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Diversity of Freshwater Shrimp in Toaya Village, Sindue District, Donggala Regency Based on Phenotypic Data

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Abstract

Freshwater shrimp are aquatic resources that play important ecological and economic roles and exhibit considerable species diversity, characterized by variations in phenotypic traits. Information regarding the diversity of freshwater shrimp species and phenotypic variation in Toaya Village remains limited; consequently, data on the level of phenotypic diversity among species are still largely unavailable. This study aimed to identify the diversity of freshwater shrimp species and analyze their phenotypic characteristics, including morphometric and meristic traits, using a multivariate analytical approach. This research employed a descriptive-exploratory design with random sampling conducted across three observation stations. The collected freshwater shrimp specimens were identified based on morphological characteristics using established scientific literature as references and were subsequently measured using 40 phenotypic characters. The resulting data were analyzed using Principal Component Analysis (PCA) and the Unweighted Pair Group Method with Arithmetic Average (UPGMA). The results revealed the presence of four freshwater shrimp species, namely Macrobrachium mammilodactylus, Macrobrachium empulipke, Macrobrachium equidens, and Macrobrachium rosenbergii. These four species exhibited a phylogenetic relationship with a similarity coefficient of approximately 0.78. At the species level, individuals showed high phenotypic similarity (0.97–0.98), reflecting the consistency of phenotypic traits within each species. Principal Component Analysis demonstrated that the first two principal components accounted for the majority of phenotypic variation, with the greatest contributions originating from specific morphometric and meristic characters. This study concludes that the multivariate analytical approach applied was both effective and efficient in revealing diversity patterns based on phenotypic characteristics.

Keywords: Diversity; Freshwater Shrimp; PCA; UPGMA; Sulawesi.

INTRODUCTION

Freshwater shrimp are aquatic organisms belonging to the subphylum Crustacea, class Malacostraca, and order Decapoda, which play important ecological and economic roles (Zaini et al., 2025). In general, shrimp habitats are classified into two main types, namely freshwater and marine environments (Fahlevi et al., 2021). The natural habitats of freshwater shrimp include various aquatic ecosystems such as rivers, lakes, and wetlands (Hurriyani et al., 2022). Within aquatic ecosystems, shrimp contribute significantly to food web dynamics, facilitate the decomposition of organic matter, and serve as indicators of environmental quality and ecosystem health (Bachry et al., 2023; Mawardi et al., 2024). Freshwater shrimp species diversity can be distinguished through phenotypic characteristics, including body shape, morphometric measurements, meristic traits, and body coloration, all of which function as distinguishing features among species (Listia et al., 2023). Morphological structures such as the rostrum, antennae, chelae, and walking legs represent observable phenotypic traits that can be used to differentiate species within the same genus (Putri et al., 2023). These phenotypic variations reflect the genetic constitution of organisms and contribute to species diversity as an essential component of biodiversity (Baderan et al., 2022; Asril et al., 2022). This phenomenon is particularly evident in Indonesia, especially on Sulawesi Island, which harbors a rich diversity of freshwater shrimp species with a high level of endemism (Carstensen et al., 2012).

Numerous studies on freshwater shrimp diversity have been conducted across Indonesia; however, most have primarily focused on species identification and distribution patterns. In Central Sulawesi, several investigations have documented the occurrence and distribution of freshwater shrimp in different aquatic habitats. Dwiyanto et al. (2018) reported several shrimp species inhabiting the Batusuya River based on morphological identification. Similarly, research conducted by Samsudin et al. (2024) in Tolitoli Regency documented the presence of seven species belonging to the genera *Macrobrachium* and *Caridina* using a descriptive approach. Studies in Lake Lindu by Annawaty (2024) emphasized the abundance and distribution of the invasive shrimp species *Macrobrachium lanchesteri*, while Milasari and Annawaty (2025) examined the distribution patterns and population characteristics of the endemic shrimp *Caridina kaili* in several inlet rivers. In general, these studies relied mainly on descriptive analyses and did not employ multivariate analytical approaches such as Principal Component Analysis (PCA) and Unweighted Pair Group Method with Arithmetic Average (UPGMA) to investigate phenotypic variation in greater detail based on morphometric and meristic characteristics among species.

Information regarding freshwater shrimp species diversity is essential not only for determining the number of species present within a particular habitat but also for assessing phenotypic differences among species as a basis for biodiversity analysis. To support such assessments, multivariate analytical techniques, including Principal Component Analysis (PCA) and Unweighted Pair Group Method with Arithmetic Average (UPGMA), can be applied. PCA is widely used to reduce data dimensionality and identify the principal characters contributing to morphological variation among species (Fadhilah et al., 2023), whereas UPGMA is utilized to construct dendrograms based on Euclidean distance matrices in order to illustrate the degree of similarity among species (Uno et al., 2019). Despite their effectiveness, studies employing these approaches remain relatively limited, particularly in Central Sulawesi. Consequently, comprehensive information regarding phenotypic diversity among freshwater shrimp species is still lacking. A similar situation exists in Toaya Village, Sindue District, Donggala Regency, an area characterized by river systems and freshwater bodies that potentially provide suitable habitats for a variety of freshwater shrimp species. Nevertheless, information on freshwater shrimp diversity in this region remains scarce, particularly with regard to phenotypic characteristics based on morphometric and meristic traits. Such information is crucial for biodiversity inventory programs, sustainable aquatic resource management, and the conservation of local species. Therefore, this study aimed to identify the diversity of freshwater shrimp species and to analyze interspecific phenotypic characteristics using a multivariate analytical approach.

MATERIALS AND METHODS

Study Area

This study was conducted in October in Toaya Village, Sindue District, Donggala Regency, Central Sulawesi, Indonesia (Figure 1). The study area is characterized by freshwater ecosystems, including rivers and small streams that provide suitable habitats for various freshwater shrimp species. These aquatic environments support diverse biological communities and play an important role in maintaining local biodiversity.

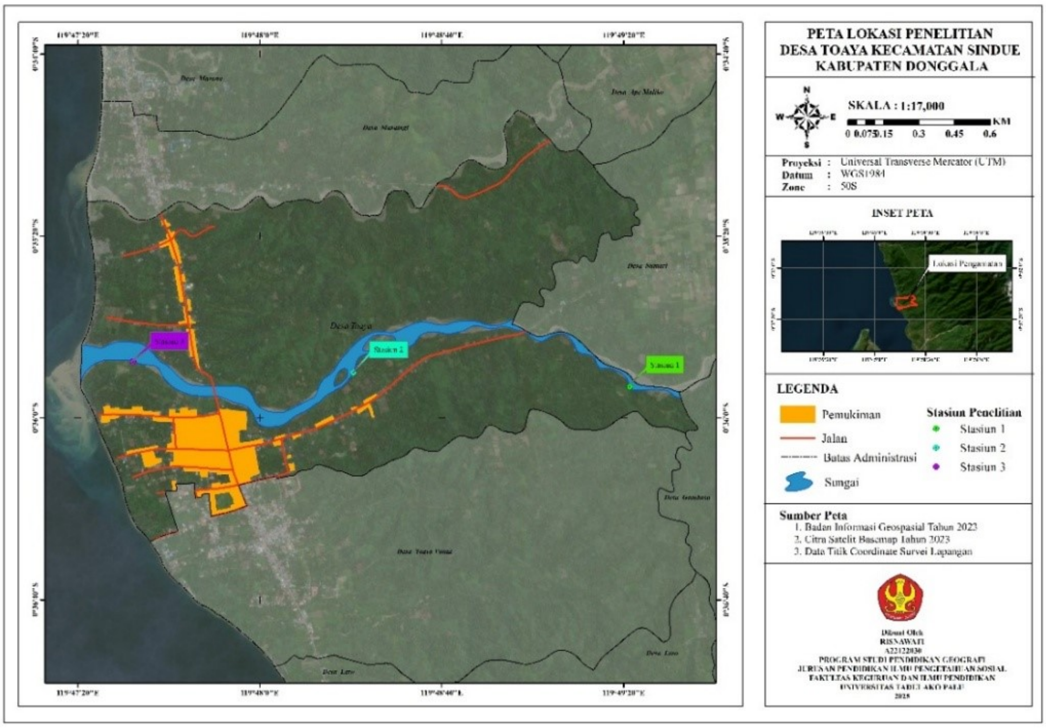


Figure 1. Map of the research location in Toaya Village, Donggala Regency, Central Sulawesi, Indonesia.

Procedures

Data Collection Techniques

Data collection began with field observation at the study site to assess the aquatic conditions and the presence of freshwater shrimp. Subsequently, sampling was carried out using a hand net (scoop net) employing a random sampling method without specific spatial restrictions. From all freshwater shrimp encountered in the study area, only 24 individuals were selected as the main samples.

Species Identification of Shrimp

Species identification of freshwater shrimp was conducted by observing the morphological characteristics of each individual and comparing them with descriptions in identification guides and relevant scientific literature as taxonomic references. From a total of 24 examined individuals, four freshwater shrimp species were successfully identified. The identification results were then used as the basis for further analysis of phenotypic variation among freshwater shrimp in the study area.

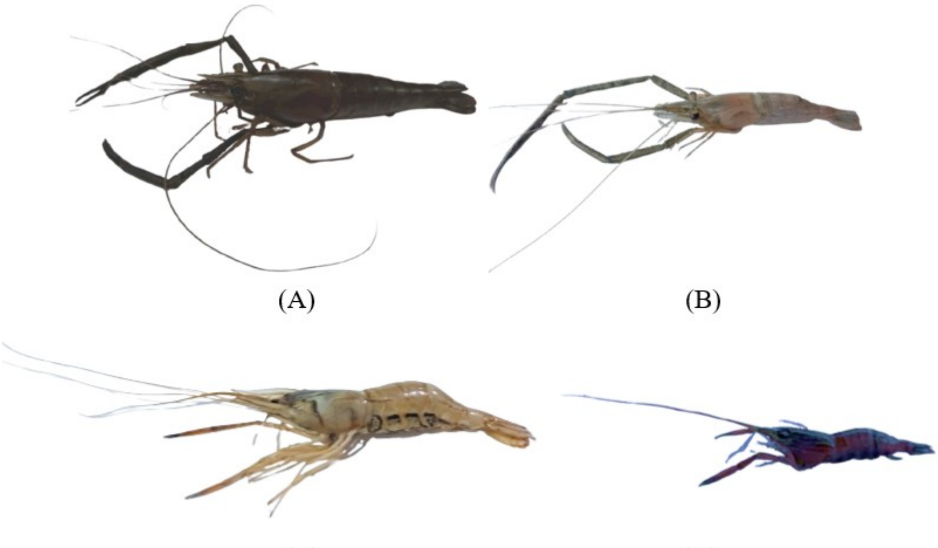
Data Analysis

Data processing involved the measurement of 40 phenotypic characters, including morphometric and meristic traits, across all shrimp samples. The resulting data were tabulated using Microsoft Excel to systematically organize the dataset and ensure data completeness and consistency. Subsequently, data analysis was performed using PAST software version 4.03. Principal Component Analysis (PCA) was applied to reduce data dimensionality and to identify phenotypic characters contributing to morphological variation. In addition, cluster analysis using the Unweighted Pair Group Method with Arithmetic Average (UPGMA) was conducted based on a distance matrix. The results were presented in the form of a dendrogram to illustrate grouping patterns based on phenotypic characteristics.

RESULTS AND DISCUSSION

Diversity of Freshwater Shrimp

The results of this study showed that from all freshwater shrimp collected in the study area, a total of 24 individuals were used as the main samples and successfully identified into four different species, namely *Macrobrachium mammilodactylus*, *Macrobrachium empulipke*, *Macrobrachium equidens*, and *Macrobrachium rosenbergii* (Figure 2). All identified species belong to the genus *Macrobrachium*, which is classified under the subphylum Crustacea and order Decapoda, and is also a member of the phylum Arthropoda characterized by segmented appendages (Putra et al., 2023; Fadillah, 2024). This level of diversity reflects that the environment provides suitable habitat conditions for various species. The aquatic environment in the study area is characterized by rocky, gravelly, and sandy substrates, supported by the presence of aquatic vegetation and riparian trees along the riverbanks. In addition, water quality parameters such as temperature, light intensity, and pH were within ranges that support shrimp survival. This is consistent with Pratiwi et al. (2016), who stated that freshwater shrimp tend to inhabit areas such as spaces between large rocks with gravelly, moss-covered, and sandy river substrates. Aquatic vegetation also serves as shelter and feeding grounds for shrimp, enabling their survival (Adli et al., 2022). These findings indicate that the waters of Toaya Village support the presence of several freshwater shrimp species exhibiting phenotypic variation, thereby providing a basis for studies on freshwater shrimp diversity in line with the objectives of this research.



(A) (B)

(C) (D)

Figure 2. Freshwater shrimp species: A. *Macrobrachium mammilodactylus*, *Macrobrachium empulipke*, *Macrobrachium equidens*, and *Macrobrachium rosenbergii.* Scale: 1 cm.

UPGMA Analysis

The dendrogram results showed that individuals within the same species clustered at a high similarity level, ranging from approximately 0.97 to 0.98, indicating relatively homogeneous phenotypic characteristics. Separation among species began to appear at a similarity level of around 0.90, where *M. equidens* and *M. rosenbergii* exhibited a closer phylogenetic relationship, as they clustered together earlier compared to the other species. *M. empulipke* showed a moderate level of similarity (0.88–0.90), whereas *M. mammillodactylus* exhibited the lowest similarity, as it clustered at a range of 0.78–0.85.

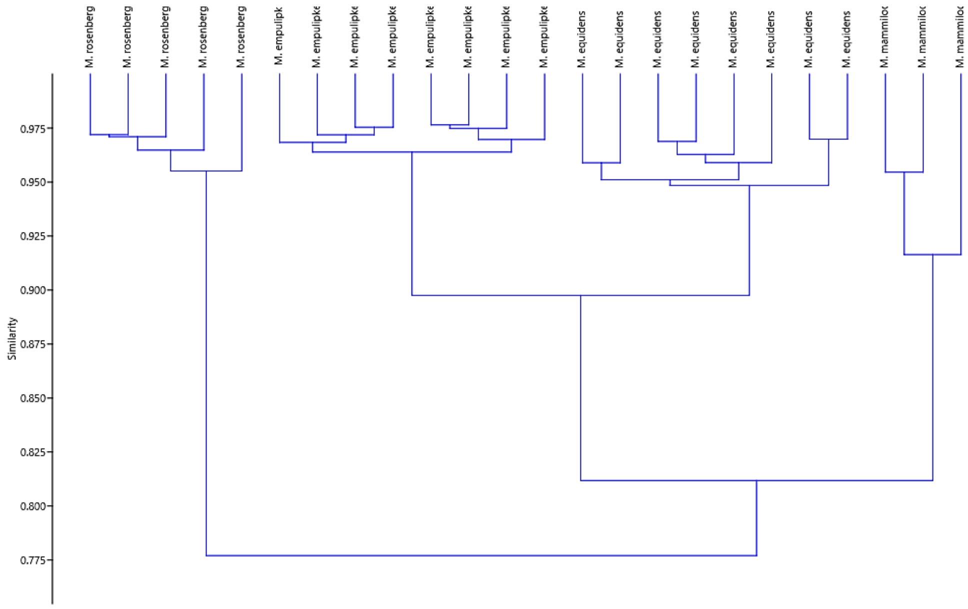


Figure 3. UPGMA analysis.

PCA Loading Plot

The results of the Principal Component Analysis (PCA) are presented in the form of loading plots, which illustrate the contribution of each morphometric character to body shape variation. This analysis included four freshwater shrimp species, namely *M. mammilodactylus*, *M. empulipke*, *M. equidens*, and *M. rosenbergii*. In the PC1 and PC2 loading plots, each variable showed different loading values. Characters such as PC, PTO, PNL, PAN, and PTK exhibited relatively high contributions to the formation of the principal components, whereas variables with lower loading values had a smaller influence on the observed morphological variation (Figures 4 and 5).

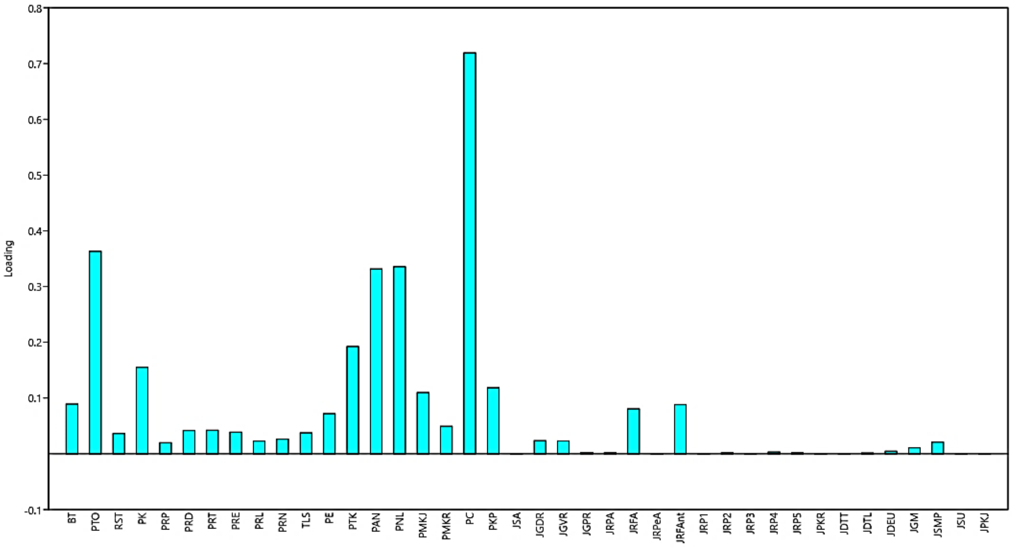


Figure 4. The Loadings Plot Componen 1.

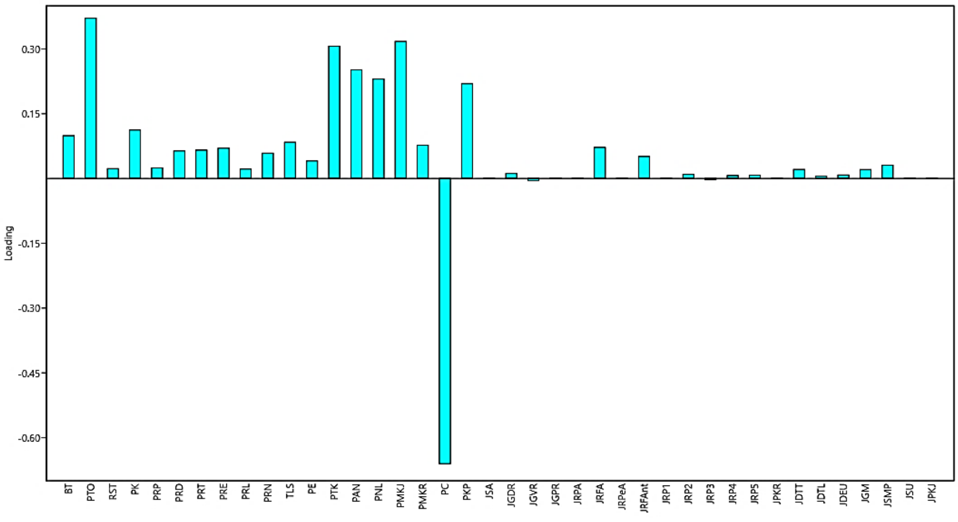


Figure 5. The Loadings Plot Componen 2.

PCA Biplot

The PCA biplot illustrates the distribution pattern of individuals based on morphometric character variation. *Macrobrachium mammillodactylus* is clearly separated from the other species, indicating the greatest degree of morphological differentiation. In contrast, *M. equidens* and *M. rosenbergii* are positioned close to each other, suggesting a high degree of similarity in their morphological characteristics. Meanwhile, *M. empulipke* occupies a distinct position with a moderate level of differentiation. This pattern is consistent with the clustering results obtained from the dendrogram (Figure 6).

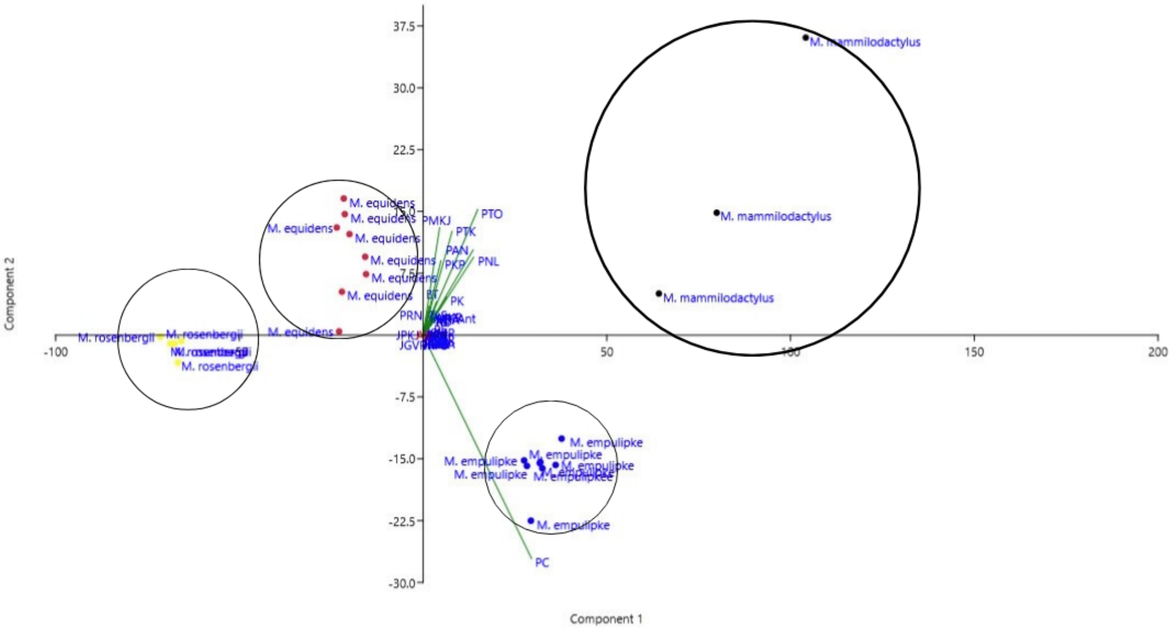


Figure 6. PCA results of freshwater shrimp analysis in a biplot representation.

Discussion

The results showed that from all freshwater shrimp collected in the study area, a total of 24 individuals were used as the main samples and successfully identified into four different species, namely *M. mammillodactylus*, *M. empulipke*, *M. equidens*, and *M. rosenbergii*. This indicates that the waters of Toaya Village possess freshwater shrimp diversity, supported by suitable environmental conditions that enable the coexistence of multiple species within a single habitat. Putra et al. (2023) stated that healthy river habitat conditions play an important role in supporting the life of various freshwater shrimp species, particularly those of the genus *Macrobrachium*, as suitable environments facilitate their survival and distribution. According to Lige et al. (2022), biodiversity is influenced by both internal and external factors. External factors include physical environmental conditions such as temperature, light intensity, humidity, and food availability, while internal factors relate to the organism's physiological responses to environmental influences. Appropriate environmental conditions allow freshwater shrimp to survive, actively move, and reproduce effectively (Rachman et al., 2025). Dirham and Trianto (2020) also reported that unpolluted waters tend to show a relatively even distribution of individuals across species.

The UPGMA analysis revealed clustering patterns indicating phenotypic differences among freshwater shrimp species. Individuals within the same species clustered at a similarity level of 0.97–0.98, indicating relatively homogeneous morphological characteristics. Separation among species began to appear at a similarity level of approximately 0.90, where *M. equidens* and *M. rosenbergii* clustered closely, indicating higher morphological similarity. *Macrobrachium empulipke* showed a moderate similarity level (0.88–0.90), while *M. mammillodactylus* was separated at a range of 0.78–0.85, indicating the greatest phenotypic difference compared to the other species. The observed variation in this study is based on morphological characteristics; therefore, the results reflect the phenotypic condition of organisms in the field (Patigu et al., 2019; Burhanuddin et al., 2025). Morphological traits represent the expression of phenotypes derived from genetic information; thus, morphometric analysis can be used to assess genetic effects within a species (Dahlia et al., 2022). The UPGMA method in this study effectively produced consistent clustering based on similarity among individuals (Raihannabil et al., 2025). The clustering pattern in the UPGMA dendrogram indicates phenotypic variation among species as an indicator of biodiversity. A lower similarity value between species corresponds to a higher degree of morphological differentiation, thereby strengthening the evidence of phenotypic diversity among freshwater shrimp in the study area.

The loading plot results showed that each morphometric character contributed differently to the formation of principal components. This can be observed from the length of the bars in the plot; higher bars indicate greater contributions of the respective characters to group separation (Hikmah et al., 2023). The loading plots for PC1 and PC2 revealed that claw length (PC) was the most dominant character in shaping morphological variation among shrimp. In PC1, claw length showed the highest loading value, indicating a major contribution to overall variation, while in PC2 it also showed the largest negative loading value, indicating an opposite directional contribution. This suggests that claw length not only contributes to size variation but also plays a key role in distinguishing morphological patterns among species. Therefore, claw length can be considered a primary character in species grouping, while other characters act as supporting variables. These findings indicate that phenotypic diversity is not only evident among species but is also influenced by specific dominant morphological traits.

The distribution of individuals in the PCA biplot showed a pattern consistent with the UPGMA results, where *M. mammillodactylus* was clearly separated along the main axis, indicating the greatest morphological differentiation. In contrast, *M. equidens* and *M. rosenbergii* were positioned close to each other, indicating high phenotypic similarity, while *Macrobrachium empulipke* occupied a separate position with a moderate level of differentiation. This analytical approach is used to identify the most influential characters in determining distribution patterns among individuals (Yaldiz and Camlica, 2020). Based on the biplot results, vector length represents the magnitude of each character's contribution to group separation (Hikmah et al., 2023). In the present study, claw length (PC) exhibited a prominent vector, indicating its important role in group separation. The biplot also revealed separation of individuals into different quadrants (Agustin et al., 2024), where *M. mammillodactylus* was clearly separated on the right side, *M. rosenbergii* on the left side, *M. empulipke* in the lower quadrant, and *M. equidens* positioned near the center to upper area. This separation indicates phenotypic diversity among species, as each species occupies different positions influenced by different dominant characters. This is consistent with Dwipurwani et al. (2022), who stated that closely positioned objects tend to share similar characteristics, while vector length reflects the level of character variability. Therefore, these results confirm that the observed diversity is not only determined by species richness but also influenced by variations in phenotypic traits.

CONCLUSIONS

This study successfully identified four freshwater shrimp species, namely *Macrobrachium mammillodactylus*, *M. empulipke*, *M. equidens*, and *M. rosenbergii*. The UPGMA analysis revealed that individuals within the same species exhibited a high level of similarity, with similarity values ranging from 0.97 to 0.98. *M. equidens* and *M. rosenbergii* showed the closest relationship at approximately 0.90, while *M. empulipke* exhibited a moderate level of similarity ranging from 0.88 to 0.90. Meanwhile, *M. mammillodactylus* showed the lowest similarity values (0.78–0.85), indicating the most pronounced phenotypic differences. The PCA biplot analysis also demonstrated that claw length (PC) is the main character contributing to the differentiation of phenotypic variation among species.

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Competing Interests: The authors declare that there are no competing interests.

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