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GENETIC DIVERSITY OF MAHSEER (*Tor* spp.) IN JAMBI: A DNA BARCODING APPROACH FOR CONVERSATION

KEANEKARAGAMAN GENETIK MAHSEER (*Tor* spp.) DI JAMBI: PENDEKATAN DNA BARCODING UNTUK KONSERVASI

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Abstract

Genetic-based management is a critical approach to maintain the sustainability of mahseer fish (*Tor tambra* and *T. tambroides*), which are facing threats from habitat degradation and overfishing in Jambi Province. This study aims to analyze the genetic diversity and population structure of mahseer using the COI gene markers. A total of 18 specimens were collected from six locations in the Jambi rivers (June-August 2024). DNA sequencing results showed 98.51–99.85% similarity to the references *T. tambra* and *T. tambroides* in GenBank. Phylogenetic analysis confirmed the grouping of this species, with a bootstrap value of 100% and closeness to the species *Barbonymus gonionotus* and *Hampala macrolepidota*. There were 11 haplotypes with the highest diversity at stations 3 and 6 (Hd= 0.90000), while moderate genetic differentiation (Fst= 0.109–0.141) was found between station 2 and other locations, indicating isolation due to habitat fragmentation. Water quality parameters (dissolved oxygen 6.3–7.1 mg/L, pH 7.0–7.3, current velocity 0.2–0.4 m/s) support habitat suitability, but anthropogenic activities potentially threaten genetic connectivity. These findings underscore the need for genetic data-driven conservation strategies, such as restocking of highly diverse populations and protection of critical habitats. Further research is needed to monitor long-term genetic dynamics.

Keywords: Genetic diversity; Habitat fragmentation; *Tor tambra*; *Tor tambroides*

Abstrak

Pengelolaan berbasis genetik merupakan pendekatan penting untuk menjaga keberlanjutan ikan mahseer (Tor tambra dan T. tambroides) yang menghadapi ancaman degradasi habitat dan penangkapan berlebih di Provinsi Jambi. Penelitian ini bertujuan untuk menganalisis keragaman genetik dan struktur populasi ikan mahseer dengan menggunakan penanda gen COI. Sebanyak 18 spesimen dikumpulkan dari enam lokasi di sungai area penghubung di Jambi (Juni-Agustus 2024). Hasil sekuensing DNA menunjukkan kemiripan 98,51–99,85% dengan referensi T. tambra dan T. tambroides di GenBank. Analisis filogenetik mengkonfirmasi pengelompokan jenis ini dengan nilai bootstrap 100% dan kedekatan dengan jenis Barbonymus gonionotus dan Hampala macrolepidota. Terdapat 11 haplotipe dengan keragaman tertinggi di stasiun 3 dan 6 (Hd= 0.90000), sementara diferensiasi genetik moderat (Fst= 0.109–0.141) ditemukan di antara stasiun 2 dan lokasi lainnya, yang mengindikasikan adanya isolasi akibat fragmentasi habitat. Parameter kualitas air (oksigen terlarut 6,3–7,1 mg/L, pH 7,0–7,3, kecepatan arus 0,2–0,4 m/detik) mendukung kesesuaian habitat, namun aktivitas antropogenik berpotensi mengancam konektivitas genetik. Temuan ini menggarisbawahi perlunya strategi konservasi berbasis data genetik, seperti kegiatan restocking dengan populasi beragam, dan perlindungan habitat kritis.

Kata Kunci*: Fragmentasi habitat; Keragaman genetik; Tor tambra; Tor tambroides*

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INTRODUCTION

Tor fish, scientifically referred to as mahseer, is a freshwater fish endemic to the mountain rivers of Sumatra Island, Java Island, and Kalimantan Island, where it is known by various local names (Yanto, 2016). Mahseer possesses significant commercial value and is widely appreciated in Indonesia and other Asian countries (Radona et al., 2015). There are four species found in Indonesia, namely *Tor soro*, *Tor tambra*, *Tor douronensis*, and *Tor tambroides* (Nazarah et al., 2022) out of 20 species of mahseer in Asia (Sudarmaji et al., 2016). *Tor soro* is currently classified as *Neolissochilus soro* (Jaafar et al., 2021).

The natural habitat of mahseer fish is generally fast-flowing rivers with high clarity and rocky and sandy substrates (Haser et al., 2021). In Jambi Province, mahseer (local name known as semah fish) is found in upstream areas such as Sekalo River (Bukit Tiga Puluh Tebo Ecosystem), Batang Merangin River, and Kerinci Region (Syaiful, 2017; Yusrizal et al., 2018). However, mahseer populations are threatened by overfishing (Nazarah et al., 2022), forest destruction, pollution, illegal gold mining activities, and land conversion (Dudgeon, 2011; Pinder & Raghavan, 2013). These anthropogenic factors not only disrupt habitat but also have the potential to cause population fragmentation and decreased genetic diversity.

One of the emerging approaches in aquatic resource management is genetically-based conservation. Genetic conservation aims to keep the genetic diversity of a species high to ensure its long-term survival (Fahmi, 2015; Yusron, 2005). Genetic diversity is the most basic level of biodiversity and an important foundation for species adaptation and survival. This study aims to analyze the genetic diversity and population structure of mahseer fish (*Tor tambra* and *T. tambroides*) in Jambi Province using Cytochrome Oxidase I (COI) gene markers through a DNA barcoding approach. With this approach, it is expected to identify the existence of genetic fragmentation due to environmental pressures and the potential location of population sources that have high genetic diversity.

The results of this study are expected to make a scientific contribution to genetically-based fisheries management in Indonesia, especially in formulating conservation strategies such as restocking, habitat corridor protection, and location-specific stock management units. Given the limited genetic data of mahseer in Jambi, this study also serves as an initial step for long-term monitoring of the genetic dynamics of the species in the future.

MATERIALS AND METHODS

This study was conducted at six mahseer fish habitat sites in Jambi Province from June to August 2024. The locations included (Figure 1) Batang Merao River (station 1), Tributaries of Batang Merangin River (Talang Kemulun, station 2), Upstream Batang Merangin (Pandan Island, station 3), Muara Hemat Market (station 4), Kerinci-Merangin District Border (station 5), and Masurai Valley (station 6).

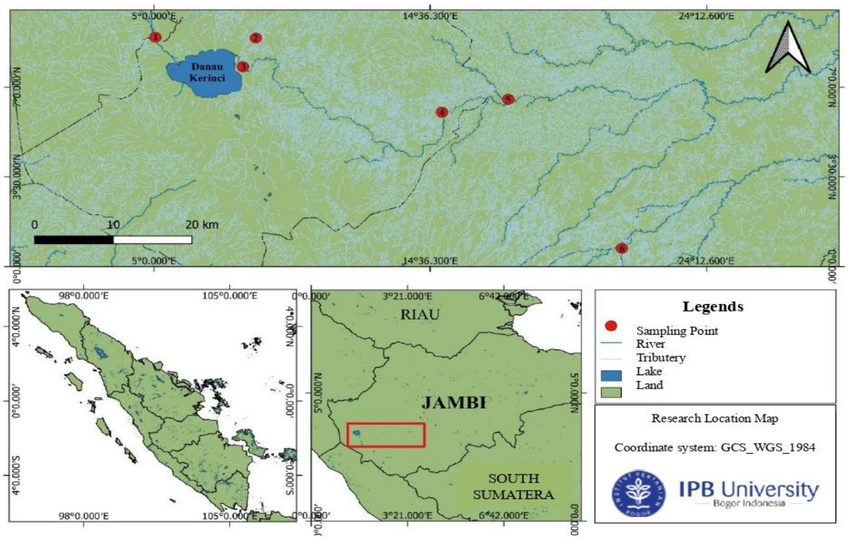

Figure 1. Fish sampling location

Site selection was done purposively based on the presence of natural mahseer habitat. A total of 18 mahseer fish individuals were captured with the help of local fishermen using gill nets, tight gill nets, and fishing rods. In addition, the research site, especially stations 3 and 4, has prohibited holes. The selection of research sites for station 5 is the river flow before the mine excavation and station 6, after the mine flow. However, at station 6 there are C excavation activities (sand and stone). Muscle samples were taken from near the dorsal fin (±30 mg), placed in microtubes containing 96% alcohol, labeled, and stored for molecular analysis. Molecular identification was carried out at the Integrated Basic Laboratory of Jambi University.

DNA Extraction and Cytochrome Oxidase I (COI) Gene Amplification

DNA was extracted using the Zymo Research Quick-DNA Miniprep Plus Kit method, then purified for further analysis. COI gene amplification was performed by PCR using FishF1/FishR1 primers. PCR conditions: initial denaturation at 95 °C (5 min), followed by 35 cycles (94 °C/30 s, 58 °C/30 s, 72 °C/1 min), and final elongation at 72 °C (10 min) (Sukmono et al., 2015). PCR products were validated by 2% agarose gel electrophoresis. Then, put it into the electrophoresis machine for 50 minutes. In making the agarose gel in the PCR quality test, redsafe is added as a dye to bind the nucleotide bases, so that when illumination uses UV, the table can be seen clearly and get good DNA quality. Each PCR reaction was accompanied by a negative control (no template DNA). Furthermore, visualization is done under UV light (100 V) to determine the success of cutting DNA bands. DNA that has good quality is sent to Fishbase/Genetica Science in Malaysia.

Habitat Survey and Water Quality

At each station, scoping of the inner and outer habitats will be conducted. The inside of the habitat is observed using a fish finder to track the presence of semah fish and measure the depth of the habitat. The outside of the habitat environmental conditions, and vegetation will be observed visually, and the coordinate points will be obtained with GPS. Habitat morphometric characters observed include river width with a range finder. Water quality is measured in-situ before fishing, including temperature and dissolved oxygen (DO), brightness, salinity, current velocity, and depth (Subagja & Marson, 2008).

Water samples were collected in 500 mL sample bottles and then tested for heavy metal content (Cd, Hg, Pb) at the Sungai Gelam Freshwater Aquaculture Center Laboratory in Jambi. In the study area, water quality is potentially affected by illegal gold mining (PETI) and the construction of the PLTA Kerinci Merangin Hydro. PETI in Jambi Province has expanded to approximately 52,059 ha and uses mercury, with some of its concentrations in water and sediments exceeding the KLHK quality standards. Meanwhile, PLTA Kerinci Merangin Hydro alters flow patterns and may increase sediment retention, thereby increasing the likelihood of heavy metal accumulation in water bodies. This situation underscores the importance of heavy metal analysis in this study to identify potential risks to the sustainability of semah fish (*Tor* spp.).

Data Analysis

Bioinformatic Analysis

DNA fragments that were successfully amplified were then sequenced. The sequences were aligned using the ClustalW method in MEGA X software. Validation was performed with BLASTn against the GenBank database (NCBI). Phylogeny was constructed using the Neighbor-Joining method with 1,000 bootstrap times.

Analysis of Genetic Diversity and Population Structure

Genetic diversity analysis was conducted by calculating haplotype diversity (Hd) and nucleotide diversity (π) using DnaSP 5.0 software (Rahayu et al., 2022). Population structure was analyzed using Fst values to measure genetic differentiation between stations, based on the Nei and Jin (1989) approach.

Habitat Survey and Water Quality Analysis

The water quality and habitat characteristic data that have been measured are then analyzed using the descriptive method, where the water quality samples studied are compared with previous research.

RESULTS

DNA amplification of the COI gene in *Tor tambra* and *T. tambroides* was successful, with strong bands observed across all 18 samples (Figure 2), indicating good DNA quality and high total DNA concentration. The sequences obtained ranged from 600 to 700 bp, and alignment with forward and reverse primers using MEGA 11 resulted in a final uniform length of 652 bp. Table 1 shows the results of uploading the nucleotide sequence of each mahseer fish sample to Genbank/NCBI, which showed that the mahseer fish samples were 99.56–99.85% close to the species *T. tambra* (accession number: NC_036511.1) and 98.51–99.70% to the species *T. tambroides* (accession numbers: KC905001.1 and KC905020.1).

The result of phylogeny tree analysis using MEGA 11 of mahseer fish (*T. tambra* and *T. Tambroides*) is shown in Figure 3. Table 2 shows the result of genetic diversity (haplotype and nucleotide diversity) of mahseer, while Table 3 shows the result of population structure analysis (Fst) of mahseer fish using DnaSP 5.0. software.

Table 1. BLAST process result of the mahseer fish

Sample ID	Species	Identify	Species on genbank
ISJ 1 ST. 1	*Tor tambra*	99.85%	NC_036511.1 (Tor tambra)
ISJ 1 ST. 2	*Tor tambra*	99.70%	NC_036511.1 (Tor tambra)
ISJ 2 ST. 2	*Tor tambra*	99.70%	NC_036511.1 (Tor tambra)
ISJ 3 ST. 2	*Tor tambroides*	99.55%	KC905001.1 (Tor tambroides)
ISJ 4 ST. 2	*Tor tambra*	99.56%	NC_036511.1 (Tor tambra)
ISJ 5 ST. 2	*Tor tambra*	99.70%	NC_036511.1 (Tor tambra)
ISJ 1 ST. 3	*Tor tambroides*	99.55%	KC905001.1 (Tor tambroides)
ISJ 2 ST. 3	*Tor tambroides*	99.25%	KC905001.1 (Tor tambroides)
ISJ 3 ST. 3	*Tor tambra*	99.85%	NC_036511.1 (Tor tambra)
ISJ 4 ST. 3	*Tor tambra*	99.56%	NC_036511.1 (Tor tambra)
ISJ 5 ST. 3	*Tor tambroides*	99.70%	KC905001.1 (Tor tambroides)
ISJ 1 ST. 4	*Tor tambroides*	98.81%	KC905020.1 (Tor tambroides)
ISJ 1 ST. 5	*Tor tambroides*	98.81%	KC905020.1 (Tor tambroides)
ISJ 1 ST. 6	*Tor tambroides*	98.51%	KC905020.1 (Tor tambroides)
ISJ 2 ST. 6	*Tor tambroides*	98.82%	KC905020.1 (Tor tambroides)
ISJ 3 ST. 6	*Tor tambra*	99.85%	NC_036511.1 (Tor tambra)
ISJ 4 ST. 6	*Tor tambra*	99.85%	NC_036511.1(Tor tambra)
ISJ 5 ST. 6	*Tor tambroides*	98.96%	KC905001.1 (Tor tambroides)

Table 2. Haplotype diversity analysis

Location	N	Hn	Hd	Π
Station 2	5	3	0.70000	0.01258
Station 3	5	4	0.90000	0.01840
Station 6	5	4	0.90000	0.01779
All Populations	15	11	0.86667	0.01724

Note: N= total sample; Hn= total *haplotype*; Hd= genetik diversity; π= nucleotide diversity

Table 3. Structure populations (Fst) analysis of mahseer fish

	Station 2	Station 3	Station 6
Station 2	-	0.109173	0.14063
Station 3		-	0.00338
Station 6			-

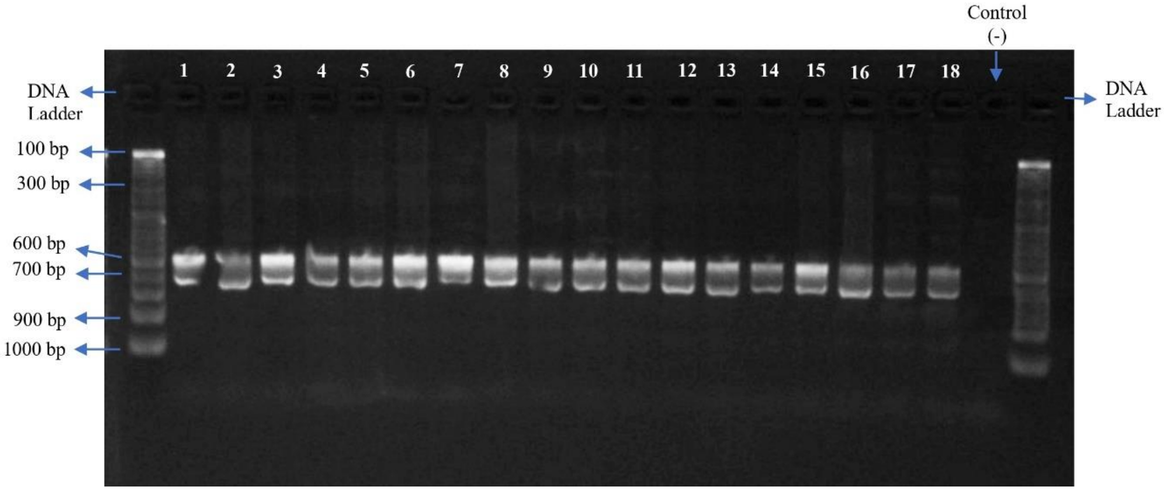

Figure 2. Results of Cytochrome Oxidase I (COI) gene amplification using DNA barcode primers FishF1 and FishR1 with 600 bp to 700 bp

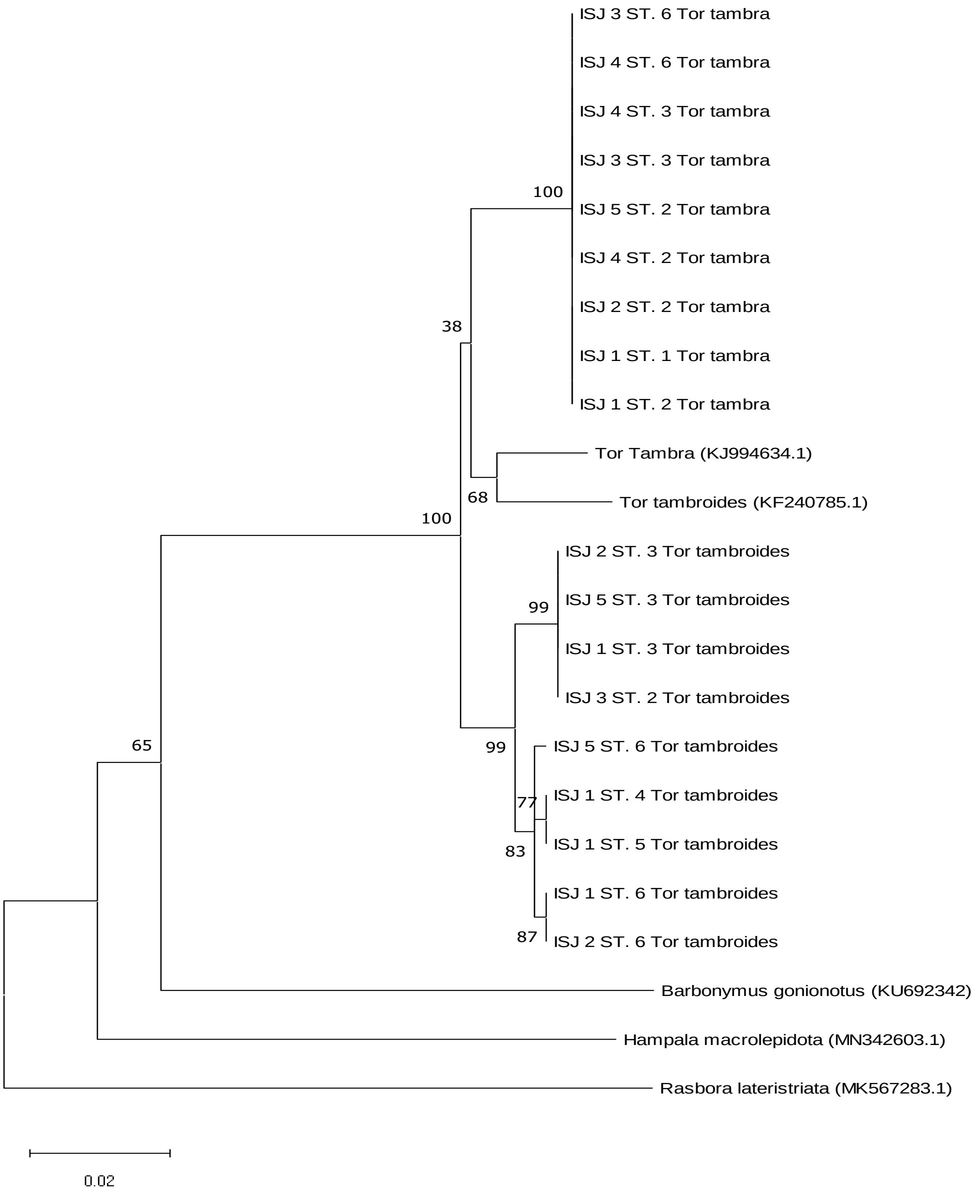

Figure 3. Phylogenetic tree of mahseer fish based on genetic distance from COI gene DNA sequences using the maximum likelihood method with 1,000× Bootstrap Kimura-2-parameter model

Based on observations (Table 5) and interviews with the community, it can be seen that the mahseer habitat has relatively the same water characteristics at each station, namely sandy and rocky with fast currents of 0.115–1.5 m/s. High brightness is characterized by a pH value of 6.93–8.60, a dissolved oxygen (DO) value that is also high, namely 3.2–12.2 mg/L, low water temperature 23.1–25.8 °C, and water brightness values ranging from 30–124 cm. The research site was subjected to rigorous measurement of heavy metal content, yielding the following results: a range of cadmium (Cd) 0.0491–0.0602 mg/L, mercury (Hg) 0.8770–1.0506 mg/L. However, lead (Pb) was not detected. The highest values were observed at station 2 (Talang Kemulun) for Cd and station 1 (Batang Merao River) for Hg.

Table 5. Observation of habitat characteristics and water quality parameters of the mahseer fish

Parameters	Observation station					
	Batang Merao River	Pandan Island	Talang Kemulun	Muara Hemat Market	Kerinci-Merangin Border	Masurai Valley
Temperature (°C)	24.30	25.80	23.10	24.80	23.10	23.80
pH	6.93	7.27	7.33	7.50	7.80	8.94
Brightness (cm)	41	92	50	57	124	30
DO (mg/L)	20.70	9.40	32.20	4.20	4	13.70
Current speed (m/s)	0.786	0.783	0.685	0.60	1.50	0.115
Depth (m)	7.01	2.50	1	4.20	3.60	5.60
River width (m)	13.80	23.50	4.50	48.60	32	19.30
Substrate character	Muddy, gravelly	Sandy, rocky	Sandy, rocky	Sandy, rocky	Sandy, rocky	Sandy, rocky
Weather	Overcast	Clear	Clear	Clear	Clear	Rain
Heavy metals						
Pb (lead) (mg/L)	Nd	Nd	Nd	Nd	Nd	Nd
Cd (cadmium) (mg/L)	0.0527	0.0555	0.0602	0.0585	0.0557	0.0491
Hg (mercury) (mg/L)	1.0506	0.8770	0.9683	0.9277	0.9516	0.9036

Note: Nd=not detected

DISCUSSION

The molecular validation results are in line with Muchlisin et al. (2021), which suggested that semah fish from Aceh showed 98–100% identification value as *Tor tambra* and *T. Tambroides*. These results indicate that the semah fish in the study site are *T. tambra* and *T. Tambroides* species because they have a distance difference of less than 3% (Hebert et al., 2003). Bootstrap or bootstrap value can be used as a benchmark in determining the level of confidence in phylogenetic tree construction. The higher the bootstrap value, the higher the confidence level of the phylogenetic tree construction results (Sahaba et al., 2021). Similar results were revealed by Jaafar et al. (2021), who based on the COX1 gene, *T. tambra* and *T. tambroides* ,Mahseer (*T. tambra* and *T. Tambroides*), which has a closer kinship with other species, can occur because mahseer and the three species have similarities in their habitat characteristics, namely liking swift, clear, high dissolved oxygen and sandy and rocky bottom waters. These results are in line with Muhtadi et al. (2017) *T. tambra* habitat is a shallower, swift-flowing river with rocky substrates. This is also in line with research findings showing that *T. tambra* is commonly found at stations 2 and 3 at depths ranging from 1 to 2.5 meters. Adaptation to environmental conditions allows phenotypic plasticity to occur (Pinder et al., 2019; Hoang et al., 2015). The significant difference between *T. tambra* and *T. tambroides* is the barbel and color. *T. tambra* has short barbel with olive or dark olive and reddish color while *T. tambroides* have long barbel with silver bronze, reddish and dark fin color (Jaafar et al., 2021).

The relatively high values of haplotype and nucleotide diversity in all populations indicate that there is considerable genetic variation. This variation can be influenced by environmental factors, the evolutionary history of the population, and the migration dynamics of individuals in the ecosystem (Sadler et al., 2023; Tamario et al., 2019). Previous studies have shown that high haplotype diversity is often associated with long-term population stability and adaptation to environmental change (Excoffier & Lischer, 2010).

Based on the genetic structure analysis, there was genetic differentiation between several populations in the study site, as indicated by the Fst value. The Fst values between station 2 and station 3 (0.109173) and between station 2 and station 6 (0.14063) indicate significant genetic differences, while the low Fst value between station 3 and Station 6 (0.00338) indicates high genetic similarity between these two populations. In the context of aquatic resource management, these results suggest that mahseer populations at station 2 experience higher genetic isolation compared to populations at stations 3 and 6. This genetic isolation can be caused by geographical factors, habitat fragmentation, or differences in environmental selection that occur at each location (Weeks et al., 2016). The high genetic differentiation at station 2 is likely due to geographical barriers and habitat fragmentation that limit gene flow, such as differences in river connectivity, water flow patterns, and physical barriers such as rapids or waterfalls. Additionally, differences in environmental conditions, such as water quality, substrate type, and riparian vegetation cover, may also act as selective pressures that reinforce this genetic divergence.

The high genetic similarity between station 3 and station 6 indicates better connectivity and greater opportunities for gene flow, possibly due to similar habitat characteristics at both locations. The clear differences between station 2 and the other stations confirm the role of spatial and ecological factors in shaping the population structure of mahseer. In the context of water resource management, these findings indicate that the population at station 2 requires special conservation attention due to its higher level of isolation, while the populations at stations 3 and 6 can be considered as more connected units. Therefore, a conservation strategy that considers these genetic differences is needed to avoid a decrease in genetic diversity due to inbreeding, which can reduce the population's resistance to environmental change and disease (Hohenlohe et al., 2021).

According to Wright (1978) and Hall (2022), Fst values between 0.05 and 0.15 indicate moderate genetic differentiation, while values below 0.05 indicate low genetic differences between populations. Fundamentally, the Fst value can be used as a basis for discussions regarding population differentiation within a species. This parameter can indicate whether a population has significant genetic differences that require separate conservation efforts, or conversely, has a high enough level of genetic similarity that it is possible to combine them under the same management strategy. Therefore, these results indicate that station 2 has greater genetic differences compared to station 3 and station 6, which may be due to geographic isolation or differences in environmental selection that can be used as a basis for restoration strategy or mahseer fish release. Previous studies have shown that populations with high genetic diversity have a greater chance of surviving under changing environmental conditions (Forester et al., 2018). Therefore, populations from stations 3 and 6 could be candidates for restocking programs to strengthen populations in other declining areas. These findings support the use of genetic information in defining stock management units (Lynch et al., 2016) and highlight the importance of site-specific conservation efforts based on genetic structure.

Mahseer habitat is known as fast-flowing rocky streams distinguished by crystal-clear freshwater and high oxygen levels. The mahseer’s habitat is defined by swift currents and fast-flowing water, rendering it an exceptional swimmer capable of navigating rapids with speeds of 20–25 knots (Abass et al., 2024). The result (Table 5) of this study is in line with Hendrik et al. (2021) where the water quality data revealed that the river is still normal and has not been polluted. The depth of the river ranged from 0.3–1.2m, very clear, the current speed ranged from 0.2–0.4 m/s, and the temperature ranged from 22–28 °C with rocky riverbed, gravel and sand. The highest temperature was recorded at Pulau Pandan station (25.8 °C) and the lowest at Talang Kemulun and the Kerinci-Merangin Border (23.1 °C). These temperature variations are influenced by factors such as depth, riparian vegetation cover, and solar intensity during measurements, where shallow and open waters tend to be warmer than deeper and sheltered waters.

The pH values at all stations were in the neutral to slightly alkaline range (6.93–8.94), which supports the metabolism of semah fish, in line with the ideal range according to Summerfelt (1998), which is 6.5–8.5. The highest turbidity was found at the Kerinci-Merangin Border (124 cm) and the lowest at the Masurai Valley (30 cm), influenced by turbidity, suspended particles, and rainfall (Effendi, 2003). DO values ranged from 4–32.2 mg/L, with high values in Talang Kemulun due to strong currents and intensive photosynthesis, while low values in Muara Hemat Market (4.2 mg/L) and the Kerinci-Merangin Border (4 mg/L) indicated high organic load (Summerfelt, 1998). Current speeds ranged from 0.115–1.5 m/s, with the highest currents at the Kerinci-Merangin Border and the lowest in the Masurai Valley. According to Kottelat et al. (1993), semah fish prefer moderate to strong currents, while slow currents can serve as feeding grounds for juveniles or other species. The substrate varies from muddy-gravelly to sandy-rocky, which is important as a spawning and feeding habitat for mahseer. Variations in environmental parameters such as current speed, bottom substrate, and dissolved oxygen levels can affect the genetic distribution of fish in different locations (Morrissey & de Kerckhove, 2009). Unfortunately, overfishing (Nazarah et al., 2022), forest destruction, water pollution, mining activities, water volume fluctuations, land transformation, and several anthropogenic factors can cause the decline of mahseer populations in their natural habitat (Dudgeon, 2011; Pinder & Raghavan, 2013; Andriyanto & Yulianti, 2020).

Heavy metal measurement results show that Pb was not detected at all stations (Nd). This is a positive indication because Pb is toxic to fish and humans if it accumulates in the food chain. Cd levels ranged from 0.0491 to 0.0602 mg/L, exceeding the Class I water quality standard threshold of 0.01 mg/L as specified in Government Regulation No. 22 of 2021. Although the levels are low, long-term exposure can cause chronic effects in fish and humans. Cadmium sources typically originate from industrial waste, phosphate fertilizers, or mining activities. Mercury concentrations at all stations were extremely high (0.8770–1.0506 mg/L), far exceeding the quality standard threshold (0.002 mg/L). These concentrations are dangerous because Hg easily undergoes biomagnification through the food chain (Boening, 2000). In the interior of Sumatra, the main source of Hg pollution is often associated with small-scale gold mining using mercury amalgamation (Rahmayani et al., 2014).

The alteration of habitats due to anthropogenic activities has been demonstrated to impede the genetic exchange between populations, thereby enhancing genetic isolation and reducing genetic diversity within a population (Su et al., 2021). A study by Yang et al. (2025) indicates that habitat connectivity plays a crucial role in maintaining genetic diversity, and the reduction of connectivity can result in an elevated risk of local extinction.

Although these results indicate the existence of genetic differentiation between populations, the limited number of samples (18 individuals) caused by limited access to locations and the low presence of the target population may affect the accuracy of genetic parameter estimates. This data remains relevant as an initial description of the genetic condition of mahseer populations in Jambi Province. Therefore, these results need to be interpreted carefully and confirmed through further studies with a wider range of samples and locations.

CONCLUSION

The results successfully analyzed the genetic diversity and population structure of mahseer fish (*Tor tambra* and *Tor tambroides*) in Jambi using COI gene markers. The study identified these species with high similarity to GenBank references and showed close kinship within the same family through phylogenetic analysis. The investigation revealed a high degree of genetic diversity, particularly at stations 3 and 6, suggesting the potential for population resilience. However, moderate genetic differentiation between station 2 and other sites indicated isolation due to habitat fragmentation. These results underscore the significance of genetically-based conservation strategies, such as critical habitat protection and restocking programs with diverse populations, which serve as a foundational step for long-term monitoring of mahseer genetic dynamics in the region.

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REFERENCES

Abass, Z., Shah, T. H., Bhaat, F. A., Ramteke, K., Magloo, A. H., Hamid, I., … Somasundharam, I. (2024). The mahseer: The tiger of water-an angler's delight in the Himalayas and the undisputed king of sport fishing. *Fisheries Research*, *279*, 0165-7836. doi: 10.1016/j.fishres.2024.107147.

Andriyanto., & Yulianti, E. (2020). Identifikasi bakteri probiotik pada saluran pencernaan ikan semah (*Tor* sp.). *Jurnal Pendidikan Biologi dan Sains*, *3*(2), 120-131.

Boening, D. W. (2000). Ecological effects, transport, and fate of mercury: A general review. *Chemosphere*, *40*(12), 1335-1351.

Dudgeon, D. (2011). Asian river fishes in the Anthropocene: Threats and conservation challenges in the era of rapid environmental change. *Journal of Fish Biology*, *79*, 1487-1524.

Effendi, H. (2003). *Telaah kualitas air: Bagi pengelolaan sumberdaya dan lingkungan perairan*. Yogyakarta: Kanisius.

Excoffier, L., & Lischer, H. E. L. (2010). Arlequin suite ver 3.5: A new series of programs to perform population genetics analyses under Linux and Windows. *Molecular Ecology Resources*, *10*(3), 564-567, doi: 10.1111/j.1755-0998.2010.02847.x.

Fahmi, M. R. (2015). Konservasi genetik ikan sidat tropis (*Anguilla* spp.) di Perairan Indonesia. *Jurnal Penelitian Perikanan Indonesia*, *21*(1), 45-54.

Forester, B. R., Lasky, J. R., Wagner, H. H., & Urban, D. L. (2018). Comparing methods for detecting multilocus adaptation with multivariate genotype-environment associations. *Molecular Ecology*, *27*(9), 2215-2233. doi: 10.1111/mec.14584.

Hall, S. J. G. (2022). Genetic differentiation among livestock breeds-values for Fst. *Animals*, *122*(1115), 1-19. doi: 10.3390/ani12091115.

Haser, T. K., Nurdin, M. H., Supriyono, E., Radona, D., Azmi, F., Nirmala, K., … Valentine, R. Y. (2021). Reproductive biology of mahseer (*Tor tambroides*) from Atu Suasah and Lawe Melang Rivers in Aceh Province to support sustainable fisheries management. *Pakistan Journal of Zoology*, *54*(2), 561-567.

Hebert, P. D. N., Ratnasingham, S., & deWaard, J. R. (2003). Barcoding animal life: Cytochrome c oxidase subunit 1 divergences among closely related species. *Proceedings of the Royal Society*, *270*(suppl. 1), 96-99. doi: 10.1098/rsbl.2003.0025.

Hendrik, H., Fauzi, M., Ramadona, T., Hendrizal, A., & Effendi, I. (2021). Local wisdom and conservation status of *Tor* Thai mahseer fish (*Tor tambroides* Blkr) in the Batang Haluan River, West Sumatra, Indonesia. *International Journal of Conservation Science*, *12*(4), 1547-1556.

Hoang, H. D., Pham, H. M., Durand, J. D., Tran, N. T., & Phan, P. D. (2015). Mahseers genus *Tor* and *Neolissochilus* (*Teleostei: Cyprinidae*) from Southern Vietnam. *Zootaxa*, *4006*, 551-568.

Hohenlohe, P. A., Funk, W. C., & Rajora, O. P. (2021). Population genomics for wildlife conservation and management. *Molecular Ecology*, *30*(1), 62-82. doi: 10.1111/mec.15720.

Jaafar, F., Na-Nakorn, U., Srisapoome, P., Amornsakun, T., Duong, T-Y., Gonzales-Plasus, M. M., … Parhar, I. S. (2021). A current update on the distribution, morphological features, and genetic identity of the Southeast Asian Mahseers, Tor species. *Biology*, *10*(286), 1-30.

Kottelat, M., Whitten, A. J., Kartikasari, S. N., & Wirjoatmodjo, S. (1993). *Freshwater fishes of Western Indonesia and Sulawesi*. Hong Kong: Periplus Editions.

Lynch, M. (2016). Mutation and human exceptionalism: Our future genetic load. *Genetics*, *202*(3), 869-875. doi: 10.1534/genetics.115.180471.

Morrissey, M. B., & de Kerckhove, D. T. (2009). The maintenance of genetic variation due to asymmetric gene flow in dendritic metapopulations. *American Naturalist*, *174*, 875-889. doi: 10.1086/648311.

Muhtadi, A., Dhuha, O. R., Desrita, D., Siregar, T., & Muammar, M. (2017). Kondisi habitat dan keragaman nekton di hulu Daerah Aliran Sungai Wampu, Kabupaten Langkat, Provinsi Sumatera Utara. *DEPIK Jurnal Ilmu-Ilmu Perairan, Pesisir dan Perikanan*, *6*(2), 90-99.

Muchlisin, Z. A., Nur, F. M., Maulida, S., Handayani, L. S., & Rahayu S. R. (2021). *Mahseer, the history of the king of the river*. Paper presented at The 10th International Conference on Multidisciplinary Research (ICMR) in conjunction with The 2nd International and National Symposium on Aquatic Environment and Fisheries (INSAEF). Retrieved from https://www.e3s-conferences.org/articles/e3sconf/abs/2022/06/e3sconf_10icmr-2insaef2022_03006/e3sconf_10icmr-2insaef2022_03006.html.

Nazarah, I., Akmal, Y., & Muliari, M. (2022). Morfologi neorocranium *Tor tambroides*, *Tor douronensis*, *Tor tambra*, dan *Tor soro*. *Jurnal Ilmiah Program Studi Perairan*, *4*(1), 61-68.

Nei, M., & Jin, L. (1989). Variances of the average numbers of nucleotides substitutions within and between populations. *Molecular Biology and Evolution*, *6*(3), 290-300. doi: 10.1093/oxfordjournals.molbev.a040547.

Pinder, A. C., & Raghavan, R. (2013). Conserving the endangered mahseers (*Tor* spp.) of India: The positive role of recreational fisheries. *Current Science*, *104*(11), 1472-1475.

Pinder, A. C., Britton, J. R., Harrison, A. J., Nautiyal, P., Bower, S. D., Cooke, S. J., … Ranjeet, K. (2019). Mahseer (*Tor* spp.) fishes of the world: Status, challenges and opportunities for conservation. *Reviews in Fish Biology and Fisheries*, *29*, 417-452. doi: 10.1007/s11160-019-09566-y.

Radona, D., Subagja, J., & Arifin, O. Z. (2015). Performa reproduksi induk dan pertumbuhan benih ikan *Tor* hasil persilangan (*Tor soro* dan *Tor douronensis*) secara resiprokal. *Jurnal Riset Akuakultur*, *10*(3), 335-343.

Rahayu, D. W., Nugroho, E. D., Azrianingsih, R., & Kurniawan, N. (2022). Molecular characterization of genus *Tor* from Indonesia based on 16S rRNA. *Edubiotik Jurnal Pendidikan Biologi Terapan*, *7*(01), 51-62.

Rahmayani, S., Rahmalia, S., & Dewi, Y. (2014). Kejadian penyakit kulit pada masyarakat pengguna air kuantan. *Jurnal Online Mahasiswa Program Studi Ilmu Keperawatan*, *1*(2), 1-8.

Sadler, D. E., Watts, P. C., & Uusi-Heikkila, S. (2023). The riddle of how fisheries influence genetic diversity. *Fishes*, *8*(510), 1-14, doi: 10.3390/fishes8100510.

Sahaba, M. A. B., Abdullah, A., & Nugraha, R. (2021). DNA barcoding untuk autentikasi produk hiu segar dari Perairan Nusa Tenggara Barat. *Indonesian Journal of Aquatic Product Technology*, *24*(3), 425-432.

Su, G., Logez, M., Xu, J., Tao, S., Villéger, S., & Brosse, S. (2021). Human impacts on global freshwater fish biodiversity. *Science*, *376*(6589), 1155-1159. doi: 10.1126/science.abd3369.

Subagja., & Marson. (2008). Identifikasi dan habitat ikan semah (*Tor* sp.) di Sungai Lematang, Sumatera Selatan. *BAWAL*, *2*(3), 113-116.

Sudarmaji, S. (2016). Teknik pembenihan ikan *Tor soro*, *Tor douronensis*, dan persilangannya. *Buletin Teknik Litkayasa Akuakultur*, *13*(2), 83-86.

Summerfelt, R. C. (1998). Water quality considerations for aquaculture. United States: Department of Animal Ecology, Iowa State University.

Sukmono, T., Duryadi, D., Rahardjo, M. F., & Affandi, R. (2015). Fish diversity of the *Cyprinidae* family based on DNA barcodes in Harapan Rainforest, Jambi. Paper presented at The First International Conference on Life Science and Biotechnology (ICoLIB) (pp. 134-138), Jember University. Retrieved from https://repository.unja.ac.id/48427/.

Syaiful, A. (2017). Lubuk Larangan sebagai bentuk kearifan lokal di Kabupaten Bungo. Paper presented at the Prosiding Simposium Nasional Ikan dan Perikanan Perairan Daratan, Masyarakat Iktiologi Indonesia.

Tamario, C., Sunde, J., Peterson, E., Tibblin, P., & Forsman, A. (2019). Ecological and evolutionary consequences of environmental change and management actions for migrating fish. *Frontiers*, *7*(271), 1-24.

Weeks, A. R., Stoklosa, J., & Hoffmann, A. A. (2016). Conservation of genetic uniqueness of populations may increase extinction likelihood of endangered species: The case of Australian mammals. *Frontiers in Zoology*, *13*(31). doi: 10.1186/s12983-016-0163-z.

Wright, S. (1978). *Evolution and the genetics of populations, volume 4: Variability within and among natural populations*. Chicago: University of Chicago Press.

Yanto, H. (2016). Kebutuhan vitamin c dalam pakan dan pengaruhnya terhadap peningkatan vitalitas dan pertumbuhan benih ikan semah (*Tor douronensis*) selama domestikasi. *Jurnal Akuatik Indonesia*, *1*(2),130-139.

Yang, C., Qi, Y., Guo, J., Peng, L., Xiong, N., Zhang, W., & Zhao, W. (2025). Habitat fragmentation increases the risk of local extinction of small reptiles: A case study on *Phrynocephalus przewalskii*. *Ecotoxicology and Environmental Safety*, *290*, 1-10.

Yusrizal, A., Ilham, Z., & Rahardjo, M. F. (2018). Morfologi tulang anggota gerak (ossaappendicularis) ikan keureling, *Tor tambroides* (Bleeker, 1854). *Jurnal Iktiologi Indonesia*, *18*(3), 261-274.

Yusron, E. (2005). Pemanfaatan keragaman genetik dalam pengelolaan sumberdaya hayati laut. *Oseana*, *30*(2), 29-34.