

Population structure of yellowfin seabream (*Acanthopagrus latus*) in Central Vietnam through morphological and genetic analyses

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Abstract. Ty N, Ngan NMK, Loi BV, Thanh ND, Huy NX, Giang TV. 2025. Population structure of yellowfin seabream (*Acanthopagrus latus*) in Central Vietnam through morphological and genetic analyses. *Biodiversitas* 26: 2402-2409. The yellowfin seabream (*Acanthopagrus latus* (Houttuyn, 1782)) is a key species found along the coastal waters of Central Vietnam, where it plays an important role in local fisheries and ecosystems. Understanding its taxonomy and population dynamics is crucial for effective management and conservation. This study aimed to investigate the morphological and genetic characteristics of *A. latus* populations across three regions in Central Vietnam (Thua Thien Hue, Quang Binh, and Nghe An) to enhance knowledge of the species' diversity and structure. Morphological identification was based on 11 meristic counts, which revealed distinct species-specific traits, such as a slender, laterally flattened body, comb-like scales, and yellow fins. Genetic analysis of mitochondrial Cytochrome Oxidase I (mtCOI) sequences identified high genetic similarity (99.54%-100%) with references in NCBI GenBank, confirming the species identification. A total of six haplotypes were found, with Thua Thien Hue exhibiting the greatest genetic diversity, while Quang Binh showed no detectable nucleotide variation. AMOVA results indicated that 95.75% of the genetic variation occurred within populations, suggesting weak differentiation among regions ($F_{st} = 0.04247$). Neutrality tests indicated population expansion or purifying selection in Thua Thien Hue and Nghe An, while Quang Binh experienced a reduction in genetic variation. These findings offer valuable insights for the conservation and management of *A. latus* populations, emphasizing the need for strategies that account for both genetic connectivity and regional variability. The study also contributes to understanding the species' ecological interactions and provides a foundation for future research to monitor long-term changes in genetic diversity.

Keywords: Central Vietnam, genetic diversity, meristic counts, mtCOI, yellowfin seabream

INTRODUCTION

Based on significant differences in physical traits such as body shape and fin morphology, the yellowfin seabream (*Acanthopagrus latus* (Houttuyn, 1782)), belonging to the Sparidae family, is broadly found throughout the Indo-West Pacific, encompassing regions from the Persian Gulf to the coasts of Japan and Australia (Iwatsuki and Heemstra 2010). *Acanthopagrus latus* is known for its ecological and economic significance; it is highly valued in commercial and artisanal fisheries, particularly in coastal and estuarine areas. Its high adaptability to differential environmental conditions and habitat utilization has made it a key species in biodiversity and fisheries management studies (Wang et al. 2020; Tang et al. 2023). In Vietnam, *A. latus* is primarily found in the coastal waters, river mouths, coastal lagoons, and downstream of major rivers in the northern provinces (Hau et al. 2019), contributing significantly to local livelihoods through fisheries.

Acanthopagrus latus has broad research tolerance to variable salinities and temperatures, reflecting the remarkable adaptability of this species, allowing it to thrive

in diverse habitats (Lu et al. 2022). Its omnivorous diet further supports this adaptability, enabling it to exploit many food resources in different waters (Sourinejad et al. 2015). It can successfully and resiliently colonize various aquatic ecosystems by adjusting its reproductive strategies to environmental conditions.

Studying the morphological and genetic characteristics of *A. latus* allows us to gain insights into its population dynamics, adaptability, and evolutionary history. Its scale forms are often shaped by environmental factors, such as salinity, water temperature, and habitat type (Tang et al. 2023). Differences between populations are critical for identifying and revealing how species adapt to varying environmental conditions.

Numerous studies worldwide have examined the morphology and taxonomy (Iwatsuki 2013), biological characteristics (Tran 2019; Li et al. 2020), genetic diversity, and population genetic structure (Liu et al. 2021; Song et al. 2021; Rahim et al. 2023) of *A. latus*. The use of molecular markers such as mitochondrial DNA, especially the mitochondrial Cytochrome Oxidase subunit I (mtCOI) gene, has been recognized as a key component in

establishing a universal system for animal taxonomy (Xiao et al. 2016; Bingpeng et al. 2018). Through this genetic data, it is possible to understand population connectivity and evolutionary history and ensure the sustainability of the species through conservation measures and fisheries management.

Central Vietnam's coastal and lagoon ecosystems are recognized as vital habitats for marine biodiversity and local livelihoods. These areas compose brackish waters, mangroves, and seagrass beds and serve as crucial breeding and nursery grounds for species such as *A. latus* and other economically significant fish and crustaceans. Fisheries and aquaculture are being supported, and these ecosystems contribute significantly to biodiversity and the local community's economic well-being (Nguyen et al. 2022b). However, overfishing, pollution, and climate change pose an increasing threat, which risks disrupting ecological balance and jeopardizing local livelihoods (Giang and Khanal 2024).

These threats have a particular impact, which is evident in species like *A. latus*. Because of habitat degradation and overexploitation, *A. latus* populations are declining (Yan et al. 2021; Peng et al. 2023). *A. latus* population decline poses broader ecological and economic risks, as it plays a critical role in local fish populations and supports regional biodiversity (Liu et al. 2021; Dang et al. 2023). A deeper understanding of its morphological and genetic characteristics is essential to ensure the long-term viability of *A. latus* in this region. Such knowledge will aid in developing effective conservation measures and maintaining these vital ecosystems' ecological and economic stability. Therefore, this study investigated the morphology and genetics of *A.*

latus in Central Vietnam to understand its population structure and adaptability. Its findings can aid conservation efforts, habitat preservation, and policy-making for species protection.

MATERIALS AND METHODS

Sample collection

A total of 160 fish samples were gathered from three study areas in Central Vietnam: Nghe An, Quang Binh, and Thua Thien Hue, between January 2023 and June 2024. Repeated sampling was conducted at specific sites to ensure adequate representation (Figure 1, Table 1). Specifically, 50 samples were obtained from Nghe An (NA1, NA2), 52 from Quang Binh (QB1, QB2), and 58 from Thua Thien Hue (HUE1, HUE2). The specimens were analyzed for morphological characteristics, and tissue samples (skeletal muscle and pectorfins) were collected for genetic analysis at the Laboratory of Zoology, Faculty of Biology, University of Education, Hue University. The samples were obtained directly from fishing activities with the assistance of local fishermen actively working in the research areas. This method ensured the collection of diverse and representative samples across the surveyed regions. The study received approval from the Animal Ethics Committee at Hue University (HUVN0036), and all experimental procedures adhered to the guidelines outlined in the Handbook for the Welfare of Laboratory Animals (Nguyen et al. 2022a).

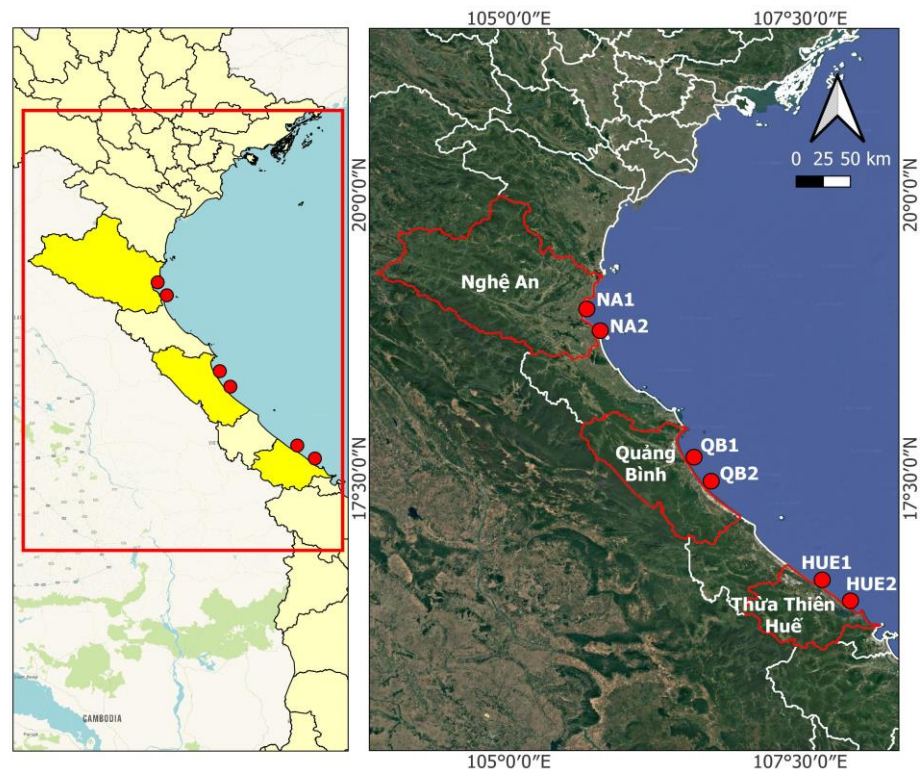


Figure 1. Sampling locations along the coast of Central Vietnam

Table 1. The fish samples were used for total DNA extraction from Central Vietnam

Location	Site on map (Figure 1)	Coordinates	Number of samples	Sample code
Nghe An	NA1	18°58'19.57"N, 105°38'5.53"E	8	5225, 5226, 5228, 5229, 6402, 6403, 6404, 6405
	NA2	18°48'49.86"N, 105°45'7.77"E		
Quang Binh	QB1	17°42'46.81"N, 106°30'26.39"E	8	4106, 4107, 4108, 4109, 3125, 3126, 3127, 3128
	QB2	17°29'10.43"N, 106°38'9.87"E		
Thua Thien Hue	HUE1	16°35'48.19"N, 107°37'13.86"E	8	1001, 1002, 1003, 1005, 2124, 2125, 2126, 2127
	HUE2	16°21'59.57"N, 107°56'30.14"E		

Morphological identification of *Acanthopagrus latus*

Acanthopagrus latus was identified from the collected fish samples based on the dichotomous keys provided by Iwatsuki and Heemstra (2010). The morphological criteria and meristic counts described by Iwatsuki (2013) were also referenced to confirm and select the species. The classification system of Fricke et al. (2023) was utilized to ensure accuracy and alignment with international standards. Key morphological features, such as body structure, fin counts, spines, and specific meristic indices, were carefully compared against standard species descriptions for precise and reliable identification (Iwatsuki 2013).

Genomic DNA extraction, PCR, and sequencing

Genomic DNA was extracted from 24 fish samples confirmed as *A. latus* based on morphological identification (Table 1). Pectoral fin tissues were dissected, preserved in 96% ethanol in Eppendorf tubes, and stored at -20°C until needed. Total DNA was extracted using the GenJET Genomic DNA Purification Kit (Thermo Fisher Scientific) according to the manufacturer's guidelines. DNA quality was evaluated via 0.8% agarose gel electrophoresis with Safe-dye™, and bands were visualized using a UV transilluminator.

The Polymerase Chain Reaction (PCR) mixture (15 µL) comprised 1.5 µL of DNA template, 7.5 µL of 2× PCR Master Mix buffer, 0.75 µL of both forward (Fish F1) and reverse (Fish R1) primers (Ward et al. 2005), and 4.5 µL of distilled water. The PCR was performed using an ESCO thermal cycler under the following conditions: an initial denaturation at 94°C for 5 minutes; 30 cycles of 94°C for 30 seconds, 53°C for 40-55 seconds, and 72°C for 1 minute; and a final extension at 72°C for 5 minutes. The PCR products were analyzed by 0.8%-1.4% agarose gel electrophoresis with Safe-dye™ (1 µL/20 mL gel) and visualized with a UV transilluminator.

The PCR products were purified using a PCR Purification Kit (Intron) according to the manufacturer's instructions. Purified PCR amplicons were visualized on 1.4% agarose gels treated with Safe-dye™ and observed under UV light. DNA sequencing using the Sanger method was conducted using capillary electrophoresis at First Base (Malaysia).

Sequence analysis and phylogenetic tree construction

The mtCOI gene segment sequences were validated using the Basic Local Alignment Search Tool (BLAST) program to confirm their identity and similarity with known sequences. After validation, the sequences were edited and

aligned using the MEGA X software (Kumar et al. 2018). The number of variable sites (S), number of mutations (η), average number of nucleotide differences (k), number of haplotypes (h), nucleotide diversity (π), and haplotype diversity (Hd) were calculated within and between each sampling region using the DnaSP 6 software (Rozas et al. 2017).

Fu's F_s and Tajima's D were calculated using the Arlequin 3.5 software (Excoffier and Lischer 2010) to investigate population expansion patterns in *A. latus*. Fu's F_s evaluates haplotype distributions, while Tajima's D compares pairwise sequence differences to infer allele frequency dynamics. Genetic divergence (Fixation Index [F_{st}]) and genetic variability within and between populations were explored using Analysis of Molecular Variance (AMOVA) with the Arlequin 3.5.2.2 software (Excoffier and Lischer 2010).

The evolutionary distances were computed using the p -distance method with the MEGA X software (Kumar et al. 2018). A Bayesian phylogenetic tree was constructed using the BEAST 2.7 software (Bouckaert et al. 2019), utilizing the HKY substitution model and the coalescent Bayesian skyline tree prior. The Markov chain Monte Carlo analysis ran for 1,000,000 generations with a 10% burn-in. Finally, the phylogenetic trees were visualized and refined using the FigTree 1.4.4 software (<http://tree.bio.ed.ac.uk/software/figtree/>).

RESULTS AND DISCUSSION

Taxonomic identification of *Acanthopagrus latus* based on morphological and meristic analyses

The identification of *A. latus* was confirmed by analyzing 11 meristic counts from 160 fish samples collected from coastal regions in Central Vietnam with their weight and standard length ranging from 4.1 to 511.2 g and 7.31 to 23.23 cm, respectively. The key morphological features of this species include a slender, elongated body flattened laterally, comb-like body scales with an anterior edge near the arch, a slightly slanted mouth with thick lips, a pointed snout, and two distinct nostrils in front of the eyes (a round anterior nostril and a slit-like posterior nostril). The pelvic fin, anal fin, and caudal fin exhibit a characteristic yellow coloration (Figure 2). These morphological traits align with the descriptions of *A. latus* in taxonomic literature, confirming its identification (Iwatsuki 2013).

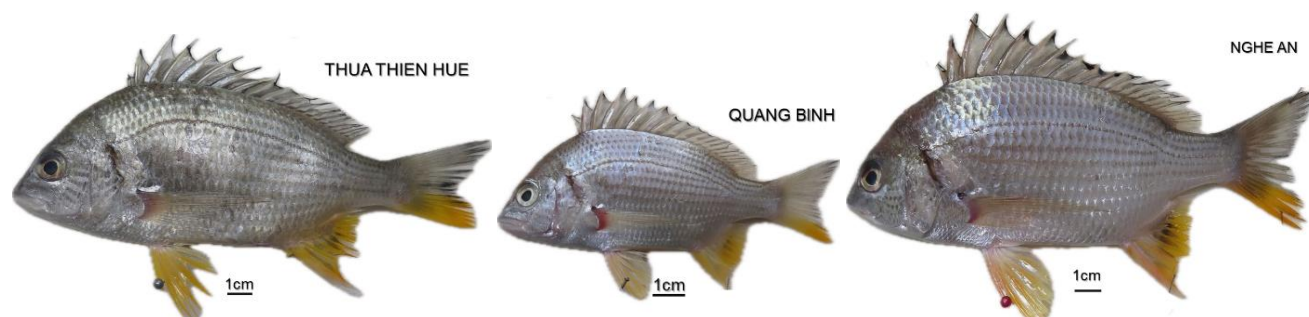


Figure 2. External morphology of *Acanthopagrus latus* from Thua Thien Hue, Quang Binh and Nghe An of Central Vietnam

Table 2. Meristic counts of *Acanthopagrus latus* distributed in Central Vietnam

Meristic counts	Thua Thien Hue	Quang Binh	Nghe An
Dorsal fin spines	XI	XI	XI
Dorsal fin rays	12	12	12
Caudal fin rays	18	18	18
Anal fin spines	III	III	III
Anal fin rays	9	9	9
Pelvic fin spines	I	I	I
Pelvic fin rays	5	5	5
Pectoral fin rays	15	15	15
Lateral line scales with pores	43-46	44	40-44
Scale rows from the fifth dorsal-fin spine base to the lateral line	3½	3½	3½
Scale rows from the ninth dorsal-fin spine base to the lateral line	3½	3½	3½

Meristic counts across regions demonstrate notable consistency. The dorsal fin consistently had 11 spines and 12 rays, while the anal fin included three spines and nine rays across all samples. The caudal fins were uniform, with 18 rays, and the pelvic fins consistently comprised one spine and five rays. The pectoral fins consistently had 15 rays in all fish across regions. Lateral line scales with pores ranged from 43-46 in Thua Thien Hue, 44 in Quang Binh, and 40-44 in Nghe An. Scale rows from the fifth dorsal-fin spine base to the lateral line and from the ninth dorsal-fin spine base to the lateral line were consistently measured as 3.5 across all regions (Table 2). Together with the key morphological features, these consistent meristic traits reinforce the identification of the studied samples as *A. latus*.

The genetic analysis of *A. latus* in Central Vietnam

Comparison of mtCOI gene sequences in *A. latus* samples from Central Vietnam with GenBank references

The BLAST analysis of the mtCOI gene sequences demonstrated high genetic similarity between the studied samples and reference sequences in the GenBank database (accession numbers NC_056780.1 and EF506764.1) with E-values = 10^{-6} . It revealed significant genetic resemblance

among the 24 mtCOI gene segments derived from *A. latus* samples collected in Central Vietnam. As shown in Table 3, all gene segments measured 655 base pairs (bp) in length, with a query coverage of 100%, indicating that the complete sequences of the genes were successfully compared. The nucleotide similarity ranged from 99.54% to 100%, indicating a close genetic match to *A. latus*. The lowest similarity was found for Haplotype 5 (Sample 5225) at 99.54%, while the highest similarity was observed for Haplotype 2 (which accounted for most samples) at 100%. The *A. latus* sequences from GenBank were closely aligned with the genetic consistency of the studied populations.

Genetic diversity

The genetic diversity analysis revealed distinct patterns across the three regions: Thua Thien Hue, Quang Binh, and Nghe An. Thua Thien Hue and Nghe An showed apparent genetic variation, with an *S* of three and five, respectively, while no variation was detected in Quang Binh. The patterns in η mirrored these results, with three and five mutations observed in Thua Thien Hue and Nghe An, respectively, and none in Quang Binh. Similarly, *k* was highest in Nghe An (3.7474), moderate in Thua Thien Hue (0.6522), and 0 in Quang Binh. In addition, π was 0.00115 ± 0.00041 in Thua Thien Hue, 0.00191 ± 0.00093 in Nghe An, but 0 in Quang Binh. *Hd* was highest in Thua Thien Hue (0.643 ± 0.184) with an *h* of four, followed by Nghe An (0.464 ± 0.200) with an *h* of three, while *h* was zero in Quang Binh. Six haplotypes were identified across all regions, giving an overall *Hd* of 0.380 ± 0.125 . Neutrality tests suggested contrasting evolutionary processes. Tajima's *D* was negative in both Thua Thien Hue (-1.44751) and Nghe An (-1.59524), indicating potential population expansion or purifying selection, but no result was available for Quang Binh. Fu's *F_s* provided further evidence, being significantly negative in Thua Thien Hue (-1.832) and slightly positive (0.617) in Nghe An (Table 4), giving an overall negative value (-0.405). These findings suggest that genetic differences exist across regions. The genetic diversity appears moderate in Thua Thien Hue and Nghe An, but absent (homogenous) in Quang Binh. These differences may be related to demographic or ecological factors shaping population structure in particular regions.

Table 3. BLAST analysis of the mtCOI gene sequences of the 24 samples from Central Vietnam and the GenBank reference sequences

Haplotype No.	Sample code	Gene size (bp)	Query coverage (%)	Nucleotide similarity (%)
Hap_1	1001	655	100	99.85
Hap_2	1002 1005 2125 2126 2127 3125 3126 3127 3128 4106 4107 4108 4109 5226 5228 5229 6403 6404 6405	655	100	100
Hap_3	1003	655	100	99.85
Hap_4	2124	655	100	99.85
Hap_5	5225	655	100	99.54
Hap_6	6402	655	100	99.69

Table 4. Genetic diversity of *Acanthopagrus latus* populations in Central Vietnam based on mtCOI sequences

Value	Thua Thien Hue	Quang Binh	Nghe An	Total
Number of samples	8	8	8	24
Number of variable sites (<i>S</i>)	3	-	5	6
Number of mutations (<i>η</i>)	3	-	5	6
Average number of nucleotide differences (<i>k</i>)	0.6522	-	3.7474	1.2500
Nucleotide diversity per site (π)*	0.00115±0.00041	-	0.00191±0.00093	0.00100±0.00041
Number of haplotypes (<i>h</i>)	4	-	3	6
Haplotype (gene) diversity (<i>Hd</i>)*	0.643±0.184	-	0.464±0.200	0.380±0.125
Tajima's <i>D</i> **	-1.44751 (0.072)	-	-1.59524 (0.018)	-1.01425 (0.363)
Fu's <i>F_s</i> **	-1.832 (0.009)	-	0.617 (0.612)	-0.405 (-)

Note: *: Presented as the mean±standard deviation; **: Presented as the value (p-value)

Table 5. AMOVA of *A. latus* populations in Central Vietnam

Source	Degree of freedom	Sum of squares	Variance components	Percentage of total variance (%)
Among populations	2	0.500	0.00818 Va	4.25
Within populations	21	3.875	0.18452 Vb	95.75
Total	23	4.375	0.19271	
Fixation Index (<i>F_{st}</i>)	0.04247	<i>P</i> = 0.3235±0.01641		

Table 6. The *F_{st}* of *A. latus* populations in Central Vietnam

Population	Thua Thien Hue	Quang Binh	Nghe An
Thua Thien Hue	***	0.20117	0.99902
Quang Binh	0.14286	***	0.46484
Nghe An	-0.04202	0.07143	***

Note: The *F_{st}* is shown below the diagonal, and the *P*-value is shown above the diagonal

Population genetic structure and variation

The AMOVA of *A. latus* populations in Central Vietnam revealed that most genetic variation was found within rather than between populations. Specifically, 95.75% of the total genetic variance occurred within populations, while only 4.25% occurred between populations (Table 5). *F_{st}* was estimated at 0.04247 and nonsignificant (*P* = 0.3235), indicating weak genetic differentiation among populations. Pairwise *F_{st}* further supported this conclusion, showing low genetic differentiation between populations (Table 6). The *F_{st}* was positive between Thua Thien Hue and Quang Binh (0.14286) and slightly negative between Thua Thien Hue and Nghe An (-0.04202), suggesting

negligible differentiation or shared genetic variation. Similarly, differentiation was estimated to be low between Quang Binh and Nghe An (*F_{st}* = 0.07143). The associated *P*-values ranged from 0.20117 to 0.99902, confirming that these differences were not significant. In general, these findings indicate that *A. latus* populations in Central Vietnam are essentially genetically homogenous, with most genetic diversity distributed within rather than between them.

Phylogenetic relationships

The Bayesian phylogenetic tree (Figure 3) shows the genetic relationships among the analyzed samples; distinct haplotype clusters were found (Hap_1 to Hap_19), and a well-defined outgroup was used as a reference. The color coding of the haplotypes demonstrates clear genetic differentiation between groups. As indicated by the black circles on the branches, the posterior probabilities range from 0.8 to 1.0, with high values (>0.95) indicating robust phylogenetic inferences for the most significant clades. Short branch lengths within specific haplotypes, such as Hap_1 and Hap_2, suggest close genetic relationships among samples, whereas longer branches separating clusters indicate greater genetic divergence. Hap_2 accounted for most of the samples in this study and the reference samples from GenBank, most of which originate from coastal regions of China. Hap_3, Hap_1, Hap_11, and Hap_9 contained six, five, four, and three samples, respectively, while the remaining haplotypes included only one or two samples each. Well-supported haplotype clusters reflect significant genetic structure within the population, consistent with potential evolutionary or demographic processes. The outgroup provides a reference point, reinforcing the tree's topology and confirming the relationships among haplotypes.

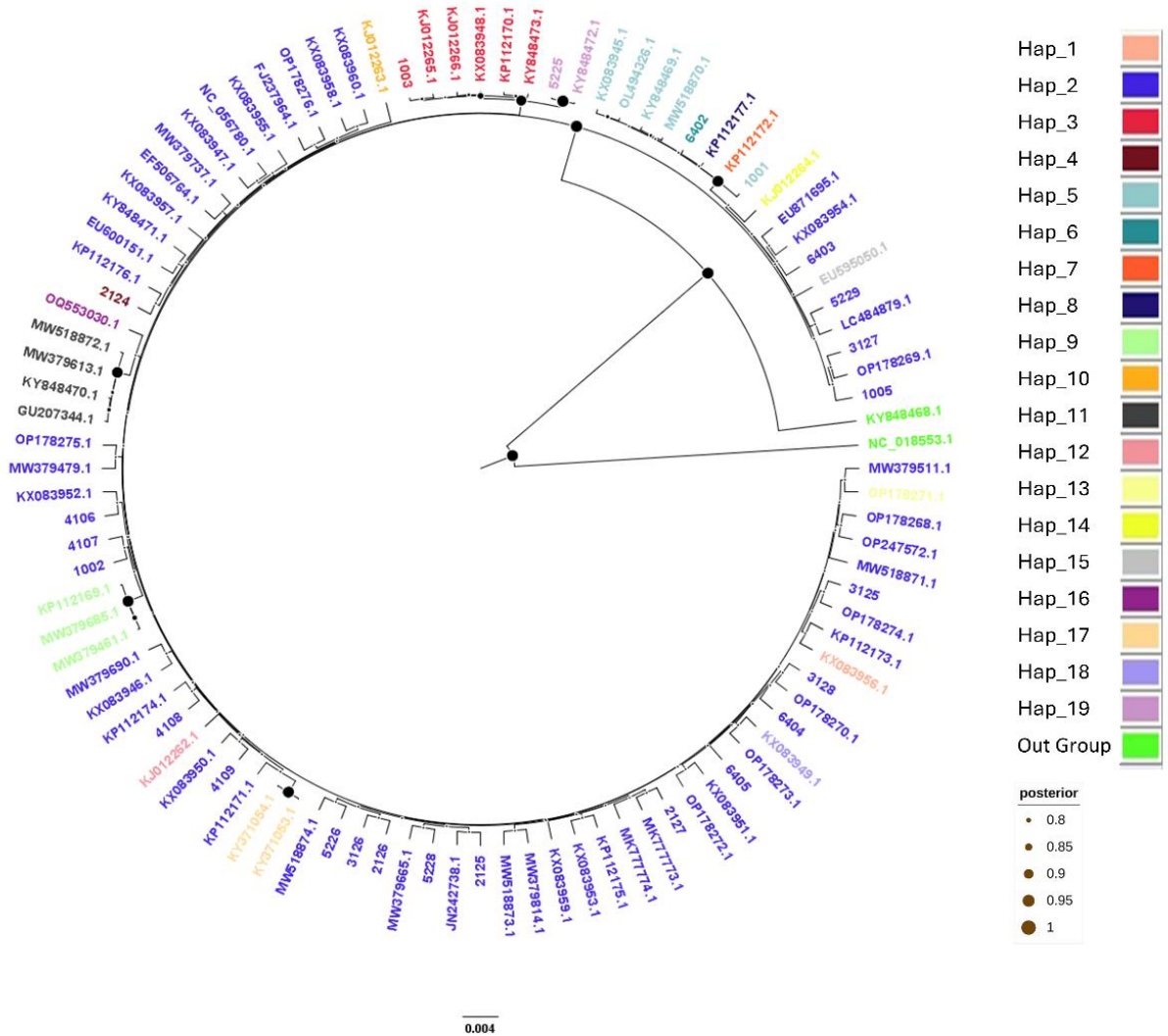


Figure 3. Phylogenetic tree based on mtCOI gene sequences of samples from *Acanthopagrus latus* populations in Central Vietnam (numerical symbol) and reference sequences on GenBank (accession numbers)

Discussion

Our results provide further insights into the morphological and genetic characteristics of *A. latus* populations in Central Vietnam, offering critical insights for taxonomic classification, population dynamics, and conservation planning. Morphological analyses highlighted the uniformity of key traits, including a slender and elongated body, laterally flattened shape, and distinctive yellow fins. The scales, characterized by their comb-like shape, and the nostrils, with their unique structure, further corroborate the identity of *A. latus* as described in prior taxonomic studies (Iwatsuki and Heemstra 2010). These morphological features, consistent with taxonomic literature, underscore the reliability of morphological methods in identifying species, especially for fisheries management and ecological studies.

Meristic data, including dorsal, anal, pelvic, and caudal fin counts, demonstrated significant uniformity across Thua Thien Hue and Quang Binh, with minor variations in Nghe An. The slight regional differences may be influenced by

ecological variables such as salinity, temperature, and habitat type, which are known to drive morphological plasticity in fish populations (Seebacher et al. 2016). This similarity in morphological and meristic traits is also supported by observations of *A. latus* populations in other Indo-West Pacific regions, which further supports the taxonomic accuracy of our study.

Genetic analyses provided additional layers of evidence supporting the identification of *A. latus*. The mtCOI gene, a broadly recognized molecular tool for identifying species, confirmed the genetic similarity of our samples to global reference sequences in the GenBank database (Heller et al. 2018; Bai et al. 2020). High sequence identity (99.54%-100%) across samples demonstrates robust genetic consistency, aligning with findings of similar studies in other parts of Asia (Song et al. 2021). This genetic consistency underscores the stability of the *A. latus* genome, even in geographically dispersed populations, likely due to its migratory behavior and broad ecological tolerance.

Six distinct haplotypes were identified across the three sampling regions, indicating moderate genetic diversity. While genetic diversity was greatest in Thua Thien Hue ($Hd = 0.643 \pm 0.184$), this region may have served as a genetic frontier. However, Quang Binh showed no detectable nucleotide diversity, potentially indicating a recent population bottleneck or founder effect. This pattern of uneven genetic diversity across regions has been observed in other fish species and reflects the complex interplay of historical, ecological, and demographic factors (Ghasemi et al. 2019; Liu et al. 2021).

The AMOVA indicated that most genetic variation (95.75%) occurs within populations, whereas just 4.25% occurs between populations. This finding and a low F_{st} (0.04247) highlight the weak genetic differentiation among *A. latus* populations in Central Vietnam. Such homogeneity is likely a result of gene flow facilitated by the species' mobility and connectivity among habitats in the coastal and lagoon systems of the region. This finding aligns with studies on other marine fish species in the Indo-West Pacific, where ocean currents and larval dispersal contribute to high levels of genetic mixing (Vahabnezhad et al. 2016; Pan et al. 2021).

Interestingly, the neutrality tests revealed region-specific evolutionary patterns among *A. latus* populations in Central Vietnam. In Thua Thien Hue, Tajima's D was negative (-1.44751, $p = 0.072$), suggesting an excess of low-frequency alleles that may reflect recent population expansion or purifying selection (Tajima 1989). Supporting this, Fu's F_s was significantly negative (-1.832, $p = 0.009$), indicating an excess of rare haplotypes typically associated with recent demographic expansion (Fu 1997). These combined results provide statistical support for a recent expansion event in this population. In contrast, the population in Nghe An showed a negative and statistically significant Tajima's D (-1.59524, $p = 0.018$), suggesting similar evolutionary processes. However, Fu's F_s was positive and non-significant (0.617, $p = 0.612$), indicating no substantial deviation from neutrality. This suggests that, while Tajima's D points to potential population expansion or selection, the lack of supporting evidence from Fu's F_s weakens the case for a strong recent demographic event. Therefore, additional studies employing alternative molecular markers are needed to validate these evolutionary hypotheses more comprehensively in this region.

A phylogenetic analysis confirmed the species' identity, with genotypes clustering closely with reference sequences from China and other regions of the Indo-West Pacific (Figure 3). Due to its wide geographical distribution, the species has high genetic connectivity, consistent with its ability to adapt to various environments. The adaptability of *A. latus* may be vital in response to environmental changes, including other factors caused by climate change and human activities.

Our results indicate that *A. latus* populations in Central Vietnam have a relatively stable genetic structure, which benefits their long-term survival from a conservation perspective. However, concern is indicated in some areas, such as Quang Binh, which shows reduced genetic diversity; therefore, there is a likely vulnerability due to environmental

changes and genetic bottlenecks. Thus, populations' genetic diversity and resilience will require site-specific management strategies. To better inform these efforts, further research using alternative molecular markers or whole-genome analyses is recommended.

In conclusion, our findings demonstrate the importance of combining morphological and genetic approaches to understand the physiology and population dynamics of *A. latus*. These approaches have provided unique and complementary insights into the species' taxonomic identity, genetic structure, and evolutionary potential. Our study contributes to the growing body of literature on the genetic diversity and connectivity of marine species in Southeast Asia, providing vital information for fisheries management and conservation. It highlights that *A. latus* populations will require continuous monitoring and adaptive management to survive the increasing environmental pressures on coastal ecosystems in Central Vietnam.

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