



ABSTRAK BIODIVERSITAS BERSUMBER DARI PANGKALAN DATA NASIONAL

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BALAI BESAR PELATIHAN KESEHATAN HEWAN

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Abstrak Indikatif jurnal Biodiversitas ini disusun dalam rangka menyediakan layanan teknis kepada para ASN BBPKH Cinagara yang fokus terhadap *Agricultural and Biological Sciences Animal Science and Zoology Plant Science Biochemistry, Genetics and Molecular Biology Molecular Biology*. Abstrak Indikatif Jurnal Biodiversitas sangat baik disitasi sebagai acuan untuk keperluan riset maupun kegiatan layanan jasa pada unit perpustakaan Balai Besar Pelatihan Kesehatan Hewan (BBPKH) – Cinagara, karena sudah berupatasi internasional dengan reputasi Q-2 Scopus dan merupakan jurnal dari Indonesia.

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1. Assessing forest biomass and diversity of tree populations in Tekam Forest Reserve, Pahang, Malaysia/ **Ruziman H.H.; Mohti A.; Nik Ali N.N.B.N.A.; Ismail A.; Pardi F.** Biodiversitas. ISSN:1412033X 9 v.25 28212827 (2024) Final

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85208578371&doi=10.13057%2fbiodiv%2fd250901&partnerID=40&md5=60d154c702126f28d266a930bedf07fa

Abstract: Free Air CO₂ Enrichment (FACE) experiments are long-term monitoring projects to comprehend the response of forest ecosystems to future atmospheres with CO₂ enriched. Therefore, the research aims to determine the forest biomass and species diversity in the FACE system of Tekam Forest Reserve (TFR), Pahang, Malaysia. The sampling plots of 25 m × 20 m were established in TekamFACE as experimental plot and control plot in TFR. Allometric equation, Shannon-Wiener, and Evenness indices were used to estimate the standing biomass, carbon stock and species diversity, respectively. Tekam FACE system recorded total forest biomass of 54.38 ton/ha, contributed by 42.82 tons/ha of Above-Ground Biomass (AGB) and 11.56 tons/ha of Below-Ground Biomass (BGB). High carbon stock was also estimated at both forest plots with 27.19 tons/ha in TekamFACE and 17.35 tons/ha in control plot. These values indicated that the forest has high biomass, which can contribute to carbon sequestration that help mitigate the impacts of climate change. Further, this forest recorded high Species Diversity (H') and Species Evenness (E) at TekamFACE (H' = 4.04; E = 0.93) and control plot (H' = 3.53; E = 0.83). Overall, this research emphasized that forests with rich biodiversity have substantial carbon sequestration capacity for the adaptation of forest ecosystems to future atmospheric changes. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Climate change; FACE; forest; species diversity; Tekam Forest Reserve

2. Potential of antimicrobial-producing endophytic bacteria from Balikpapan endemic ginger (*Etlingera balikpapanensis* A.D. Poulsen)/ **Fatimah; Asritafriha L.; Salsabila S.; Dewi E.K.; Ni'matuzahroh; Gerald A.; Ramadhan R.; Suwito H.; Rahman A.; Riyadi L.** Biodiversitas. ISSN:1412033X 9 v.25 30053013 (2024) Final

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85208581661&doi=10.13057%2fbiodiv%2fd250922&partnerID=40&md5=de0962d53c808f43d909baca1ef894bc

Abstract: *Etlingera balikpapanensis* A.D. Poulsen is a new species of the Zingiberaceae family, which was discovered as an endemic species in the Balikpapan, Kalimantan. This study aimed to isolate endophytic bacteria from endemic Balikpapan ginger (*E. balikpapanensis*) and evaluate its antimicrobial activity against *Escherichia coli*, *Staphylococcus aureus*, and *Candida albicans* and to identify the most promising antimicrobial isolates. Plant samples include roots, stems, and leaves. The process of isolating bacteria from various plant parts, such as roots, stems, and leaves, involved repeated subculturing until pure isolates were obtained. Seven pure isolates were successfully obtained, coded as 6D, 5R, 2R, 3D1, 10D, 4R2, and 2D. Macroscopic, microscopic, and biochemical characterization of the seven isolates was carried out. The seven endophytic bacteria had varied macroscopic characteristics and were Gram-positive. The disc diffusion method was used to determine the ability of isolates to produce antimicrobial agents. The isolates showed antibacterial activity against *E. coli* and *S. aureus*. Isolates 3D1 and 5R showed the highest antibacterial activity against *E. coli* (8.20±0.47 mm and 8.57±0.08 mm), and 5R also showed the highest antibacterial activity against *S. aureus* (8.14±0.49 mm). These results demonstrate the potential of these isolates as effective antimicrobial agents. The 16S rRNA gene analysis revealed that isolate 3D1 was identified as *Bacillus cereus* strain

PJA4.2 and isolate 5R as *Micrococcus luteus* strain SGAir0127 with similarity of 99.55% and 100%, respectively. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: 16S rRNA gene; Antimicrobial agent; endemic ginger; endophytic bacteria; *Etlingera balikpapanensis*

3. Diversity of Diptera in mixed-used agroforestry area of Tun Razak Agricultural Research Centre, Pahang, Malaysia/ Sahrir P.R.M.; Mustaffa M.; Izam N.A.M.; Nasir D.M.; Hatta S.K.M.; Abdullah N.A.. Biodiversitas. ISSN:1412033X 10 v.25 35763584 (2024) Final

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Link: <https://www.scopus.com/inward/record.uri?eid=2-s2.0-85209173787&doi=10.13057%2fbiodiv%2fd251019&partnerID=40&md5=662b779f86f37ed228449049eb218d79>

Abstract: Sahrir PRM, Mustaffa MB, Izam NAM, Nasir DM, Hatta SKM, Abdullah NA. 2024. Diversity of Diptera in mixed-used agroforestry area of Tun Razak Agricultural Research Centre, Pahang, Malaysia. Biodiversitas 25: 3576-3584. The order Diptera, comprising flies, mosquitoes, midges, and gnats, plays a significant role in the agricultural ecosystem as pests and pollinators. With agricultural activities posing a threat to insect populations globally, there is a need for studies on the potential of managed agroecosystems as habitats for this order. This study provides preliminary information on Diptera diversity in a mixed-used agroforestry area at the Tun Razak Agricultural Research Centre (Pusat Penyelidikan Pertanian Tun Razak/PPPTR), Pahang, Malaysia. The diversity assessment was conducted using malaise traps in various areas within the PPPTR, including a small forest fragment, a rubber plantation, an oil palm plantation, and an orchard, over two weeks in February and March 2023 yielded promising results. A total of 1,077 individuals representing 17 families, 36 genera, and 82 morphospecies of Diptera were collected during the research. The most abundant family recorded was Dolichopodidae, with 429 individuals, followed by Phoridae (140 individuals) and Calliphoridae (130 individuals). Notably, rubber plantations exhibited the highest diversity of Diptera ($H'=3.228$), while forest fragments showed the lowest diversity ($H'=2.745$), as indicated by the Shannon-Wiener Diversity Index. These findings highlight the potential of managed agroforestry areas as crucial Diptera conservation habitats, instilling hope and optimism in the scientific community. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Entomofauna; flies; fragmented forest; horticulture

4. A comprehensive study of phytonematodes of grape plants in the conditions of the Surkhandarya Valley, Uzbekistan/ Khuramov A.; Bobokeldieva L.; Choriyeu S.; Rakhmatullaev B.; Khimmatov N.; Raimov S.; Narzullaeva G.; Bobokeldiyeva S.; Mukhiddinova M.; Karshieva M.. Biodiversitas. ISSN:1412033X 11 v.25 40334042 (2024) Final

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Abstract: Article analyzes the faunal complex of grape phytonematodes collected from 2018 to 2020 from 14 districts and 28 farms of the Surkhandarya Valley, Uzbekistan. Sample collection was carried out using the route (collecting samples by going to predetermined areas in a certain direction) method generally accepted in modern faunal studies. The Berman funnel method was used to isolate nematodes permanent and temporary preparations for

determination of the type and gender of nematodes were prepared according to the Seinhorst method; when determining the species of phytonematodes, the works of domestic and foreign authors were used, as well as morphometric indicators obtained using the generally accepted de Mann formula. During the study period, we found 118 species of phytonematodes belonging to 54 genera, 33 families, 9 orders, and 2 subclasses on grape agrocenoses. The discovered nematodes are distributed among the orders as follows: The order Monhysterida is represented by 5 species: Enoplida-1, Mononchida-6, Dorylaimida-23, Alaimida-5, Rhabditida-7, Teratocephalida-25, Aphelenchida-19 and the order Tylenchida-27 species. The degree of dominance of registered phytonematodes in the roots and root soil of grapes was studied. According to the frequency of occurrence of the detected species of phytonematodes in root and soil samples, there were no dominant or eudominant species; in the root soil of grapes; of the subdominants 10 species and 108 species were classified as subprecedents. In the root system of grapes, the subdominants are total 10 species. In the root system of grapes, all other species of phytonematodes registered (74 species) are classified as subprecedents. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Degree of dominance; ecological classification; fauna; grapes; phytonematodes

5. Diversity of epipellic microalgae in a shallow, tropical estuary of Northern Mindanao, Philippines/ **Tuong E.J.A.; Tubio E.G.; Leopardas V.E.**. Biodiversitas. ISSN:1412033X 9 v.25 32373245 (2024) Final

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Abstract: Tuong EJA, Tubio EG, Leopardas VE. 2024. Diversity of epipellic microalgae in a shallow, tropical estuary of Northern Mindanao, Philippines. Biodiversitas 25: 3237-3245. Microphytobenthos are important primary producers in many of the most critical ecosystems, including the estuary. However, environmental variables, including season, influenced their abundance and diversity. In this study, spatial and temporal patterns of epipellic microalgae in Talabaan Estuary Naawan, Misamis Oriental, were conducted last October 2016 and February 2017 to represent wet and dry seasons, respectively. The species composition and diversity of epipellic microalgae samples were assessed using an improvised corer (2 cm, inner diameter). Only the upper 10 mm. of the cored sample was analyzed. Forty-eight species belonging to 33 families and 35 genera were identified and documented in the estuary. Diatoms (Class Bacillariophyta) were found to be the most dominant group, with about 90% of the epipellic microalgae community composed mainly of chains of cells and formed in colonies. Navicula sp. and Nitzschia sp. were among the species found in all sampled stations. The common occurrence of this species across all stations in wet and dry seasons indicated that they are the typical euryhaline species of this tropical estuary. The abundance and diversity of the epipellic microalgae community were found to vary across stations and seasons ($p < 0.05$), but the interaction between these variables did not differ significantly. When abiotic and biological factors were regressed, a significant relationship was found with temperature, while all other factors exhibited no considerable variation. This highlights the effect of seasons in shaping benthic microalgae communities and is an essential factor in structuring microphytobenthic communities in an estuary. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Algae; diatoms; dry season; Talabaan estuary; wet season

6. Bird communities in the tropical peri-urban landscape of Bogor, Indonesia/ **Nugroho S.P.A.; Mardiasuti A.; Mulyani Y.A.; Rahman D.A.**. Biodiversitas. ISSN:1412033X 12 v.24 69866998 (2024) Final

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Abstract: Nugroho SPA, Mardiasuti A, Mulyani YA, Rahman DA. 2023. Bird communities in the tropical peri-urban landscape of Bogor, Indonesia. *Biodiversitas* 24: 6986-6998. Amidst the urbanization threat, peri-urban landscapes can play an important role in biodiversity conservation, particularly among birds. Therefore, to study species and functional diversity of bird communities in the tropical peri-urban landscape, we observed four habitat types (forest, plantation, built-up area, and farmland) in the Ciampea-Dramaga Landscape, Bogor, Indonesia, from September to December 2020 and September to December 2021. A standard point method was used to observe birds, and several diversity indices were used for data analysis. Altogether, we recorded 11,290 individual birds of 61 species and 33 families. The species diversity tended to be higher in the increasing habitat succession stages. Forest had the highest species diversity ($H'=3.17$), followed by plantation ($H'=2.87$), built-up area ($H'=2.54$), and farmland ($H'=2.23$). Meanwhile, functional diversity revealed that all feeding guilds can be observed in the forest. The species richness of frugivore-insectivores dominated all habitats, and their abundance are also dominated in forest and plantation habitats. In contrast, granivores dominated farmland, and fly-catching insectivores dominated built-up areas. Due to its relatively high bird diversity in the study area, it needed to be conserved, including habitat management at the landscape scale, strengthening policies and conservation actions, and raising public awareness. © 2023, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Bird; conservation; diversity; ecology; urbanization

7. Diversity and ethnobotany of plants used as natural dye in traditional woven by local community in Belu District, Indonesia/ **Seran W.; Kaho L.M.R.; Pellondo'u M.E.; Mau A.E.; Aini Y.; Riwu Kaho N.P.L.B.; Soimin M.** *Biodiversitas*. ISSN:1412033X 11 v.25 44154424 (2024) Final

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Abstract: Natural dye plants used by indigenous people for coloring woven fabrics are considered an important and unique Traditional Ecological Knowledge (TEK), especially in East Nusa Tenggara, Indonesia, which has high biodiversity and endemism. This study is aimed to document the diversity, conservation status and ethnobotanical knowledge of dye-producing plant species used by local community in Belu District, East Nusa Tenggara Province. We used in-depth interviews with local weavers to collect data on plants used as natural dyes and observed the processes of extracting dyes and coloring the yarn. We documented 18 plant species used as dye for traditional tenun ikat (tied woven). The coloring process includes oiling the yarn, tying, measuring, dyeing, and drying, followed by weaving processes. Stems and leaves are the most used part for producing dyes (each with 39%), followed by rhizomes (11%), fruits (6%) and roots (5%). Based on conservation status, only one species is conservation concern with status of endangered, i.e., *Tectona grandis* L.f., which produce purple and red colors. This study is useful as a record to preserve the rich ethnobotanical knowledge on the use of plants for coloring materials in the eastern region of Indonesia, and to raise awareness of the importance of documenting and conserving traditional plant-based practices. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Conservation; dye plant; ethnobotany; local weaver

8. Species diversity, mosquito behavior, and microfilariae detection in vectors and reservoirs in filariasis-endemic areas of Bengkulu, Indonesia/ **Kermelita D.; Hadi U.K.; Soviana S.; Tiuria R.; Novianto D.** Biodiversitas. ISSN:1412033X 9 v.25 31253131 (2024) Final

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[85208551337&doi=10.13057%2fbiodiv%2fd250934&partnerID=40&md5=466e2b14d0767a6396dce1da52d29a20](https://www.scopus.com/inward/record.uri?eid=2-s2.0-85208551337&doi=10.13057%2fbiodiv%2fd250934&partnerID=40&md5=466e2b14d0767a6396dce1da52d29a20)

Abstract: Filariasis, recognized by the WHO as a neglected tropical disease, remains a significant global health challenge, particularly in Southeast Asia. In Bengkulu Province, Indonesia, 66 cases of filariasis were reported between 2010 and 2020, with the highest prevalence found in Mukomuko and Seluma Districts. This study analyzed the vector behavior and detection of filariasis reservoirs in endemic areas of Bengkulu Province. Human landing and resting collections were employed for mosquito collection for 12 h (18:00-06:00), and blood sampling was performed on reservoir animals (*Canis familiaris*, *Felis catus* Linnaeus, 1758, and *Macaca fascicularis* (Raffles, 1821)). Mosquito diversity was analyzed using several diversity indices. *Filaria* larvae in mosquitoes were detected using Polymerase Chain Reaction (PCR) methods, and filaria in reservoir animals were detected using blood smears with Giemsa staining. The result showed that 17 mosquito species were captured in the filariasis-endemic regions of Bengkulu Province: *Culex quinquefasciatus* Say, 1823; *Culex hutchinsoni* Barraud, 1924; *Culex gelidus* Theobald, 1901; *Culex pseudovishnui* Colless, 1957; *Culex vishnui* Theobald, 1901; *Armigeres subalbatus* (Coquillett, 1898); *Aedes aegypti* (Linnaeus, 1762); *Aedes albopictus* (Skuse, 1894); *Anopheles tessellatus* Theobald, 1901; *Anopheles vagus* Döntiz, 1902; *Anopheles minimus* Theobald, 1901; *Anopheles indefinitus* (Ludlow, 1904); *Anopheles sundaicus* (Rodenwaldt, 1948); *Anopheles barbirostris* Wulp, 1884; *Anopheles maculatus* Theobald, 1901; *Anopheles* sp., and *Mansonia annulata* Leicester, 1908. *Culex pseudovishnui* exhibited the highest indoor density among the mosquito species, whereas *C. quinquefasciatus* exhibited the highest outdoor density. *Filaria* larvae were not detected in all mosquito sample pools based on the PCR results, whereas microfilariae of *Dirofilaria immitis* (Leidy, 1856) Railliet & Henry, 1911 were identified in the reservoir (Canine) blood samples. Thus, the presence of microfilariae in reservoir animals must be monitored because they can transmit filariasis to the community. Control strategies should be developed for endemic regions in Bengkulu Province. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Detection microfilaria; *Dirofilaria immitis*; neglected tropical diseases

9. Genetic diversity of black soldier flies in Vietnam based on DNA COI sequence/ **Nguyen T.N.; Tran T.B.N.; Tran H.N.** Biodiversitas. ISSN:1412033X 12 v.24 67276732 (2024) Final

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[85183661475&doi=10.13057%2fbiodiv%2fd241235&partnerID=40&md5=a0e63c59a01c70b3234a9414f2ea438e](https://www.scopus.com/inward/record.uri?eid=2-s2.0-85183661475&doi=10.13057%2fbiodiv%2fd241235&partnerID=40&md5=a0e63c59a01c70b3234a9414f2ea438e)

Abstract: The Black Soldier Fly (BSF), *Hermetia illucens* (Linnaeus, 1758), is found in temperate and tropical regions of the world. In recent years, BSF has been cultivated as fodder in some areas of Vietnam. The genetic diversity of BSF in Vietnam has not yet been assessed. This study aimed to investigate the nucleotide diversity in COI sequences of BSF in Vietnam. We examined the COI nucleotide sequences of 22 BSFs using flies or larval tissue samples for DNA extraction and subsequent sequencing. Our analysis showed that the nucleotide composition of BSF consisted of 25.36% A, 36.04% T, 21.25% C, and 17.35% G, with a significant prevalence of A+T nucleotides of 61.40% compared to 38.60% for G+C nucleotides. Among 22 individual BSFs samples collected from ten provinces and cities, spanning

seven agro-ecological regions in Vietnam, we identified 9 different haplotypes, which were distributed in five clades but mainly clustered in two main clades: E and F. Clade E, prominently represented by branch E, showed a higher abundance in Asia, while Clade F has been identified in Europe, Uganda, South Korea, Oceania and North America. Our results highlight the relatively high genetic diversity of the Vietnamese BSF population. In addition, the COI nucleotide sequences of these Vietnamese BSF samples were similar to those of Asian and Australian countries, showing significant similarities to the Palearctic and Oriental regions. These results provide valuable insights to inform BSF breeding and development in Vietnam. © 2023, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Black soldier fly; DNA-COI sequence; genetic diversity

10. A mid-Holocene pollen record of mangrove diversity on the coast of Ujung Genteng, the southern edge of Sunda Shelf, Indonesia/ **Nugroho S.H.; Rizal Y.; Zaim Y.; Yulianto E.; Putra P.S.; Riyanto A.M.; Amar.** Biodiversitas. ISSN:1412033X 10 v.25 36533664 (2024) Final

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Abstract: Nugroho SH, Rizal Y, Zaim Y, Yulianto E, Putra PS, Riyanto AM, Amar. 2024. A mid-Holocene pollen record of mangrove diversity on the coast of Ujung Genteng, the southern edge of Sunda Shelf, Indonesia. Biodiversitas 25: 3653-3664. The Sunda Shelf provides the most informative data for studying mangrove ecosystems. However, the southern edge of the Sunda Shelf adjacent to the Sunda megathrust zone has yet to be studied. This study aimed to provide a paleoecology record of the Ujung Genteng mangrove ecosystem during the mid-Holocene (over 6,300 cal year BP (Before Present)). We looked at changes in a mangrove ecosystem using pollen and radiocarbon data from the UG 7B core. *Rhizophora* sp. initially dominated at c. 6,200-6,100 cal year BP. The ecosystem gradually declined, transitioning to a back mangrove environment. A decrease in the mangrove and back mangrove pollen since 4,200 cal year BP, indicating a shift away from the mangrove forest. In contrast, higher non-mangrove pollen frequency indicates a closer distance to the lowland. By 400 cal year BP, all mangrove pollen vanished, and the environment became almost completely terrestrial. The implications of this research contribute to improved insights into mangrove resilience and resistance to environmental and anthropogenic stressors, aiding effective coastal management and adaptation strategies. Our study also highlights the unique conditions of Sunda Shelf paleoecology, contributing to a more comprehensive regional knowledge and offering an important reference for further investigations on coastal ecosystem dynamics. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Biodiversity; coast of Ujung Genteng; mid-Holocene; pollen; *Rhizophora*; Sunda Shelf

11. Amplicon metagenome comparison of Tandag River, Surigao del Sur, Philippines, based on high-throughput parallel DNA sequencing analysis of bacterial communities/ **Eupeña-Caray R.G.; Ramos G.B.; Panduyos J.B.; Bacquial L.S.; Tabugo S.R.M..** Biodiversitas. ISSN:1412033X 10 v.25 34643472 (2024) Final

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Abstract: Rivers serve as a vital freshwater reservoir for the environment and human consumption. Biomonitoring based on eDNA is essential for aquatic ecosystems. The present study investigates the bacterial taxonomic diversity of this ecosystem using the V1-V3 16S rRNA regions obtained from paired-end Illumina MiSeq reads. A total of nine amplicon libraries (U1, U2, U3, M1, M2, M3, D1, D2, D3) were constructed corresponding to the sites (U-upstream, M-midstream, D-downstream) of the Tandag River. After post-quality control and processing, there were 608,099 amplicon sequence variants (ASVs), representing 1194 families and 2090 genera. Results showed that the most abundant ASVs were affiliated with genera *Bacillus*, *Pseudomonas*, *Ralstonia*, *Alcaligenes*, and *Pseudarcicella*, along with unclassified bacteria derived from Gammaproteobacteria, Alphaproteobacteria, Verrucomicrobia subdivision, Flavobacteria, and Pseudomonadaceae. The bacterial alpha diversity was ranked upstream>midstream>downstream. An increase in the abundance of *Bacillus* (Firmicutes) and Gammaproteobacteria in an urbanized zone indicated a high level of human activity and an important threat to public health. Noteworthy is that the alkaline environment characterized by increased pH levels favors the occurrence of alkaliphilic bacteria. Microbial community structure was influenced by anthropogenic interference and selective pressure from loads of urban discharge in the area. The functional prediction of bacterial communities by Parallel-Meta Suite (PMS) using the PICRUSt algorithm suggests functions related to metabolism and environment information processing. The presence of xenobiotic biodegradation bacteria highlights future possible applications. Findings contribute to understanding microbial communities in response to rapid urbanization. This is the first account of high-throughput sequencing analysis of bacterial communities in an urban river under anthropogenic stress in the Philippines. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: amplicon sequencing; ASV; functional prediction; PMS; river

12. Species composition and diversity along the elevational gradient of a low tropical hill in Teramuo Hill, Bau, Sarawak, Malaysia/ **Noweg T.; Grinang J.; Nelson J.; Philip B.; Felix S.E.; Kalu M.** Biodiversitas. ISSN:1412033X 9 v.25 33203330 (2024) Final

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Abstract: Noweg T, Grinang J, Nelson J, Philip B, Felix SE, Kalu M. 2024. Species composition and diversity along the elevational gradient of a low tropical hill in Teramuo Hill, Bau, Sarawak, Malaysia. Biodiversitas 25: 3320-3330. Numerous efforts have been made to study the diversity pattern of trees in Nature Reserves in the Bau District of Sarawak, Malaysia. However, studies on tree diversity along the elevational gradient in the district's low tropical hills still need to be completed. This study sought to evaluate the composition and diversity of tree species on a low tropical rainforest hill in the Bau District of Sarawak. The study's specific objectives include: (i). Identifying the species composition at different elevations and (ii). Measuring the species diversity and richness across different elevational gradients. The study site was Teramuo Hill, a 9.2-hectare local recreational area in Bau District, Sarawak, belonging to a Bidayuh village community. The hill encompasses three forest types (primary, secondary, and agroforest) and has suffered degradation from both human activity and natural causes. A total of 28 sampling sites were arranged in six vertical lines along the elevational gradient, with the lowest elevation being below 45 meters above sea level (m asl.) and the highest about 100 m asl.. The study found that the species composition and species types dominating at different elevations varied. A distinct pattern emerged in species diversity and richness across the elevational gradient. Between 61 and 75 m asl., the mid-elevation zones exhibited the highest species diversity. These results suggest that the main influences are ecological factors and habitat physical variability at different elevations. The findings are essential for understanding how minor elevation changes affect tree communities in tropical forest

environments. This knowledge can assist in planning targeted conservation programs and dictate community priorities in the Bau District of Sarawak, Malaysia. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Borneo; community-managed; diversity; elevation; species composition

13. Response of transgenic tobacco with P5CS gene expression to polyethylene glycol-induced drought stress/ Riduan A.; Santoso D.; Sudarsono. Biodiversitas. ISSN:1412033X 10 v.25 39743984 (2024) Final

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[85210104394&doi=10.13057%2fbiodiv%2fd251057&partnerID=40&md5=118e410a15d397325a73ed2ed21d55f8](https://www.scopus.com/inward/record.uri?eid=2-s2.0-85210104394&doi=10.13057%2fbiodiv%2fd251057&partnerID=40&md5=118e410a15d397325a73ed2ed21d55f8)

Abstract: Drought stress, a significant obstacle in plant growth and production, can be effectively addressed with the use of polyethylene glycol (PEG). This treatment has shown promise in screening plant germplasm responses to drought stress. The objectives of this experiment were to determine the effects of stress due to PEG treatment at 0%, 5%, or 10% concentration on growth, leaf proline content, and their correlation to stress responses in the T1 seedlings derived from five T0 transgenic Gombel Shili (GS) tobacco P5CS. Positive results of total nucleic acid PCR analysis in T1 seedling populations derived from each of the T0 plants indicated that the regenerated T0 plants were transgenic tobacco integrating P5CS transgene. Results of the experiment revealed that the effects of stress due to PEG treatment indicated stress due to PEG treatment (5% or 10%) reduced the growth plants of all tobacco plants. The stress sensitivity index categorized the T1 plants P5CS transgenic GS tobacco into tolerance, medium tolerance, and sensitivity against PEG-induced stress. Notably, the T1 plants P5CS transgenic GS tobacco exhibited better growth with higher plant height, leaf, biomass, and root dry weight compared to non-transgenic tobacco under stress and non-stress conditions. The over-expression of the P5CS gene led to a significant increase in leaf proline content after drought stress was observed in all transgenic tobacco compared to non-transgenic tobacco. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Agrobacterium-mediated genetics transformation; PEG-induced drought stress; proline accumulation; sensitivity index; transgenic tobacco P5CS

14. The potential of cold plasma technology for weed control in the pre-growth and post-growth phases/ Bukhori A.; Guntoro D.; Sudradjat; Sugiarto A.T.. Biodiversitas. ISSN:1412033X 10 v.25 36283636 (2024) Final

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[85208921019&doi=10.13057%2fbiodiv%2fd251024&partnerID=40&md5=b995dc90ddb55f94e9fba3756e35673e](https://www.scopus.com/inward/record.uri?eid=2-s2.0-85208921019&doi=10.13057%2fbiodiv%2fd251024&partnerID=40&md5=b995dc90ddb55f94e9fba3756e35673e)

Abstract: Efforts to reduce the use of herbicides can be made by using cold plasma technology. This technology produces heat energy through the emission of UV plasma light, generated by electrical energy. This research investigates the potential of various cold plasma treatments to inhibit germination, inhibit the growth of weed seeds in soil media, and suppress weed growth. The study was conducted at the Ecotoxicology Laboratory and Seed Propagation Laboratory, Institut Pertanian Bogor, Bogor, Indonesia, from March to September 2023. Three types of weeds used were *Asystasia gangetica* (L.) T.Anderson, *Cyperus rotundus* L., and *Eleusine indica* (L.) Gaertn. Three experiments were designed for this study. The first experiment tested cold plasma on weed seeds, the analysis was

conducted using a single-factor completely randomized designed with varying doses of cold plasma and four replications. The second experiment tested cold plasma technology in soil media, the analysis was conducted using a single-factor completely randomized designed with various doses of cold plasma and seven replications. The third experiment tested cold plasma on the growth of each weed, the analysis was conducted using a single-factor randomized block design with various doses of cold plasma and four replications. The research shows that the application of cold plasma at a dose of 14 kV for 85 seconds can inhibit germination and weed growth in soil media of each type of weed *A. gangetica*, *C. rotundus*, and *E. indica*. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: *Asystasia gangetica*; *Cyperus rotundus*; *Eleusine indica*; weed germination; weed growth

15. Species composition, stand structure, and carbon stock in the agroforestry system of Wana Lestari Community Forestry, West Nusa Tenggara, Indonesia/ **Akdah R.D.; Wijayanto N.; Hartoyo A.P.P.**. Biodiversitas. ISSN:1412033X 9 v.25 33503358 (2024) Final

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Abstract: Climate change is characterized by shifting climate patterns that result in erratic weather phenomena. One of the major consequences of climate change is the reduction in biodiversity and the increased concentration of greenhouse gases (GHGs), primarily carbon. Agroforestry systems (AF) have emerged as a potential solution to mitigate these effects by conserving biodiversity and enhancing carbon stocks. This study aims to analyze the species composition and structure of tree stands and estimate the carbon stock in the AF of the community forest (HKm). The methods used employed included vegetation analysis, stand structure measurement using the Spatially Explicit Individual-based Forest Simulator (SEI-FS), and carbon stock estimation using allometric equations and destructive approaches for seedlings and understory levels. A total of 25 plots, each measuring 20×20 m, were used for data collection. The results show that the species composition in HKm Wana Lestari consists of 63 plant species from 40 families. The highest importance value index (IVI) was recorded for durian (*Durio zibethinus* Murray) at the pole growth level (90.34%), while coffee (*Coffea robusta* L.Linden) emerged as the dominant species within the agroforestry system. The diversity index (H') ranged from 0.40 to 2.29, indicating a medium category of diversity. The stand structure did not follow the expected "J" curve pattern. The total biomass and carbon stock across all growth levels were found to be 228.35 and 107.22 tons/ha, respectively. In conclusion, the agroforestry system in HKm Wana Lestari demonstrates notable species diversity and carbon storage potential, although its stand structure deviates from the ideal "J" curve, suggesting opportunities for further forest management improvements. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Aboveground carbon; *Coffea robusta*; FOLU Net Sink; forest farming; SEI-FS

16. Amino acid profile and potential utilization purposes of albumin from four types of freshwater fish in Makassar, South Sulawesi, Indonesia/ **Nurfaidah; Asikin A.N.; Kasmianti; Angraeni.** Biodiversitas. ISSN:1412033X 11 v.25 41994207 (2024) Final

DOI: 10.13057/biodiv/d251119

Link: <https://www.scopus.com/inward/record.uri?eid=2-s2.0-85211381737&doi=10.13057%2fbiodiv%2fd251119&partnerID=40&md5=f62c7b0772f5cf628fa001463ee8dd0f>

Abstract: Nurfaidah, Asikin AN, Kasmiati, Angraeni. 2024. Amino acid profile and potential utilization purposes of albumin from four types of freshwater fish in Makassar, South Sulawesi, Indonesia. *Biodiversitas* 25: 4199-4207. Albumin, a high-quality protein, is known for its complete amino acid profile, which is essential for numerous biological functions, including immune response and nutritional status maintenance. This study investigates the amino acid composition of albumin in four freshwater fish species commonly found in Indonesia: *Cyprinus carpio*, *Pangasius pangasius*, *Channa striata*, and *Trichopodus trichopterus* to assess their potential utilization in sustainable food resources and nutritional and health-related products. Albumin extraction was performed using homogenization and incubation techniques, followed by amino acid analysis using High-Performance Liquid Chromatography (HPLC). The results revealed the presence of 18 amino acids, including 9 essential and 9 non-essential amino acids. The most abundant amino acids were glutamic acid, aspartic acid, leucine, and lysine, with lysine being particularly noteworthy for its role in wound healing and protein synthesis. Significant variations in the amino acid composition were observed across the species, influenced by factors such as diet, habitat, and species-specific physiology. *P. pangasius* exhibited the highest lysine content (12.01%), while *C. carpio* had the highest glutamic acid content (24.55%) of total amino acid. These findings suggest that the albumin from these freshwater fish species is a valuable source of high-quality protein, with potential applications in developing nutraceuticals, functional foods, and dietary supplements aimed at improving health and nutritional status. Importantly, the study highlights the potential of these fish species as a sustainable source of protein, contributing to food security and supporting the development of affordable, protein-rich products that can enhance public health while reducing the reliance on conventional livestock-based proteins. This study provides new insights into the amino acid composition of fish albumin from Indonesian freshwater species, contributing to the broader understanding of the nutritional value of local fish resources and their role in promoting sustainable food systems. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Functional food; nutraceutical; nutritional evaluation; protein quality

17. State of sediment transport and seagrass distribution under the combined action of velocity and current direction/ **Umar W.; Hasim H.; Moka W.J.C.**. *Biodiversitas*. ISSN:1412033X 11 v.25 45154524 (2024) Final

DOI: 10.13057/biodiv/d251150

Link: <https://www.scopus.com/inward/record.uri?eid=2-s2.0-85212087457&doi=10.13057%2fbiodiv%2fd251150&partnerID=40&md5=466a255d4afdb3148935b90dfeaa8386>

Abstract: This research delves into the intricate dynamics of sediment transport and seagrass distribution on the West Coast of Bone Bay, Indonesia, specifically focusing on the profound influence of ocean currents. Our data, meticulously collected from Karang-Karangan, Siwa, and Sembilan Island, reveal a compelling narrative. We employed quantitative methods, including measuring ocean current speeds using Marotte current meters, which recorded velocities ranging from 0.1 to 0.5 m/s. Sediment samples were analyzed for grain size, with median sizes ranging from 233 μm (fine sand) to 626 μm (coarse sand). Sedimentation rates, a key indicator, were measured using sediment traps, recorded between 10 and 50 $\text{mg}/\text{cm}^2/\text{day}$. Seagrass cover was assessed through line transect sampling, revealing cover percentages from 28 to 45% across the study sites. The results, a testament to the power of scientific inquiry, indicate that Sembilan Island had the highest sedimentation rates and seagrass coverage, which correlates with its unique hydrodynamic conditions, particularly the southward-directed currents. These findings underscore the critical relationship between ocean currents, sediment transport, and seagrass ecosystems, which are essential for the proposed designation of Bone Bay as a marine protected area. This research underscores the

importance of combining quantitative data with a thorough understanding of environmental interactions to effectively manage and conserve coastal ecosystems. Further studies are recommended to explore the detailed mechanisms of these interactions, paving the way for a deeper understanding of our natural world. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Bone Bay; current; seagrass; sedimentation

18. Morphometric variation and ecological niche differentiation in *Hyophila apiculata* and *H. involuta* from karst microhabitats in Kanchanaburi, Thailand/ **Sawangproh W..** Biodiversitas. ISSN:1412033X 11 v.25 45514560 (2024) Final

DOI: 10.13057/biodiv/d251154

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Abstract: Karst environments, characterized by limestone and dolomite formations, host diverse ecosystems shaped by unique geological features such as sinkholes, caves, and underground rivers. These landscapes foster adaptations among flora and fauna, showcasing phenotypic plasticity that enables species to thrive in challenging conditions. This study examines the morphometric variation between *Hyophila apiculata* M.Fleisch. and *H. involuta* (Hook.) A.Jaeger in arid karst microhabitats of Kanchanaburi Province, Thailand. Surveys conducted across 86 sampling points revealed predominantly allopatric populations, with *H. apiculata* present in 26 sites (30%) and *H. involuta* in 58 sites (68%). Sympatric occurrences were rare, found at only two points (2%). Leaf morphometric analyses demonstrated that *H. involuta* exhibits wider leaves and larger leaf areas compared to *H. apiculata*, which features longer and wider median and apical leaf cells with thicker cell walls. Principal Component Analysis (PCA) indicated distinct morphological clusters for the two species, though some overlap was observed, suggesting the possibility of hybridization or transitional forms. These findings underscore the ecological niche differentiation and adaptive strategies of these moss species, enhancing our understanding of plant diversity and resilience in calcareous environments. This research contributes to the broader conservation efforts in these sensitive areas, emphasizing the need for preserving karst ecosystems that harbor unique biological communities and serve as indicators of environmental health. Such insights are critical for developing effective conservation strategies aimed at safeguarding the rich biodiversity found in karst landscapes. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: *Hyophila apiculata*; *Hyophila involuta*; microclimates; morphometric analysis; Western Thailand

19. Human-macaque conflicts at a human settlement in Riau Province, Indonesia/ **Metananda A.A.; Sutopo; Gunawan; Nurjaman; Dani R.; Ruhyat Y.; Sutopo; Ahmad; Aprianto A.; Naibaho J.; Afrianto W.F..** Biodiversitas. ISSN:1412033X 9 v.25 29502958 (2024) Final

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Abstract: Various human activities have caused the loss and degradation of the natural habitat of macaques, resulting in their share habitat with high levels of human activities. The proximity of macaque habitats to human activities may

increase potential human-macaque conflicts. This research aims to observe the conflict between humans and macaques, especially *Macaca fascicularis* (Raffles 1821), by identifying macaque population parameters, including the number of groups, group distribution, home range, sex ratios, and age structure in the Pertamina Official Housing (POH) complex, Dumai District, Riau Province, Indonesia. Population data were acquired through a census inventory using concentration count and exploration methods. The results showed the population of 461 macaque individuals belonging to 19 groups which were spread over 17 points in the study area. Based on the sex ratio, juveniles were the most predominant group with 104 individuals. The distribution of individuals indicated that there were several groups with varying numbers and structures at one observation point. Factors that caused macaque disturbance include food availability, habitat space availability, community habits and behavior, and safety. Macaque disturbance included attacks on children, damage to lighting, roofs, fruit trees, vegetable plants, and the presence of *M. fascicularis* groups in large numbers in the area traversed by residents. We recommend improving the management of *M. fascicularis* habitat, conducting population control, and educating the community about behaviors that can trigger disturbances. In addition, mitigation measures and regular monitoring must be carried out to find effective long-term solutions. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Distribution; disturbance; *Macaca fascicularis*; population; sex ratio

20. Comparative investigation of biological indices and biochemical compounds of reproductive indicators in male and female *Pangasius nasutus*/ **Torsabo D.; Ataguba G.A.; Iber B.T.; Noordn N.M.; Idris N.; Koh I.C.C.; Abduh M.Y.; Piah R.M.; Abol-Munafi A.B..** Biodiversitas. ISSN:1412033X 9 v.25 31053115 (2024) Final

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Abstract: *Pangasius nasutus* (Bleeker, 1863) is an emerging freshwater aquaculture species with known difficulties in the aspect of reproduction in captivity. This study examined biological, biochemical, and fatty acid profiles of *P. nasutus* obtained from cage culture systems in Pahang, Malaysia as indicators of sexual maturity. A total of 73 samples (43 females and 30 males) of fish were used to collect data on biological indices, biochemical composition, and fatty acid percentages. Otolith growth marks were examined and counted under a microscope for age determination. The results showed a female to male sex ratio of 1.5:1 and the age structure skewed towards three years old fish. The Gonadosomatic Index (GSI) was significantly high for females and with a significantly low difference in the Coelomic Fat Index (CFI) in comparison with the males. Protein and lipid were found to be highest in the testes of males and the liver of females respectively. Saturated Fatty Acids (SFA) and Monounsaturated Fatty Acids (MUFA) significantly differ between males and females in the liver and gonads, in addition to highest Polyunsaturated Fatty Acids (PUFA) also recorded in the gonads of 3 years fish. The current study reveals that *P. nasutus* reaches sexual maturity at a minimum age of 3 years, with an average body weight of 1099.27 ± 21.5 g and an average total length of 48.36 ± 0.45 cm. Significant differences between fatty acid groups highlight the need for lipid nutrition in the broodstock of *P. nasutus* for the supply of adequate energy and essential fatty acids for their gonad development. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Age; captive stock; coelomic fat index; fatty acid; gonad development; otoliths; *Pangasius nasutus*

21. Relationship analysis and genetic diversity of tea *Camellia sinensis* germplasm from illegitimate seeds based on morphological characters/ Maxiselly Y.; Bakti C.; Murgayanti; Ernah; Wahyudin A.A.; Prayoga M.K.; Karuniawan A.. Biodiversitas. ISSN:1412033X 8 v.25 34863495 (2024) Final

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[85202522324&doi=10.13057%2fbiodiv%2fd250820&partnerID=40&md5=196a618b901d885009caa2fb42108d21](https://www.scopus.com/inward/record.uri?eid=2-s2.0-85202522324&doi=10.13057%2fbiodiv%2fd250820&partnerID=40&md5=196a618b901d885009caa2fb42108d21)

Abstract: Tea (*Camellia sinensis* (L.) O. Kuntze) is a plant with self-incompatible traits and requires significant efforts to assemble superior clones. The generation of the superior clone is from seed-derived genetic material that demands comprehensive information on population variance, genetic diversity, and the level of relationship among accessions. Therefore, this research aimed to determine population variances, genetic diversity, and relationships of tea germplasm accessions based on morphological characteristics. The experiment was conducted from August 2023 to January 2024 at the Indonesian Research Institute Tea and Cinchona, Mekarsari Village, Pasir Jambu District, Bandung Regency, West Java, Indonesia. An experimental method, "no layout design," was used to identify morphological traits of 36 characters in 50 selected accessions from the population. Observational data were analyzed to determine variance values, principal component analysis (PCA), heatmap correlation, and cluster analysis using XLSTAT software. The results showed a wide variation of 50% among the 36 characters, with genetic diversity in the 2 Principal Components (PC) at 38.99%. The cluster analysis of accessions had an Euclidean distance range, measuring a measure of the straight line distance between two points of 2.23 to 12.86. This variation was caused by a high correlation of some characteristics, such as leaf length, width, and leaf area, as the potential to develop the new tea clone. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Accession; cluster analysis; euclidean distance; principal component analysis; variance

22. Diversity of *Vibrio* spp. as pathogenic bacteria and their antimicrobial resistance profile isolated from *Penaeus vannamei* ponds/ Amalia R.; Windarto S.; Sibero M.T.; Saputra D.. Biodiversitas. ISSN:1412033X 11 v.25 44504461 (2024) Final

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[85212114997&doi=10.13057%2fbiodiv%2fd251144&partnerID=40&md5=e0968b0c2bf8dd4f334951feac672841](https://www.scopus.com/inward/record.uri?eid=2-s2.0-85212114997&doi=10.13057%2fbiodiv%2fd251144&partnerID=40&md5=e0968b0c2bf8dd4f334951feac672841)

Abstract: Vibriosis is one of the most severe diseases affecting brackish aquaculture systems. The objective of this study was to investigate the diversity of unspciated *Vibrio* spp. and antimicrobial resistance patterns of pathogenic *Vibrio* sp. bacteria isolated from *Penaeus vannamei* Boone 1931 ponds. Water and sediment samples were collected from several intensive ponds at the Marine Science Techno Park (MSTP), Universitas Diponegoro, Jepara, Indonesia. The result showed that the total vibrio count (TVC) ranged from 0.46×10^7 to 7.07×10^7 CFU mL⁻¹ in water samples and from 4.73×10^7 to 20.07×10^7 (2.01×10^8) CFU mL⁻¹ in sediment samples. In total, 150 bacterial cultures were successfully isolated. Furthermore, yellow, greenish-yellow, green, and dark green bacterial colonies were observed on the TCBS agar. Four out of the 150 isolates bacteria, T3.S.1, T1.B.1, T2.S.1, and TK.A.1 were selected based on different genetic profiles and identified by 16S rRNA sequencing. These isolates belonged to the genus *Vibrio* and were closely related to *Vibrio alginolyticus*, *Photobacterium damsela*, *Vibrio parahaemolyticus*, and *Vibrio harveyi*. The results of antibiotic resistance revealed that gentamicin (Cn); ampicilin (Amp); ciprofloxacin (Cip); tetracycline (Te); chloramphenicol (C); and amoxcicilin (Aml) were ineffective against *V. alginolyticus*, *P. damsela*, *V. parahaemolyticus*, and *V. harveyi*, finding indicates that these bacteria were resistant to antibiotics. Only *P. damsela*

showed intermediate resistance to chloramphenicol (C). Further research is necessary to detect antibiotic resistance genes and virulence genes in these isolates. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: 16S rRNA; antibiotic resistance bacteria; Antibiotics; *Penaeus vannamei* ponds; *Vibrio* sp.

23. Natural association of the entomopathogenic fungi *Aschersonia placenta* with spiralling whitefly (*Aleurodicus dugesii*) in Bali, Indonesia/ **Sudiarta I.P.; Suputra I.P.W.; Mertaningsih N.P.; Wirya G.N.A.S.; Selangga D.G.W.; Utama I.W.E.K.; Gargita I.W.D.; Klett K.; Yudha I.K.W..** Biodiversitas. ISSN:1412033X 11 v.25 40674073 (2024) Final

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Abstract: Sudiarta IP, Suputra IPW, Mertaningsih NP, Wirya GNAS, Selangga DGW, Utama IWEK, Gargita IWD, Klett K, Yudha IKW. 2024. Natural association of the entomopathogenic fungi *Aschersonia placenta* with spiralling whitefly (*Aleurodicus dugesii*) in Bali, Indonesia. Biodiversitas 25: 4067-4073. The whitefly is one of the most common pests in agriculture, and one highly polyphagous species is the spiral whitefly (*Aleurodicus* sp.). The fungal genus *Aschersonia* can be used to control *Aleurodicus* sp.. This research has potential applications in agriculture because it can produce a new environmentally friendly method to control whitefly infestations. The aim of this study was to analyze the morphology and molecular characteristics of *Aschersonia* and their hosts in Bali. The samples were taken from several areas in Bali Province. Morphological identification was carried out at the Plant Pathology Laboratory, Faculty of Agriculture, Universitas Udayana. The conidia of *Aschersonia* were fusoid with tapered ends, 9-16 µm long and 1.5-2 µm wide, and the color of the culture was white to yellowish white. Molecular analysis exhibited that DNA bands measuring between 500-600 bp were successfully amplified with universal primers ITS1/ITS4. *Aschersonia* infected spiralling whiteflies has never been reported in mulberry plants. Further phylogenetic analysis showed that *Aschersonia*-infected spiralling whiteflies were in the same group as *Aschersonia placenta*/ *Hypocrella raciborskii* isolates from Thailand and India. *Aleurodicus dugesii* Cockerell 1896 had morphological characteristics, such as vasiform orifice with lingula extending beyond the borders of orifice, compound pores present on puparia, and thoracic legs with claws. The results of morphological analysis showed that *A. dugesii* from Bali (LC491422) had the closest kinship to *A. dugesii* from the USA (AY521251). This is the first report of the identification of *Aschersonia placenta* associated with *A. dugesii* in Indonesia. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: *Aschersonia placenta*; biological control; insect pest; molecular; morphological; whitefly

24. Wing geometric morphometric analysis of dwarf honeybee (*Apis florea*) populations in Thailand/ **Soipijit S.; Sopaladawan P.N..** Biodiversitas. ISSN:1412033X 10 v.25 35683575 (2024) Final

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Link: <https://www.scopus.com/inward/record.uri?eid=2-s2.0-85208992878&doi=10.13057%2fbiodiv%2fd251018&partnerID=40&md5=004f2b7b4b4487e597671a3a5a1b082b>

Abstract: The dwarf honeybee, *Apis florea* Fabricius, 1787, is native to Thailand and distributed throughout the country. It plays a vital role in agriculture and the environment as an excellent pollinator of crops and economic plants in Thailand. Deforestation and insecticide usage have decreased populations of *A. florea*. There is a need for

more information about the diversity of this species in Thailand, particularly its morphological diversity. This study aimed to determine variation among *A. florea* populations in Thailand based on geometric morphometrics of right forewings. Samples of adult *A. florea* worker were collected from 81 colonies across Thailand. Forewing shape variation was examined based on 19 landmark coordinates. The results revealed that landmark number 15 had the highest variance, followed by landmark numbers 14 and 16 with the $S^2=0.00004646$, 0.00004436 , and 0.00004024 , respectively. Principal component analysis (PCA) showed that *A. florea* populations were distributed as one group, consistent with discriminant and cluster analyses. In addition, multivariate analysis of variance (MANOVA, $\alpha=0.05$) was not significantly different among populations. In summary, *A. florea* in Thailand had less morphological diversity than *Apis cerana* Fabricius, 1793 and *Apis mellifera* Linnaeus, 1758. This exciting information provides valuable insight for conserving *A. florea* in Thailand. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Discriminant analysis; landmark; principal component analysis; right forewing

25. Isolation, screening, and molecular characterization using 16S rDNA gene of feather-degrading bacteria isolated from poultry soil in Basrah Province, Iraq/ **Ahmed Al-Amery N.M.; Alyousif N.A.** Biodiversitas. ISSN:1412033X 9 v.25 32173226 (2024) Final

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Link: <https://www.scopus.com/inward/record.uri?eid=2-s2.0-85206813055&doi=10.13057%2fbiodiv%2fd250944&partnerID=40&md5=2b95c37d0f11b306b35e11ac614c720c>

Abstract: Al-Amery NMA, Alyousif NA. 2024. Isolation, screening, and molecular characterization using 16S rDNA gene of feather-degrading bacteria isolated from poultry soil in Basrah Province, Iraq. Biodiversitas 25: 3217-3226. Bioremediation of feathers based on the production of keratinase enzyme is one of the most promising methods and has gained increasing interest in biotechnology. This study aimed to isolate, identify, and screen the bacteria that can potentially degrade feathers from the soil in Basrah province, Iraq using 16S rDNA gene. Ten soil samples were collected from various poultry fields and 97 bacterial isolates have been isolated from the samples. Seventy-four protease-producing isolates were found among isolates. The highest number of bacterial isolates that were found to be able to break down feathers were B6, E1, F7, M6, and J9 according to the values of keratinase activity were 42.1 U/mL, 29.1 U/mL, 28.8 U/mL, 28.1 U/mL, and 28.1 U/mL, respectively. The isolate B6 was the most promising isolate, because it was the best isolate with a higher value of 42.1 U/mL. Based on the sequencing of the 16S rDNA gene, these 5 isolates were identified as *Bacillus amyloliquefaciens*, *B. subtilis*, *B. licheniformis*, *B. subtilis*, and *B. pumilus*, respectively. Eleven bacterial isolates have been reported as new strains and recorded in NCBI GenBank. The current study reported several isolates that have the potential to produce keratinase with different capabilities for the first time in the world. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: 16S rDNA sequencing; Feathers degradation; keratin; keratinase; keratinolytic bacteria

26. LC-MS/MS analysis and antioxidant activity of ethanol fraction of *Aglaonema modestum* leaves/ **Silaban S.; Nainggolan B.; Ikhwan J.; Harliananda N.; Simorangkir M.** Biodiversitas. ISSN:1412033X 12 v.25 47564762 (2024) Final

DOI: 10.13057/biodiv/d251211

Link: <https://www.scopus.com/inward/record.uri?eid=2-s2.0-85213043435&doi=10.13057%2fbiodiv%2fd251211&partnerID=40&md5=94586d3e23b0648a561f494b14dc7248>

Abstract: Free radicals are one of the triggers of various diseases. Excessive free radicals have the potential to cause oxidative stress, such as diabetes, heart disease, Alzheimer's, and Parkinson's disease. Antioxidants can be used to prevent free radicals. Synthetic antioxidants have unnecessary side effects, and natural antioxidants can be a safer alternative. Natural antioxidants can come from plants, which contain phenolic compounds in the form of flavonoids. *Aglaonema modestum*, with the local name simargaolgaol, contains this compound. This plant is often found in Barus, North Sumatra, Indonesia, and is usually used by the community as traditional medicine for internal and external wounds. This study aims to identify the potential antioxidant activity of the leaves ethanol fractions of *A. modestum*. Purification was done using the standard column chromatography method, antioxidant activity analysis using the 2,2-Diphenyl-1-picrylhydrazyl (DPPH) method with vitamin C as a control, and fraction compound analysis using LC-MS/MS. Antioxidant activity value (IC₅₀) of ethanol fraction of *A. modestum* consecutively at 30.953 ppm (very strong), 109.809 ppm (moderate), and vitamin C with an IC₅₀ value of 2.304 ppm (very strong). The results of LC-MS/MS analysis of the ethanol fraction identified three compounds, namely Cadsurenin K (RT 5.91 minutes), Methyl ophiopogonone B (RT 6.37 minutes), and Schizandrin C (RT 7.30 minutes). The ethanol fraction of *A. modestum* leaves has alternative potential as a natural antioxidant. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: *A. modestum*; antioxidant; chromatography; DPPH; LC-MS/MS

27. Polyploidization of three Chrysanthemum varieties in vitro at various levels of colchicine soaking length/ Haring F.; Farid M.; Ridwan I.; Anshori M.F.; Fadhilah A.N.; Hartanto K.B.. Biodiversitas. ISSN:1412033X 8 v.25 34963503 (2024) Final

DOI: 10.13057/biodiv/d250821

Link: <https://www.scopus.com/inward/record.uri?eid=2-s2.0-85202533530&doi=10.13057%2fbiodiv%2fd250821&partnerID=40&md5=49eee3315b99d6bd23f2051d9c7e336f>

Abstract: The demand for new types and varieties of chrysanthemums with unique characteristics, such as various colors, shapes, and sizes, continues to increase. One approach that can be taken to achieve this diversity is through mutation techniques using chemical mutagens such as colchicine to obtain polyploid plants. This research, which aims to determine the best varieties and soaking time for colchicine in forming polyploid plants in vitro, has the potential to impact the field of Chrysanthemum breeding significantly. The research was arranged in a split-plot design (SPD), with the main plot being the Chrysanthemum variety (v), consisting of the Pinka Pinky (v1), Lollipop (v2), and Maruta (v3) varieties. The subplot is the soaking time at a colchicine concentration of 0.05%, which consists of 0 hours (t0), 4 hours (t1), 8 hours (t2), and 12 hours (t3). The parameters observed were the number of shoots, number of leaves, number of roots, time to sprout, time to root, time to form plantlets, and polyploidy analysis. Chromosome doubling in chrysanthemum plants after 0.05% colchicine induction with different soaking times produced mixoploid plants or the highest chromosome doubling of 9.18% + 18.82%, namely in the Lollipop variety with a soaking time of 12 hours. Meanwhile, other treatments did not show chromosome doubling and remained diploid but had different levels of chromosome variation. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Chrysanthemum; colchicine; in vitro; mutation; polyploidization

28. Molecular identification of rhizospheric Actinomycetes from karst ecosystems of Gorontalo, Indonesia, and its seed germination induction capability of *Zea mays* var. *doti*/ **Retnowati Y.; Katili A.S.; Kandowangko N.Y.; Pembengo W..** Biodiversitas. ISSN:1412033X 12 v.25 47634771 (2024) Final

DOI: 10.13057/biodiv/d251212

Link: <https://www.scopus.com/inward/record.uri?eid=2-s2.0-85213042742&doi=10.13057%2fbiodiv%2fd251212&partnerID=40&md5=cfd4471edcaecb8da8e2b7f887ea468c>

Abstract: Karst, as an extreme ecosystem, was a source of diverse Actinomycetes with varied biological activities. This study explored the plant-growth-promoting potential of rhizospheric Actinomycetes from the karst ecosystem of Gorontalo, with a focus on inducing seed germination in *Zea mays* var. *doti*. Four locations in Gorontalo were selected to explore Actinomycetes, targeting approximately 20 different rhizospheric plant species to isolate these microorganisms. Among the 25 isolates obtained, representing diverse morphological types from 12 rhizospheric plants, eight actinomycete isolates exhibited phosphate-solubilizing activity and produced indole-3-acetic acid (IAA). The 16S rRNA gene sequence analysis showed that approximately 75% of the isolates belonged to the *Streptomyces* genus, including *Streptomyces cavourensis* strain KRZm-02, *Streptomyces* sp. strain KRZm-03, *Streptomyces pratensis* strain KRLI-01, *Streptomyces carpaticus* strain KRIt-01, *Streptomyces* sp. strain KRIt-02, and *Streptomyces aquilus* strain KRPa-01. Additionally, 12.5% of the isolates were identified as *Nocardiopsis alba* strain KRZm-01 and *Micromonospora* sp. strain KRPt-01, respectively. The two isolates with the highest plant-growth-promoting potential, *Streptomyces pratensis* strain KRLI-01 and *Streptomyces carpaticus* strain KRIt-01, were further tested for their ability to promote germination of *Zea mays* var. *doti* seeds over 7 days. Among the two, *Streptomyces carpaticus* strain KRIt-01 exhibited the highest germination-inducing potential. Overall, the karst ecosystem of Gorontalo offers a valuable reservoir of biological resources with the potential for Plant-Growth-Promoting Rhizobacteria (PGPR). Further studies on the application of these actinomycete isolates as biofertilizers in agricultural and plantation crops could significantly contribute to improving crop growth and productivity, thereby revolutionizing agricultural practices. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Actinomycetes; karst ecosystem; rhizosphere; seed germination; *Zea mays* var. *doti*

29. Insects found in different ages of coconut *viridis* variety in Sri Tiga Village, Banyuasin District, South Sumatra, Indonesia/ **Anggraini E.; Sinaga T.M.; Irsan C.; Herlinda S.; Muslim A.; Hamidson H.; Sefrila M.; Kurnianingsih A.; Aryani D.; Antoni M.; Ikhsan Z..** Biodiversitas. ISSN:1412033X 8 v.25 26372647 (2024) Final

DOI: 10.13057/biodiv/d250836

Link: <https://www.scopus.com/inward/record.uri?eid=2-s2.0-85202553937&doi=10.13057%2fbiodiv%2fd250836&partnerID=40&md5=903dc5df7af1112c9163204823dc6840>

Abstract: Coconut (*Cocos nucifera* L.) is a high-value export commodity and has promising potential on the global market. The existence of insect species is very important in coconut cultivation. The coexistence of insects and plants is interconnected because plants provide habitat and food sources for insects. However, the correlation between plants and insects still needs to be discovered to many people. Therefore, a comprehensive assessment of insect biodiversity in an environment is important to be carried out. This study revealed the structure of the insect community associated with coconut plants and weeds around coconut trees. Therefore, this is a novel and pioneering study that aims to determine the insects associated with coconut plants. This study was conducted by surveying community-owned coconut plantations in Sri Tiga Village, Sumber Marga Telang Sub-district, Banyuasin District, South Sumatra, Indonesia. The observation was carried out during July and September of 2023. The data-gathering process involved identifying three coconut plantations with varying ages of coconut trees (8, 5, and 2 years old). Data

collection was carried out using the purposive sampling method by direct observations and using traps such as insect nets, light traps, and pheromone traps. Collected specimens were identified using a microscope in the Laboratory of Entomology, Department of Plant Pests and Disease, Faculty of Agriculture, Universitas Sriwijaya. The results of this study found 12 insect species in coconut trees, namely *Oryctes rhinoceros* Linnaeus 1758, *Aspidiotus* sp., *Nipaecoccus nipae* Maskell 1893, *Aleurocanthus* sp., *Apis cerana* Fabricius 1793, *Cotesia congregata* Say 1836, *Dolichoderus thoracicus* Smith 1860, *Oecophylla smaragdina* Fabricius 1775, *Provespa* sp., *Pteroma pendula* de Joannis 1929, *Metura* sp., *Metisa plana* Walker 1883. The predominant insect pests identified were *Aspidiotus* sp., *N. nipae*, and *Aleurocanthus* sp. Furthermore, the most predominant insects that served as insect scavengers were *Polyrhachis* sp. and *O. smaragdina*. Meanwhile, in the weeds around coconut trees, there were found six insect species, namely *Aulacophora lewisii* Baly 1866, *Eumorphus westwoodi* Guérin 1858, *Mactrotermes* sp., *Conocephalus* sp., *Dianemobius* sp., and *Tettigidea* sp. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Coconut; *Cocos nucifera*; insects; viridis variety

30. Diurnal activity patterns of painted storks (*Mycteria leucocephala*) in an urban artificial wetland in Malaysia/ **Limin N.A.; Abidin M.Z.Z.; Kamar N.N.S.; Amran M.A.A.; Yusof N.M.** Biodiversitas. ISSN:1412033X 12 v.25 48784885 (2024) Final

DOI: 10.13057/biodiv/d251224

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Abstract: The increasing population of painted storks (*Mycteria leucocephala*) in Malaysia poses potential risks to native waterbird species, such as the milky stork. Despite their growing presence in urban artificial lakes, such as those in Putrajaya and Selangor, our understanding of their activity patterns remains limited, highlighting the importance of this research. Therefore, this study closely investigated the diurnal activity patterns of painted storks in an urban artificial wetland in Malaysia. Stork behavior was observed using instantaneous scanning and focal sampling methods for over 20 days. Results indicated that preening was the most common activity (30%), followed by foraging (24%), vigilance (23%), walking (15%), and other behaviors (8%). Storks displayed significantly more preening in the morning, though the durations were shorter compared to the afternoon and late afternoon. They also spent more time foraging and being vigilant in the morning than at other times. Furthermore, during all sessions, the number of individuals observed in the grassy areas was much higher than in the lake or on nearby rooftops. This study provides valuable insights into the behavior of painted storks, which could inform management strategies for waterbird species in urban artificial wetlands. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Activity budget; behavior sampling; urban ecosystem; waterbird

31. Evaluation of a newly isolated thermophilic microalga *Chlorella sorokiniana* UNM-IND1 as biodiesel feedstocks/ **Ramadani N.Z.; Indrayani; Zainuddin E.N.** Biodiversitas. ISSN:1412033X 9 v.25 33393349 (2024) Final

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Link: <https://www.scopus.com/inward/record.uri?eid=2-s2.0-85207171320&doi=10.13057%2fbiodiv%2fd250956&partnerID=40&md5=a23e4abe99138c6d9bb0651272e0f38d>

Abstract: Microalgae contain lipids and fatty acids that can be used as an alternative energy for biodiesel. Efforts to increase lipid productivity in microalgae can be done by conditioning the microalgae under certain stress conditions. Temperature is one of the environmental factors that can stimulate lipid production in microalgae. This study aims to analyze the effect of different temperatures on the growth, biomass, lipid productivity and fatty acid composition of a newly isolated microalgae *Chlorella sorokiniana* Shihira & Krauss, 1965 UNM-IND1 and to evaluate the potential of the microalga as biodiesel feedstocks. The *C. sorokiniana* UNM-IND1 was initially cultured at three different temperature conditions namely culture room temperature (25-26°C), ambient room temperature (28-32°C) and drying room temperature (32-48°C) (phase I). In phase II, the cultures were transferred to lower temperature conditions and incubated for 3 days. The parameters measured were cell density, specific growth rate, biomass productivity, lipid content, lipid productivity and fatty acid composition. The results showed that all cultures can grow at all culture conditions tested. The highest specific growth rate and biomass productivity were achieved at drying room temperature treatment at 0.790 d⁻¹ and 0,166 g.L⁻¹.d⁻¹, respectively. The highest lipid productivity (0.0674 g.L⁻¹.d⁻¹) was obtained at culture room temperature. After the temperature shift, the lipid yield, lipid content and lipid productivity of all cultures increased. Fatty acid analysis showed that the alga consists of mainly palmitic acid, linolenic acid and linoleic acid. Based on the growth, biomass, lipid and fatty acid composition, the *C. sorokiniana* UNM-IND1 has potential as a biodiesel feedstock. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Biodiesel feedstocks; *Chlorella sorokiniana*; fatty acids; lipid; thermophilic

32. Phytochemicals' compound and antioxidant activities in the food of *Pongo tapanuliensis* from Batang Toru Forest, North Sumatra, Indonesia/ **Sianipar H.F.; Widoretno W.; Hakim L.; Amolia R.R.; Fatchiyah F.** Biodiversitas. ISSN:1412033X 10 v.25 34543463 (2024) Final

DOI: 10.13057/biodiv/d251007

Link: <https://www.scopus.com/inward/record.uri?eid=2-s2.0-85209202811&doi=10.13057%2fbiodiv%2fd251007&partnerID=40&md5=730586732cd78a625313d7652c8ffc32>

Abstract: Sianipar HF, Widoretno W, Hakim L, Amolia RR, Fatchiyah F. 2024. Phytochemicals' compound and antioxidant activities in the food of *Pongo tapanuliensis* from Batang Toru Forest, North Sumatra, Indonesia. Biodiversitas 25: 3454-3463. *Camposperma auriculatum* (Blume) Hook.fil. and *Agathis borneensis* Warb. are food for *Pongo tapanuliensis* Nurcahyo, Meijaard, Nowak, Fredriksson & Groves, 2017 found in the Batang Toru Forest, Indonesia. Studying the phytochemical properties of both plant species is important part of conservation framework for Tapanuli orangutans because information regarding their nutrient contents and benefits still needs to be investigated. This research examined the closest components, amino acids, and phytochemicals compounds that have antioxidant activity. The *C. auriculatum* and *A. borneensis* fruit were tested for proximate, amino acid, phytochemical, total flavonoid content, LC-MS/MS, and FRAP to determine antioxidant activity. The results of proximate and amino acid tests showed that *C. auriculatum* has higher contents of carbohydrates (74.49%), protein (7.54%), lipids (3.73%), energy from fat (33.57Kcal/100 g), total energy (361.71Kcal /100g), L-Histidine (1704.975ppm), L-Leucine (3759.28ppm), and L-Lysine (2099.038ppm) compared to *A. borneensis*. The phytochemical tests of both samples were positive for containing alkaloids, flavonoids, saponins, steroids, tannins, phenolics, and quinolines. The higher flavonoid content is found in *C. auriculatum* (94.44±2.77mg QE/g). LC-MS/MS results for both samples, *C. auriculatum* that is (3 α ,20R,24Z)-3-Hydroxy-21-oxoeupha-8,24-dien-26-oic acid, terpenoid group, and *A. borneensis*, that is Procyanidin B2, the flavonoid group. The higher antioxidant capacity was found in *C. auriculatum* (4.63±0.111 μ g/mL). The *C. auriculatum* has excellent potential as a natural source of nutrition and antioxidants for the Tapanuli orangutan; therefore, it is necessary to develop a strategy by cultivating these two

plants and using them in pharmacognosy for *P. tapanuliensis*. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Antioxidant; food; nutrition; orangutans; phytochemicals

33. Determining the hybrid diversity between Bali cattle (*Bos javanicus*) and Wagyu cattle (*Bos taurus*) breeds using specific microsatellite markers/ **Jakaria; Dairoh; Setyani N.M.P.; Sutikno; Ulum M.F.; Priyanto R.** Biodiversitas. ISSN:1412033X 9 v.25 30483055 (2024) Final

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Abstract: This study aimed to determine hybrid diversity between Bali and Wagyu cattle using microsatellite markers. Total blood samples were collected from Bali purebreds (n=32 heifers), Wagyu×Bali crossbreeds, which consist of 2 bulls and 9 heifers (n=11), and Wagyu purebreds (n=6 dams). The four microsatellite markers (INRA035, ILST006, ETH225, and HEL9) were used to determine genetic diversity among cattle populations, which is part of what is recommended by FAO (Food and Agriculture Organization). GenAlex, CERVUS, MEGA10, UPGMA, and RStudio software were used for data analysis. Thirty-one alleles were identified at the four microsatellite loci used in this study. All identified alleles were polymorphic and informative. This study found 283 bp and 300 bp (ILST006) and 139 bp (ETH225), demonstrating the private alleles for Wagyu×Bali crossbreeds; 104 bp (INRA035), 284 bp (ILST006), 155 bp, 159 bp, and 167 bp (ETH225) were private alleles for Bali purebred, while 288 bp (ILST006), 145 bp (ETH225), and 162 bp (HEL9) were private alleles for Wagyu purebred. Based on Neighbor Joining and PCA analysis, the Wagyu purebred exhibited at the different clusters in both Wagyu×Bali crossbred and Bali purebred. These findings highlight that microsatellite markers effectively distinguished between Bali purebred, Wagyu x Bali crossbred, and Wagyu purebred cattle, providing valuable insights for breeding programs tailored to each population. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Bali cattle; crossbreeding; genetic hybrid; microsatellite marker; Wagyu cattle

34. Species diversity and the spread of invasive fish in the Upper Bengawan Solo River, Central Java, Indonesia/ **Haqqi M.R.A.; Sholichah D.M.; Armando M.F.; Sani M.F.; Aprianto M.K.; Dewangga A.; Yap C.K.; Dadiono M.S.; Setyawan A.D.** Biodiversitas. ISSN:1412033X 10 v.25 40004010 (2024) Final

DOI: 10.13057/biodiv/d251060

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Abstract: Haqqi MRA, Sholichah DM, Armando MF, Sani MF, Aprianto MK, Dewangga A, Yap CK, Dadiono MS, Setyawan AD. 2024. Species diversity and the spread of invasive fish in the Upper Bengawan Solo River, Central Java, Indonesia. Biodiversitas 25: 4000-4010. Bengawan Solo is the largest and longest river in Java, Indonesia, and has a major role in supporting the life of communities around it. To understand the quality of the Bengawan Solo River environment, the study can be done from physical, chemical, and biological aspects. This research was carried out to inventory the species and the spread of invasive fish found in the Upper Bengawan Solo River, Central Java, Indonesia.

This research was conducted from November to December 2023 and settled on 5 sampling stations located on main body of Bengawan Solo River, including (i) northern spillway of Gajah Mungkur Reservoir, Wonogiri, (ii) Colo Reservoir, Sukoharjo, (iii) Demangan Floodgate, Surakarta, (iv) Tlumpuk, Karanganyar, and (v) Jati, Sragen. Data collection was performed using Visual Encounter Survey (VES) and direct catch with several fishing tools, collected species identified using iNaturalist, and several books such as Jenis Ikan Introduksi dan Invasif Asing di Indonesia, Ikan Air Tawar di Ekosistem Bukit Tigapuluh, Ensiklopedia Populer Ikan Air Tawar, and Baku Saku Pengolah Data Jenis Ikan. Identification also carried out by interviewing local people at study area location to match out vernacular names. The results showed 20 species of fish from 12 families were found, dominated by Cyprinidae. The most fish captured is tilapia (*Oreochromis niloticus*), which can be obtained from all the sampling stations. A species with high conservation status according to IUCN Red List was also found, namely *Rasbora lateristriata* with Vulnerable (VU) status. As many as 6 species discovered were categorized as invasive, including snakehead fish (*Channa striata*), red devil fish (*Amphilophus citrinellus*), tilapia (*O. niloticus*), catfish (*Clarias gariepinus*), sailfin catfish (*Pterygoplichthys pardalis*), and guppy (*Poecilia reticulata*). Their invasive characteristics are usually due to their predatory trait, well adaptability, and high population. The introduction of invasive fish in the Upper Bengawan Solo River was caused by several reasons, such as intentional release for stocking population, escaping fish from nearby farms, and wild releases from fish keepers. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Bengawan Solo River; diversity; ecosystem; fish; invasive

35. Satellite remote sensing techniques for mapping and estimating mangrove carbon stocks in the small island of Gili Meno, West Nusa Tenggara, Indonesia/ **Karang I.W.G.A.; Nuarsa I.W.; Hendrawan I.G.; Dewi N.M.N.B.S.; Yasa P.K.; Krisnanda I.M.D.** Biodiversitas. ISSN:1412033X 9 v.25 31893200 (2024) Final

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Abstract: Estimating mangrove carbon stocks is crucial for effective conservation and management but presents challenging, particularly on small islands. Satellite remote sensing offers a powerful tool for assessing mangrove ecosystems, though its application in small island environments remains underutilized. This study aims to explore and evaluate the effectiveness of satellite remote sensing techniques, specifically using Sentinel-2, for mapping and estimating mangrove carbon stocks on the small island of Gili Meno, West Nusa Tenggara, Indonesia. The Random Forest technique was employed to distinguish between mangrove and non-mangrove areas by analyzing multiple parameters. Additionally, a semi-empirical method was used to evaluate and map the Above Ground Carbon (AGC) of mangroves, with general allometric equations applied to calculate AGC values. Six vegetation indices were assessed to develop a model for estimating mangrove AGC using linear regression equations. The accuracy of the model predictions was evaluated using the Root Mean Square Error. The study identified that the mangrove forest area in Gili Meno covers approximately 6.88 ha. Notably, the research revealed that the IRECI model, with an R^2 value of 0.76 and RMSE of 17.14 ton/ha, was the most effective for AGC estimation when utilizing red edge bands. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Above ground carbon; Random Forest; Sentinel-2; small islands; vegetation indices

36. Analysis of the relationship between the population size of Kalimantan orangutan (*Pongo pygmaeus*) and land cover changes in Central Kalimantan, Indonesia/ **Openg E.B.L.; Santosa Y.; Jaya I.N.S.**. Biodiversitas. ISSN:1412033X 8 v.25 34683475 (2024) Final

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85202517498&doi=10.13057%2fbiodiv%2fd250818&partnerID=40&md5=c2bc0c8a915f9667f05fea4d5081ba91

Abstract: Land cover change, a major driver of habitat change, significantly influences the distribution of wildlife species, including the Kalimantan orangutan (*Pongo pygmaeus* Linnaeus, 1760) in Central Kalimantan, Indonesia. This analysis, aimed at quantitatively assessing the relationship between changes in land cover and the population of Kalimantan orangutans in 2014-2019, underscores the urgent need for orangutan conservation. Using data on the population of Kalimantan orangutans and updated Landsat images with land cover data from the Indonesian Ministry of Environment and Forestry, we conducted a multiple linear regression analysis to unveil the relationship between the two. The research results from three specific conservation area locations reveal a decrease in the orangutan population in Lamandau, with the largest increase in open land cover types, a trend largely influenced by anthropogenic factors. Conversely, an increase in population was observed in Sebangau, with the largest increase in the swamp land cover type, and population fluctuations occurred in Tanjung Puting, with the largest increase in the open land cover type. The decline in the orangutan population is attributed to anthropogenic factors and natural predators, while the population increase occurs naturally and through orangutan reintroduction activities. The analysis concludes that secondary swamp forests, bushes, and open land cover are closely related to the size of the Kalimantan orangutan population at the research location, thereby highlighting the urgency and concern for orangutan conservation. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Conservation area; forest cover; multiple linear regression; orangutan population

37. Association and distribution patterns of nipah (*Nypa fruticans*) in a degraded protected mangrove forest/ **Eddy S.; Milantara N.; Setiawan A.A.; Taufik M.; Rosanti D.; Putri S.A.D.; Rahmawati.** Biodiversitas. ISSN:1412033X 11 v.25 45254534 (2024) Final

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85212112445&doi=10.13057%2fbiodiv%2fd251151&partnerID=40&md5=1655b4cc60ebe6f733ca8de30a982661

Abstract: Eddy S, Milantara N, Setiawan AA, Taufik M, Rosanti D, Putri SAD, Rahmawati. 2024. Association and distribution patterns of nipah (*Nypa fruticans*) in a degraded protected mangrove forest. Biodiversitas 25: 4525-4534. The invasion of nipah (*Nypa fruticans*) serves as an indicator of mangrove forest degradation that has occurred globally, impacting biodiversity. Therefore, understanding the population dynamics of nipah is essential for controlling its growth. This study aims to classify land cover types in the Air Telang Protected Forest (ATPF), analyze the association of nipah with other plants, and examine its distribution patterns. We employed a descriptive research method, utilizing Geographic Information Systems (GIS) for land cover change analysis, alongside field surveys to collect data on plant species associated with nipah. Drone photography was used to document nipah populations across various land cover types. Our findings revealed four land cover types in ATPF: primary forest, secondary forest, open area (shrub), and plantation, with 29 plant species associated with nipah. Nipah has spread across various land cover types through multiple mechanisms. We estimate that nipah will dominate nearly all degraded areas of ATPF and hinder the succession process if restoration efforts are not implemented promptly. However, with the right strategies, there is hope for successful restoration. This research contributes to understanding nipah's population

dynamics, the implications of its dominance, and strategies for controlling its growth. In addition, this study is more widely useful for information on mangrove ecosystem management, ecological risk assessment, ecosystem restoration efforts, and conservation policy development. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Air Telang Protected Forest; association and distribution patterns; invasive species; mangrove forest; nipah

38. Arbuscular Mycorrhizal Fungi (AMF) diversity and population in UPV Nature Trail, Miagao, Iloilo, Philippines/ **De Asis E.P.T.; Demetillo F.M.M.; Paguntalan D.P.**. Biodiversitas. ISSN:1412033X 12 v.24 66926703 (2024) Final

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Abstract: Arbuscular Mycorrhizal Fungi (AMF) are soil microorganisms that form the most prevalent mutualistic associations with plant species. Studies revealed its global distribution in various terrestrial habitats, but available local literature remains few. This study investigated AMF diversity in the University of the Philippines Visayas (UPV) Nature Trail, Miagao, Iloilo, Philippines. AMF spores were isolated using wet sieving, decanting, and centrifugation. A total of 2815 individual spores were documented, with 114 distinct morphospecies representing 16 genera, nine families, and four orders classified. *Glomus clarum*, *Acaulospora* sp.7, and *Scutellospora pellucida* tallied the highest abundance across all points. *Scutellospora pellucida* (FOC=83.3%) recorded the highest species richness, followed by *Ambispora* sp. (FOC=77.78%), then *Acaulospora mellea* and *Glomus australe* (FOC=72.22%). Overall, Shannon-Weiner diversity index ($H=3.6019$) and Simpson diversity index ($D=0.0420$) revealed a very high AMF diversity in the trail, while the Pielou evenness index ($J=0.7605$) suggested a semi-balanced number of individuals among each morphospecies. A more abundant, even, and diverse, albeit not statistically significant, AMF community was recorded in forested areas compared to non-forested areas of the trail. Results generally suggest that the AMF community is diverse and abundant regardless of the location, ecosystem type, and faunal association. © 2023, Society for Indonesian Biodiversity. All rights reserved.

Keyword: AMF abundance; Arbuscular Mycorrhizal Fungi (AMF); diversity; morphospecies; UPV Nature Trail

39. Gamma-ray irradiation alters the morphology, anatomy and agronomic characters of the groundnut (*Arachis hypogaea*) bison cultivar in M1 generation/ **Nilahayati; Handayani R.S.; Nazimah; Neni; Saputra D.**. Biodiversitas. ISSN:1412033X 11 v.25 41794189 (2024) Final

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Abstract: Groundnut is the world's most important agricultural commodity, serving as a major source of protein and vegetable oil. Enhancing the genetic diversity of groundnuts is essential for improving yield, early maturity and environmental resistance such as drought tolerance. This study aims to determine the effect of gamma irradiation on the morphological and agronomic diversity of bison groundnut cultivar in the M1 generation. Gamma irradiation

was carried out at the Radiation Process Technology Research Center, National Research and Innovation Agency of Indonesia, Jakarta. This research was designed using a single-factor Randomized Complete Block Design. The dose of gamma irradiation was 0 Gray (Gy), 100 Gy, 200 Gy, and 300 Gy, with three replications. Consequently, there were a total of 12 experimental units. We generated 600 groundnut plants in total. The observed variables included morphological diversity such as variation in leaf, stem, seed color and seed shape. The agronomic variability was recorded to the seed growth percentage, plant height, number of branches, flowering age, harvesting age, number of pods, number of empty pods, dry pod weight per plant, dry seed weight per plant, 100 seed weight per plot, dry seed weight per plot, length, width, and number of leaf stomata. The results showed that gamma irradiation treatment induced morphological and agronomic changes in the bison groundnut cultivar. Morphological changes included alterations in leaf color, pod shape, and seed coat color. Higher doses of gamma irradiation can negatively impact certain agronomic traits such as plant height and yield, beginning at 200 Gy, but at 100 Gy all parameters slightly increased. Higher dose of gamma irradiation also delayed the flowering and harvesting time. Further studies are also needed to evaluate the heritability of these traits in the M2 generation to ensure the stability of desirable traits. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: M1 generation; mutant; mutation breeding; seed-coat; variation

40. Aquaculture infection of *Kappaphycus alvarezii* by *Vibrio alginolyticus* causing ice-ice disease/ **Prasetyo E.N.; Permanasari Y.; Basyirah A.; Fitriya S.A.; Jadid N.; Zullaikah S.; Ekawati I.; Isdiantoni; Koentjoro M.P.**. Biodiversitas. ISSN:1412033X 11 v.25 40864094 (2024) Final

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Abstract: The occurrence of ice-ice disease on seaweed (*Kappaphycus alvarezii* (Doty) Doty ex P.C.Silva) tissue is indicated by the presence of bleaching and softening symptoms on thallus, which attracts microbial infection. In addition, it is often caused by unfavorable environmental conditions during specific seasons and is characterized by fragmentation as well as a reduction in biomass. To prevent the disease, several studies have suggested the use of ice-ice disease-resistant seeds. Therefore, the aim of this study was to investigate the resistance level of seaweed seeds to microbial infection, particularly *Vibrio alginolyticus*, which is responsible for ice-ice disease in different aquaculture areas in Sumenep District. Data were collected from four different villages, including Brakas, Padike, Tanjung, and Lobuk, followed by analysis using descriptive qualitative method. *K. alvarezii* seeds collected from four villages were infected with *V. alginolyticus* using the in vitro method. Thallus of seaweed was then observed and water samples were taken every 6 hours for 24 hours post-infection. The results showed that seeds from Brakas had the lowest (11%) infection rate, followed by Tanjung (67%), and Padike and Lobuk (89% each). This indicated that *K. alvarezii* seeds from Brakas possessed a prominent activity against *V. alginolyticus* infection with no sign of chlorosis or tissue softening on thallus. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Aquaculture; ice-ice disease; infection; *Kappaphycus alvarezii*; *Vibrio alginolyticus*

41. Diversity and spatial distribution of Lauraceae tree species in Lower Montane Forest at Doi Suthep-Pui National Park, Northern Thailand/ **Srisuwan S.; Sungkaew S.; Wachrinrat C.; Asanok L.; Kamyo T.; Thinkampheang S.; Kachina**

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Abstract: Montane forests are characterized by high plant diversity, including a notable representation by the Lauraceae family, which offers a variety of ecological and economic benefits. This study aimed to assess the species diversity, spatial distribution, and habitat suitability of the Lauraceae family in the Doi Suthep-Pui National Park, Northern Thailand. A Generalized Linear Model (GLM) was employed to determine the spatial distribution of the dominant Lauraceae species, whereas the Maximum Entropy (MaxEnt) model was used to assess habitat suitability for key species. A total of 24 species across 10 genera were found. The most species-rich genera were *Cinnamomum* and *Litsea*, followed by *Cryptocarya*, *Machilus* and *Phoebe*, and *Actinodaphne*, *Persea*, *Beilschmiedia*, and *Neocinnamomum*. Habitat suitability for important Lauraceae species was categorized into low-, medium-, and high-potential areas. The elevation and soil organic matter were the most significant factors influencing species abundance. Additionally, soil properties also played a role in species distribution. The spatial distribution of Lauraceae species was primarily influenced by elevation. However, this distribution is also influenced by the interplay between elevation, soil properties, climate, and human activity. Thus, a comprehensive knowledge of these determinants can inform conservation strategies and ensure the long-term viability of Lauraceae populations in montane forests. © 2024, Society for Indonesian Biodiversity. All rights reserved.

Keyword: Ecological niche; forest dynamic plots; Generalized Liner Model; habitat suitability; long-term ecological research