BIBLIOMETRIC ANALYSIS OF DROSOPHILIDAE RESEARCH IN WALLACEA: REPRODUCTIVE ISOLATION, SPECIATION, AND FUTURE DIRECTIONS IN NORTH MALUKU, INDONESIA

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Abstract: The Wallacea region, positioned between the Asian (Sunda) and Australian (Sahul) continental shelves, is a globally significant biogeographic transition zone marked by high endemism and complex evolutionary histories. Although *Drosophilidae* are established model organisms in evolutionary biology, their diversity, reproductive isolation, and speciation in Wallacea – particularly North Maluku – remain poorly explored. This study presented the first systematic bibliometric mapping of global and regional Drosophilidae research in relation to Wallacea. Using Google Scholar (2000–2025) *via* Publish or Perish, records were retrieved with combined taxonomic, evolutionary, and geographic search terms, cleaned in OpenRefine, verified in Mendeley, and analyzed with VOSviewer and Bibliometrix R. Network visualizations revealed thematic clusters, collaboration networks, and temporal trends, while overlay and density maps identified emerging topics. A total of 519 publications formed 37 keyword clusters, comprising 1,437 links and a total link strength of 3,507. Three dominant thematic areas emerged: (1) genetics and molecular evolution, (2) reproductive isolation mechanisms, and (3) island biogeography. Wallacea-focused research accounted for less than 2% of all publications. Notable gaps include limited study of Wallacean endemic taxa, poor integration of genomic and ecological datasets, and minimal consideration of marine biogeographic barriers such as the Maluku Strait and Halmahera Sea. The findings underscore the need for integrative molecular, ecological, and behavioral research to investigate speciation in insular systems. Addressing these gaps could position Wallacea as a pivotal reference for island evolution studies across the Asia–Australia transition zone.

Keywords: *Drosophila*, Wallacea, North Maluku, reproductive isolation, speciation, biogeography.

INTRODUCTION

The Wallacea region is a transitional biogeographic zone positioned between the Asian (Sunda) and Australian (Sahul) continental shelves. Its islands, separated by deep marine barriers, exhibit exceptionally high levels of endemism and unique evolutionary

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trajectories shaped by complex geological and climatic histories. The geographical isolation among islands in Wallacea provides a natural setting to examine mechanisms of divergence and speciation in various taxa (Shipton *et al.*., 2021), including *Drosophila*.

Fruit flies (*Drosophilidae*) are among the most studied organisms in evolutionary biology and genetics due to their short generation time, high fecundity, and ease of laboratory culture (Hales *et al.*, 2015). Beyond their role as a global model organism, certain *Drosophila* species in Wallacea offer unique opportunities for field-based studies of reproductive isolation in insular environments.

For example, research on *Drosophila melanogaster* populations from Ternate and Tidore – two islands in North Maluku separated by a narrow sea channel – showed a sexual isolation index of only 0.1, indicating no significant reproductive isolation between the populations despite the presence of a geographic barrier (Suparman *et al.*, 2018). This suggests that while the two populations are geographically allopatric, the marine barrier between them is insufficient to drive substantial prezygotic isolation. Similar results have been observed in other *Drosophila* systems, where geographically separated populations do not always evolve reproductive barriers (Kim *et al.*, 2013); (Nanda & Singh, 2012).

Studies in other parts of Wallacea also highlight the region's biogeographic distinctiveness. For instance, Doorenweerd *et al.* (Doorenweerd *et al.*, 2020) found that nearly half of Dacini fruit fly species in Sulawesi are endemic, fitting Lydekker's Line yet supporting Wallacea as a coherent biogeographic unit. Such findings reinforce the idea that Wallacea is a unique evolutionary arena, though systematic studies on *Drosophila* remain sparse.

Given the paucity of research on *Drosophila* in North Maluku, there is a clear opportunity to integrate molecular, ecological, and behavioral approaches to study speciation processes in the region. This is especially relevant for testing hypotheses about the role of marine barriers, elevational gradients, and habitat heterogeneity in shaping reproductive isolation and genetic divergence.

This study is designed to provide a comprehensive mapping of the global and regional research landscape concerning *Drosophilidae*, with particular attention to reproductive isolation, speciation, and evolutionary dynamics. By employing bibliometric and network analysis, the research seeks to reveal dominant themes, collaboration patterns, and emerging trends in this field. Special emphasis is placed on identifying existing gaps in the literature related to Wallacea, a region whose complex biogeographic history remains underexplored in the context of *Drosophila* research. Furthermore, the study aims to highlight and articulate specific opportunities for future investigations in North Maluku, integrating molecular, ecological, and behavioral approaches to better understand how geographic barriers and environmental gradients influence evolutionary processes in island ecosystems. Ultimately, this work provides the first systematic bibliometric assessment of *Drosophila* research with an explicit focus on Wallacea, offering a novel framework to guide targeted field studies and genomic investigations in one of the world's most unique yet understudied biogeographic regions.

METHODS

DATA SOURCES

All bibliographic data for this study were retrieved from Google Scholar using the *Publish or Perish* (PoP) software (Harzing, 2007) which enables the systematic extraction of publication metadata from the Google Scholar index. Google Scholar was selected as the primary data source due to its broad coverage, which includes both peer-reviewed journal articles and region-specific grey literature that are often underrepresented in commercial databases such as Web of Science or Scopus (Martín-Martín *et al.*, 2018). The literature search employed controlled vocabulary and Boolean operators, using three groups of keywords: taxonomic terms (*"fruit fly"*, *"Drosophilidae"*, *"Drosophila"*), evolutionary concepts (*"reproductive isolation"*, *"speciation"*, *"evolution"*), and geographic focus (*"Wallacea"*, *"North Maluku"*, *"Maluku Utara"*). The search covered publications from January 2000 to February 2025.

DATA EXTRACTION

All bibliographic records retrieved from the search were exported in RIS format via Publish or Perish, ensuring compatibility with bibliometric analyses. The dataset included complete metadata such as titles, authors, year, abstract, journal, keywords, and citation counts. Prior to analysis, duplicates were removed and metadata fields – especially author names, affiliations, and keywords – were standardized to ensure consistency and accuracy. Data cleaning and normalization were performed using *OpenRefine* (Verborgh & De Wilde, 2013), which allowed for efficient handling of inconsistencies and preparation of the dataset for integration into the bibliometric software environment.

DATA PROCESSING AND ANALYSIS

Before bibliometric processing, all cleaned RIS files were imported into *Mendeley Reference Manager* for additional verification and organization of the metadata. The use of Mendeley allowed for systematic checking of author names, institutional affiliations, and publication details to ensure consistency across the dataset, while also facilitating the identification and removal of any remaining duplicates or incomplete records (Kwon *et al.*, 2015); (Ivey & Crum, 2018). Following this preparatory stage, bibliometric and network analyses were conducted using two primary tools. The first was **VOSviewer** (van Eck & Waltman, 2010), which was employed to construct and visualize co-authorship networks at the author, institution, and country levels; generate keyword co-occurrence maps to identify thematic clusters; and develop citation networks to highlight influential publications within the dataset.

The second tool was the Bibliometrix R package (Aria & Cuccurullo, 2017), which was used to analyze annual publication trends, determine the most productive authors, institutions, and countries, and produce thematic evolution maps to track changes in research topics over time. These complementary approaches provided both structural and temporal perspectives on the research landscape, allowing for a more comprehensive understanding of scholarly activity in the field.

PARAMETER SETTINGS

Network mapping and clustering were performed in VOSviewer using parameter settings optimized for bibliometric visualization. A minimum keyword occurrence of three was applied to build the co-occurrence network, reducing noise and highlighting key research topics (van Eck & Waltman, 2010). In co-authorship analysis, only authors with at least two publications were included. Clustering resolution was set at the default 1.0 to balance granularity and thematic cohesion, while normalization employed the association strength method for more accurate representation of node relationships (Perianes-Rodriguez *et al.*, 2016). The analyses produced outputs on publication trends, influential authors and articles, thematic clusters, and collaboration network density across authors, institutions, and countries. The bibliometric analysis followed four main steps (Fig. 1): (1) data retrieval from Google Scholar using Publish or Perish; (2) data cleaning and standardization in OpenRefine; (3) data verification in Mendeley; and (4) visualization of keyword networks, overlay maps, and density maps in VOSviewer.

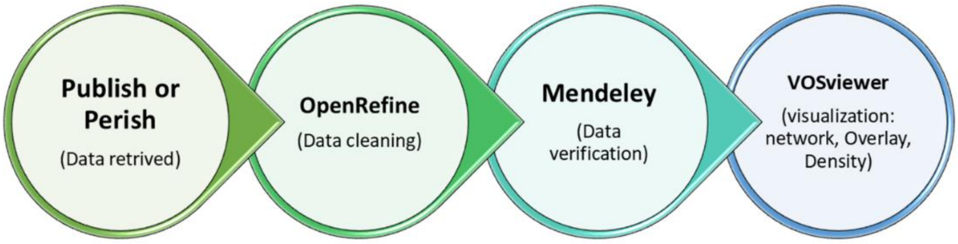

Figure 1. Flowchart of the bibliometric analysis process. The upper text indicates the software used, while the lower text describes its function.

LIMITATIONS

While Google Scholar offers extensive coverage, its indexing is less standardized than that of curated databases like Web of Science or Scopus. This may result in metadata inconsistencies and occasional inclusion of non-scholarly materials. Nevertheless, previous evaluations have shown that Google Scholar is particularly effective for capturing regionally relevant literature, including grey literature and local journals, which is crucial for studies focusing on underrepresented geographic areas such as Wallacea (Martín-Martín *et al*., 2018); (Haddaway *et al*., 2015).

RESULTS

The bibliometric analysis conducted with VOSviewer identified a total of 519 keyword items distributed across 37 clusters, with 1,437 interconnections and an overall link strength of 3,507.

NETWORK VISUALIZATION

In the network visualization (Fig. 2), the central position in the network was dominated by the keyword *biogeography*, represented by the largest node size, indicating both a high frequency of occurrence and extensive connectivity to other terms. Other highly connected and thematically significant keywords included *melanogaster species group*, *incipient sexual isolation*, *natural selection*, *molecular evolution*, *allopatric speciation*, *reproductive isolation barrier*, *mate choice*, and *evolution canyon*. Certain clusters appeared relatively isolated from the main network, such as the cluster containing *natural populations* and *speciation genetic* (brown), the cluster linking *atlantic coastal forest* and *drosophila polymorpha population* (light purple), and the cluster featuring *locus* and *insect pheromone* (yellow).

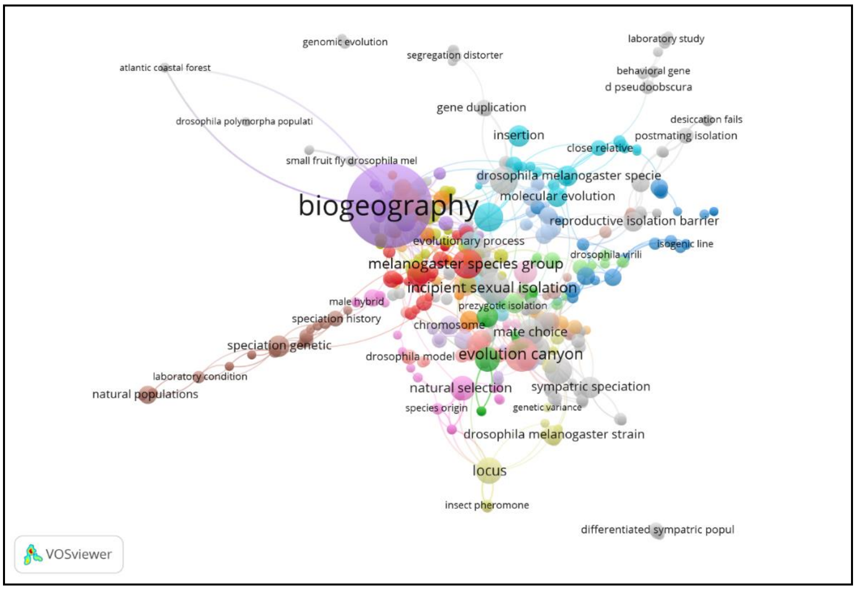

Figure 2. Network Visualization of Keyword Co-occurrence in Global Research on *Drosophila*, Speciation, and Biogeography (2000–2025) with a Focus on Wallace.

OVERLAY VISUALIZATION

The overlay visualization (Fig. 3) revealed the temporal distribution of keywords. Early-stage research, between 2005 and 2010 (dark blue), was characterized by terms such as *natural populations*, *speciation genetic*, and *evolutionary experimentation*. In the intermediate period from 2010 to 2015 (green), emerging topics included *molecular evolution*, *mate choice*, *evolution canyon*, and *allopatric population*. The most recent trends, spanning 2018 to 2020 (yellow), highlighted keywords such as *laboratory study*, *drosophila genus*, and specialized themes related to *gene duplication* and *behavioral gene*.

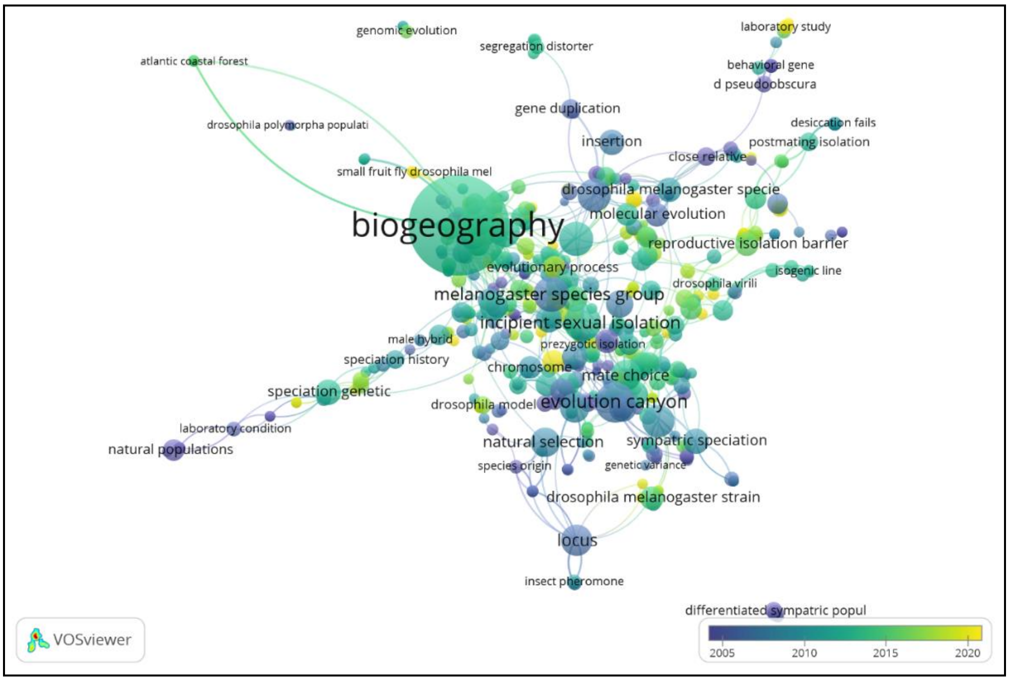

Figure 3. Overlay Visualization Showing Temporal Distribution of Keywords in *Drosophila* and Biogeography Research (2000–2025) with a Focus on Wallace.

DENSITY VISUALIZATION

The density visualization (Fig. 4) indicated that the highest-intensity areas (bright yellow–green) were concentrated around *biogeography*, followed by *melanogaster species group*, *incipient sexual isolation*, *mate choice*, and *evolution canyon*. Lower-density zones were associated with peripheral keywords such as *atlantic coastal forest*, *insect pheromone*, and *natural populations*, reflecting less central but potentially niche research areas.

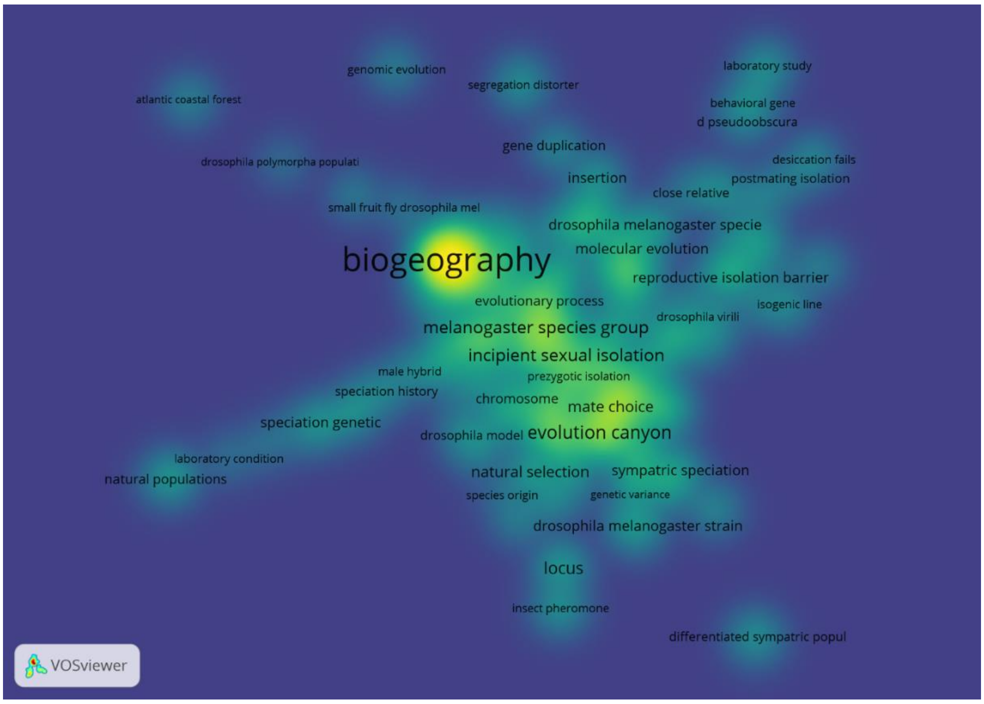

Figure 4. Density Visualization Highlighting High-Intensity Research Themes in *Drosophila* and Biogeography Studies (2000–2025) with a Focus on Wallace.

PUBLICATION TRENDS (2000–2025) AND AUTHORS

The global research output on *Drosophilidae* in evolutionary and speciation contexts shows a consistent upward trend, with peak growth between 2018 and 2023. However, studies explicitly mentioning “Wallacea” or “North Maluku” remain under 2% of total publications. Top contributors include research groups from Japan, USA, and Australia, with emerging contributions from Indonesia (notably Bogor Agricultural University and Universitas Pattimura). International collaborations dominate, with limited intra-Indonesia collaboration. Few joint publications between Wallacea-based institutions and global research centers were recorded.

KEYWORD CO-OCCURRENCE

The keyword co-occurrence analysis revealed three major thematic clusters representing the core research foci in *Drosophila* and biogeography studies.

The first cluster centers on **genetics and molecular evolution**, encompassing terms such as *mitochondrial DNA*, *phylogeography*, and *genetic* *drift*. This cluster reflects the prominence of molecular genetic approaches in elucidating phylogenetic relationships, population histories, and evolutionary dynamics of *Drosophila* species. The frequent use of molecular markers, particularly mitochondrial DNA, underscores a strong emphasis on reconstructing phylogenies and detecting patterns of divergence among geographically distinct populations.

The second cluster focuses on **reproductive isolation mechanisms**, with keywords including *prezygotic barriers*, *hybrid sterility*, and *sexual selection*. This thematic area highlights research investigating the genetic and behavioral processes that restrict gene flow – both pre- and post-fertilization – ultimately contributing to speciation. Studies within this cluster often combine cross-breeding experiments, mating behavior assays, and genetic analyses to disentangle the mechanisms underlying reproductive isolation in *Drosophila*.

The third cluster emphasizes **biogeography and Wallacea studies**, incorporating terms such as *island biogeography*, *endemism*, and *Maluku Islands*. This cluster reflects research addressing the role of geographic barriers, colonization processes, and speciation across island systems, particularly within the Wallacea region. The occurrence of the term *Maluku Islands* indicates that, while still underrepresented in the literature, there is an emerging interest in exploring the diversity and distribution of *Drosophila* in North Maluku.

Overall, these findings illustrate the strong interconnection between molecular evolutionary studies, reproductive isolation research, and island biogeography analyses. At the same time, they reveal a clear research gap in the Wallacea region, presenting a significant opportunity for future work focusing on underexplored island ecosystems such as North Maluku.

RESEARCH GAP ANALYSIS

The bibliometric mapping highlights major gaps in Drosophila research within Wallacea, especially North Maluku. First, Wallacea and North Maluku are poorly represented in global studies; core clusters feature terms like *biogeography*, *melanogaster species group*, and *molecular evolution*, while region-specific terms (e.g., Halmahera, Tidore, Ternate) are absent. Second, research remains dominated by laboratory model species such as *D. melanogaster*, with little focus on Wallacean endemics that may exhibit unique isolation mechanisms. Third, genomic studies are weakly integrated with ecological research, limiting insights into how genetic variation relates to adaptation and speciation in natural island systems. Finally, marine biogeographic barriers – such as the Maluku Strait and Halmahera Sea – are underexplored despite their importance for understanding dispersal and divergence in island populations.

DISCUSSION

The bibliometric analysis highlights significant **research gaps** in *Drosophila* studies concerning the Wallacea region, especially **North Maluku**, underscoring several key implications for future work.

UNDERREPRESENTATION OF WALLACEA AND NORTH MALUKU IN DROSOPHILA RESEARCH

Despite Wallacea's pivotal role as a biogeographic transition zone between Asia and Australasia, regions such as North Maluku remain conspicuously underrepresented in Drosophila research (Lohman *et al*., 2011). A keyword co-occurrence analysis reveals a dominance of themes like biogeography, the *melanogaster* species group, and molecular evolution, while regional terms such as Wallacea, Ternate, or Tidore are notably absent (Holmquist, 2023) This oversight is striking given Wallacea's complex geological history and its status as one of the world's largest centers of endemism, offering a natural laboratory for evolutionary studies (Lambert, 2017) (Coates & Bishop, 1998)

Field surveys conducted across Halmahera, Tidore, Ternate, Morotai, and Bacan have documented a rich diversity of *Drosophila* species, including endemics and isolated populations shaped by volcanic terrains and varying elevations (Irham, 2012); (Prawiradilaga, 2020)). Such biodiversity underscores the potential for Drosophila species to exhibit unique evolutionary traits in response to these ecological pressures (Rutgrink *et al*., 2018)

Integrating molecular, behavioral, and spatial data within North Maluku could not only enhance our understanding of island evolution but also establish Wallacea as a benchmark for speciation and adaptive evolution in biodiversity-rich, insular environments (Lohman *et al*., 2011).

BIAS TOWARD GLOBAL MODEL SPECIES

Our analysis indicates a predominant focus on established laboratory models, particularly *Drosophila melanogaster*. While these species have provided foundational insights into genetics and development, they may not accurately represent the evolutionary dynamics present in Wallacean endemic taxa. Island endemics often exhibit unique reproductive isolation mechanisms and adaptive traits linked to insular selection pressures – phenomena well-documented in other archipelagic taxa ((Warren *et al*., 2015) Redirecting focus toward these neglected taxa could uncover novel speciation processes.

DISCONNECT BETWEEN GENOMIC DATA AND FIELD ECOLOGY

The current literature reveals a pronounced gap between genomic investigations (*e.g.*, molecular evolution, gene duplication) and field-based ecological research. Many studies remain confined to laboratory-centered approaches, which, while offering controlled insights into genetic mechanisms, fail to capture how genetic variation translates into ecological adaptation in natural habitats. This disconnect is particularly evident in insular tropical ecosystems, where adaptive divergence and speciation are strongly shaped by environmental heterogeneity – a dynamic frequently documented in island diversification models (Gillespie, 2016). Integrating high-resolution genomic tools with ecological field surveys is now recognized as a critical frontier for evolutionary biology (Theissinger *et al.*, 2023); (Patiño *et al.*, 2017). Without such integration, genomic signals risk being misinterpreted or decontextualized from the selective pressures acting in the wild (Nosil & Feder, 2012) Population genomics frameworks explicitly emphasize combining molecular data with in situ environmental measurements to disentangle the drivers of divergence across space and time (Johnson *et al.*, 2018). In the context of Wallacea, where geographic and oceanographic barriers interact with fine-scale ecological gradients, coupling genomic datasets with behavioral, spatial, and environmental observations could significantly advance our understanding of speciation processes and adaptive evolution in natural island systems.

UNDERSTUDIED MARINE BIOGEOGRAPHIC BARRIERS

Although Wallacea's defining marine straits – such as the Maluku Strait, Halmahera Sea, and Seram Sea – are recognized as barriers of dispersal and genetic exchange, bibliometric analysis reveals weak representation of terms like marine barriers or island isolation. Yet, studies on other taxa illustrate the influence of these barriers on population structure and genetic differentiation, including seagrass populations delineated by Wallace's Line and reef fish distributions (Hernawan *et al.*, 2017); (Wainwright *et al.*, 2024); (McCullough *et al.*, 2022). Applying seascape genetics in Drosophila could significantly enhance our understanding of speciation dynamics in marine-influenced island systems.

OPPORTUNITIES FOR FUTURE RESEARCH

North Maluku presents a unique setting for integrative research aimed at understanding the evolutionary dynamics of Drosophila. Molecular phylogenetic studies can be employed to reconstruct evolutionary lineages across the islands, providing insights into historical diversification and biogeographic patterns (Hervas *et al.*, 2017) Complementarily, population genetic analyses are essential to evaluate gene flow and assess the genetic structure of local populations, revealing how isolation and environmental heterogeneity shape genetic variation (Matute & Coyne, 2010). Behavioral ecological studies can further elucidate mechanisms of reproductive isolation and mating preferences, which are often key drivers of speciation in insular systems. Finally, long-term ecological monitoring is critical for assessing the impacts of environmental changes – such as habitat alteration, climate variability, or invasive species – on fruit fly populations, thereby linking genetic and ecological dynamics in a comprehensive evolutionary framework.

SYNTHESIS AND OUTLOOK

Our findings illuminate a mismatch between *Drosophila* research emphases and the evolutionary potential of Wallacea. A strategic research pivot is therefore warranted – toward regional integration of molecular, behavioral, and spatial data within North Maluku. Such an approach would not only enrich understanding of island evolution but also position Wallacea as a benchmark for speciation and adaptive evolution in biodiversity-rich, insular environments.

RESEARCH IMPLICATIONS

1. Addressing the Wallacea gap. North Maluku offers a “natural laboratory” to empirically test island speciation, addressing the scarcity of Wallacea-focused biogeographic studies.
2. Linking ecological and genomic scales. This work bridges island ecology (marine barriers, elevational gradients) with reproductive isolation and population genomics, filling a gap between laboratory and tropical field studies.
3. From generalist to endemic inference. By testing whether patterns in *Drosophila melanogaster* apply to other Wallacean taxa (e.g., *D. ananassae* complex, tropical *D. suzukii*, local *Sophophora*), we extend evolutionary biogeographic insights across the Asia–Australia transition.

CONCLUSION

This bibliometric study reveals a growing global interest in Drosophilidae evolutionary research but a marked underrepresentation of the Wallacea region, particularly North Maluku. With its exceptional biodiversity and distinctive geographic context, North Maluku offers significant untapped opportunities for advancing evolutionary biology. Strengthening local research capacity and fostering international collaboration are critical to unlocking this potential. Integrating molecular, ecological, and behavioral approaches will not only refine island biogeography theory but also provide essential guidance for biodiversity conservation. These insights can directly inform policy actions aimed at safeguarding Wallacea's unique evolutionary heritage amid accelerating environmental change.

REFERENCES

1. Aria, M., & Cuccurullo, C. (2017). bibliometrix: An R-tool for comprehensive science mapping analysis. *Journal of Informetrics*, *11*(4), 959–975. https://doi.org/10.1016/j.joi.2017.08.007.
2. Coates, B. J., & Bishop, K. D. (1998). A Guide to the Birds of Wallacea: Sulawesi, The Moluccas and Lesser Sunda Islands, Indonesia. *The Auk*, *115*(3), 811–813.
3. Doorenweerd, C., Ekayanti, A., & Rubinoff, D. (2020). The dacini fruit fly fauna of sulawesi fits lydekker's line but also supports wallacea as a biogeographic region (Diptera, tephritidae). *ZooKeys*, *2020*(973), 103–122. https://doi.org/10.3897/zookeys.973.55327.
4. Gillespie, R. G. (2016). Island time and the interplay between ecology and evolution in species diversification. In *Evolutionary Applications* (Vol. 9, Issue 1, pp. 53–73). Wiley-Blackwell. https://doi.org/10.1111/eva.12302
5. Haddaway, N. R., Collins, A. M., Coughlin, D., & Kirk, S. (2015). The Role of Google Scholar in Evidence Reviews and Its Applicability to Grey Literature Searching. *PLoS ONE*, *10*(9). https://doi.org/10.1371/journal.pone.0138237.
6. Hales, K. G., Korey, C. A., Larracuente, A. M., & Roberts, D. M. (2015). Genetics on the fly: A primer on the drosophila model system. *Genetics*, *201*(3), 815–842. https://doi.org/10.1534/genetics.115.183392.
7. Harzing, A. W. (2007). *Publish or Perish*. Https://Harzing.Com. https://harzing.com.
8. Hernawan, U. E., van Dijk, K. J., Kendrick, G. A., Feng, M., Biffin, E., Lavery, P. S., & McMahon, K. (2017). Historical processes and contemporary ocean currents drive genetic structure in the seagrass Thalassia hemprichii in the Indo-Australian Archipelago. *Molecular Ecology*, *26*(4), 1008–1021. https://doi.org/10.1111/mec.13966.
9. Hervas, S., Sanz, E., Casillas, S., Pool, J. E., & Barbadilla, A. (2017). PopFly: the Drosophila population genomics browser. *Bioinformatics (Oxford, England)*, *33*(17), 2779–2780. https://doi.org/10.1093/bioinformatics/btx301.
10. Holmquist, A. J. (2023). *A tale of three hotspots-the interplay of ecological and evolutionary processes in shaping arthropod communities of Sulawesi, Hawaii, and California*.
11. Irham, M. (2012). Avifauna diversity at Central Halmahera North Maluku, Indonesia. *Zoo Indonesia*, *21*(1), 17–31.
12. Ivey, C., & Crum, J. (2018). Choosing the right citation management tool: EndNote, Mendeley, RefWorks, or Zotero. *Journal of the Medical Library Association*, *106*(3). https://doi.org/10.5195/jmla.2018.468.
13. Johnson, J. S., Krutovsky, K. V., Rajora, O. P., Gaddis, K. D., & Cairns, D. M. (2018). *Advancing Biogeography Through Population Genomics* (pp. 539–585). https://doi.org/10.1007/13836_2018_39.
14. Kim, Y. K., Phillips, D. R., & Tao, Y. (2013). Evidence for no sexual isolation between Drosophila albomicans and D. nasuta. *Ecology and Evolution*, *3*(7), 2061–2074. https://doi.org/10.1002/ece3.619.
15. Kwon, Y., Lemieux, M., McTavish, J., & Wathen, N. (2015). Identifying and removing duplicate records from systematic review searches. *Journal of the Medical Library Association*, *103*(4), 184–188. https://doi.org/10.3163/1536-5050.103.4.004.
16. Lambert, F. (2017). Birds of the Indonesian Archipelago: Greater Sundas and Wallacea James A. Eaton, Bas van Balen, Nick W. Brickle and Frank E. Rheindt. 2016. Lynx Editions, Barcelona. 496 pages. ISBN-13: 978-84-941892-6-5. *Kukila*, 23–26.
17. Lohman, D. J., De Bruyn, M., Page, T., Von Rintelen, K., Hall, R., Ng, P. K. L., Shih, H. Te, Carvalho, G. C., & Von Rintelen, T. (2011). Beyond Wallaces line: Genes and biology inform historical biogeographical insights in the Indo-Australian archipelago. *Annual Review of Ecology, Evolution, and Systematics*, *42*, 205–226. https://doi.org/10.1146/annurev-ecolsys-102710-145001.

18. Martín-Martín, A., Orduna-Malea, E., Thelwall, M., & Delgado López-Cózar, E. (2018). Google Scholar, Web of Science, and Scopus: A systematic comparison of citations in 252 subject categories. *Journal of Informetrics*, *12*(4), 1160–1177. https://doi.org/10.1016/j.joi.2018.09.002.
19. Matute, D. R., & Coyne, J. A. (2010). Intrinsic Reproductive Isolation Between Two Sister Species of Drosophila. *Evolution*, *64*(4), 903–920. https://doi.org/10.1111/j.1558-5646.2009.00879.x
20. McCullough, J. M., Oliveros, C. H., Benz, B. W., Zenil-Ferguson, R., Cracraft, J., Moyle, R. G., & Andersen, M. J. (2022). Wallacean and Melanesian Islands Promote Higher Rates of Diversification within the Global Passerine Radiation Corvides. *Systematic Biology*, *71*(6), 1423–1439. https://doi.org/10.1093/sysbio/syac044.
21. Nanda, P., & Singh, B. N. (2012). Behavioural reproductive isolation and speciation in Drosophila. *J Biosci*, *37*, 359–374. https://doi.org/https://doi.org/10.1007/s12038-012-9193-7
22. Nosil, P., & Feder, J. L. (2012). Genomic divergence during speciation: Causes and consequences. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *367*(1587), 332–342. https://doi.org/10.1098/rstb.2011.0263.
23. Patiño, J., Whittaker, R. J., Borges, P. A. V., Fernández-Palacios, J. M., Ah-Peng, C., Araújo, M. B., Ávila, S. P., Cardoso, P., Cornuault, J., de Boer, E. J., de Nascimento, L., Gil, A., González-Castro, A., Gruner, D. S., Heleno, R., Hortal, J., Illera, J. C., Kaiser-Bunbury, C. N., Matthews, T. J., … Emerson, B. C. (2017). A roadmap for island biology: 50 fundamental questions after 50 years of The Theory of Island Biogeography. *Journal of Biogeography*, *44*(5), 963–983. https://doi.org/10.1111/jbi.12986.
24. Perianes-Rodriguez, A., Waltman, L., & van Eck, N. J. (2016). Constructing bibliometric networks: A comparison between full and fractional counting. *Journal of Informetrics*, *10*(4), 1178–1195. https://doi.org/10.1016/j.joi.2016.10.006.
25. Prawiradilaga, D. M. (2020). Diversity and threats to endemic birds in the Wallacean region, Indonesia. *IOP Conference Series: Earth and Environmental Science*, *473*(1). https://doi.org/10.1088/1755-1315/473/1/012064.
26. Rutgrink, A. L. J., Visser, M., & van Welzen, P. C. (2018). Differences between the floras of the North and South Moluccas (Indonesia). *Journal of Systematics and Evolution*, *56*(6), 652–662. https://doi.org/10.1111/jse.12301.
27. Shipton, C., O'Connor, S., & Kealy, S. (2021). The biogeographic threshold of Wallacea in human evolution. *Quaternary International*, *574*, 1–12. https://doi.org/10.1016/j.quaint.2020.07.028.
28. Suparman, S., Roini, C., & Saban, J. (2018). Indeks isolasi sexual antara lalat buah (drosophila melanogaster (meigen)) dari moya, pulau ternate dan gurabunga, pulau tidore. *Saintifik@ Jurnal Ilmiah MIPA*, *3*(1), 41–48.
29. Theissinger, K., Fernandes, C., Formenti, G., Bista, I., Berg, P. R., Bleidorn, C., Bombarely, A., Crottini, A., Gallo, G. R., Godoy, J. A., Jentoft, S., Malukiewicz, J., Mouton, A., Oomen, R. A., Paez, S., Palsbøll, P. J., Pampoulie, C., Ruiz-López, M. J., Secomandi, S., … Zammit, G. (2023). How genomics can help biodiversity conservation. In *Trends in Genetics* (Vol. 39, Issue 7, pp. 545–559). Elsevier Ltd. https://doi.org/10.1016/j.tig.2023.01.005.
30. van Eck, N. J., & Waltman, L. (2010). Software survey: VOSviewer, a computer program for bibliometric mapping. *Scientometrics*, *84*(2), 523–538. https://doi.org/10.1007/s11192-009-0146-3.
31. Verborgh, Ruben., & De Wilde, Max. (2013). *Using OpenRefine : the essential OpenRefine guide that takes you from data analysis and error fixing to linking your dataset to the Web* (1st ed.). Packt Publishing.
32. Wainwright, B. J., Leon, J., Vilela, E., Hickman, K. J. E., Caldwell, J., Aimone, B., Bischoff, P., Ohran, M., Morelli, M. W., Arlyza, I. S., Marwayana, O. N., & Zahn, G. (2024). Wallace's line structures seagrass microbiota and is a potential barrier to the dispersal of marine bacteria. *Environmental Microbiome*, *19*(1). https://doi.org/10.1186/s40793-024-00568-3.
33. Warren, B. H., Simberloff, D., Ricklefs, R. E., Aguilee, R., Condamine, F. L., Gravel, D., & Thébaud, C. (2015). Islands as model systems in ecology and evolution: prospects fifty years after MacArthur–Wilson. *Ecology Letters*, *18*(2), 200–217. https://doi.org/https://doi.org/10.1111/ele.12398.