, Thailand

*Corresponding author, e-mail: kannika.si@ku.th

ABSTRACT:

The banteng (*Bos javanicus*) is a wildlife species native to Southeast Asia including Thailand. Its biodiversity plays important roles in maintaining ecosystem balance, especially for the survival of the top predator in a food chain. Currently classified as critically endangered by the IUCN, the global population of banteng has declined alarmingly in recent decades. The situation observed in Thailand is worsen as a recent study has shown that only few haplotypes are left. Major threats of extinction include illegal hunting, habitat loss, and hybridization with domestic cattle. Somatic cell nuclear transfer of banteng has been reported, so that banking of cells enables conservation efforts through such advanced biotechnology. Skin tissue biopsies of four bantengs located at the Khao Nam Phu wildlife and nature education center (Kanchanaburi province) were submitted for cell isolation. Three specimens were obtained from live animals under anesthesia, while the other was from a carcass. Skin fibroblasts were successfully isolated from all specimens. All primary cells were successfully cultivated for up to passage 5 and cryopreserved. These cultured cells exhibited fibroblast-like characteristics. The doubling times of all isolates ranged from 1.2 to 2.0 days. Cumulative population doubling levels exceeded 10 to 13 at the time the cultivation intentionally suspended. As a result, 166 vials of banteng fibroblast cells have been stored in the Kasetsart University Veterinary Animal Cell Bank (KUVACB), thus ensuring a valuable genetic resource for future applications. These preserved somatic cells not only can support genetic studies but also warrant a backup pool of biodiversity for the future. This biobanking effort provides a foundation for restoring genetic diversity and in turn guiding population management strategies. Despite technical and ethical challenges, such initiatives highlight the potential of biotechnology in wildlife conservation and position Thailand as a leader in safeguarding endangered species.

KEYWORDS:

Banteng (*Bos javanicus*); skin fibroblasts; cell cryopreservation; cell bank.

Disentangling the role of ectomycorrhizal fungi in plant nutrient acquisition along a Zn gradient using X-ray imaging

Erwin Afrendi^{1,*}

¹Tottori University, Japan

*Corresponding author, e-mail: kannika.si@ku.th

ABSTRACT:

Zinc (Zn) is an essential micronutrient that plays critical roles in plant growth, enzyme activity, and DNA/RNA function. Its uptake and homeostasis in plants are managed through redox-based and chelation-based strategies involving microbial and plant root activity. Ectomycorrhizal fungi (EMF), which form symbiotic relationships with many forest trees, assist in the uptake of Zn and other minerals, helping plants cope with both deficiency and toxicity. For instance, EMF can enhance Zn uptake by upregulating specific transporters or buffer excess Zn to protect host plants. Interactions with other nutrients, such as Cu and Ca, also affect Zn dynamics due to shared transport pathways. Despite known benefits of EMF in nutrient regulation, how they influence the spatial distribution of Zn within plant root tissues remains poorly understood. This study aims to fill that gap by exploring nutrient uptake patterns and Zn localization in the *Suillus*–*Pinus* symbiosis under both low and high Zn conditions. Using synchrotron-based imaging, researchers visualized how Zn is distributed across ectomycorrhizal and non-ectomycorrhizal roots, providing empirical evidence on EMF's role in shaping nutrient flow at the plant-mycorrhiza-rhizosphere interface. This study shows that *Suillus luteus* regulates nutrient uptake and transport in pine roots depending on external zinc (Zn) concentrations. At low Zn levels, it enhances the absorption of Zn, calcium, copper, and iron, while at high Zn levels, it limits their uptake, likely through detoxification and barrier functions of the fungal sheath. Iron uptake is favored under low Zn, possibly due to fungal siderophores or competition at transport sites. However, *S. luteus* offers limited protection at extreme Zn concentrations, as seedlings did not survive 10 mM Zn exposure.

KEYWORDS:

Micronutrient, homeostasis, Ectomycorrhizal fungi

SESSION 6

BIODIVERSITY MANAGEMENT TO OVERCOME GLOBAL CRISIS



INVITED SPEAKER 6-1:



Enhancing Biodiversity Conservation and Sustainable Tourism in Thailand through Local Government Financing Solution

Niran Nirannoot

United Nations Development Programme, 14th Floor UN Building, Rajdamnern Nok Avenue, Bangkok, 10200, Thailand

*Corresponding author, e-mail: niran.nirannoot@undp.org

Abstract:

Over half of global GDP—\$44 trillion is reliant on nature, yet the degradation of natural ecosystems has accelerated significantly over the past 50 years due to the failure to integrate biodiversity into planning and decision-making process. Efforts to achieve the biodiversity targets were largely unmet, exacerbated by a chronic biodiversity financing gap, estimated at \$700 billion annually. In Thailand, biodiversity management is fragmented across 60 government agencies, with spending declining from 0.53% of total government expenditures in 2016 to 0.36% in 2023.

To address this challenge, the Kunming-Montreal Global Biodiversity Framework calls for mobilizing at least \$200 billion annually by 2030. In response, Thailand developed its Biodiversity Finance Plans, prioritizing biodiversity finance solutions to increase funding, eliminate harmful subsidies, and enhance financial resource allocation. A key initiative under this framework is the Koh Tao Sustainable Finance Model.

The model introduces a self-financing mechanism in the form of tourist user charges, a transformative approach to conservation funding, especially in non-protected areas. Revenue generated supports coral reef preservation—a critical asset for the island's tourism—and promotes sustainable tourism. Since its launch in April 2022, the pier service fee has funded pier operations, tourist assistance, waste management, and volunteer diving teams for underwater debris removal.

This initiative exemplifies how local governments can shift from a nature-negative to a nature-positive economic framework. By leveraging tourism-based revenues, Thailand is addressing funding gaps for biodiversity while building a scalable model for conservation in non-protected areas, nature-based tourism sites, and national parks. The Koh Tao case demonstrates the potential for local financing to bridge biodiversity funding shortfalls, fostering long-term sustainability and resilience for both ecosystems and economies.

KEYWORDS:

Biodiversity finance, Sustainable tourism, Nature-positive economy

INVITED SPEAKER 6-2:

Managing Biodiversity in Common Pool Resources: Insights from Experimental Economics to Address Global Crises



Witsanu Attavanich¹, Yohei Mitani^{2,*} and Ken Miura²

¹Department of Economics, Faculty of Economics, Kasetsart University, Bangkok, 10900, Thailand

²Division of Natural Resource Economics, Graduate School of Agriculture, Kyoto University, Kyoto, 606-8502, Japan

*Corresponding author, e-mail: mitani.yohei.7w@kyoto-u.ac.jp

ABSTRACT:

Forests and fisheries, as vital common pool resources, are central to addressing global crises such as climate change, food insecurity, and biodiversity loss. Effective management of these resources strengthens ecological resilience, sustains livelihoods, reduces greenhouse gas emissions, and mitigates risks that transcend national boundaries. Understanding how communities govern forests and fisheries is therefore essential for crafting solutions to interconnected global challenges. This panel discussion will present findings from a systematic review of 48 field experimental studies on community-based management of fishery and forest common-pool resources to synthesize trends and insights for sustainable management. This review highlights the power of field experiments in measuring social capital and its influence on collective action, resource sustainability, and policy formulation. Key findings reveal that trust-building interventions consistently improve adherence to resource management regulations, and communities with strong social capital exhibit enhanced collective action and resource sustainability. While both monetary and non-monetary incentives prove effective, their impact varies depending on the context and resource type. Critically, the analysis demonstrates that interventions tailored to local social and ecological contexts produce the most robust outcomes. Based on these findings, the study proposes policy recommendations to address common challenges in forest and fishery management, along with resource-specific strategies adapted to their unique ecological and socio-economic environments.

KEYWORDS:

pool resources, global crises, climate change, food insecurity, biodiversity loss

How Youth Can Shape the Future of Biodiversity?

Pasut To-ying¹, Nunnapus Pongwitoon¹, Bhabordee Ngamphuek¹, Thanakit Suparat¹, Kittikun Saksung¹ and Suchada Kosavisutte^{1,*}

¹Global Youth Biodiversity Network for Thailand (GYBN Thailand), Bangkok, Thailand

*Corresponding author, e-mail: suchada.ksvs@gmail.com

ABSTRACT:

Today, youth recognise biodiversity loss as a critical issue affecting economic, social, health, and well-being outcomes. However, a significant disconnect persists between environmental awareness and concrete conservation action among young people. The interest of youth in Thailand's biodiversity conservation remains understudied. Our national chapter aims to increase youth engagement in biodiversity, evaluate contribution to national biodiversity and climate strategies, and identify pathways for transforming awareness into effective action. Notably, numerous environmental engagements of young people have been shaped by global climate momentum, with climate activism serving as an entry point before transitioning to biodiversity-focused work. Two significant outcomes from our work were the Local Conference of Youth (LCOY) in 2024 and the 2025 Children and Youth Environment Survey (CYES). We present results incorporating active citizenship and initiatives that engage children, youth, and families in biodiversity data collection across multiple communities nationwide. The LCOY results show that youth are eager to strengthen biodiversity-related skills in ecotourism, monitoring, urban green spaces, and fair forest resource policy. The CYES indicates that most youth are willing to participate in environmental actions, although few take the initiative, and only some are unsure where to start. Key strategies include government promotion of youth policy involvement, private sector support for green skills training, civil society network creation, and educational sector integration of hands-on ecological learning. Our surveys reveal substantial youth commitment to Thailand's NBSAP implementation and KMGBF framework goals. These findings demonstrate that young people act as environmental agents rather than passive observers, possessing both motivation and capacity for meaningful action. The critical need now lies in institutional responsiveness, developing platforms that channel youth expertise into policy implementation and creating educational frameworks that support their conservation leadership potential.

KEYWORDS:

National biodiversity and climate strategies, Youth engagement, Policy implementation

POSTER PRESENTATION

SESSION 6



Coral recovery following the 2024 coral bleaching event in Mu Ko Chumphon National Park, the Western Gulf of Thailand

Charernmee Chamchoy^{1,*}, Wichin Subpala¹, Makamas Sutthacheep¹, Laongdow Jungrak¹, Wanlaya Klinthong¹, Wiphawan Aunkhongthong¹ and Thamasak Yeemin¹

¹Marine Biodiversity Research Group, Department of Biology, Faculty of Science, Ramkhamhaeng University, Huamark, Bangkok, 10240, Thailand

*Corresponding author, e-mail: charernmee1707@gmail.com

ABSTRACT:

Coral bleaching driven by global warming has become a major threat to coral reef resilience worldwide. This widespread phenomenon not only compromises coral survival and reef structure but also diminishes the ecosystem services that millions of people rely on, including food security, coastal protection, and livelihoods. Understanding the patterns and drivers of bleaching events is therefore critical for developing effective conservation strategies. Targeted monitoring and adaptive management approaches are essential to enhance reef resilience in the face of accelerating climate change. This study aims to assess the incidence of coral bleaching at Ko Ngam Yai, Ko Ngam Noi, and Ko Kachiu in Mu Ko Chumphon. The findings revealed that the incidence of coral bleaching across the surveyed sites ranged between 75% and 95%, reflecting severe thermal stress on local coral communities. Several coral species were affected by bleaching, including *Acropora muricata*, *Fungia fungites*, *Galaxea fascicularis*, colonies were estimated at 70% to 85%, whereas mortality rates ranged from 5% to 10%, indicating considerable variability in resilience among different coral taxa and morphologies. These results highlight the vulnerability of coral reefs in Mu Ko Chumphon to thermal anomalies associated with climate change. The study underscores the critical need for the implementation of continuous monitoring programs and the development of adaptive management strategies aimed at enhancing resilience and ensuring the long-term conservation of coral reef ecosystems. Such concerted efforts are essential not only to mitigate the adverse impacts of climate-induced bleaching events but also to safeguard the vital ecological functions, ecosystem services, and biodiversity that coral reefs provide to coastal communities and marine organisms.

KEYWORDS:

coral bleaching, Chumphon, monitoring, mortality, recovery rate

Environmental DNA metabarcoding for stock assessment and conservation of fish species in the Southern Region, Philippines

Rodelyn M. Dalayap^{1,*}, Ziljih M. Molina¹, Rande B. Dechavez² and Sharon Rose M Tabugo³

¹Department of Biology, Faculty, Sultan Kudarat State University, Tacurong City, Philippines

²Department of Biology, Faculty, Sultan Kudarat State University, Kalamansig, Sultan Kudarat, Philippines

³Department of Biological Science, Faculty, Mindanao State University-Iligan Institute of Technology, Iligan City, Philippines

*Corresponding author, e-mail: rodelyndalayap@sksu.edu.ph

ABSTRACT:

Mindanao is located in the southern region of the Philippines and is recognized as one of the marine biodiversity hotspots. However, marine ecosystems face significant challenges due to anthropogenic activities and climate change, leading to biodiversity loss in marine habitats. This study was conducted in selected areas of the southern Philippines to assess fish species in marine ecosystems for conservation purposes using Environmental DNA (eDNA) metabarcoding. Thirty fish species belonging to 19 families have been documented. One fish species was categorized as vulnerable and twenty-nine of them were considered of least concern and not evaluated. These results demonstrate that eDNA metabarcoding can be used to detect vulnerable species in marine environments, thereby providing a basis for effective conservation management. These findings contribute to the promotion of ecologically and economically sustainable marine fisheries.

KEYWORDS:

biodiversity, environmental DNA, fisheries, marine ecosystem, sustainable, vulnerable

Environmental DNA (eDNA) and Global Biodiversity Information Facility (GBIF) (data infrastructure for monitoring of fish species in Bongo Island, Maguindanao, Mindanao, Philippines)

Sharon Rose Tabugo^{1,2,*}, Mayvel Suan³, Noel John Ian Feben Maguate^{1,2} and Janece Jean Manubag⁴

¹Department of Biological Sciences, College of Science and Mathematics, Mindanao State University-Iligan Institute of Technology (MSU-IIT), Tibanga, Iligan City, Philippines

²Molecular Systematics and Conservation Genomics Laboratory, Center for Biodiversity Studies and Conservation, Premier Research Institute of Science and Mathematics, MSU-IIT, Tibanga, Iligan City, Philippines

³Caraga State University (CSU), Butuan City, Philippines

⁴JCI Iligan Maria Cristina, Iligan City, Philippines

*Corresponding author, e-mail: sharonrose.tabugo@g.msuiit.edu.ph

ABSTRACT:

The Global Biodiversity Information Facility (GBIF) data infrastructure serves as a global platform aggregating and providing access to biodiversity data, while eDNA technologies offer a non-invasive method for detecting and characterizing organisms based on genetic material present in their environment. By linking GBIF data infrastructure to eDNA studies, researchers benefit from a wealth of information contributed by diverse sources worldwide. GBIF's extensive databases include taxonomic, spatial, and temporal information, providing a comprehensive baseline for biodiversity assessments. Integrating eDNA data into this infrastructure enhances the accuracy and completeness of biodiversity records, contributing valuable insights into the distribution and ecology of species. This study aimed to identify fish and other aquatic organisms in a specific area using eDNA and GBIF. The High-throughput sequencing eDNA approach, employing the 12S rRNA (MiFish-U) marker, was utilized to identify fish communities and vulnerable or threatened species. Data preprocessing and MiSeq raw reads were analysed using the MitoFish pipeline. It automatically processes and visualizes biodiversity indices. In this study, fish species were detected, representing twelve families, namely Pomacentridae, Siganidae, Acanthuridae, Atherinidae, Clupeidae, Engraulidae, Cyprinidae, Xenocypridae, Serranidae, Salmonidae, Scombridae, and Syngnathidae. The outcomes derived from the synergistic approach offer valuable insights into identifying significant fish species, including detecting *Hippocampus comes* (tiger-tail seahorse), classified as a threatened species by the IUCN. Traditional methods should complement synergistic approaches for enhanced taxonomic resolution and community analysis. Results served as baseline data for crafting of policies for management strategies.

KEYWORDS:

MitoFish, 12S rRNA, Environmental DNA (eDNA), MiSeq

Interspecific Hybridization Between Pearl Danio and Zebrafish Leads to Novel Research Models and Environmental Concern

Chonphoom Phan-poe¹, Juthathip Jurutha¹, Yanika Piyasanthi¹, Kornkanok Sritabtim¹, Suparat Chaipipat¹, Rungthiwa Sinsiri¹, Kannika Siripattrarapravat^{1,2} and Sukumal Prukudom^{1,3,*}

¹Center for Veterinary Diagnostic Laboratory - Bangkhen, Faculty of Veterinary Medicine, Kasetsart University, Bangkok 10900, Thailand

²Department of Pathology, Faculty of Veterinary Medicine, Kasetsart University, Bangkok 10900, Thailand

³Department of Anatomy, Faculty of Veterinary Medicine, Kasetsart University, Bangkok 10900, Thailand

*Corresponding author, e-mail: sukumal.pru@ku.th

ABSTRACT:

Pearl danio (*Danio albolineatus*), also known as the White-lined danio or Rearing danio, is a freshwater fish native to northern Thailand. It belongs to the family Danionidae, the same family as the zebrafish (*Danio rerio*), a renowned model in scientific research. Pearl danio holds potential as an alternative model organism, given the high costs and strict regulations currently associated with the import of zebrafish laboratory strain, whose continuous use has led to extensive inbreeding over generations. This study aimed to explore breeding strategies of Pearl danio, which included developing reproductive techniques and generating zebrafish-pearl danio hybrid offspring. Approximately 1-year-old broodstock were used, females were induced to ovulate through natural mating with males. Gametes were then collected from anesthetized male and female of both species. *In vitro* fertilization (IVF) was performed via reciprocal crosses between zebrafish and pearl danio. Fertilized embryos were incubated at 28°C until hatch, and the survival ratio as well as morphological abnormalities were monitored daily. Crossing male zebrafish with female pearl danio resulted in 97.5% (195/200) of the offspring exhibited pericardial edema and died at 3-day-old. The remaining five larvae showed signs of weakness, including incomplete swim bladder inflation, leading to loss of equilibrium and inability to ingest food. These larvae died following the post-larval stage (15-day-old). In contrast, hybrids from male Pearl danio crossed with female zebrafish showed no abnormalities, with approximately 70% of larvae fully developed into adults. Phenotypic observation indicated a tentative sex ratio of 90% males and 10% females. Arranged mating were induced to evaluate their reproductive soundness; however, no sign of courtship was observed, suggesting sterility. At six months of age, gonadal tissues of representative individual will be subjected to histological assessment (H&E staining) to confirm a presence or absence of gametogenesis. Taken together, our results demonstrated that interbreeding zebrafish and pearl danio was successful only when combination of zebrafish eggs and pearl danio milt were used, and thus led a new biological inquiry on the maternal role of teleost development. The hybrids produced, if sterile, could serve as a model for developmental research such as gametocyte migration and surrogate technology, potentially contributing to advancements in aquatic reproductive biology. However, if they are fertile, it highlights the potential genetic hybridization threats to other danio species when pet zebrafish, which is an alien species, contaminate natural water sources in Thailand.

KEYWORDS:

In vitro fertilization (IVF); Pearl danio (*Danio albolineatus*); Reproductive biology model; Sterile teleost hybrids; Zebrafish hybridization.

Modeling species distribution and range shifts of Negros Island endemics within protected areas in response to changing climate

Mistee Emille Iana Init^{1,*}

¹College of Forestry and Natural Resources, University of the Philippines Los Baños, Laguna, Philippines

*Corresponding author, e-mail: minit@up.edu.ph

ABSTRACT:

Protected areas (PAs) are vital for biodiversity conservation, offering habitats for endemic species. In the Philippines, PAs and key biodiversity areas (KBAs) face increasing threats from urban development and climate-induced ecosystem changes. These pressures imply consequences for endemic wildlife populations confined to remaining forest fragments within such areas, including the Visayan Warty Pig (*Sus cebifrons*), Visayan Tarictic Hornbill (*Penelopides panini*), and Negros Forest Frog (*Platymantis negrosensis*). This study used species distribution modeling (SDM) to address gaps in understanding the current and future distributions of these species under changing climate conditions on Negros Island. By projecting range shifts and habitat changes under two climate scenarios (SSP126 and SSP585), potential climate refugia, or areas likely to remain ecologically stable, were identified. Ensemble models indicated habitat losses for all three species, with *S. cebifrons* projected to face the most pronounced decline. In contrast, *P. panini* and *P. negrosensis* showed potential for habitat expansion within and beyond PA and KBA boundaries. The findings emphasize the importance of existing PA boundaries in sustaining these species and the critical role of KBAs as potential climate refugia. Recommendations include implementing standardized protections for KBAs and conducting field validation to identify suitable areas for habitat expansion within established PA boundaries, thereby furthering the formulation of management strategies that ensure the effectiveness and adaptability of these systems under changing environmental conditions in the coming decades.

KEYWORDS:

climate change, climate refugia, endemic wildlife, key biodiversity areas, protected areas, species distribution modeling

How warming temperature affect the survival and developmental rate of common cutworm (*Spodoptera litura*)?

Rungtip Wonglersak^{1,*} and Nopparat Pongjun¹

¹Office of Natural History Research, National Science Museum, Pathum Thani, 12120, Thailand

*Corresponding author, e-mail: Rungtip.w@nsm.or.th

ABSTRACT:

The common cutworm (*Spodoptera litura*) is an agricultural pest that causes widespread damage to important crops and is found worldwide in many regions. Temperature is a crucial physical factor affecting the development and survival of *S. litura*, as its internal biological processes largely depend on the surrounding environmental temperature. Therefore, this research aims to study the impact of climate change, particularly the warming temperature, on the developmental rate, survival rate, and body size of *S. litura*. The experiment was conducted in a laboratory with four different controlled temperatures: 20°C, 25°C, 30°C, and 35°C ($\pm 3^\circ\text{C}$), under 60% humidity and a photoperiod of 10 hours light and 14 hours dark (10L:14D). Observations included the duration of each developmental stage (eggs, larvae, pupae, and adults), the number of days required to reach each stage, and the size of the adult moths. These data were then used to analyze the larval developmental rate and the effect of temperature on the adult body size. We found that the larval development is highest at 30°C, while the larvae cannot survive under 20 and 25°C. The findings from this study will contribute valuable knowledge and serve as a foundation for planning pest outbreak management in the future. Additionally, the results will support further research on the effectiveness of both biological and chemical insecticides against this pest.

KEYWORDS:

climate change, common cutworm, developmental rate, *Spodoptera litura*, survival rate

Assessment of the biodiversity credit potential of Chulalongkorn University Centenary Park using Verra's methodology

Chintisan Chotjira-anan¹, **Nakulkan Singhoah¹**, **Natsorrachat Muangmo¹**, **Chawatat Thanoosing¹**, **Nipada Ruankaew Disyatat¹**, and **Pongchai Dumrongrojwatthana^{1,*}**

¹Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok, 10330, Thailand

*Corresponding author, e-mail: pongchai.d@chula.ac.th

ABSTRACT:

Biodiversity loss is one of the most pressing global problems. The Kunming-Montreal Global Biodiversity Framework has been established with goals to protect and sustainably use biodiversity by 2030 and beyond. This framework encourages organizations to adopt nature-positive approaches by increasing biodiversity, improving environmental quality, and sequestering carbon through various legal and financial mechanisms, including biodiversity credits and markets. Biodiversity credits are a form of environmental credits designed to quantify and represent measurable improvements in biodiversity outcomes, encouraging investment in conservation through tradable units. Although relatively new, biodiversity credits are gaining global attention to accelerate funding for biodiversity conservation and restoration. Currently there are over 50 schemes and methodologies to evaluate biodiversity credits, including Cercarbono, Terrasos, and Verra's methodologies. In Thailand, biodiversity credits are still a relatively new concept with limited research. There is still a lack of pilot studies or case studies calculating the value of biodiversity credits in areas where biodiversity conservation activities are being implemented. Therefore, this study aims to estimate initially the biodiversity credit potential at Chulalongkorn University Centenary Park by applying Verra's methodology, which considers ecosystem type, area size, condition quality, and biodiversity significance. The methodology includes defining the ecosystem type and area size, selecting and measuring condition indicators at the project start, establishing reference values, standardizing indicators relative to these values, and calculating the area-adjusted condition. This approach provides a standardized assessment framework for evaluating biodiversity improvements in urban ecosystems. Relevant data collected from the park, such as canopy cover, species richness, and above-ground biomass, were used to assess the biodiversity credit value. The calculation results are presented with the limitations of this study. A guide for future research and targeted activities to enhance biodiversity within the park will be proposed, along with recommendations for scaling up similar assessments in other urban contexts in Thailand.

KEYWORDS:

Bangkok; biodiversity assessment; biodiversity credits; conservation; urban ecosystem; Verra's methodology

Developing Prototype Competency-Enhancing Biodiversity Activities for Thai High School Students: Reflections from Teachers and Students

Thanate Kerdkaew^{1,*}

¹Chemistry and Biology Unit, The Institute for the Promotion of Teaching Science and Technology, Bangkok, 10110, Thailand

*Corresponding author, e-mail:thker@ipst.ac.th

ABSTRACT:

In Thailand, biodiversity is part of the high school biology curriculum and is important for students to understand, as it is not only essential for maintaining natural systems but also provides invaluable benefits to humans through services such as food security, human health and well-being, and economic value. This study developed two competency-enhancing activities. Activity 1, Causes of Biodiversity Loss, helps students understand the concept of the 'extinction vortex', discuss key threats, and propose relevant case studies or examples using reliable sources with proper citations, thereby promoting thinking and communication competencies. Activity 2, What Species Can Be Found?, involves surveying organisms in a selected habitat using citizen science tools like Seek by iNaturalist and databases such as GBIF, TH-BIF, the IUCN Red List, etc., thereby promoting competencies in thinking, communication, and technology use. Students recorded both local and alien species they found, then used their findings to create media about a selected organism, share it on social media, and present their ideas.

The activities were piloted with 12th-grade students from two schools (School 1: 12 students; School 2: 30 students) to gather feedback for further development. After completing the activities, students responded to a 5-point rating scale questionnaire, and teachers submitted classroom reflection reports. Results revealed that in Activity 1, most students found the activity engaging and aligned with active learning, though they felt that classroom time was somewhat limited. Similarly, in Activity 2, students appreciated the active learning approach but again reported time constraints. Reflection reports indicated positive collaboration and task management among most students, particularly in group work. However, some students were less enthusiastic due to familiarity with the activity format, while others showed high interest, especially in Activity 1. While both activities supported communication skill development, Activity 2 enhanced students' technological skill through the use of digital tools for biodiversity monitoring.

Common challenges included limited analytical thinking, difficulties in information search and citation, and insufficient time for media creation. In some cases, data inaccuracies during fieldwork affected the outputs. Teachers addressed these issues by offering clear guidance and ongoing support.

For further activity development, in Activity 1, students should be encouraged to explain why the selected case study is relevant to biodiversity loss, to enhance their reasoning and analytical thinking. In Activity 2, students could be shown how to use the application and databases prior to the main activity to ensure familiarity. Providing additional training in research and citation skills, as well as offering detailed teacher guidance, may further support student success and reduce time constraints. These findings highlight the importance of well-structured, interactive learning environments that may promote both content understanding and competency development in biodiversity education.

KEYWORDS:

Biodiversity Education; Competency-Based Learning; Citizen Science

Calibration of thermal dissipation probes for water use measurements in *Terminalia catappa* and *Tabebuia rosea*: A preliminary study of tropical urban forest species

Chomchan Sittikit¹, Palita Kunchorn² and Pantana Tor-ngern^{3,4,*}

¹Chulalongkorn University Demonstration Secondary School, Bangkok, 10330, Thailand

²International Program in Hazardous Substance and Environmental Management, Graduate School, Chulalongkorn University, Bangkok, 10330, Thailand

³Department of Environmental Science, Faculty of Science, Chulalongkorn University, Bangkok, 10330, Thailand

⁴Water Science and Technology for Sustainable Environment Research Unit, Chulalongkorn University, Bangkok, 10330, Thailand

*Corresponding author, e-mail: pantana.t@chula.ac.th

ABSTRACT:

Forest ecosystems worldwide face increasing pressure from climate change, making accurate monitoring of tree health essential for biodiversity conservation. *Terminalia catappa* (tropical almond) and *Tabebuia rosea* (pink trumpet tree) are common urban forest species that provide critical wildlife habitat while delivering key environmental benefits including carbon storage, air purification, and temperature regulation. Understanding water use patterns in these trees is crucial for developing effective forest management strategies that protect both biodiversity and ecosystem health. Thermal dissipation probes (TDPs) are widely used to measure tree water use through stem monitoring, relying on empirical functions originally derived from three conifer species. However, recent studies indicate that TDPs require species-specific calibration, as wood properties vary among species and may affect measured values. Given the important ecological roles of *T. catappa* and *T. rosea* in supporting urban wildlife and their increasing use in urban planning, establishing accurate calibration methods for these species is essential for reliable tree monitoring and effective conservation management. We conducted a calibration study using four *T. catappa* and four *T. rosea* potted saplings with stem circumferences ranging from 13 to 19 cm, grown on a building balcony at Chulalongkorn University. All saplings were equipped with self-constructed TDPs and automatic weighing scales, with twice-daily watering via an automated irrigation system. Data from both systems were recorded by data loggers every 30 minutes from June 11 to June 17, 2025. For each species, we analyzed the relationship between actual water uptake rates from weighing scales (Fd_{actual}) and TDP values (K) using regression analysis. Results revealed a significant linear relationship for *T. catappa* ($Fd_{actual} = 46.264K + 11.395$, $R^2 = 0.1415$, $p < 0.0001$) and a significant quadratic relationship for *T. rosea* ($Fd_{actual} = 1214.1K^2 - 244.58K + 43.486$, $R^2 = 0.1820$, $p < 0.0001$). However, low R^2 values suggest substantial data variation, indicating that long-term data collection across diverse environmental conditions and phenological stages (wet vs dry seasons, leaf development phases) would strengthen these relationships. This study represents an initial investigation into calibrating TDP equations for tropical trees in Thailand, where such research remains limited. Expanding the dataset and incorporating additional variables could enhance the precision of water-use estimations, contributing to more informed urban forest management and conservation strategies under climate change pressures.

KEYWORDS:

Thermal dissipation probe; Sap flux density; Gravimetric measurement; *Terminalia catappa*, *Tabebuia rosea*.

Evaluation of plant growth promoting activities of actinomycetes under drought stress for the development of bioinoculant

Waranya Butdee¹, Ratchanee Mingma^{2,3} and Kannika Duangmal^{1,3}

¹Department of Microbiology, Faculty of Science, Kasetsart University, Bangkok 10900, Thailand

²Department of Microbiology, Faculty of Liberal Arts and Science, Kasetsart University, Nakhon Pathom 73140, Thailand

³Biodiversity Center Kasetsart University (BDCKU), Kasetsart University, Bangkok 10900, Thailand

*Corresponding author: fscikkd@ku.ac.th

ABSTRACT:

Drought is one of the main abiotic factors affecting global agricultural productivity. The application of bioinoculants containing plant growth promoting actinomycetes (PGPA) is considered a promising and environmentally friendly approach to enhancing plant resistance to drought stress. This study aimed to explore the potential of actinomycete strains isolated from various habitat for the production of bioinoculant in the application to enhance plant growth under drought condition. Four actinomycete strains were subjected to drought tolerance tests at different concentrations of polyethylene glycol (PEG)-6000, and assessed for their plant growth promoting activities. The result showed that all strains exhibited drought tolerance at 10%, 30%, and 50% concentrations of PEG-6000. Additionally, these strains demonstrated the ability to produce indole-3-acetic acid (IAA), siderophore, ammonia, and 1-aminocyclopropane-1-carboxylate (ACC) deaminase, including nitrogen fixation and phosphate solubilization properties at 28, 37, and 42°C. The 16S rRNA gene sequences analysis revealed that all strains belonged to the genus *Streptomyces*, including *Streptomyces deserti* LD1.3-S2 (from mangrove), *Streptomyces ardesiacus* PH3-1 (from shrimp pond), *Streptomyces sulphureus* LD1.1-S2 (from mangrove), and *Streptomyces yokosukanensis* KK5PN1 (from peat swamp forest). The formulation of these isolates as a bioinoculant was investigated using sodium alginate-based formulation. The isolates were cultivated on broken-milled rice for 7 days at 28 °C and then prepared as freeze-dried powder. These inoculums were gently mixed under aseptic conditions with a 2% (w/v) sodium alginate solution at a ratio of 1:6 for the preparation of alginate beads. The result showed that encapsulated strains maintained high viability after the storage at 4°C for three months. The co-cultivation of bioinoculants to promote plant growth under drought stress are under investigation. These bioinoculants could serve as alternative methods for sustainable agriculture.

KEYWORD:

Actinomycete, *Streptomyces*, Plant growth promoting, Drought stress, Bioinoculants

Diversity of Invertebrate-Pathogenic Fungi in and around the Pha Daeng Mine, Tak Province, Thailand

Suchada Mongkolsamrit^{1,*}, Kanoksri Tasanathai¹, Donnaya Thanakitpipattana¹, Kanraya Liangsiri¹, Jennifer Luangsa-ard¹ and Nattawut Boonyuen¹

¹National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), 111 Thailand Science Park, Phahonyothin Road, Khlong Nueng, Khong Luang, Pathum Thani, 12120, Thailand

*Corresponding author, e-mail: suchada@biotec.or.th

ABSTRACT:

The Pha Daeng Mine, located in Tak Province, northwestern Thailand, is a former zinc mining site that has ceased operations and is currently undergoing ecological restoration to regain its natural fertility. This area presents a unique opportunity to explore microbial diversity, particularly invertebrate-pathogenic fungi, which may play an important role in natural habitats. This study aimed to investigate the diversity of invertebrate-pathogenic fungi in and around the Pha Daeng Mine. Field surveys were conducted during the rainy season of 2024, covering six nature trails and one agricultural area. Fungal samples were identified based on morphological characteristics under a microscope and molecular techniques. A total of 26 species of invertebrate-pathogenic fungi were recorded. The family Ophiocordycipitaceae showed the highest species richness with 13 species, followed by Cordycipitaceae (7 species), Clavicipitaceae (5 species), and Polycephalomycetaceae (1 species). Notably, two new species of *Metarhizium* were isolated from cicada cadavers. The discovery of local strains of *Beauveria* and *Metarhizium* highlights their potential for development as biocontrol agents. These findings provide valuable insights into the diversity and ecological significance of invertebrate-pathogenic fungi in a post-mining landscape undergoing ecological restoration. Continued surveys across additional trails and habitats in the region are recommended to achieve a more comprehensive understanding of fungal diversity and to support the conservation and sustainable use of biological resources.

KEYWORDS:

Diversity; ecological restoration; invertebrate-pathogenic fungi

Ethnomycology of Macrofungi in Selected Areas of South Cotabato, Mindanao, Philippines

Eiza V. Barotas¹, Orlando D. Sakam¹, Annie D. Francisco¹, MS, Ziljih S. Molina¹ and **Rodelyn M. Dalayap, PhD^{1,*}**

¹Department of Biology, Sultan Kudarat State University, City of Tacurong, Province of Sultan Kudarat, Mindanao 9800, Philippines

*Corresponding author, e-mail: rodelyndalayap@sksu.edu.ph

ABSTRACT:

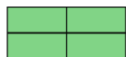
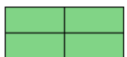
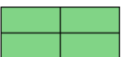
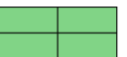
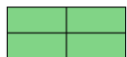
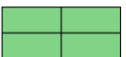
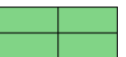
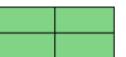
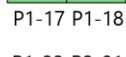
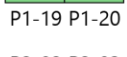
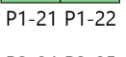
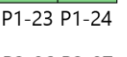
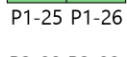
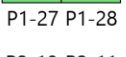
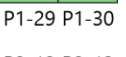
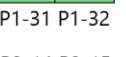
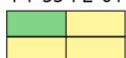
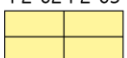
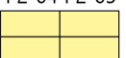
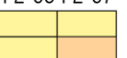
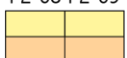
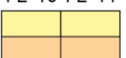
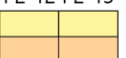
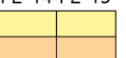
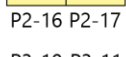
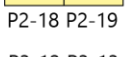
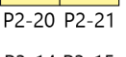
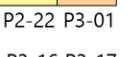
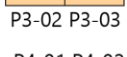
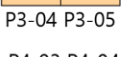
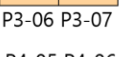
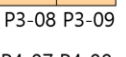
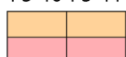
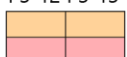
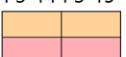
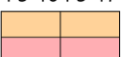
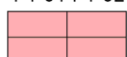
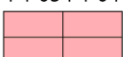
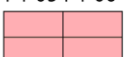
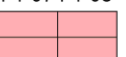
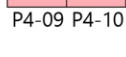
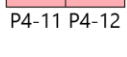
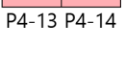
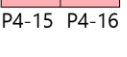
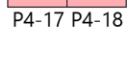
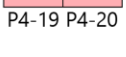
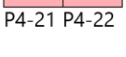
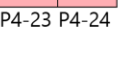
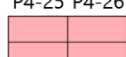
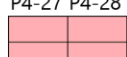
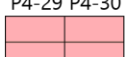
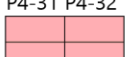
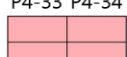
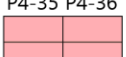
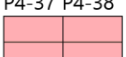
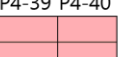
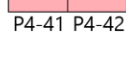
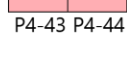
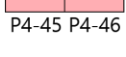
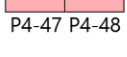
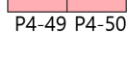
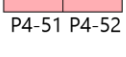
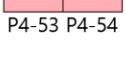
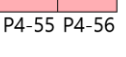
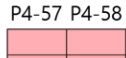
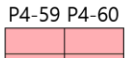
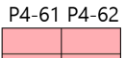
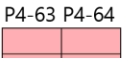
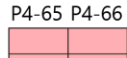
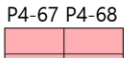
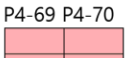
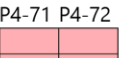
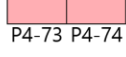
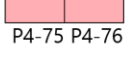
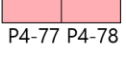
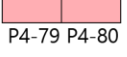
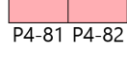
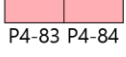
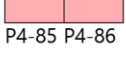
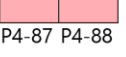
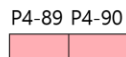
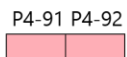
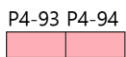
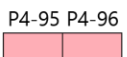
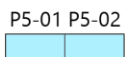
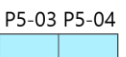
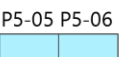
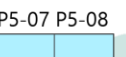
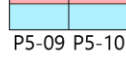
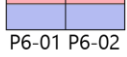
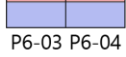
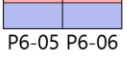
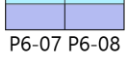
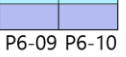
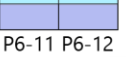
Macrofungi are one of the most diverse group of organisms inhabiting all types of ecosystems. They have significant ecological, cultural, and economic importance. Identification and classification of macrofungi was conducted at selected areas of Norala and T-boli South Cotabato. Collection and photo-documentation of macrofungi species were done along the established transect lines. The collected macrofungi species were classified, identified and verified by expert. Result showed 10 families with 21 species namely *Auricularia auricula-judae*, *Auricularia mesenterica*, *Auricularia polytricha*, *Ganoderma carnosum*, *Ganoderma lucidum*, *Ganoderma applanatum*, *Termitomyces clypea* *Cymatoderma* sp., *Volvariella volvacea*, *Earliella scabrosa*, *Favolus emeric*, *Microporus xanthopus*, *Trametes ellipsospora*, *Trametes hirsute*, *Trametes elegans*, *Trametes gibbosa*, *Trametes ochracea*, *Coprinellus disseminatus*, *Cookeina tricholoma*, *Tremella* sp. and *Daldinia concentrica*. The different macrofungi species have various uses such as for culinary and food; medicine bioremediation, decomposition or degradation for nutrient cycling, clothing, fire starter, cosmetics and ornamental.

KEYWORDS:

Macrofungi, ethnomycology, economic importance, South Cotabato, Mindanao

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