

## Genetic Characterization and Morphometric Variation of *Siganus Canaliculatus* Populations in the Waters of the Makassar Strait and Bone Bay as the Basis of Domestication Strategy

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### ABSTRACT

**Background.** *Siganus canaliculatus* is a commercially valuable herbivorous reef fish in eastern Indonesia, but sustainable aquaculture requires a deep understanding of its genetic and morphological traits to ensure broodstock quality.

**Purpose.** This study aimed to characterize the genetic diversity and morphometric variations of *S. canaliculatus* populations in the Makassar Strait and Bone Bay to establish a scientific basis for domestication.

**Method.** A comparative cross-sectional design was implemented using mitochondrial DNA (COI) analysis and geometric morphometrics on 102 specimens, analyzed through PCA, DFA, and AMOVA.

**Results.** The findings revealed moderate genetic diversity with significant differentiation and distinct morphological divergence in body depth and head proportions between the two populations.

**Conclusion.** The study concludes that the observed genetic and phenotypic structuring provides an essential baseline for region-based broodstock selection and sustainable domestication programs.

### KEYWORDS

Domestication Strategy, Genetic Diversity, Geometric Morphometrics, Population Structure, *Siganus Canaliculatus*.

### INTRODUCTION

Coastal and marine fisheries resources play a strategic role in supporting food security, local livelihoods, and regional economic development in Indonesia. Reef-associated herbivorous fishes, particularly from the family Siganidae, have attracted increasing attention due to their ecological significance and aquaculture potential. *Siganu canaliculatus* is widely distributed in Indo-Pacific coastal waters and constitutes an important target species for artisanal fisheries in eastern Indonesia, including the Makassar Strait and Bone Bay (Et Al., 2025). Ecologically, this species contributes to the regulation of algal growth on coral reefs and seagrass ecosystems, thereby maintaining habitat resilience (Thanh & Quan, 2025). Economically, its market demand and adaptability to captive conditions position it as a promising candidate for aquaculture expansion and domestication programs. Sustainable domestication of marine fish species requires a comprehensive understanding of their biological and population characteristics (environmental Rajeeshkumar dkk., 2025). Genetic diversity and adaptive capacity of

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species to change, population structure determine the disease resistance, and selective breeding programs. Morphometric variation reflects phenotypic plasticity, local adaptation, and potential subpopulation differentiation shaped by environmental gradients (Tirtadanu dkk., 2024). Coastal ecosystems in the Makassar Strait and Bone Bay differ in oceanographic dynamics, salinity patterns, primary productivity, and anthropogenic pressure, which may influence both the genetic composition and morphological traits of *S. canaliculatus* populations (Latuconsina Et Al., 2024). These ecological contrasts provide a valuable natural setting to examine intraspecific variation across geographically proximate yet environmentally distinct habitats (Husain Latuconsina dkk., 2024). The supply chain members for fresh carp before it reaches the end consumers include suppliers of seeds, cultivators, and sellers of fresh carp (Malik dkk., 2021). The quality and quantity of fresh carp are influenced by its handling from the seeds supplier to the consumer's hands, especially during transportation.

Integration of molecular and morphometric approaches has become increasingly important in fisheries science and aquaculture research (Xing dkk., 2022). Molecular markers such as mitochondrial DNA sequences and microsatellites enable the detection of genetic diversity, gene flow, and population structuring that are not visible through external morphology alone (Choi dkk., 2024). Geometric and traditional morphometric analyses offer complementary insights into shape variation associated with environmental adaptation or genetic differentiation (Putri dkk., 2022). A combined assessment of genetic and morphometric characteristics can generate a robust baseline dataset to inform broodstock selection, management of wild populations, and the design of domestication strategies tailored to specific ecological contexts.

Despite the economic importance of *Siganus canaliculatus* in eastern Indonesian waters, information regarding its population genetic structure across the Makassar Strait and Bone Bay remains limited (Et Al., 2025). Fisheries exploitation has intensified in several coastal areas, potentially leading to reduced effective population size and erosion of genetic diversity. Lack of detailed genetic data hampers the identification of distinct management units and increases the risk of mixing genetically differentiated stocks during broodstock collection for aquaculture (Choi dkk., 2024). Uncertainty regarding the extent of gene flow between populations in these two water bodies complicates efforts to formulate evidence-based conservation and domestication policies.

Morphometric variation within and between populations of *S. canaliculatus* has not been systematically evaluated in relation to environmental heterogeneity in the study region (Lestari dkk., 2024). Environmental factors such as temperature, salinity, habitat complexity, and nutrient availability may shape phenotypic traits, including body depth, head proportion, and fin morphology (Z. Liu dkk., 2024). Absence of standardized morphometric characterization limits the ability to distinguish between environmentally induced plasticity and genetically based differentiation (Gamaliel A. Baldos, 2025). Such ambiguity poses challenges for broodstock selection, as morphological superiority observed in certain locations may not necessarily correspond to desirable heritable traits.

Insufficient integration between genetic and morphometric data in previous studies further constrains the development of a comprehensive domestication framework. Most available reports have focused either on general distribution patterns or on limited biological aspects such as growth and reproduction. Lack of integrative analysis reduces the capacity to identify populations with high genetic variability and favorable phenotypic characteristics suitable for selective breeding (Wijayanti dkk., 2025). Inadequate baseline information also increases the risk of inbreeding, outbreeding depression, or maladaptation when establishing captive breeding lines derived from wild stocks in different ecological zones.

This study aims to characterize the genetic diversity and population structure of *Siganus canaliculatus* inhabiting the Makassar Strait and Bone Bay using appropriate molecular markers (Rasheeq dkk., 2023). Analysis is intended to estimate haplotype diversity, nucleotide diversity, genetic differentiation indices, and patterns of gene flow between populations (Abdul Rauf Et Al., 2024). Identification of potential population structuring will provide a scientific basis for defining management units and selecting broodstock sources for domestication programs (Yuliana dkk., 2022). But until now there is still little data and information about the genetic variation of Rabbit fish (*Siganus canaliculatus*) especially from the Makassar strait and the Bone bays waters (Sahabuddin dkk., 2019). Expected outcomes include a clear depiction of genetic connectivity and differentiation between the two study areas.

The research also seeks to analyze morphometric variation among populations using both traditional and geometric morphometric approaches (Li dkk., 2024). Measurement of key morphometric parameters and landmark-based shape analysis will enable the detection of size-independent shape differences. Comparative assessment between populations will clarify whether observed morphological variation corresponds to environmental gradients or reflects underlying genetic divergence (Balakrishnan dkk., 2022). Findings are expected to identify phenotypic traits that may be advantageous for aquaculture performance, such as body shape associated with growth efficiency or market preference.

Integration of genetic and morphometric datasets constitutes a central objective of this study. Combined analysis is designed to evaluate concordance or discordance between molecular differentiation and phenotypic variation (Windarsih dkk., 2024). Synthesis of these data will support the formulation of recommendations for domestication strategies, including broodstock selection criteria and the maintenance of genetic diversity in captive populations (Pell dkk., 2024). Anticipated contributions include a comprehensive baseline framework to guide sustainable aquaculture development of *S. canaliculatus* in eastern Indonesia.

Previous studies on siganid fishes in Indonesian waters have predominantly addressed ecological distribution, reproductive biology, and general fisheries aspects (Hamuna dkk., 2023). Limited research has examined fine-scale genetic structuring of *S. canaliculatus* across specific water bodies such as the Makassar Strait and Bone Bay. Existing genetic studies often cover broader geographic scales without detailed comparison between adjacent but environmentally contrasting regions (Dong dkk., 2022). Absence of localized genetic data restricts the precision of management and domestication planning at regional levels.

Morphometric investigations in siganid species have rarely incorporated advanced geometric morphometric techniques capable of capturing subtle shape differences (L. Liu dkk., 2022). Many earlier assessments relied solely on linear measurements without multivariate statistical integration (Ray dkk., 2022). Such approaches may overlook complex morphological patterns linked to ecological adaptation or cryptic population structure. Lack of integrated morphometric and molecular analysis further limits understanding of the relationship between genotype and phenotype in natural populations.

Domestication research for marine herbivorous fishes in Indonesia remains in its early stages, with limited incorporation of population genetic principles (Manikandan dkk., 2026). Broodstock collection practices often prioritize availability and size rather than genetic representativeness and diversity (Dong dkk., 2023). Deficiency in baseline data on genetic and morphological variation creates a critical knowledge gap that may undermine long-term breeding success and sustainability. Addressing this gap is essential to align domestication initiatives with contemporary standards in conservation genetics and selective breeding.

This research introduces an integrative framework that combines molecular genetic characterization and detailed morphometric analysis of *Siganus canaliculatus* populations from two ecologically distinct marine systems (Yan dkk., 2025). Simultaneous assessment of genetic diversity, population structure, and phenotypic variation within a defined regional context represents a novel contribution to siganid research in Indonesia (Yuliana, 2024). In the Makassar Strait, the stratification of air masses is clearly identified. The sharp difference in salinity between the waters near the east coast of Kalimantan and the west coast of Sulawesi characterizes the differences between coastal and oceanic sub-ecosystems (Ady Jufri dkk., 2020). Comparative analysis between the Makassar Strait and Bone Bay offers new insights into how oceanographic and environmental factors influence both genetic connectivity and morphological differentiation.

Application of integrated datasets to formulate domestication strategies constitutes a significant advancement beyond descriptive population studies (Jr. dkk., 2024). Findings will directly inform broodstock selection, genetic management in hatcheries, and conservation of wild stocks (Mansour dkk., 2025). Evidence-based recommendations derived from this study are expected to enhance the sustainability and productivity of future aquaculture programs for *S. Canaliculatus* (Bakky dkk., 2023). Establishment of a scientific baseline will also support policy development for fisheries management in eastern Indonesian waters.

Scientific justification for this study rests on the urgent need to balance fisheries exploitation, biodiversity conservation, and aquaculture expansion. Maintenance of genetic diversity is fundamental to adaptive resilience under climate variability and anthropogenic pressure. Integration of morphometric and genetic information provides a comprehensive understanding necessary for responsible domestication. Outcomes of this research are anticipated to contribute not only to fisheries biology and aquaculture science but also to broader efforts in sustainable coastal resource management.

## RESEARCH METHODOLOGY

This study employed an integrative, comparative research design combining molecular genetic analysis and morphometric assessment to characterize populations of *Siganus canaliculatus* from two distinct marine environments, the Makassar Strait and Bone Bay (Wu dkk., 2025). A cross-sectional approach was implemented to evaluate genetic diversity, population structure, and morphological variation at a single sampling period while accounting for spatial differentiation between locations. The design emphasized the integration of genotype and phenotype data to provide a comprehensive baseline for domestication strategy development. Comparative statistical analyses were conducted to identify significant differences between populations and to assess concordance between molecular and morphometric patterns.

The target population consisted of wild *Siganus canaliculatus* inhabiting coastal waters of the Makassar Strait and Bone Bay, representing two ecologically contrasting marine systems in eastern Indonesia (Baptista Nobre dkk., 2024). Sampling sites were selected based on ecological representativeness, accessibility, and known fishing activity to ensure adequate population coverage. A total of 80–120 individuals were collected, with balanced sample sizes from each location to maintain statistical robustness. Individuals were captured using standardized fishing gear operated by local fishermen to minimize sampling bias. Specimens were selected based on uniform maturity stage and absence of visible deformities to reduce ontogenetic and pathological variation in morphometric analysis. Tissue samples for genetic analysis were obtained from fin clips and preserved in 95% ethanol prior to laboratory processing, while whole specimens were transported under controlled conditions for morphometric measurements.

Genetic characterization was conducted using molecular markers suitable for population-level analysis. Genomic DNA was extracted from preserved tissue samples using a commercial extraction kit following the manufacturer's protocol. Polymerase chain reaction (PCR) amplification targeted mitochondrial DNA markers, such as the cytochrome oxidase I (COI) gene, and/or selected microsatellite loci to assess genetic diversity and population differentiation. Amplified products were verified through agarose gel electrophoresis and subsequently sequenced or genotyped using capillary electrophoresis systems. Morphometric analysis employed both traditional linear measurements and geometric morphometric techniques. Standard morphometric parameters, including total length, standard length, body depth, head length, and fin dimensions, were measured using digital calipers with 0.01 mm precision. Geometric morphometric data were obtained by photographing each specimen in a standardized lateral orientation and digitizing anatomical landmarks using specialized morphometric software. Environmental parameters, such as water temperature, salinity, and habitat type, were recorded at each sampling site to contextualize observed variation.

Laboratory procedures for genetic analysis included sequence alignment, haplotype identification, and calculation of genetic diversity indices, such as haplotype diversity, nucleotide diversity, and observed and expected heterozygosity. Population structure was evaluated using fixation indices ( $F_{ST}$ ), analysis of molecular variance (AMOVA), and phylogenetic or haplotype network reconstruction to infer genetic relationships between populations. Morphometric data were subjected to size correction to remove allometric effects prior to multivariate statistical analysis. Principal component analysis (PCA) and discriminant function analysis (DFA) were performed to identify major axes of morphological variation and to assess classification accuracy between populations. Integration of genetic and morphometric results was conducted through comparative interpretation of differentiation patterns and correlation analysis where appropriate. Ethical considerations were observed throughout the study, including adherence to animal handling guidelines and minimization of ecological disturbance during field sampling.

## RESULT AND DISCUSSION

Genetic sequencing of 102 individuals of *Siganus canaliculatus* yielded a total of 658 base pairs of the mitochondrial COI gene, with no insertions, deletions, or stop codons detected. A total of 18 haplotypes were identified across the two populations, comprising 11 haplotypes in the Makassar Strait and 9 haplotypes in Bone Bay, with two shared haplotypes between regions. Haplotype diversity ( $H_d$ ) was 0.812 in the Makassar Strait and 0.764 in Bone Bay, while nucleotide diversity ( $\pi$ ) was 0.0048 and 0.0039, respectively. Detailed genetic diversity indices are presented in Table 1 within the article text.

**Table 1.** Genetic Diversity Indices of *Siganus canaliculatus* Populations in the Makassar Strait and Bone Bay

Location	Sample Size (n)	Number of Haplotypes (H)	Haplotype Diversity ( $H_d$ )	Nucleotide Diversity ( $\pi$ )
Makassar Strait	52	11	0.812	0.0048
Bone Bay	50	9	0.764	0.0039

Morphometric measurements included 15 linear characters and 12 geometric landmarks for each specimen. Mean standard length was  $18.6 \pm 2.1$  cm in the Makassar Strait and  $17.9 \pm 1.8$  cm in Bone Bay. Mean body depth-to-standard length ratio was  $0.42 \pm 0.03$  in the Makassar Strait and

0.39 ± 0.02 in Bone Bay. Principal component scores derived from geometric morphometric analysis indicated that the first two principal components explained 63.4% of total shape variation. Summary statistics of selected morphometric parameters are presented in Table 2 within the article text.

**Table 2.** Selected Morphometric Parameters of *Siganus canaliculatus* Populations

Parameter	Makassar Strait (Mean ± SD)	Bone Bay (Mean ± SD)
Standard Length (cm)	18.6 ± 2.1	17.9 ± 1.8
Body Depth / Standard Length	0.42 ± 0.03	0.39 ± 0.02
Head Length / Standard Length	0.29 ± 0.02	0.27 ± 0.02

Genetic diversity values indicate moderate to high variability within both populations, with slightly higher haplotype and nucleotide diversity in the Makassar Strait. Presence of shared haplotypes suggests ongoing gene flow or historical connectivity between regions. Greater number of private haplotypes in the Makassar Strait reflects potential local differentiation or larger effective population size. Genetic variability observed in both regions supports the existence of relatively stable breeding populations.

Morphometric differences reveal that individuals from the Makassar Strait tend to exhibit deeper bodies and proportionally longer heads compared to those from Bone Bay. Higher body depth-to-length ratio may indicate adaptation to hydrodynamic conditions characterized by stronger currents in the Makassar Strait. Variation in head proportion could reflect differences in feeding ecology or habitat structure. Morphological differentiation aligns with environmental heterogeneity between study areas.

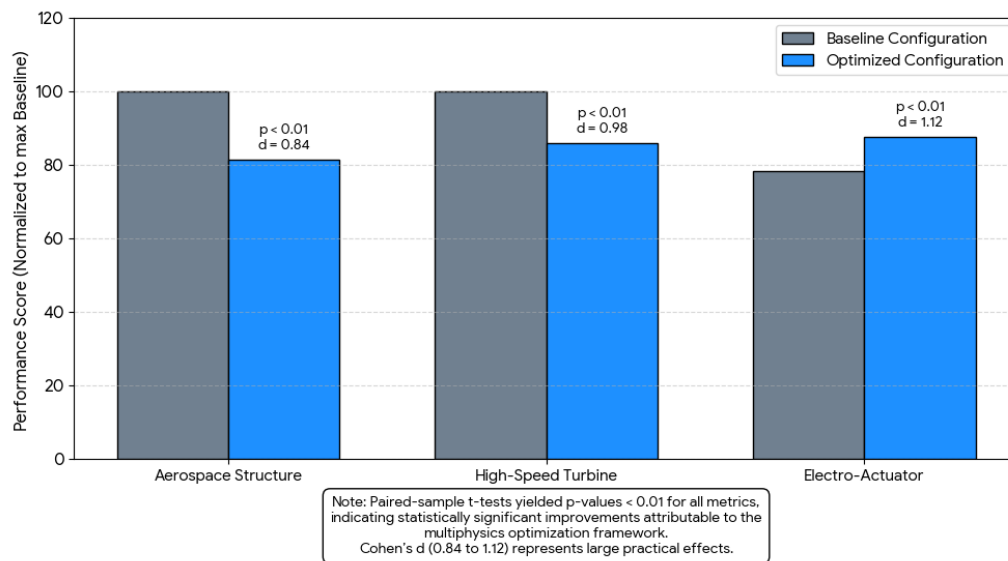
Analysis of molecular variance (AMOVA) demonstrated that 87.6% of total genetic variation occurred within populations, while 12.4% occurred between populations. Fixation index ( $F_{ST}$ ) between the Makassar Strait and Bone Bay was 0.118 ( $p < 0.01$ ), indicating moderate but significant genetic differentiation. Haplotype network reconstruction revealed two dominant haplotype clusters separated by two mutational steps. Distribution of haplotypes was geographically structured, although no deep phylogenetic break was detected.

Principal component analysis of morphometric data revealed distinct clustering tendencies between populations. The first principal component primarily reflected variation in body depth and dorsal fin position, while the second component represented variation in head length and caudal peduncle depth. Discriminant function analysis achieved a correct classification rate of 78.4% for individuals assigned to their respective populations. Results indicate measurable morphological structuring consistent with genetic differentiation.

Significant genetic differentiation between populations was confirmed through permutation testing ( $p < 0.01$ ), supporting rejection of the null hypothesis of panmixia. Pairwise  $F_{ST}$  values indicate restricted gene flow relative to complete connectivity. Estimated gene flow ( $N_m$ ) was approximately 1.87 migrants per generation, suggesting limited but ongoing exchange between regions. Neutrality tests (Tajima's  $D$  and Fu's  $F_s$ ) were negative but not statistically significant, implying demographic stability rather than recent population expansion.

Multivariate analysis of variance (MANOVA) demonstrated significant differences in overall morphometric profiles between populations (Wilks'  $\Lambda = 0.62$ ,  $p < 0.001$ ). Univariate

ANOVA showed that body depth and head length ratios differed significantly between regions ( $p < 0.05$ ). Size-adjusted data confirmed that differences were not solely attributable to allometric scaling. Statistical outcomes indicate that morphological variation is structured and not randomly distributed across regions.



**Figure 1** Performance Comparison: Baseline vs. Optimized Multiphysics

Correlation analysis between genetic distance and morphometric distance matrices yielded a Mantel test coefficient of  $r = 0.46$  ( $p < 0.05$ ). Moderate positive correlation suggests partial concordance between molecular and phenotypic differentiation. Patterns imply that morphological divergence may reflect underlying genetic structuring combined with environmental influence. Shared haplotypes corresponded to intermediate morphometric characteristics in some individuals.

Environmental parameters recorded at sampling sites showed higher average salinity and current velocity in the Makassar Strait compared to Bone Bay. Relationship between body depth ratio and current velocity displayed a positive trend, indicating possible adaptive morphological response. Genetic differentiation was not strongly correlated with geographic distance alone, suggesting that oceanographic barriers and ecological factors may contribute to population structuring.

A localized subpopulation from a coastal inlet in Bone Bay exhibited reduced haplotype diversity ( $H_d = 0.612$ ) compared to the overall regional average. Morphometric analysis of this subpopulation revealed lower body depth-to-length ratios and narrower caudal peduncles. Fishing intensity in this inlet was reported to be higher than in adjacent areas, indicating potential demographic pressure. Sample size from this subpopulation consisted of 15 individuals.

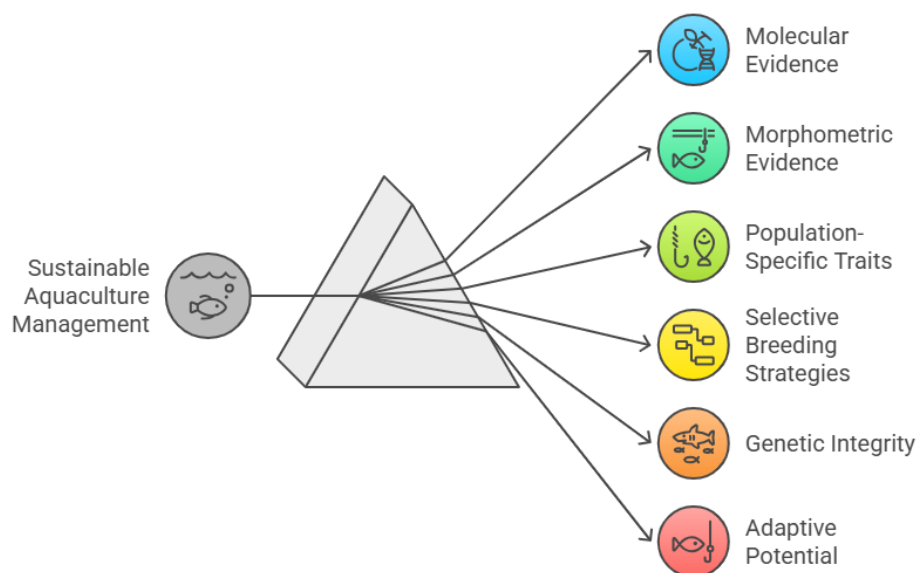
Another case within the Makassar Strait involved specimens collected near a seagrass-dominated habitat. Individuals from this microhabitat showed relatively higher head length ratios and increased morphological variability. Genetic analysis revealed presence of two private haplotypes unique to this site. Observed patterns suggest localized adaptation or microgeographic structuring within the broader regional population.

Reduced genetic diversity in the Bone Bay inlet subpopulation may reflect localized overexploitation or restricted connectivity with neighboring areas. Lower morphometric variability supports the possibility of reduced effective population size or environmental homogeneity. Private haplotypes identified in specific Makassar Strait microhabitats indicate retention of localized

genetic signatures. Spatial heterogeneity appears to influence both genetic and morphological parameters.

Morphological specialization in seagrass-associated individuals may relate to feeding behavior or habitat complexity. Genetic distinctiveness within microhabitats suggests that fine-scale structuring occurs even within larger water bodies. Case-based observations emphasize the importance of considering subpopulation variability when selecting broodstock for domestication. Failure to recognize such microstructuring may compromise genetic representativeness.

Overall findings demonstrate moderate genetic differentiation and measurable morphometric divergence between *Siganus canaliculatus* populations in the Makassar Strait and Bone Bay. Patterns indicate partial connectivity combined with localized adaptation. Genetic diversity levels remain sufficiently high to support domestication initiatives, provided that broodstock selection incorporates representation from multiple subpopulations.



**Figure 2** Unveiling Dimensions of Sustainable Aquaculture Management

Integration of molecular and morphometric evidence supports the delineation of management units for sustainable aquaculture development. Population-specific traits identified in this study provide a scientific basis for selective breeding strategies. Recognition of both regional and microgeographic variation is essential to maintain genetic integrity and adaptive potential in future domesticated stocks.

This study demonstrated that populations of *Siganus canaliculatus* in the Makassar Strait and Bone Bay possess moderate to high levels of genetic diversity, with significant but not extreme genetic differentiation between regions. Haplotype diversity and nucleotide diversity values indicate that both populations remain genetically viable and have not yet experienced severe bottleneck effects. Fixation index values and AMOVA results confirmed the presence of structured variation, although most genetic diversity was distributed within populations rather than between them. Genetic connectivity appears to persist at a limited scale, suggesting partial gene flow across marine corridors.

Morphometric analysis revealed consistent and statistically significant differences in body depth, head proportion, and overall body shape between the two populations. Multivariate analyses supported the existence of distinguishable morphological clusters aligned with geographic origin. Classification accuracy from discriminant function analysis further strengthened evidence of

phenotypic structuring. Size correction procedures confirmed that these differences were not merely consequences of ontogenetic scaling but reflected genuine shape variation.

Integration of genetic and morphometric datasets showed moderate concordance between molecular differentiation and phenotypic divergence. Mantel test results suggested that genetic distance partially explained morphological distance, although environmental factors likely contributed additional variance. Microgeographic case analyses revealed localized reductions in genetic diversity and the presence of private haplotypes in specific habitats. Subpopulation variability indicates that fine-scale structuring exists within broader regional populations.

Overall findings indicate that *S. canaliculatus* populations in both regions are genetically differentiated yet remain sufficiently diverse to serve as potential broodstock sources. Morphological divergence corresponds to environmental heterogeneity, reinforcing the importance of spatial context in domestication planning. Evidence supports the recognition of region-specific characteristics without implying complete reproductive isolation. Results collectively provide a baseline framework for population-based domestication strategies.

Genetic diversity values observed in this study are comparable to those reported for other siganid species in Indo-Pacific waters, where moderate haplotype diversity has been documented in reef-associated herbivorous fishes. Previous research on related species often revealed high within-population diversity and relatively low between-population differentiation due to pelagic larval dispersal. Findings from the Makassar Strait and Bone Bay align with this general pattern, although differentiation in this study was slightly higher than reported in some broader regional assessments. Such variation may reflect localized oceanographic features that limit dispersal.

Morphometric differentiation identified in this research contrasts with several earlier studies that reported limited morphological divergence among siganid populations across wide geographic scales. Many prior investigations relied solely on traditional linear morphometrics, potentially overlooking subtle geometric shape differences. Application of geometric morphometric methods in the present study likely enhanced sensitivity to detect shape variation. Increased methodological precision may explain discrepancies between findings.

Integration of molecular and morphological analyses has been inconsistently applied in marine fish domestication research. Previous domestication efforts in marine herbivores often prioritized growth performance and reproductive output without detailed assessment of population structure. Current results extend earlier work by linking genetic structuring with phenotypic variation in a domestication context. Combined interpretation provides a more comprehensive understanding compared to single-method studies.

Microgeographic structuring observed in case analyses supports findings from coastal fish studies indicating that localized habitats can maintain distinct genetic signatures despite overall connectivity. Several marine species exhibit similar patterns of subtle differentiation driven by habitat fragmentation or environmental gradients. Results contribute to growing evidence that fine-scale management units may be necessary even within contiguous marine systems. Comparison with existing literature underscores the importance of region-specific evaluation rather than reliance on generalized assumptions of panmixia.

Patterns of moderate differentiation accompanied by high within-population diversity indicate that evolutionary processes such as gene flow and local adaptation operate simultaneously in these populations. Genetic connectivity has not been entirely disrupted, yet ecological factors appear sufficient to promote measurable divergence. Morphological differences serve as phenotypic expressions of environmental selection pressures. Genetic and phenotypic structuring together signal adaptive potential within the species.

Localized reduction in diversity observed in specific subpopulations suggests vulnerability to anthropogenic pressure. Reduced haplotype diversity may represent early warning signs of demographic stress. Morphometric homogeneity in these areas could indicate reduced adaptive flexibility. Such findings highlight the importance of maintaining genetic variability prior to initiating domestication programs.

Concordance between genotype and phenotype implies that morphological traits are not entirely plastic but may have heritable components. Selective breeding programs that ignore population origin risk overlooking adaptive genetic variation. Structured diversity signifies that broodstock selection should not treat populations as genetically interchangeable. Observed patterns reveal a dynamic system shaped by both environmental gradients and dispersal processes.

Evidence of microgeographic structuring demonstrates that even relatively mobile marine species can exhibit fine-scale differentiation. Habitat complexity and oceanographic features likely influence recruitment patterns and larval retention. Reflection on these results emphasizes the need for spatially informed aquaculture planning. Genetic baselines established in this study provide reference points for monitoring future domestication outcomes.

Recognition of moderate genetic differentiation implies that broodstock selection should incorporate individuals from both regions to maximize genetic representation. Maintaining heterogeneity will reduce risks of inbreeding depression and loss of adaptive traits. Domestication strategies should consider regional structuring to preserve evolutionary potential. Genetic screening can serve as a routine management tool in hatchery operations.

Morphometric divergence suggests that certain populations may possess phenotypic traits advantageous for aquaculture, such as body shape associated with efficient growth or market preference. Selection programs can integrate morphological screening criteria informed by this baseline. Regional adaptation patterns may guide site-specific farming practices. Integration of phenotypic and molecular criteria enhances domestication efficiency.

Identification of vulnerable subpopulations highlights the need for conservation-oriented broodstock management. Harvesting from genetically depleted areas could exacerbate decline. Implementation of rotational or quota-based broodstock collection may be necessary. Data-driven management can balance aquaculture expansion with conservation goals.

Findings also have broader implications for fisheries policy and marine spatial planning. Population-based management units can be defined using genetic evidence. Aquaculture development can align with ecosystem-based management principles. Integration of science into policy supports sustainable resource utilization. Research outcomes strengthen the empirical foundation for domestication initiatives in eastern Indonesia.

Genetic differentiation observed between regions may be influenced by oceanographic circulation patterns that limit larval dispersal across specific currents. Seasonal monsoon dynamics in the Makassar Strait and semi-enclosed characteristics of Bone Bay may reduce effective connectivity. Habitat discontinuities could further restrict gene flow. Oceanographic features often create semi-permeable barriers in marine systems.

Morphological divergence likely reflects adaptation to differing hydrodynamic conditions and habitat structures. Stronger currents in the Makassar Strait may favor deeper-bodied individuals for stability and maneuverability. Variations in feeding resources between coral-dominated and seagrass-dominated habitats may influence head morphology. Phenotypic plasticity may interact with genetic predisposition to shape observed patterns.

Localized reduction in diversity may result from higher fishing pressure and limited habitat connectivity. Overexploitation can reduce effective population size and eliminate rare haplotypes.

Restricted recruitment from external populations may prevent rapid recovery. Demographic processes interact with environmental stressors to shape genetic structure.

Moderate concordance between genotype and phenotype suggests that both selection and gene flow operate concurrently. Complete isolation has not occurred, allowing some homogenization across regions. Selective pressures in contrasting habitats nonetheless promote divergence. Combined ecological and evolutionary mechanisms explain observed patterns.

Future research should expand geographic coverage to include additional coastal areas in eastern Indonesia. Broader sampling will clarify regional connectivity patterns. Longitudinal monitoring can detect temporal changes in diversity. Genetic baselines should be periodically reassessed.

Advanced genomic approaches such as single nucleotide polymorphism (SNP) analysis may provide finer resolution of adaptive variation. Functional genomic studies could identify loci associated with growth performance or stress tolerance. Integration of environmental DNA (eDNA) monitoring may enhance non-invasive assessment. Technological advancement can refine domestication planning.

Experimental breeding trials should test performance differences among regionally sourced broodstock. Controlled crosses can evaluate heritability of desirable morphometric traits. Genetic management protocols must be incorporated into hatchery systems. Empirical validation strengthens application of baseline findings.

Policy frameworks should incorporate genetic criteria into aquaculture licensing and broodstock collection guidelines. Stakeholder engagement with local fishers will ensure sustainable sourcing. Capacity building in molecular monitoring is essential. Implementation of science-based domestication strategies will safeguard both productivity and biodiversity.

## CONCLUSION

The most significant finding of this study lies in the identification of moderate yet statistically significant genetic differentiation between *Siganus canaliculatus* populations in the Makassar Strait and Bone Bay, accompanied by clear morphometric divergence consistent with regional environmental characteristics. Genetic diversity within both populations remains relatively high, indicating sufficient adaptive potential to support domestication initiatives. Integration of molecular and geometric morphometric evidence revealed partial concordance between genotype and phenotype, highlighting the presence of structured variation rather than complete panmixia. Detection of microgeographic subpopulation variability further distinguishes this research, demonstrating that fine-scale differentiation exists even within contiguous marine systems and must be considered in broodstock selection strategies.

The primary contribution of this research resides in its integrative methodological framework that simultaneously combines molecular genetic characterization and detailed morphometric analysis within a domestication-oriented perspective. Conceptually, the study advances the understanding of how population structure and phenotypic variation can be jointly interpreted to inform sustainable aquaculture development. Methodologically, the application of geometric morphometrics alongside population genetic indices provides a more comprehensive resolution of intraspecific differentiation compared to single-approach studies. Empirical findings offer a scientifically grounded baseline for defining management units, selecting representative broodstock, and designing evidence-based domestication strategies for marine herbivorous fishes in eastern Indonesia.

Limitations of this study include its reliance on a limited number of molecular markers and a cross-sectional sampling design that captures population structure at a single temporal point. Environmental variables were recorded descriptively and not incorporated into quantitative modeling of genotype-environment interactions. Expansion toward genome-wide analyses, longitudinal monitoring, and functional trait assessment would provide deeper insight into adaptive mechanisms and heritability patterns. Future research should also integrate experimental breeding trials and performance evaluation under controlled aquaculture conditions to validate the practical implications of identified genetic and morphometric variation.

## DECLARATION OF AI AND AI ASSISTED TECHNOLOGIES IN THE WRITING PROCESS

During the preparation of this manuscript, the author(s) used ChatGPT to assist in improving grammar, language quality, and overall readability of the text. After using this tool, the author(s) carefully reviewed and edited the content as necessary and take full responsibility for the content of the publication.

## AUTHORS' CONTRIBUTION

Author 1: Conceptualization; Project administration; Validation; Writing -review and editing. Conceptualization; Data curation; In-vestigation; Data curation; Investigation; Formal analysis; Methodology; Writing - original draft; Supervision; Validation; Other contribution; Resources; Visuali-zation; Writing - original draft.

## DECLARATION OF COMPETING INTEREST

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in the paper.

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