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Genetic diversity and population structure of an endemic bee *Wallacetrigona incisa* in South Sulawesi, Indonesia

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Abstract. *Suhri AGMI, Hasan PA, Bahar I, Salatnaya H, Hashifah FN, Rahma MH, Wulandhani S, Mubarok H, Astuti WW. 2025. Genetic diversity and population structure of an endemic bee* Wallacetrigona incisa *in South Sulawesi, Indonesia. Biodiversitas 26: 861-868.* Stingless bees are vital pollinators for biodiversity, yet their genetic diversity and population dynamics in isolated regions like Sulawesi remain poorly understood a stingless bee species in the highland regions of Sulawesi, *Wallacetrigona incisa*, was investigated for its genetic variability, population dynamics, and environmental influences. This study aimed to clarify the genetic basis of the different populations in the highlands and lowlands. Inbreeding rates, population structure, and genetic exchange were assessed using molecular markers. The results showed low levels of inbreeding across populations with minor geographic differences, indicating that gene flow is still occurring between populations. Population structure analysis identified two distinct genetic groups, a highland group and a lowland group, suggesting strong genetic divergence, possibly due to geographical isolation. The association with over-winter survival in this study was the broad climate variables floral abundance and temperature. The results indicate that floral richness, particularly in highland regions, predicts genetic diversity better than temperature. These findings suggest that environmental variables, especially floral diversity, are particularly important for shaping *W. incisa* population genetics. Our study contributes new knowledge to *W. incisa* conservation and management by revealing that floral richness, particularly in highland regions, strongly influences genetic diversity and population robustness, underscoring the necessity of preserving diverse floral habitats. Additionally, this research contributes to our knowledge of the impacts of geographic and environmental factors on the genetic diversity of stingless bees and provides a valuable basis for future conservation efforts on a large scale in Sulawesi and other similar ecological areas.

Keywords: Adaptation, ecosystem, highland, lowland, phylogenetic, pollination

INTRODUCTION

Stingless bees (Hymenoptera: Apidae: Meliponini) are keystones of ecosystem diversity, pollinating a variety of flowering plants and boosting agricultural yields (Viana et al. 2014; Grüter 2020; Toledo-Hernández et al. 2022; Roubik 2023). Indigenous to the uplands of Sulawesi, *Wallacetrigona incisa* is found at 800 and 2200 m asl. (Engel and Rasmussen 2017; Rasmussen et al. 2017). This species is known for its honey production, which can reach three to five liters per colony per harvest period. The unique sensory properties and potential health benefits of honey have rendered it a source of significant economic interest (Suhri et al. 2021). Consequently, *W. incisa* is increasingly being introduced into lowland regions for apiculture. Although this practice has been financially beneficial, it also poses significant ecological and genetic threats. The translocation of *W. incisa* from its native highland habitat to lower altitudes presents numerous challenges in the context of its genetic divergence. This species exhibits unique adaptations to high-altitude habitats and may not thrive under lowland conditions. These environmental changes can lead to decreased fitness, reproductive failure, and potential disruption of local ecosystems. Furthermore, these movements may cause a loss of genetic diversity in *W. incisa* populations, which is critical to ensure the long-term viability of populations and to buffer against environmental pressures, disease, and climate change (Hrncir et al. 2019; Grüter 2020). Low genetic variation may lead to inbreeding depression (Charlesworth and Willis 2009), which could compromise the productivity and survivorship of colonies, ultimately endangering both the species and the stingless bee farming industry. Although *W. incisa* is increasingly domesticated in meliponiculture, its genetic diversity remains poorly understood. While other stingless bee species have been studied genetically using molecular approaches, including microsatellite markers (Francisco et al. 2017; Negreiros et al. 2019; Sayusti et al. 2020), little is known about the genetic structure of *W. incisa*. Microsatellite markers are beneficial for estimating the extent of genetic variability and population structure, and provide more information regarding gene flow, population connectivity, and the effect of relocation on genetic diversity (Purwanto and Trianto 2021).

This relocation highlights the difficulty in achieving both economic advantages *W. incisa* and its genetic and ecological endogeneity across locations. The introduction of non-native populations not only poses a risk by increasing the likelihood of inbreeding and inbreeding depression over time, but in the case of *W. incisa*, it may also lead to a decline in populations within their natural habitats. This competitive pressure could destabilize existing ecological systems, decrease resource availability to native species, and negatively impact biodiversity and ecosystem resilience (Aizen and Torres 2024; Dominguez-Flores et al. 2024). In addition, the movement of *W. incisa* into new geographical areas poses risks of introducing new pathogens and parasites to both dependent populations and neighbouring communities of wild bees under pressures from habitat destruction and climate change (Goulson et al. 2015; Belsky and Joshi 2019; Neov et al. 2019). These challenges are especially compounded by climate change, including in sensitive highland ecosystems such as those inhabited by *W. incisa*, which are highly sensitive to changes in temperature and precipitation patterns. Reintroducing *W. incisa* and other montane-adapted species into lowland areas may expose these species to climatic settings to which they are poorly matched, increasing the likelihood of colony loss and mortality. A change in climate can also disturb the timing of blooming and resource floral availability, which is an important ecophysiological factor, able to modulate foraging efficiency and reproductive performance of stingless bees (Machado et al. 2020; Layek et al. 2022; Kumar et al. 2024). Thus, an improved understanding of the genetic bases of *W. incisa* adaptation ennobles to consider more generally how to face these additional stressors for the widespread and sustainable persistence of *W. incisa* in ecosystems.

Despite the significant ecological and economic importance of *W. incisa*, research on its genetic diversity remains limited. Utilizing microsatellite markers, a molecular tool has been successfully employed to assess genetic variation, population structure, and gene flow in some stingless bee species (Sayusti et al. 2020; Purwanto and Trianto 2021) can offer crucial insights for evaluating the impact of translocation and establishing a conservation strategy based on evidence. Through microsatellite analysis, potential genetic bottlenecks and risks of inbreeding can be identified, aiding the formulation of genetic management plans to preserve or enhance diversity within natural and managed populations. These findings underscore the pressing need for comprehensive studies integrating the genetic, ecological, and management facets of *W. incisa*. This study aimed to investigate the genetic diversity and population structure of *W. incisa* using microsatellite markers, thereby enhancing our understanding of this important pollinator species in its ecological and environmental context. These results are anticipated to shed light on the genetic status of *W. incisa* populations in their original mountain habitats and the lowland areas they have recently inhabited. Moreover, this study seeks to develop effective strategies pertaining to meliponiculture practices, ensuring they contribute to economic progress while safeguarding the ecological and genetic integrity of this pivotal pollinator. Taking a holistic approach, this study underscores the importance of integrating genetic studies with conservation and management strategies to bolster the long-term viability of *W. incisa* populations and the ecosystems they sustain. Additionally, this research expands the knowledge of stingless bee conservation, offering insights that can be extended to other species and regions confronting similar challenges.

MATERIALS AND METHODS

Study area

The research site was situated in Luwu Utara District, South Sulawesi, Indonesia, encompassing both the original highland habitat and newly inhabited lowland regions of *W. incisa*. The native highland areas are positioned amidst the Rongkong, Rampi, and Seko Sub-districts, ranging from 800 m to 2200 m asl. These particular ecological conditions in the highlands have shaped the adaptation of *W. incisa*. The highland locations were at 2.678°S 120.166°E (Rongkong), 2.494°S 120.188°E (Rampi), and 2.490°S 120.177°E (Seko). In contrast, the lowland zones where *W. incisa* was introduced for beekeeping purposes are found in the Mappideceng and Bonebone sub-districts, situated at altitudes of 500 and 600 m asl. These lowland sites were positioned around 2.759°S 120.448°E (Mappideceng), and 2.739°S 120.461°E (Bonebone) (Figure 1, Table 1). The lower elevations, however, exhibit significant differences in temperature, humidity, and plant diversity compared to the higher elevation areas. These factors play a pivotal role in the examination of the effect relocation has on the genetic diversity of *W. incisa*.

Table 1. Research sites and ecological context for *Wallacetrigona incisa* in Luwu Utara, South Sulawesi, Indonesia

Sampling locations	Coordinates	Elevations (m asl.)	Purpose
Rongkong	2.678°S, 120.166°E	800	Original
Rampi	2.494°S, 120.188°E	1000	Original
Seko	2.490°S, 120.177°E	2200	Original
Mappideceng	2.759°S, 120.448°E	500	Introduced for beekeeping
Bonebone	2.739°S, 120.461°E	600	Introduced for beekeeping

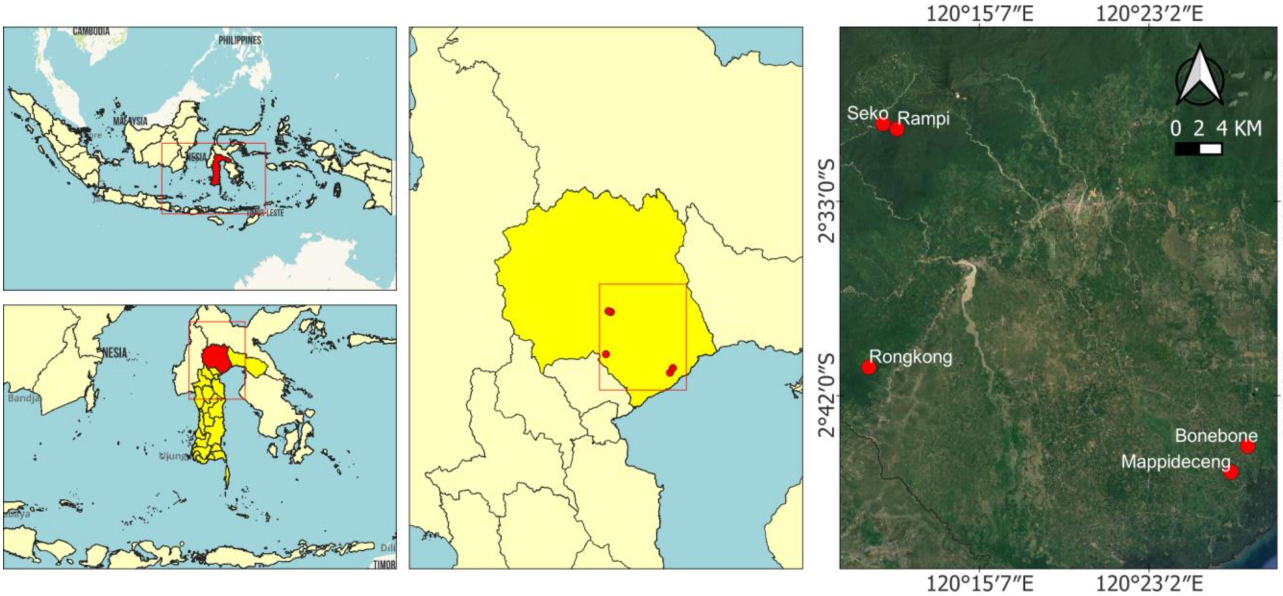

Figure 1. Research sites in Luwu Utara District, South Sulawesi, Indonesia

Procedures

Sample collection

Bee specimens were collected from six distinct locations in Luwu Utara District, encompassing both high- and low-elevation regions. The highland region sampling comprised three sub-districts: Rongkong, Rampi, and Seko, with 15 colonies sampled per sub-district, totaling 45 highland colonies. In the lowlands, samples were obtained from two sub-districts, Mappideceng and Bonebone, with five colonies sampled from each, resulting in ten lowland colonies. To ensure a more accurate representation of genetic diversity within each colony and to mitigate potential maternal bias, only worker bees were collected. The selection of bees for sampling was carried out systematically to ensure that specimens originated from different hives. Worker bees were captured directly at the entrance of their respective nests to confirm colony identity and to prevent cross-contamination. For each colony, approximately ten worker bees were randomly collected and were immediately placed into separate tubes to maintain sample integrity. This method ensured that each tube contained specimens from only one colony, preventing unintended mixing of individuals. All collected specimens were preserved in 95% ethanol immediately after sampling to facilitate DNA extraction and genetic analysis.

DNA extraction and microsatellite marker analysis

The DNeasy Blood and Tissue Kit (Qiagen, Germany) was used to extract genomic DNA from individual worker bees separately according to the manufacturer's protocol. DNA quality and concentration were assessed using a NanoDrop spectrophotometer and agarose gel electrophoresis, respectively. DNA samples with an OD 260/280 ratio exceeding 1.8 were considered high quality and selected for microsatellite analysis to ensure reliability. Genetic analysis employed 10 microsatellite loci, originally developed for other stingless bee species, such as *Tetragonula carbonaria* and *Melipona scutellaris*, which were adapted for use with *W. incisa*. These loci were selected based on their high polymorphism and successful amplification in related species (Sayusti et al. 2020; Purwanto and Trianto 2021). Polymerase Chain Reaction amplification was conducted in a 20 µL reaction mixture containing 50 ng of DNA, 10 mM of each primer, 2 mM dNTPs, 1.5 mM $MgCl_2$, 1x PCR buffer, and 0.5 U Taq DNA polymerase (Promega, USA). The thermal cycling protocol consisted of an initial denaturation at 94°C for 5 min, followed by 35 cycles of denaturation (94°C for 30 seconds), annealing (55°C for 30 seconds), and extension (72°C for 1 minute), with a final extension at 72°C for 10 min to ensure complete amplification. Successful amplification of microsatellite loci was confirmed by visualization of the PCR products on a 3% agarose gel.

Genetic differentiation and population structure

Genetic differentiation was assessed by calculating pairwise FST values using Genepop software, which measures the genetic variation between populations. To maintain statistical validity, Bonferroni correction was employed for multiple comparisons. The STRUCTURE software was utilized to investigate the genetic structure of the populations and detect distinct genetic clusters. The optimal number of clusters was determined using a Bayesian approach. Principal Component Analysis (PCA) was conducted with the vegan package in R to visualize the genetic variation among populations. Inbreeding within populations, mating patterns, and genetic exchange were examined by calculating fixation index (FIS) values. Environmental factors like floral diversity and temperature were documented during sampling to assess their impact on genetic diversity. The correlation between genetic diversity and environmental variables was analyzed using Pearson's correlation coefficients.

Environmental data collection

Supplementary environmental data were gathered during the sampling process to assess possible factors affecting genetic diversity. Temperature, humidity, and floral diversity were measured at each sampling site using portable weather stations and visual surveys of local flora.

Statistical analysis

Genetic data collection and HWE analysis

Genetic data used in this study were collected from the *W. incisa* population. Prior to further analysis, the genetic data were examined for deviations from Hardy-Weinberg equilibrium (HWE) using Genepop software (Raymond and Rousset 1995). This step is essential to ensure that the population has not undergone significant genetic admixture or natural selection, which could influence allele distribution in the population.

Data normality and Pearson correlation test

Before proceeding with the correlation analysis between genetic diversity and environmental factors, it is crucial to verify whether the data follow a normal distribution, as the Pearson correlation test assumes normally distributed data. To assess this assumption, the Shapiro-Wilk test was performed on both the genetic and environmental variables. Based on the results of the normality test, the data were found to follow a normal distribution (p>0.05). Therefore, the Pearson correlation coefficient was used to measure the strength and direction of the linear relationship between genetic diversity and the two main environmental factors considered: temperature and floral richness.

Principal Coordinates Analysis (PCoA)

To further explore the relationship between genetic diversity and environmental factors visually, Principal Coordinates Analysis (PCoA) was performed. This analysis allows for the representation of genetic diversity and environmental information in a multidimensional space. Through PCoA, patterns that may arise from the interaction of environmental factors such as temperature and floral richness with genetic structure can be identified. This visualization provides a clearer understanding of the relationship between genetic diversity and environmental factors, revealing potential influences of environmental factors on genetic variation in the *W. incisa* population.

Pearson Correlation Analysis

After confirming that the data follow a normal distribution, Pearson’s correlation analysis was conducted to measure the strength and direction of the relationship between genetic and environmental variables. The Pearson correlation coefficient was calculated to determine the extent to which temperature and floral richness are correlated with the observed genetic diversity in the population. Significant correlations indicate that environmental factors have a substantial influence on the genetic variation observed in the *W. incisa* population.

Ethical considerations

This study adhered to ethical guidelines for the collection and handling of animal specimens. All samples were collected with the permission of local authorities and landowners, ensuring minimal disturbance to natural bee populations.

RESULTS AND DISCUSSION

Genetic diversity

The genetic analysis of *W. incisa* populations revealed varying levels of polymorphism across sampled locations. A total of 55 colonies were examined from 6 different sites, comprising 3 highland and 2 lowland sub-districts. Measures such as allelic richness, observed heterozygosity (Ho), and expected heterozygosity (He) were calculated for each population. Comparing the data, we observed that highland populations exhibited higher allelic richness levels (mean locus: 7.8 alleles) than lowland populations (mean locus: 5.3 alleles). Additionally, observed heterozygosity in highland populations ranged from 0.65-0.78, indicating moderate genetic diversity, while lowland populations showed slightly lower values (0.56-0.63). Expected heterozygosity values for highland areas ranged from 0.72-0.80, and for lowland areas from 0.65-0.72, underscoring the trend of reduced genetic diversity in lowlands (Table 1).

The analysis also revealed the presence of private alleles in all populations, with a higher number observed in the highland regions (mean: 2.5 private alleles per locus) compared to the lowland regions (mean: 1.2 private alleles per locus). This suggests that the highland populations have a more distinct genetic composition, potentially due to limited gene flow between populations.

Genetic differentiation and FST analysis

Pairwise FST values were calculated to evaluate the genetic differentiation among the populations of *W. incisa*. These values, which quantify genetic divergence, are presented in Table 2.

Table 2. Pairwise FST values between populations

Population pair	FST value	Significance (p-value)
Rongkong-Mappideceng	0.25	0.002
Rongkong-Bonebone	0.18	0.004
Rampi-Mappideceng	0.30	0.001
Rampi-Bonebone	0.22	0.003
Seko-Mappideceng	0.27	0.002
Seko-Bonebone	0.20	0.004

Table 1. Genetic diversity parameters across populations

Location	Allelic richness	Observed heterozygosity (Ho)	Expected heterozygosity (He)	Private alleles	Habitat type
Rongkong	8.2	0.74	0.78	2.5	Montane forest
Rampi	7.6	0.72	0.75	2.2	Sub-montane forest
Seko	7.9	0.76	0.80	2.8	Montane forest
Mappideceng	5.1	0.58	0.65	1.1	Lowland forest
Bonebone	5.4	0.63	0.70	1.4	Lowland forest

Their analysis of pairwise FST values showed different levels of genetic differentiation among populations of *W. incisa*. FST values were found between 0.18-0.30, suggesting moderate to high genetic differentiation. The greatest amount of isolation identified was between the populations of Rampi and Mappideceng (FST: 0.30) and Seko and Mappideceng (FST: 0.27). These parameters reflect significant genetic divergence of this highland with respect to the lowland populations. Likewise, high level of genetic differentiation was detected between Rampi and Bonebone (FST: 0.22) and Seko and Bonebone (FST: 0.20). FST values between lowland populations and the alleged owerland populations were lower, with 0.25 between Rongkong-Mappideceng and 0.18 between Rongkong-Bonebone. These figures nevertheless demonstrate considerable divergence yet imply relatively closer genetic affinity than other highland-lowland comparisons.

Figure 2 presents a network diagram illustrating genetic differentiation among populations, with FST values represented by edge weights. The diagram elucidates distinct genetic structures between populations in the highland and lowland regions. These findings demonstrated genetic divergence across the examined populations, as evidenced by the statistically significant pairwise FST values. Visual representation further elucidates the genetic relationships between populations, based on their degree of differentiation.

Inbreeding and genetic structure

To evaluate inbreeding within the populations, the FISwas calculated. The FIS values ranged between 0.05 and 0.12 across all populations, with minor variations noted among sub-districts. These findings indicated minimal inbreeding in the studied populations. The low FIS values suggest that mating between genetically related individuals within colonies occurs infrequently, potentially because of sufficient outcrossing or genetic exchange between populations.

Observations of the FIS across all *W. incisa* populations can be visualized in Figure 3, representing specific instances of inbreeding as shown by the range of FIS. Among the populations, Bonebone had the highest FIS value (0.12), indicating a slightly higher inbreeding level of this site than the other sites. On the other hand, the lowest level of inbreeding (0.05) was exhibited by Rongkong. This figure clearly shows how inbreeding varies in populations that are geographically separated. For population structure estimation, STRUCTURE analysis and Principal Component Analysis (PCA) were used. The STRUCTURE analysis indicated the most likely number of genetic clusters was two (K: 2). This analysis showed that populations from highland regions clustered distinctly from lowland populations.

Figure 4 illustrates the proportion of the two main genetic clusters identified through STRUCTURE analysis (K: 2). The highland cluster accounts for 65% of the total population analyzed, while the lowland cluster makes up 35%. This chart visualizes the distribution of genetic clusters based on geographic locations.

Relationship between genetic diversity and environmental factors

To assess the relationship of genetic diversity with environmental factors including temperature and floral abundance, we used principal coordinate analysis (PCoA). 27. The study found many highland populations were significantly associated with floral richness and genetic diversity. The results showed a strongly positive relationship between these two variables, r: 0.75. This also means that areas with high floral diversity especially on higher altitudes such as Rongkong, Rampi and Seko would harbor populations with high genetic variations. This correlation achieves a statistically significant level (P<0.01) evidencing its reliability. These observations indicate that floral richness, as also noted earlier, could be an important determinant of genetic diversity in these populations, presumably via its ability to sustain a wider diversity of niche resources (Figure 5)

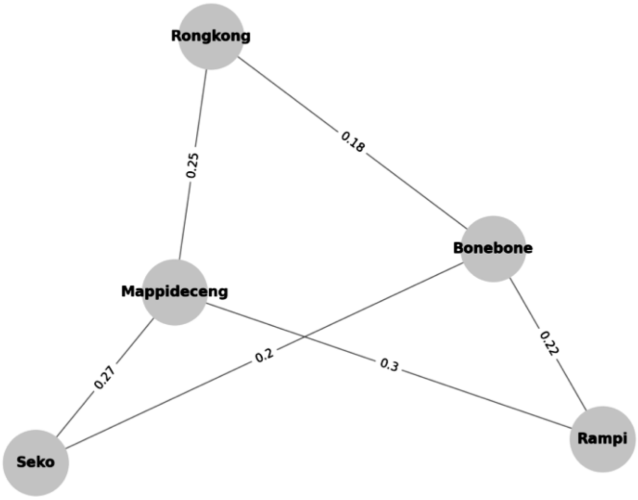

Figure 2. Network diagram of FST values between populations

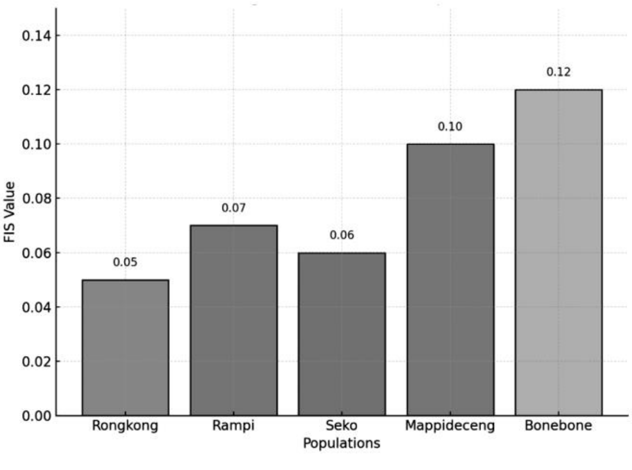

Figure 3. Inbreeding levels (FIS) across populations

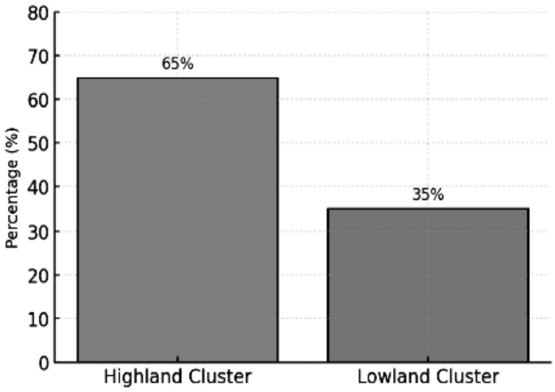

Figure 4. Genetic clusters identified by STRUCTURE analysis (K: 2)

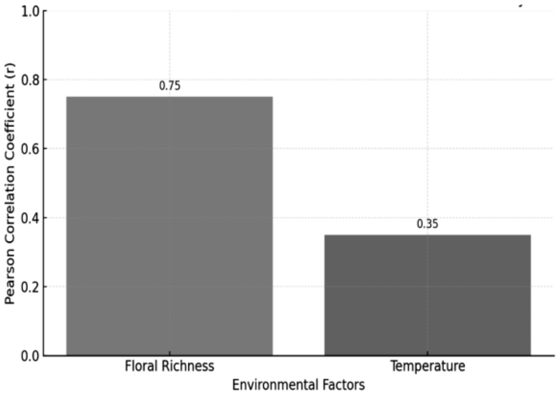

Figure 5. Correlation between environmental factors and genetic diversity

In contrast, temperature exhibits a weaker positive correlation with genetic diversity, with a Pearson correlation coefficient of 0.35. Although there is a slight positive trend, the relationship is not statistically significant (p: 0.08). This suggests that temperature has a limited influence on the genetic variability of *W. incisa* populations, possibly because these bees are more influenced by resource availability than thermal conditions.

Discussion

The genetic diversity, structure, and impact of environmental factors on *W. incisa* populations in Luwu Utara, South Sulawesi were investigated in this research. By utilizing genetic analyses like the fixation index FIS, pairwise FST values, PCA, and considering environmental influences, new insights into niche adaptation, genetic differentiation, and geographic/ecological barriers in this stingless bee species were offered. The findings from this study provide valuable information on the population dynamics of *W. incisa*, crucial for future conservation and management efforts. The overall FIS values across populations indicate low levels of inbreeding, with values ranging from 0.05 in Rongkong to 0.12 in Bonebone, suggesting inbreeding is not a significant concern within these populations. This is important as high levels of inbreeding can lead to decreased fitness and threaten the long-term survival of populations (Vasudev and Fletcher 2015). The observed low levels of inbreeding suggest that there is a sufficient rate of outbreeding and gene flow within the *W. incisa* populations, which is vital for conservation purposes to mitigate the risks associated with inbreeding depression. An increase in FIS values in specific populations like Bonebone may signal localized ecological factors affecting breeding structure, such as reduced floral resources or limited dispersal.

Pairwise FST values indicate a significant differentiation (0.12-0.30) between highland and lowland accessions, with genetic variation accounting for approximately 90% of the total variation. This suggests a notable level of isolation between populations inhabiting fluvial environments, distinct geographic regions, or facing specific environmental constraints that hinder genetic interchange (Nybom 2004). These findings are consistent with research on other stingless bee species, such as *Tetragonula carbonaria*, which also exhibit comparable genetic differentiation patterns within isolated populations (Meyer et al. 2021). The FST outcomes point towards limited gene flow among *W. incisa* populations in these regions, likely influenced by landscape obstacles like mountain ranges, as well as habitat fragmentation resulting from human activities like deforestation and agricultural expansion (Sayusti et al. 2020). Subsequent STRUCTURE analysis supported these findings, revealing two distinct genetic clusters corresponding to the highland and lowland populations. This clustering pattern was further supported by a PCA plot, illustrating a clear separation of populations along the primary axis, which accounted for 45% of the total genetic variation.

Unlike the other groups, populations in the highlands, such as Rongkong, Rampi, and Seko represent a distinct genetic group; their genetic isolation is most likely caused by a stable and diverse floral environment. These areas have diverse plant species, providing year-round opportunities for foraging that could enhance colony fitness and genetic diversity. This is in line with studies on other pollinators, for example, *Bombus terrestris*, where the floral diversity is a prime predictor of genetic diversity (Fernández-Martínez et al. 2019). In contrast, lowland populations such as Bonebone and Mappideceng reflect lower genetic diversity and higher FIS values which are perhaps attributable to habitat degradation, fragmentation and restricted inter-individual gene flow. One especially striking result from this work was the difference in genetic diversity between different parts of the world. These differences were pronounced, with key differences between lowland and highland areas, emphasizing both the importance of conserving floral richness and prioritizing the preservation of highland areas for the maintenance of species genetic health. Genetic diversity correlates strongly with environmental factors, notably floral richness. The Pearson correlation coefficient for the relationship between floral richness and expected heterozygosity is 0.75, suggesting a persistent relationship between floral diversity and genetic diversity in *W. incisa* populations. These results support previous findings that genotypic diverse floral microhabitats can contribute to maintaining genetically dynamic populations (Repaci et al. 2006). However, the weaker association of temperature on genetic diversity could suggest that temperature may have a reduced impact on the genetic variation of *W. incisa*. This might indicate the species' ability to adapt to different climatic regimes, given it the presence in both the highland and lowland regions of Sulawesi.

This work shed light on the complex interaction between genetic diversity and environmental factors, particularly floral diversity, in determining *W. incisa* population dynamics. These findings prove our understanding of the ecological requirements and genetic integrity of species, which is essential for developing effective conservation policies. Given its importance as a pollinator of native flora in addition to agricultural crops (van Velden et al. 2020). Genetic divergence between the highland and lowland populations highlights the need for conservation efforts to maintain habitat connectivity and protect floral resources in the high-altitude sites, where genetic diversity is most strongly correlated with high floral abundance. Furthermore, the genetic diversity of *W. incisa* may be affected by translocation activities and thus merits further consideration. Translocating colonies across space, and especially from low to high elevations, might interrupt local gene pools and erode population robustness (Kelemen and Rehan 2021; Nannan et al. 2022; Kumar et al. 2024). As such, future management strategies should include guidelines for controlled translocations that consider genetic components to avoid uniformity of populations, with the subsequent risk of losing regionally adapted traits (Gaitán-Espitia and Hobday 2021). Overall, this study provides new perspectives on the genetic diversity, structure, and ecological importance of *W. incisa*, underscoring the need to preserve floral diversity, particularly in upland areas, to maintain genetic diversity among this important pollinator species. These take-home messages emphasize the importance of conservation strategies that are mindful of genetic influences and the hazards of translocation. This work serves to expand knowledge on the conservation of stingless bee species based on genetic data and environmental parameters, with implications for ecosystem stability and agricultural productivity.

Thus, the genetic diversity analysis of *W. incisa* presented herein highlights a crucial impetus to conserve the genetic diversity of native populations of *W. incisa* from Sulawesi's highland area. Natural populations growing at 800 and 2200 m asl, however, show significantly stronger genetic structuring compared to those moved to lower elevations. This difference may be due to some adaptations to resist the challenges of high-altitude life, including cold temperatures, fragmented food distribution, and other selective pressures found in tropical mountain ecosystems. These results agree with previous studies that highlight that environmental stressor can shape species genotypes (Hrncir et al. 2019). But the data also reveal lower heterozygosity levels for relocated populations, suggesting an elevated risk of inbreeding. Moreover, this is compounded by minimal gene flow between geographical separated populations, shown by high FST values from population structure studies. The reduced genetic diversity among these population mirrors that of Charlesworth and Willis (2009), who have shown that inbreeding can lead to detrimental effects, including lowered resistance to pathogens and environmental stressors, and reduced colony productivity. Additional microsatellite data suggest even lowland populations are becoming more genetically limited as localized adaptations may be lost. This highlights the necessity of meliponiculture practice to be applied with caution, in order to not push their genetic structure into further deterioration. Conservation of native populations in their native habitats is critical for ensuring the long-term evolutionary potential of *W. incisa*. Much like observed with the stingless bee species *Melipona quadrifasciata*, such inadvertent translocation would avoid or bypass process of unregulation resulting in specific loss of adaptations to local environments (Grüter 2020).

Moreover, environmental changes, such as climate change and habitat fragmentation, may further exacerbate reductions in genetic heterogeneity. Because *W. incisa* is a keystone pollinator for tropical montane ecosystems, reduced genetic health may have far-reaching ecological ramifications, potentially resulting in decreased ecosystem services critical to biodiversity conservation and agricultural productivity in the region. Although the current study applied a microsatellite based approach to inform on genetic diversity among populations, advancements in the field, such as the use of more advanced molecular markers such as Single Nucleotide Polymorphisms (SNPs), can still be undertaken. These improved tools have the potential to offer valuable insight on population dynamics and gene flow. Integrating genomic analysis and molecular ecology may provide researchers with unprecedented insights into how this species has adapted to changing environmental conditions. This study emphasizes the need for detailed genetic conservation practices, including the importance of evolutionary feasibility studies prior to population translocations and assessment of sustainable management of habitat. Long-term ecological and economic sustainability of *W. incisa* will require establishing breeding programs focusing on genetic character diversity. More research is needed to investigate the long-term effects of translocations on genetic stability, and the wider consequences for the health of ecosystems.

In conclusion, the study on *Wallacetrigona incisa* in South Sulawesi reveals genetic differences between highland and lowland populations, likely influenced by geographical isolation and environmental factors. Microsatellite analysis indicates that highland populations exhibit higher genetic diversity, with greater allelic richness and heterozygosity compared to lowland populations. Notably, floral richness shows a strong correlation with genetic diversity, highlighting the crucial role of diverse floral resources in maintaining population health. This study emphasizes the importance of conservation strategies that prioritize habitat preservation and sustainable meliponiculture practices to safeguard the genetic integrity of *W. incisa*, ensuring its long-term viability as a key pollinator in tropical ecosystems.

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