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Article

Genetic Diversity and Kinship Relationships Among Black Mangrove Populations (*Rhizophora mucronata*) in West Sulawesi Based on Morphological Markers

Mukrimin*, Gusmiaty, Marwah Salam, Atisa Muslimin

Department of Forestry, Universitas Hasanuddin, Jl. Perintis Kemerdekaan No. KM. 10 Tamalanrea Regency, Makassar, South Sulawesi 90245, Indonesia
* Correspondence: mukrimin@unhas.ac.id

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Abstract. *Rhizophora mucronata* is a black mangrove with the most productive ecosystem that has benefits many people. But in reality, because of their business, some people often neglect preserving mangrove ecosystems and habitats. This study was conducted to analyze the level of genetic diversity and the relationship between *R. mucronata* in West Sulawesi based on morphological markers that will be used in future restoration efforts of black mangroves around the coast. This study used ten trees from three origins: Polewali Regency Mandar, Majene, and Mamuju. Then, several parts of the tree are used for this study, namely leaves, trunks, bark, roots, flowers, and propagules. However, the observed characteristics are leaf shape, stem shape, and color samples such as bark color, stem color, root color, color propagule (fruit and hypocotyl), and leaf color with a qualitative and quantitative approach. The results of this study show that black mangroves in Polewali Mandar, Majene, and Mamuju show high-value genetic diversity. The genetic distance between Polewali Mandar and Mamuju shows a high value of 0.13, meaning they have a distant kinship. Meanwhile, the genetic distance between Polewali Mandar and Majene shows a low value of 0.09, meaning they are close relatives. The findings of this study directly address the research urgency by highlighting the high genetic diversity of *R. mucronata* populations in West Sulawesi, despite increasing threats from anthropogenic activities. The observed genetic distances indicate significant variation among populations, particularly between Polewali Mandar and Mamuju, which suggests the need for targeted conservation strategies. The close genetic relationship between Polewali Mandar and Majene further emphasizes the importance of localized preservation efforts. These insights provide a scientific basis for future restoration initiatives, ensuring conservation programs maintain genetic resilience and adaptability within the mangrove ecosystem.

Keywords: Genetic Variability, Heterozygosity, Mangroves, Morphological Markers, *Rhizophora mucronata*

INTRODUCTION

Mangrove forest ecosystems are one of the most productive and unique ecosystems that function to protect coastal areas from various disturbances, as well as providing habitat for various animal species. As one of the most productive ecosystems, mangrove forests are inseparable from their use for human purposes. As a result of these interests, some communities ignore the ecological aspects and natural habitats of mangrove forests. Some mangrove forests have been damaged, decreasing the halophyte populations. Several mangrove forest areas are converted into cultivation areas (conventional ponds) (Wu et al., 2022; Su et al., 2025; Yang et al., 2025). Due to the large losses caused by the destruction of mangrove forests, rehabilitation measures are mandatory. Billah et al. (2020) showed that mangrove forests in Borong suffered from low tree density, with their area coverage of less than 50%. Factors such as land clearing for road construction, waste disposal, and cutting of mangrove trees by the community for daily needs have caused this damage (Sofue et al., 2025; Yap & Al-Mutairi, 2025).

There are several species of mangroves, one of which is the prima donna, namely the type of *Rhizophora mucronata* or black mangrove. *R. mucronata* is widely distributed in West Sulawesi, especially in coastal areas such as Polewali Mandar, Majene, and Mamuju. These sites have potentially good mangrove forest ecosystems, but genetic diversity information about black mangroves in these areas is needed, so that it can be used in plant breeding efforts in places where mangrove populations have begun to decline. A drastic population decline is an early symptom of a species' extinction that will result in a decline in genetic diversity (Mukrimin et al., 2021).

Genetic diversity is needed to determine the magnitude of genetic variation that exists. Genetic diversity also determines the success of populations to adapt to changing environments. Diversity analysis can be carried out with various approaches, one of which is using morphological characteristics. This type of marker can indicate the diversity of plant varieties and species observed. The advantage of this type of marker is that it is not only cheap, but also easy to apply (Fitri et al., 2018).

Research on black mangroves based on morphological markers has been conducted before, but it is limited to only three areas, namely Barru, Maros, and Pangkep (Mukrimin et al., 2021). Therefore, this research is important to be carried out to see the genetic diversity of black mangroves in different areas, namely Polewali Mandar, Majene, and Mamuju.

MATERIAL AND METHODS

Research Location

This research was carried out in March-April 2021. Sampling was conducted in several West Sulawesi districts, namely Polewali Mandar, Majene, and Mamuju. Sampling was carried out using the random sampling method. Ten samples were collected from each site. Sampling campaign was carried out in the morning and at noon, when the sea water recedes, to make it easier for researchers in the sampling process. Each tree has its leaves, trunk, bark, roots, and fruits and their coordinate points. Furthermore, the observation of genetic diversity based on morphological markers, sample measurements, and data analysis was carried out at the Laboratory of Biotechnology and Tree Breeding, Faculty of Forestry, Hasanuddin University, Makassar.

Morphological Analysis Observations

Observations and measurements were made on the variables: leaves, stems, crowns, roots, flowers, and fruits. Data collection techniques in the field are carried out in the following ways (Mukrimin et al., 2021):

Leaf

1. Leaf Length (LL): measurements are taken starting from the tip of the petiole, to the tip of the leaf using a ruler
2. Leaf Thickness (LT): measurement using a caliper
3. Leaf Weight (LW): performed using an analytical scale by measuring the initial weight and final weight of the leaf
4. Leaf Width (LW): measurement of the broadest leaf surface using a ruler
5. Leaf Shape: observations are made by observing visuals and documented with a camera
6. Leaf Tip Curve Shape: observations are made by visual observation and documented with a camera

Stem

1. Rod Diameter (RD): measure the circumference of the rod using a tape meter
2. Stem Skin Color (SSC): compare colors using MPTCC *(Munsell Plant Tissue Color Chart)* books
3. Bar Color (BC): compare colors using MPTCC books

4. Stem Straightness (SS): done by visual observation and documented with a camera
5. Stem Shape (SSH): performed by visual observation and documented with a camera
6. Stem Moisture Content: measured using the moisture content formula
7. Rod Specific Gravity: measured using the Specific Gravity formula

Height
1. Branch-free height (BFH): measured using a *Laser Distance Meter*
2. Total Tree Height (TTH): measured using a *Laser Distance Meter*
3. Propose BFH dan TTH: The TBC value is divided by the Ttot value and then multiplied by 100%

Crown
Crown Projected Area (CPA): Measurements are carried out starting from the east, south, west, and north

Root
1. Root Length: The length of the roots is measured using a tape measure. Measurements are taken from the rod to the surface of the mud
2. Root Color: Compare colors using MPTCC books
3. Air Flows Up: Using the moisture content formula obtained from the initial and final weight values of the root sample
4. Root Specific Gravity: Using the specific gravity formula

Fruit
1. Fruit Weight: Weighed using an analytical scale
2. Fruit Color: Compare colors using MPTCC books

Data Analysis

This study uses qualitative and quantitative approaches to analyze morphological data using heatmap analysis (R program software). A qualitative approach is an approach whose characteristics cannot be measured, such as leaf color, stem color, bark color, fruit color, root color, stem shape, and leaf shape. The quantitative approach is an approach whose characteristics can be measured, such as leaf length, stem length, leaf weight, stem weight, and so on.

The statistical analysis for the quantitative data used in this study is as follows:

Diameter

$$d = \frac{K}{\pi} \qquad (1)$$

where:
- d = Diameter
- K = tree circumference
- π = 3.14

Specific Gravity

$$\text{Specific Gravity} = \frac{\text{Wood density (g/cm}^3\text{)}}{\text{water density (g/cm}^3\text{)}} \qquad (2)$$

$$\text{Wood density} = \frac{\text{wood mass (g)}}{\text{wood volume (cm}^3\text{)}}$$

Note: 1 cm^3 = 1 ml

Moisture content

$$\text{Moisture content} = \frac{\text{Beginning-final weight}}{\text{final weight}} \times 100\% \quad (3)$$

Mean

To find out the average of diameter, length, height, weight, volume, and moisture content, the formula is used:

$$\bar{x} = \frac{\Sigma f}{n} \quad (4)$$

where:
- $\bar{x}$ = Average
- Σf = Amount of data (diameter, leaf area, moisture content)
- N = Number of Individuals/Sample

Heterozygosity

The heterozygosity value is calculated to determine the magnitude of genetic diversity (Kanaka et al., 2023).

$$qi = \sqrt{\frac{\text{number or individual}}{\text{total number of individual}}} \quad (5)$$

$$pi = 1 - qi$$

$$he = 1 - pi^2 - qi^2$$

where:
- qi = frequency of morphological characters appearing
- pi = Dominant frequency morphological character
- he = heterozygosity

Heatmap Analysis

Heatmap analysis is often used in data visualization studies, where heatmaps are graphical representations presented in the form of colors. Heatmap charts were generated using specific packages in the R software program, generating a high-quality matrix that can be customized and integrated with dendrograms (Galili et al., 2018).

Genetic Distance

Genetic distance is the level of gene difference between a population or species. Small genetic distance indicates a small relationship, and vice versa large genetic distance indicates a large genetic ridge (Pina & Schertzer, 2019). The formula used is:

$$D = -\ln I$$

$$I = \sum x_i y_i / \sqrt{\sum x_i^2 \sum y_i^2} \quad (6)$$

where:
- x_i^2 = The square of the frequency of morphological characters in population x

y_i^2 = The square of the frequency of morphological characters in population y
$x_i y_i$ = Multiplication of the frequency of the ith morphological character in populations x and y
I = Normal genetic identity for x and y populations
D = Genetic distance between x and y populations

RESULTS

Qualitative Data

The qualitative observations made in this study include observation of leaf shape, stem shape, and observation of sample colors such as bark color, stem color, root color, propagule color (fruit and hypocotyl), and leaf color.

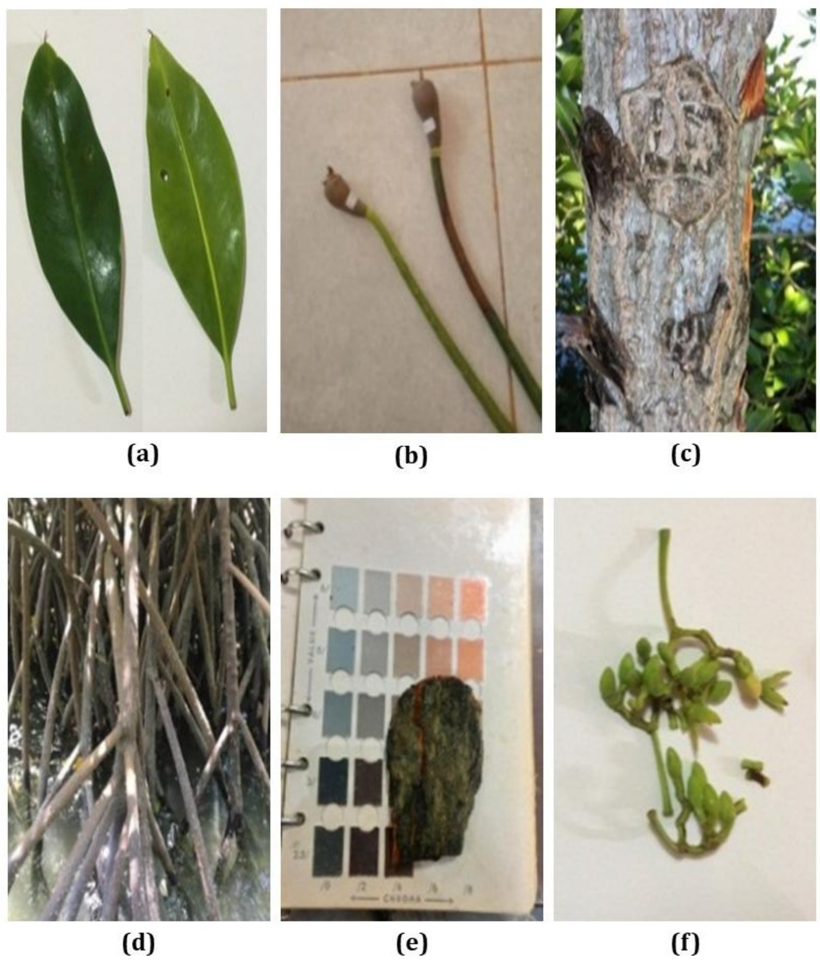

Figure 1. (a) leaves; (b) propagule; (c) Stem; (d) roots; (e) bark; (f) flowers

Determining the color of the sample is not easy because of the many types of colors and the high level of color similarity. Therefore, the Munsell Plant Tissue Color Chart (MPTCC) book is used, which contains various kinds of colors expressed in three units or criteria, namely hue, chroma, and value. The results of qualitative observations can be seen in Fig. 1.

The results of the observation of qualitative data and the average sample color per character that have been compared with the MPTCC book can be seen in Table 1. Based on Table 1. It can be seen that the morphological characteristics of the 30 mangrove plants in the three areas observed have different colors, both in different areas and in the same province.

Table 1. Average color of *R. mucronata* samples

Character		Dominant Colors		
		Polman	**Majene**	**Mamuju**
Bark Color		Bright gray	Grayish-brown	Grayish-brown
Stem Color		Red	Red	Red
Root Color		Brown	Yellow	(no dominant)
Propagation Colors	Fruit Color	Olive	Olive	Olive
	Hypocotyl Color	Olive	Olive	Olive
Flower Color		Yellow olive	Olive	(No Interest)
Leaf	Leaf Top Surface Color	Olive	Olive	Olive
	Leaf Undersurface Color	Yellow	Yellow olive	Yellow olive
	Leaf Shape	Elliptical	Elliptical	Elliptical
	Leaf Tip Curve Shape	Apiculate	Apiculate	Apiculate
	Leaf Base Curve Shape	Cuneate	Cuneate	Cuneate
	Leaf Edge Shape	Entire	Entire	Entire
Stem	Stem Shape	Teres	Teres	Teres
	Trunk Straightness	Straight	Branched out a lot	Bent/straight/tilted

Morphological Characters based on Quantitative Data

Morphological characters based on quantitative data are values obtained based on the results of measurements that have been carried out directly. The results of the observation of the morphological character of the black mangrove *R. mucronata* are shown in Table 2.

Table 2. Quantitative data of black mangrove *R. mucronata*

Observed characters	Areas			Average
	Polman	**Majene**	**Mamuju**	
Total height (m)	6.48	5.88	5.23	5.86
Branch-free height (m)	1.72	1.23	2.22	1.72
Propose ttot-tbc (%)	21.68	22.15	44.89	29.57
Diameter (m)	0.12	0.11	0.2	0.14
Tree volume (m^3)	0.06	0.04	0.12	0.07
Root length (cm)	90.9	203.2	110.5	134.87
Propagule weight (gr)	25.67	48.21	55.8	43.23
Fruit length (cm)	5.11	4.74	5.32	5.06
Hypocotyl length (cm)	16.83	37.42	45.75	33.33
Initial weight of leaves (gr)	4.25	2.61	3.65	3.50
Leaf end weight (gr)	2.48	1.67	2.25	2.13
Leaf length (cm)	14.64	11.02	12.62	12.76
Leaf width (cm)	7.23	5.43	5.44	6.03
Leaf thickness (mm)	0.42	0.41	0.47	0.43
Header Projection (m)	1.73	2.86	2.08	2.22

Table 2 shows that the observed morphological traits vary. The statistical test result of the preliminary ANOVA results indicates that the p-values for Total height and Branch-free height are all above 0.05, suggesting no statistically significant differences among the three regions for these variables. The ANOVA test results indicate that all observed characters have p-values of approximately 0.766, significantly higher than the standard significance level of 0.05. This suggests no statistically significant differences in the quantitative traits of *R. mucronata* among the three regions (Polman, Majene, and Mamuju). This result implies that despite different environmental conditions, the black mangrove populations exhibit uniform morphological traits across these locations. If needed, further analysis using a larger sample size or molecular markers may provide additional insights into genetic diversity.

Moisture Content and Specific Gravity in Bark, Stem, and Roots

The moisture content and specific gravity are obtained from the values of the initial weight, final weight, and volume. The moisture content and specific gravity values of the bark, stem, and roots of *R. mucronata* black mangrove are shown in Table 3.

Table 3. Quantitative data on moisture content and specific gravity in black Mangrove *R. mucronata* bark, stem, and root

Character		Polman	Majene	Mamuju	Rata-rata
Moisture	Bark	50.08	50.85	40.51	47.15
	Stem	78.46	71.26	61.76	70.50
	Root	79.75	86.06	58.41	74.74
Average		**69.43**	**69.39**	**53.56**	**64.13**
Specific Gravity	Bark	0.36	0.33	0.41	0.37
	Stem	0.51	0.44	0.53	0.49
	Root	0.49	0.52	0.32	0.44
Average		**0.45**	**0.43**	**0.42**	**0.43**

Based on Table 3. The moisture content and specific gravity of 30 samples were found in the bark, stem, and roots. The moisture content value is obtained from the initial weight and final weight values using the moisture content formula. The initial weight is the weight of the sample before being treated, while the final weight is the weight of the sample after being baked at 1,050 °C for 24 hours.

Genetic Diversity Values (Heterozygosity)

High genetic diversity, in addition to increasing the chances of the desired combination of good traits, also allows the improvement of plant character through direct selection (Casadebaig et al., 2014). The genetic diversity values of black mangroves in the three areas can be seen in Table 4.

Table 4. Data on the value of genetic diversity of black mangrove *R. mucronata* in Polewali Mandar, Majene, and Mamuju Areas

Areas	He	SE	Values
Polewali Mandar	0.38	0.01	High
Majene	0.35	0.01	High
Mamuju	0.36	0.01	High
Average	**0.36**	**0.01**	**High**

Information: High: He>0,30, Keep: He 0,20 – 0,30, and Low: He< 0,20 (Kinho et al., 2016).

Heatmap Analysis

Clustergram analysis with a combination of heatmap and hierarchical dendrograms simplifies the visualization of the analysis, making it easier to understand. To make it easier to perform quantitative calculations and analyze data. R software is a software suite used for data manipulation, calculations, simulations, and graph viewing, and at the same time as an interpreter programming language. The morphological observation data from the heatmap analysis can be seen in Fig. 2 and Fig. 3.

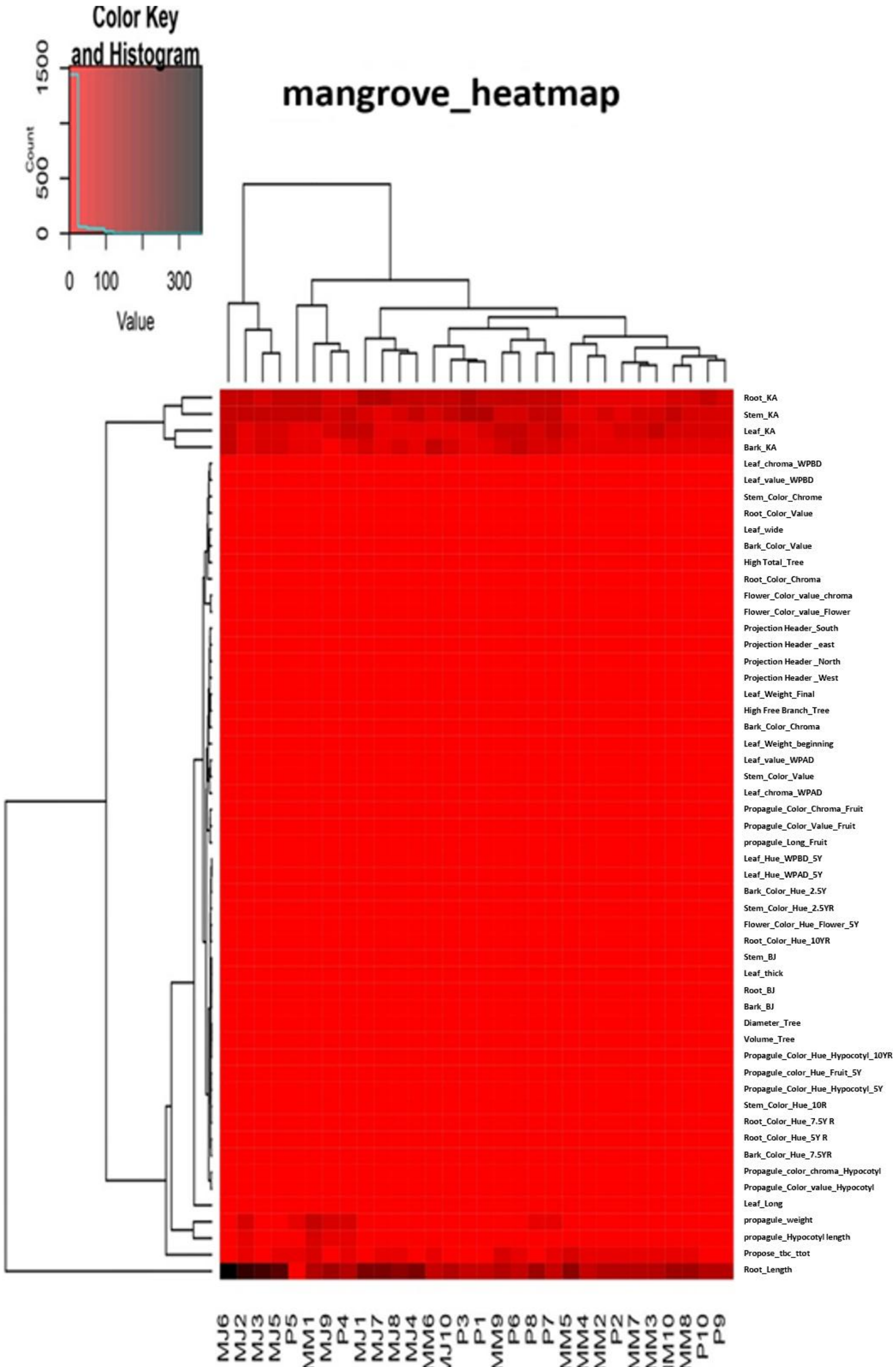

Figure 2. Cluster analysis based on morphological data of black mangrove *R. mucronata* in Polewali Mandar (P), Majene (MJ), and Mamuju (MM) Areas

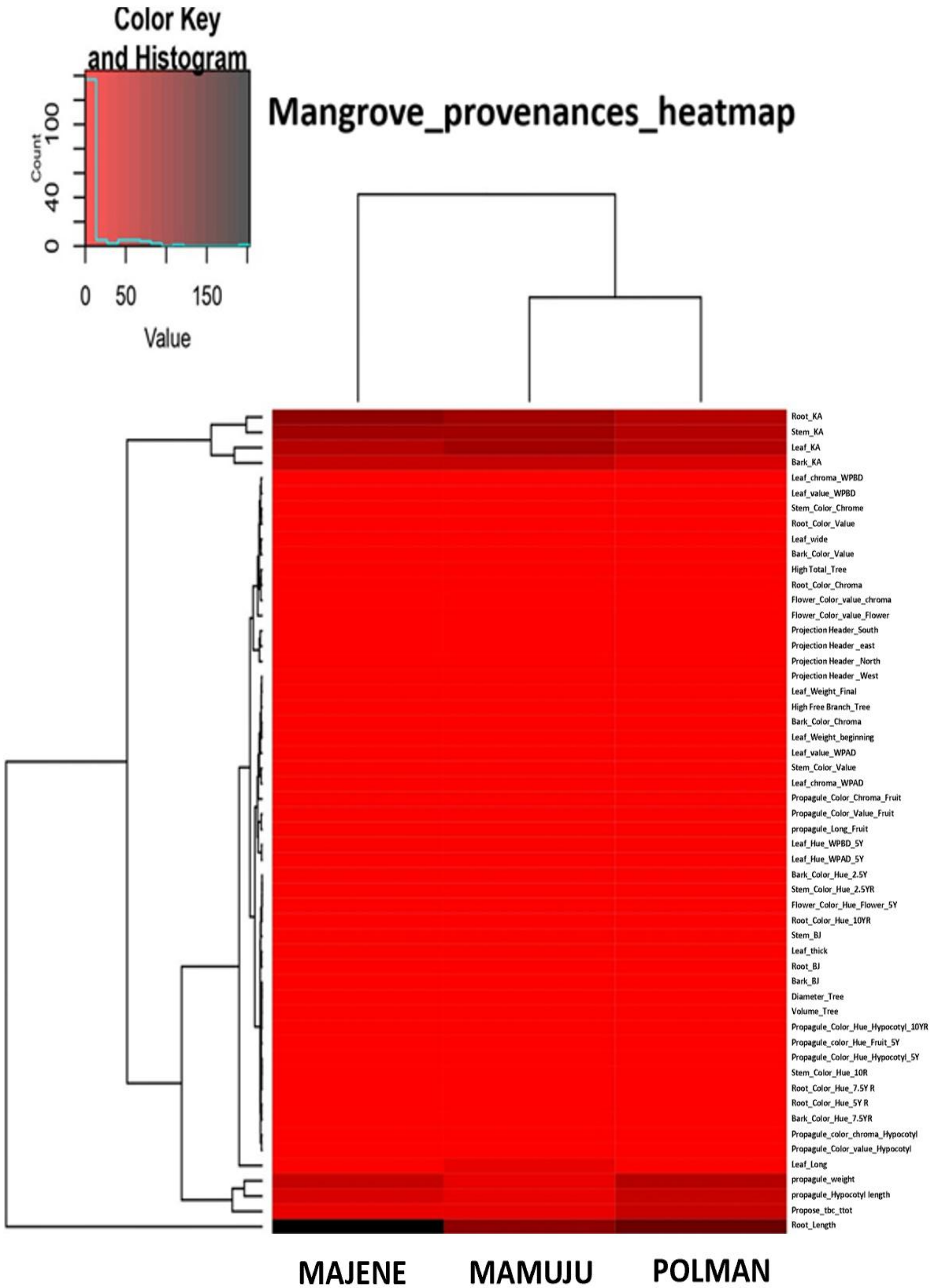

Figure 3. Cluster analysis based on average morphological data of black mangrove *R. mucronata* in each province

Based on Figs. 2 and 3, information about the characteristics of all samples from the three areas observed based on morphological markers was obtained using heatmap analysis aimed at the degree of color sharpness. Meanwhile, Fig. 3 also shows the results of the heatmap analysis, which is dominated by bright colors.

Genetic Distance

The calculation of genetic distance is carried out by comparing the characteristics between one location and another. The results of the calculation of the genetic distance of black mangroves in Polewali Mandar, Majene, and Mamuju can be seen in Table 5.

Table 5. Results of calculation of genetic distance of black mangrove *R. mucronata* in Polewali Mandar, Majene, and Mamuju

Genetics Distance	Polman	Majene	Mamuju
Polman	-		
Majene	0.09	-	
Mamuju	0.13	0.1	-

Based on Table 5 of the results of the calculation of genetic distance above, the farthest genetic distance with a value of 0.13 is between the areas of Polewali Mandar and Mamuju. As for the nearest genetic distance, it is between Polewali Mandar and Majene, which is 0.09. The less the value of the genetic distance between two organisms, the closer the kinship relationship between the two (Hernández-Velasco et al., 2025; Lee et al., 2025).

DISCUSSION

Qualitative observations made in Fig. 1 show the morphological characteristics of black mangroves on leaves, propagules, stems, roots, bark, and flowers. Data was obtained that the thirty black mangrove samples had some similarities and differences in morphological properties from several observed variables. The morphological similarities obtained are in the form of elliptical leaf shapes, apiculate *leaf tip indentations*, cuneate *leaf base indentations*, and entire *leaf edge shapes*. The difference in morphological properties is in the form of different colors on the leaf sheets. Other characters that can be seen are in the form of a *terrace* stem, an olive-yellow flower, and olive fruit. As for the straightness of the stems, in the province of Polewali Mandar, two stems are slanted, and the rest are straight. In Majene, all samples are multi-branched. As for samples for Mamuju, the straightness of the trunk is straight, bent, and oblique.

Based on Table 1, the bark of *R. mucronata* stems is generally gray to black. The young tree has gray bark, while the old tree gradually turns black with very obvious cracks. The change in bark color is related to anatomical activity. According to (Frankiewicz et al., 2021; Ohse et al. 2022; Serra et al. 2022) the color and texture of the bark are controlled by the periderm during the growth and development process of the plant. Old trees are found in Mamuju.

The color of the leaves is highly determined by chlorophyll and pigments or dyes found in the cells in the leaves. The color of the leaves depends on the dominant pigment. The leaves are generally green because the amount of chlorophyll is much more than other pigments. A wide variety of colors can be found on the same leaf blade. This is due to the variation of leaf cells (genetic), and the color is determined by specific pigments, depending on the cell (Hoban et al., 2023).

Table 2 shows that the average value is different for each character from all sampling sites. In the character of total tree height (TTH), the average value of the thirty samples was 5.86 m, with the highest value of 6.48 m, which is the average total height of the Polewali Mandar province. This is because the sampling location in Polewali Mandar has muddier soil and is also close to the estuary. This statement is in accordance with the opinion of Phong (2025); Shao et al. (2025); Zhang et al. (2025), which states that mangroves can grow optimally in coastal areas that have river mouths and mud substrates, while in coastal areas that do not have river estuaries, mangrove forests do not grow optimally.

The average data of BFH, the proportion of TTH-BFH, trunk diameter, and volume of trees in the Mamuju area are higher. This might be due to the distance between trees observed in this area, which the other two sites do not have. The planting distance is inversely proportional to the density of the trees. The wider the planting distance, the smaller the density (Li et al., 2023; Pommerening et al., 2024). Planting distance affects the size of the diameter, as evidenced by the previous studies of Pitkänen et al. (2022); Slesak et al. (2025); Zabihi et al. (2025) which states that the relationship between planting distance and average diameter is that the wider the planting distance, the more space to grow and less competition so it will produce a number of trees with a larger average diameter.

The genetic diversity data that can be seen in Table 4 is based on heterozygosity values. The heterozygosity value (He) is one of the parameters that can be used to measure the level of genetic diversity in a population. The higher the heterozygote frequency in a population, the higher the level of diversity (Hernández-Velasco et al., 2025; Lee et al., 2025). Polewali Mandar had the highest, due to its varied characteristics. This can be seen by comparing each character on the tree, especially in the propagule part. In the observations that have been made, data were obtained that the black mangroves of Polewali Mandar have more propagules compared to the other sites. The wider the diversity of a character in a population, the more varied the traits that exist in the character that reflect genetic control in the population (Meuwissen et al., 2020; Hoban et al., 2023; Yap & Al-Mutairi, 2025).

Characterization is one of the important stages in the plant breeding program. Characterization can be used as a basis for grouping plants. This grouping aims to determine the kinship relationship between plant genotypes and can be a consideration in the selection process. Selection through grouping will be effective if the characteristics of the group can be known. One method that can be used is clustergram analysis. Clustergram analysis is a multivariate s that combines several cluster analyses in a flat dimension (Fleischmann, 2023).

Based on Fig. 2, information was obtained about the characteristics of all samples from the three areas observed based on morphological markers using heatmap analysis, shown by the color brightness level. Fig. 2 of cluster analysis is predominantly bright compared to dark colors. The dark-colored part shows the highest value, while the light-colored part shows the lowest value. The dark-colored parts include root length, root moisture content, stem moisture content, leaf moisture content, and bark moisture content.

Figure 3 also shows the results of the analysis of the predominantly brightly colored heatmap. However, there are still dark parts, namely, on the length of the roots, root moisture content, stem moisture content, leaf moisture content, and bark moisture content. In Fig. 3, it can be seen that the results of the analysis show that two clusters have been formed. Cluster I was constructed by Majene samples, while cluster II is Polewali Mandar and Mamuju. The most distinguishing characteristic of the Majene area is that the root length is quite different from the root length of other areas. This is suspected to have caused Majene samples to be in different clusters. In cluster II, namely the areas of Polewali Mandar and Mamuju. The difference between these two areas from Majene is in terms of root moisture content, stem moisture content, and leaf moisture content. For the character of root length, the three areas show the length of the dark roots, but if sorted, the Majene areas are darker than the root lengths of Mamuju and Polewali areas.

This shows that the roots of black mangroves in Majene are longer than those in Mamuju and Polewali Mandar. As for the water content of roots, stems, leaves, and bark, the order from darkest to lightest was Majene, Polewali, and then Mamuju. Furthermore, based on the results of the calculation of genetic distance in Table 5, the farthest genetic distance with a value of 0.13 is between the areas of Polewali Mandar and Mamuju. As for the nearest genetic distance, it is between Polewali Mandar and Majene, which is 0.09. According to Šorgić et al. (2025) the less the value of the genetic distance between two organisms, the closer the kinship relationship between the two.

Kinship between two individuals or populations can be measured based on the similarity of a number of characters assuming that different characters are caused by differences in genetic makeup. The difference in morphological character between plants is not only influenced by genetics, but also influenced by environmental factors. The magnitude of the difference in genetic distance in the population can be caused by several factors zuch as isolation factors by distance, geography, ecology, and reproduction (Casadebaig et al., 2014; Buzatti et al., 2019; Senayai et al., 2025).

CONCLUSION

This study shows that the black mangroves of Polewali Mandar, Majene, and Mamuju had a high genetic diversity. This enhances resilience to environmental changes and diseases. It also allows for better adaptation to shifting ecosystem conditions. Black mangroves between the areas of Polewali Mandar and Mamuju have the highest value of genetic diversity, representing the farthest kinship. In the contrary, the black mangroves between the areas of Polewali Mandar and Majene had the lowest value, representing a closer kinship. This can be caused by geographical factors, such as the proximity of the location that allows the flow of genes through the dispersion of propagules or pollen by ocean currents and winds. In addition, similarities in environmental conditions, such as salinity, substrate types, as well as similar ecological pressures, can drive the same adaptation in mangrove populations in all three regions. Proper genetic distance between planted mangroves can influence the growth and survival rates of saplings. If planted too close, there can be excessive competition, while planting too far apart can reduce the likelihood of beneficial gene exchange. Considering these values, mangrove rehabilitation efforts in Polewali Mandar and Majene can be more effective and sustainable.

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AUTHOR CONTRIBUTIONS

Mukrimin: research conceptualization, research coordinator, data analysis, data interpretation, script writing; Gusmiaty: member contributor, research implementer, interpretation, manuscript writing; Marwah Salam: contributors, research implementers, mapmakers, manuscript writers; Atisa Muslimin: member of Contributor and scriptwriter.

CONFLICTS OF INTEREST

Mukrimin stated that all authors have no conflict of interest. The funding sponsor has no role in the research design, in data collection, analysis, or interpretation, in the writing of the script, and in the decision to publish the results.

REFERENCES

Billah, M., Arthana, I.W., Restu, I.W., & As-syakur, A.R. (2020). Analisis perubahan luasan dan kerapatan tajuk mangrove di Kecamatan Borong Kabupaten Manggarai Timur. *Journal of Marine and Aquatic Sciences*, 6(1), 43-50. https://doi.org/10.24843/jmas.2020.v06.i01.p06.

Buzatti, R.S.dO., Pfeilsticker, T.R., Muniz, A.C., Ellis, V.A., Souza, R.P.d, Lemos-Filho, J.P., & Lovato, M.B. (2019). Disentangling the environmental factors that shape genetic and phenotypic leaf trait variation in the tree *Qualea grandiflora* across the Brazilian Savanna. *Frontiers in Plant Science*, 10, 1–14. https://doi.org/10.3389/fpls.2019.01580.

Casadebaig, P., Trépos, R., Picheny, V., Langlade, N.B., Vincourt, P., & Debaeke, P. (2014). Increased genetic diversity improves crop yield stability under climate variability: A computational study on sunflower. arXiv:1403.2825, 1–24. https://doi.org/10.48550/arXiv.1403.2825.

Fitri, A., Basyuni, M., Wati, R., Sulistiyono, N., Slamet, B., Harahap, Z.A., Balke, T., & Peter, B. (2018). Management of mangrove ecosystems for increasing fisheries production in Lubuk Kertang Village, North Sumatra, Indonesia. *AACL Bioflux*, 11(4), 1252–64. https://pure.aber.ac.uk/ws/portalfiles/portal/27870251/2018.1252_1264docx.pdf.

Fleischmann, M. (2023). Clustergram: Visualization and diagnostics for cluster analysis. *Journal of Open Source Software*, 8(89), 5240. https://doi.org/10.21105/joss.05240.

Frankiewicz, Kamil E, John H Chau, and Alexei A Oskolski. (2021). Wood and Bark of Buddleja : Uniseriate Phellem, and Systematic and Ecological Patterns. *IAWA Journal* 42 (1): 3–30. https://doi.org/10.1163/22941932-bja10020.

Galili, T., O'Callaghan, A., Sidi, J., & Sievert, C. (2018). Heatmaply: An R package for creating interactive cluster heatmaps for online publishing. *Bioinformatics*, 34 (9), 1600–1602. https://doi.org/10.1093/bioinformatics/btx657.

Hernández-Velasco, J., Hernández-Díaz, J.C., Simental-Rodríguez, S.L., Jaramillo-Correa, J.P., Gernandt, D.S., Vargas-Hernández, J.J., Porth, I., Goessen, R., González-Elizondo, M.S., Fladung, M., Sáenz-Romero, C., Martínez-Ávalos, J.G., Carrillo-Parra, A., Mendoza-Maya, E., Blanco-García, A., & Wehenkel, C. (2025). Causes of heterozygosity excess : The case of mexican populations of Populus tremuloides. *Plant Diversity*, 47(3): 415–428. https://doi.org/10.1016/j.pld.2024.12.006.

Hoban, S., Bruford, M.W., da Silva, J.M., Funk, W.C., Frankham, R., Gill, M.J., Grueber, C.E., Heuertz, M., Hunter, M.E., Kershaw, F., Lacy, R.C., Lees, C., Lopes-Fernandes, M., MacDonald, A.J., Mastretta-Yanes, A., McGowan, P.J.K., Meek, M.H., Mergeay, J., Millette, K.L., Mittan-Moreau, C.S., Navarro, L.M., O'Brien, D., Ogden, R., Segelbacher, G., Paz-Vinas, I., Vernesi, C., & Laikre, L. (2023). Genetic diversity goals and targets have improved, but remain insufficient for clear implementation of the post-2020 global biodiversity framework. *Conservation Genetics*, 24(2), 181–191. https://doi.org/10.1007/s10592-022-01492-0.

Kanaka, K.K., Sukhija, N., Goli, R.C., Singh, S., Ganguly, I., Dixit, S.P., Dash, A., & Malik, A.A. (2023). On the concepts and measures of diversity in the genomics era. *Current Plant Biology*, 33, 100278. https://doi.org/10.1016/j.cpb.2023.100278.

Kinho, J., Na'iem, M., & Indrioko, S. (2016). Study on genetic diversity of *Diospyros rumphii* Bakh in North Sulawesi based on isoenzym markers Ebenaceae. *Jurnal Pemuliaan Tanaman Hutan*, 10(2), 95–110. https://doi.org/10.20886/jpth.2016.10.2.95-109.

Lee, Y.B., So, S., Park, Y.J., Kang, H., Lee, H.R., Kim, J.H., Gwak, H.K., Kim, K.A., & Cheon, K.S. (2025). Genetic diversity and population structure analysis of *Forsythia ovata*, a Korean Endemic, based on Genotyping-by-Sequencing. *PLoS ONE*, 13(2), 1–16. https://doi.org/10.1371/journal.pone.0317278.

Li, X., Duan, A., & Zhang, J. (2023). Long-term effects of planting density and site quality on timber assortment structure based on a 41-year plantation trial of Chinese fir. *Trees, Forests and People*, 12, 100396. https://doi.org/10.1016/j.tfp.2023.100396.

Meuwissen, T.H.E, Sonesson, A.K., Gebregiwergis, G., & Woolliams, J.A. (2020). Management of genetic diversity in the era of genomics. Frontiers in Genetics, 11, 1–16. https://doi.org/10.3389/fgene.2020.00880.

Mukrimin, M., Restu, M., DB, E.M., & Musdalifah, M. (2021). Genetic diversity of black mangrove (*Rhizophora mucronata* Lamk.) based on morphological markers in Maros, Pangkep, and Barru Provenances. *IOP Conference Series: Earth and Environmental Science*, 886(1), 1–7. https://doi.org/10.1088/1755-1315/886/1/012010.

Ohse, Megumi, Rika Irohara, Etsushi Iizuka, Izumi Arakawa, Peter Kitin, Ryo Funada, and Satoshi Nakaba. (2022). Sequent Periderm Formation and Changes in the Cellular Contents of Phloem Parenchyma during Rhytidome Development in Cryptomeria Japonica. *Journal of Wood Science*. https://doi.org/10.1186/s10086-022-02027-4.

Phong, N.T. (2025). Vegetated intertidal mudflat and existing ecological restoration perspectives to control coastal erosion: Constraints and recommendations. *Ecological Engineering*, 215, 107610. https://doi.org/10.1016/j.ecoleng.2025.107610.

Pina, V.M., & Schertzer, E. (2019). How does geographical distance translate into genetic distance? *Stochastic Processes and Their Applications*, 129(10), 3893–3921. https://doi.org/10.1016/j.spa.2018.11.004.

Pitkänen, T.P., Bianchi, S., & Kangas, A. (2022). Quantifying the effects of competition on the dimensions of scots pine and norway spruce crowns. *International Journal of Applied Earth Observation and Geoinformation*, 112. 102941. https://doi.org/10.1016/j.jag.2022.102941.

Pommerening, A., Sterba, H., & Eskelson, B.N.I. (2024). Distance and T-Square sampling for spatial measures of tree diversity. *Ecological Indicators*, 163, 111995. https://doi.org/10.1016/j.ecolind.2024.111995.

Senayai, A., Harnvanichvech, Y., Vajrodaya, S., Oyama, T., & Kraichak, E. (2025). Genetic and morphological variation among populations of duckweed species in Thailand. *Plants*, 14(13), 1–14. https://doi.org/10.3390/plants14132030.

Serra, Olga, Ari Pekka Mähönen, Alexander J Hetherington, and Laura Ragni. (2022). The Making of Plant Armor : The Periderm. *Annual Review Of Plant Biology* 73 (1): 405–32. https://doi.org/10.1146/annurev-arplant-102720-031405.

Shao, O., Li, Y., Gu, W., Zhang, R., Tang, Y., Xu, H., Shou, L., Zeng, J., & Liao, Y. (2025). Assessment of macrobenthos in evaluating the restoration effects of artificial mangrove planting on tidal flats in Zhejiang, China. *Marine Environmental Research*, 204, 106930. https://doi.org/10.1016/j.marenvres.2024.106930.

Slesak, R.A., Agne, M.C., Harrington, C.A., & Powers, M.D. (2025). Long-term effects of tree spacing during reforestation on survival and growth of three important tree species in the Pacific Northwest, USA. *Forest Ecology and Management*, 586, 122724. https://doi.org/10.1016/j.foreco.2025.122724.

Sofue, Y., Quevedo, J.M.D., Lukman, K.M., & Kohsaka, R. (2025). Identifying changes in mangrove landscapes in the Philippines and Indonesia using remote sensing and community perceptions: Towards ecosystem services management. *Regional Studies in Marine Science*, 82, 104023. https://doi.org/10.1016/j.rsma.2025.104023.

Šorgić, D., Stefanović, A., Popović, M., & Keckarević, D. (2025). From genetic data to kinship clarity: Employing machine learning for detecting incestuous relations. *Frontiers in Genetics*, 16, 1–12. https://doi.org/10.3389/fgene.2025.1578581.

Su, Z., Qiu, G., Yang, P., Yang, H., Liu, W., Tan, L., Zhang, L., Sun, D., Huang, J., & Tang, K.W. (2025). Conversion of earthen aquaculture ponds to integrated mangrove-aquaculture systems significantly reduced the emissions of CH4 and N2O. *Journal of Hydrology*, 652, 132692. https://doi.org/10.1016/j.jhydrol.2025.132692.

Wu, L., Yang, P., Luo, L., Zhu, W., Hong, Y., Tong, C., & Peñuelas, J. (2022). Conversion of mangrove forests to shrimp ponds in Southeastern China destabilizes sediment microbial networks. Geoderma, 421, 115907. https://doi.org/10.1016/j.geoderma.2022.115907.

Yang, F., Li, R., Wang, M., Zhang, L., & Wang, W. (2025). Restoration patterns and influencing factors for the vegetation structure and carbon storage in mangroves converted from abandoned ponds. *Global Ecology and Conservation*, 58, e03430. https://doi.org/10.1016/j.gecco.2025.e03430.

Yap, C.K., & Al-Mutairi, K.A. (2025). Mangrove ecosystems in Western Asia: A literature review of trends, conservation gaps, and sustainable management strategies. *Frontiers in Forests and Global Change*, 8, 1556158. https://doi.org/10.3389/ffgc.2025.1556158.

Zabihi, K., Singh, V.V., Trubin, A., Korolyova, N., & Jakuš, R. (2025). How to define spacing among forest trees to mitigate competition: A technical note. *Biology*, 14(3), 296. https://doi.org/10.3390/biology14030296.

Zhang, Z., Jiang, W., Xiao, Z., Ling, Z., Sun, J., Song, J., & Li, X. (2025). Optimal simulation of future restoration and protection spatial for mangroves and assessment of disaster prevention and mitigation functions with SDG13.1. *Journal of Cleaner Production*, 516, 145784. https://doi.org/10.1016/j.jclepro.2025.145784.