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(RESEARCH ARTICLE)

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Genetic Diversity of *Perca fluviatilis* Across Turkish Lakes and Dams

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Abstract

This study aimed to investigate the genetic diversity, phylogenetic relationships, and oxidative stress responses of *Perca fluviatilis* populations collected from 12 lakes and dams across different regions of Turkey. Molecular characterization was performed using four ISSR markers, yielding 100 scorable bands, 68% of which were polymorphic. Cluster analyses (UPGMA) and Principal Component Analysis (PCA) revealed three main genetic groups, with the Adana population showing significant isolation and genetic differentiation from other populations. Mitochondrial DNA analyses targeting *ATP6* and *cytb* gene regions confirmed species identity and demonstrated limited intraspecific variation, while closely related species (*P. schrenkii and P. flavescens*) formed distinct clades. Overall, this study provides comprehensive insights into the genetic and physiological diversity of *P. fluviatilis* populations in Turkey and emphasizes the importance of combined molecular approaches for sustainable management and conservation of perch fish populations.

Keywords: *ATP6* Gene; *cytb* Gene; Environmental Adaptation; Mitochondrial DNA; ISSR Analysis

1. Introduction

The European perch (*Perca fluviatilis* L.) is a medium-sized freshwater fish species within the family *Percidae* (McDowall 1996). The taxonomic history of the species dates back to the early 18th century, when it was initially described from Swedish lakes by Peter Artedi in 1730 and subsequently incorporated into the formal binomial nomenclature by Carl Linnaeus in 1758, largely on the basis of Artedi's pioneering ichthyological work (Thorpe 1977; Pimakhin et al. 2015). The family *Percidae* represents a diverse taxonomic group, currently comprising 10 genera and approximately 195 species distributed across Eurasia and North America (Berra 2001). Fossil evidence suggests that the evolutionary origin of the genus *Perca* can be traced back to the early Miocene, around 19.8 million years ago, indicating a long adaptive history within freshwater ecosystems (Stepien et al. 2015).

Due to its broad geographic distribution, high ecological plasticity, and significant role in both recreational fisheries and aquaculture, *P. fluviatilis* has been the focus of a substantial body of scientific literature (Pimakhin et al. 2015). Research has addressed various aspects of its physiology, growth performance, feeding ecology, and aquaculture potential, reflecting the species' economic and ecological importance. However, despite this extensive interest, detailed and integrative studies that specifically investigate the biology, ecology, and adaptive mechanisms of the species across different environments remain relatively limited. Such comprehensive investigations are critical not only for enhancing our fundamental understanding of *P. fluviatilis*, but also for identifying existing knowledge gaps, addressing methodological constraints, and clarifying the ecological drivers underlying its wide distribution across diverse freshwater habitats. Moreover, improved insights into the species' ecological interactions and environmental tolerances would contribute to more sustainable management strategies in both natural populations and aquaculture systems.

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Geographic variation in genetic traits has been documented across the distribution range of *P. fluviatilis* (Nesbo et al. 1999; Vanina et al. 2019). For instance, Nesbø et al. (1999) investigated genetic variation in 55 European populations and one Siberian population using mitochondrial DNA (*mtDNA*) D-loop sequencing and RAPD markers. Their results revealed high levels of genetic differentiation among watersheds and regions, suggesting that present-day populations in Western and Northern Europe originated from three main refugia: Northeastern Europe, Southeastern Europe, and Western Europe. Similarly, Vanina et al. (2019) analyzed genetic diversity in perch populations from Poland, the Czech Republic, and Slovakia using four mitochondrial markers and found significant genetic differentiation among populations, with the Polish population being particularly distinct.

These genetic differences are often associated with phenotypic variation among geographically distinct populations (Mandiki et al. 2004; Mélard et al. 2004; Vanina et al. 2019). For example, Mélard et al. (2004) compared growth performance under controlled experimental conditions and demonstrated that fish originating from northeastern France exhibited 76% higher body weight at day 200 compared with those from northern Italy, while Belgian populations outperformed southwestern French populations by 56%. Likewise, Mandiki et al. (2004) observed differences in growth rates and survival among European perch populations, with southern European populations showing the lowest growth potential and survival. However, it is important to note that the association between genetic and phenotypic divergence does not necessarily imply causation, as phenotypic plasticity may play a significant role in shaping observed patterns (Bergek and Björklund 2009).

Genetic markers are fundamental tools for assessing genetic diversity in fish populations (Rashed et al. 2008) and a wide range of other organisms. Among these, inter simple sequence repeat (ISSR) markers represent a dominant, polymorphic, rapid, and relatively cost-effective molecular marker system based on the amplification of DNA regions between microsatellite loci. ISSR markers have proven to be effective for evaluating the genetic structure of fish, providing valuable insights into species identification, genetic diversity assessment, population structure analysis, and breeding programs. Integrating such molecular techniques into the management of both wild and cultured fish stocks contributes to evidence-based decision-making processes (Saad et al. 2009). In this method, short primers complementary to microsatellite regions are employed in polymerase chain reaction (PCR) amplification, and the resulting banding patterns are analyzed to reveal genetic variation among individuals (Zietkiewicz et al. 1994; Pradeep Reddy et al. 2002; Maltagliati et al. 2006). ISSR markers have been widely applied to investigate genetic diversity, population structure, phylogenetic relationships, and geographic differentiation in fish species. This approach is particularly relevant for the conservation of natural stocks, taxonomic classification, and fisheries management (Elsayed et al. 2024; Khandanizadeh et al. 2025; Song et al. 2025).

The present study aims to investigate the genetic diversity and physiological responses of *P. fluviatilis* populations across various lakes and dams in Türkiye. Genetic diversity and population structure are assessed using Inter-Simple Sequence Repeat (ISSR) markers, while mitochondrial DNA regions (*ATP6* and *cytb*) are analyzed to elucidate phylogenetic relationships and species-level genetic homogeneity. By integrating molecular approaches, this study aims to provide comprehensive insights into the effects of geographic distribution and habitat-related stressors on the genetic and physiological health of perch populations, contributing to their sustainable management and conservation.

2. Materials and methods

2.1. Materials

Fish samples were collected from twelve different perch bodies in Türkiye, including Darıderesi Dam (Isparta), Yedikır Dam Lake (Amasya), Ürkmez Dam (İzmir), Tahtalı Dam (İzmir), Seyhan Dam (Adana), Şeyitler Dam (Afyon), Denizli Pond (Kocaeli), Karaağaç Pond (Uşak), Hirfanlı Dam (Kırşehir), Çamlıdere Dam (Ankara), Altınapa Dam (Konya), and Ladik Lake (Samsun). Sampling was carried out using gill nets with a mesh size of 4 mm. From each location, 25 individuals were obtained, resulting in a total of 300 specimens used in the study.

2.2. Methods

2.2.1. Phylogenetic Analysis and Molecular Characterization

Genomic DNA was extracted from caudal fin tissues using the Thermo Scientific GeneJET Genomic DNA Purification Kit (Catalog No: K0721), following the manufacturer's protocol optimized for this study. The quality and integrity of the extracted DNA were verified by electrophoresis on 2% agarose gels. Polymerase chain reaction (PCR) amplifications were performed using protocols and primers previously described by Ragauskas et al. (2023), Bachevskaya et al. (2023), and Alyamkin et al. (2022). Detailed PCR conditions and the list of primers employed in the study are presented

in Table 1 and Table 2. PCR products producing single, correctly sized bands were purified using the GenElute™ PCR Clean-Up Kit (SIGMA, Catalog No: NA1020) following the manufacturer's instructions. Purified products were re-checked on 2% agarose gels to ensure the absence of nonspecific bands or primer dimers before sequencing. Sequencing was performed by Olygomer Biotechnology A.Ş. The resulting sequences were processed using Sequencher 4.5, with forward and reverse reads aligned and manually corrected to generate consensus sequences for the *mtDNA ATP6* and *cytb* regions. Sequences were converted to FASTA format and aligned using MEGA 6.0 (Tamura, 2013). BLAST searches against the NCBI database confirmed sequence accuracy. Phylogenetic relationships and genetic distances among populations were inferred using the Neighbor-Joining method in MEGA 6.0, and nucleotide composition was calculated for each population.

For molecular characterization, PCR products were loaded on 2% agarose gels and electrophoresed at 80 V for 120 min, followed by visualization under a UV imaging system. Band presence or absence was scored to generate a binary (1–0) matrix, and similarity indices were calculated using the Dice coefficient. Cluster analysis was then performed using the Unweighted Pair-Group Method with Arithmetic Mean (UPGMA) in NTSYS software version 2.02 (Rohlf 1997), and dendrograms were constructed to illustrate genetic relationships among populations.

Table 1 ISSR markers used in molecular characterization

Primer Name	Primer Sequence	PCR Content	PCR amplification	
UBC-807	$(AG)_8T$	5 µL Genomic DNA, 1 µL primers, 5 µL Master mix (PZR buffer, 2mM $MgCl_2$, 250 µM dNTP, 0.75 U Taq DNA polymerase) ve 13 µL dH_2O. (Total 25 µL)	95°C/2 min (Initial denaturation 1 cycle)	
UBC-808	$(AG)_8C$		94°C/30 sec 47–53°C/45 sec 72°C/45 sec	(35 cycle)
UBC-809	$(AG)_8G$		72°C/5 min (Final extension: 1 cycle)	
UBC-823	$(TC)_8C$			

Table 2 Primers used to obtain *mtDNA* sequences

Primer Name	Primer Sequence	PCR Content	PCR amplification	
mtDNA ATP6	F: 5'-CCTAACGAGCCTACATCCC-3' R: 5'-TGTAAGAGGTCAAGGGCTGG-3'	5 µL Genomic DNA, 1 µL primers, 5 µL Master mix (PZR buffer, 2mM $MgCl_2$, 250 µM dNTP, 0.75 U Taq DNA polymerase) ve 13 µL dH_2O. (Total 25 µL)	95°C/2 min (Initial denaturation 1 cycle)	
mtDNA cytb	F: 5'-GTCATAATTCCTGCCAGGATTTTAACCAGG-3' R: 5'-TTTAGAATCCTAGCTTTGGGAGTTAGGGG-3'		94°C/30 sec 47–53°C/45 sec 72°C/45 sec	(35 cycle)

3. Results and Discussion

In this study, genetic variation data obtained from ISSR (Inter-Simple Sequence Repeat) analyses of perch samples collected from 12 different lakes and dams located in various geographical regions of Turkey were subjected to cluster analysis using the UPGMA (Unweighted Pair Group Method with Arithmetic Mean) method, and the results are presented in Figure 1. Molecular analyses performed with a total of four ISSR markers yielded 100 scorable bands, of which 68 were polymorphic and 32 were monomorphic, corresponding to a polymorphism rate of 68%. The obtained banding patterns revealed a clear level of genetic differentiation among the populations. According to the generated dendrogram, the samples were grouped based on genetic similarity coefficients, resulting in two main clusters. The first cluster consisted of a sub-cluster including Afyon (Şeyitler Dam), Uşak (Karaağaç Pond), and Isparta (Darıderesi Dam) populations, and another sub-cluster comprising Samsun (Ladik Lake), Amasya (Yedikır Dam Lake), and Kocaeli (Denizli Pond) populations. Two different sampling sites within İzmir (Tahtalı and Ürkmez dams) were positioned as the closest group to this cluster. This indicates that fish populations in these regions exhibit relatively closer genetic structures, likely attributable to similar environmental conditions or gene flow. The second major cluster included

populations from Konya (Altınapa Dam), Ankara (Çamlıdere Dam), Kırşehir (Hirfanlı Dam), and Adana (Seyhan Dam). Individuals in this group exhibited greater genetic distances from the other populations. In particular, the Adana population displayed the farthest genetic distance on the dendrogram, suggesting that these samples represent a more isolated population structure and are markedly differentiated from other groups in terms of genetic variation.

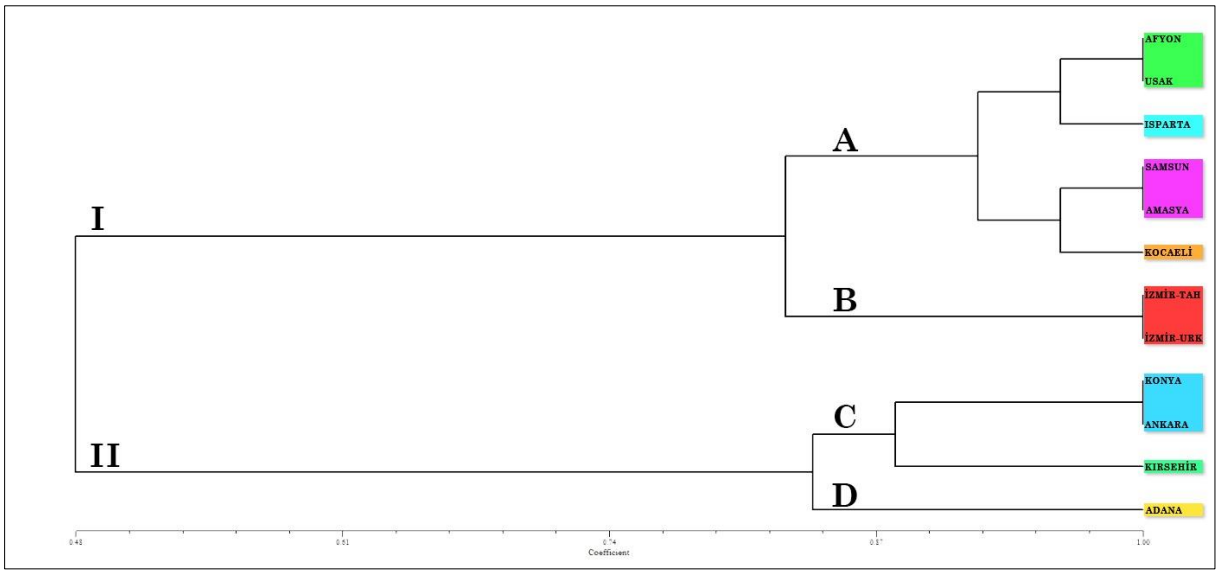

Figure 1 ISSR-based genetic similarity dendrogram of perch populations

In addition, the two-dimensional plot obtained from Principal Component Analysis (PCA) (Figure 2) was largely consistent with the dendrogram. In the PCA, populations from Afyon, Uşak, Isparta, Samsun, Amasya, and Kocaeli clustered closely in the same direction, confirming their high genetic similarity. The İzmir-Tahtalı and İzmir-Ürkmez populations were again grouped together and distinctly separated from the other populations. Konya, Ankara, Kırşehir, and Adana populations were positioned on the positive side of the PCA axis, apart from the other groups. Notably, the Adana population appeared even more distant, indicating as in the dendrogram that it possesses a more isolated and divergent genetic structure. Both analyses consistently revealed three main clusters: Group 1 (Afyon, Uşak, Isparta, Samsun, Amasya, Kocaeli), Group 2 (İzmir-Tahtalı and İzmir-Ürkmez), and Group 3 (Konya, Ankara, Kırşehir, and partly Adana). These findings suggest that genetic diversity among populations may be associated with geographical distribution, with particularly pronounced differences observed between populations from İzmir and the Central Anatolia region.

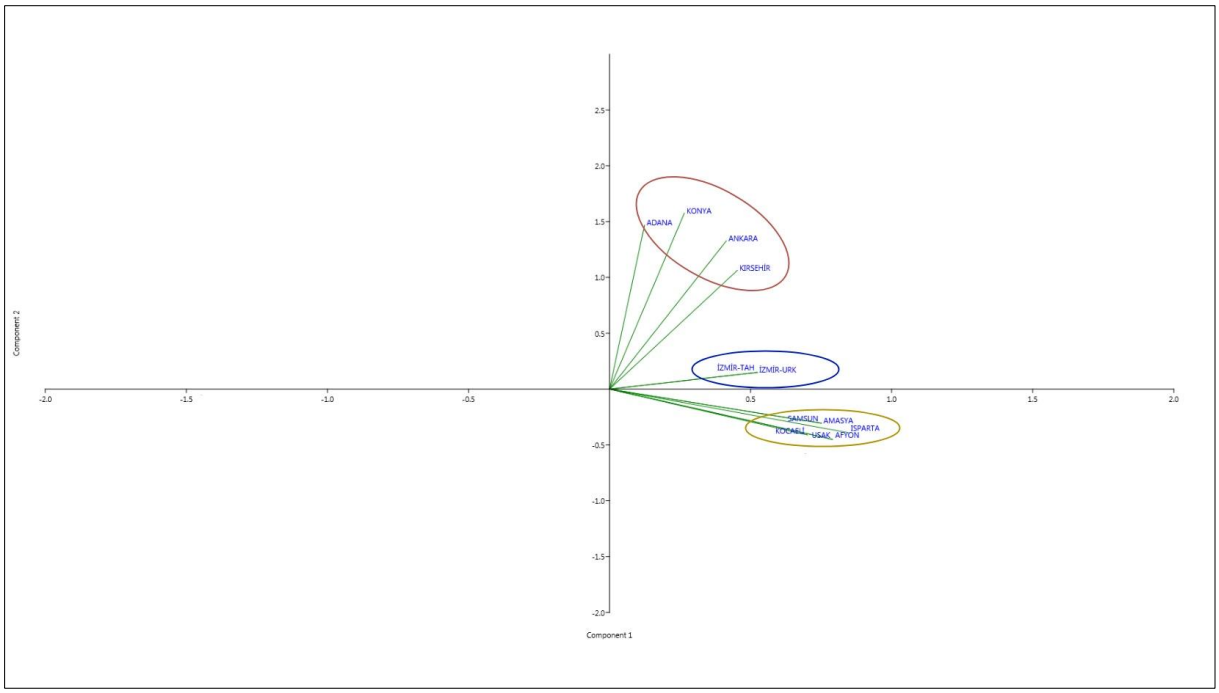

Figure 2 PCA analysis of perch populations based on ISSR data

The genetic similarity matrix based on ISSR markers is presented in Table 3. The results revealed a significant level of genetic variation among perch populations. Examination of the distance matrix showed that the genetically closest populations were Afyon–Uşak and İzmir-Tahtalı–İzmir-Ürkmez, both with 100% similarity. This indicates that fish populations from these locations share a high degree of genetic similarity, likely reflecting development under comparable environmental conditions without substantial genetic isolation.

Moreover, the Afyon, Uşak, Isparta, and Samsun populations also displayed high similarity (≥92%), and these groups were clustered within the same main branch of the dendrogram. Notably, Afyon–Samsun and Uşak–Amasya populations exhibited 92% similarity, suggesting that despite their geographical distance, their genetic structures remain alike. This could be attributed to inter-population gene flow, human-mediated translocation, or the influence of similar environmental stress factors.

In contrast, the Adana population emerged as one of the most genetically distinct, both in the distance matrix and in the dendrogram analysis. Its similarity with Kırşehir was 76%, whereas with Afyon it was only 40%. This suggests that the Adana population represents a genetically isolated group that may have undergone a process of regional adaptation. Additionally, Konya and Ankara populations exhibited 100% similarity and clustered within the same sub-group, implying either extensive genetic exchange or a shared origin. Similarly, the İzmir-Tahtalı and İzmir-Ürkmez populations showed completely overlapping genetic profiles, reflecting a common genetic pool.

In conclusion, the ISSR marker-based genetic similarity analysis demonstrated that *P. fluviatilis* populations from different geographical regions of Türkiye harbor substantial genetic diversity.

Table 3 Genetic similarity matrix based on ISSR markers

	AFYON	**KONYA**	**ISPARTA**	**SAMSUN**	**ANKARA**	**İZMİR-TAH**	**İZMİR-URK**	**USAK**	**KIRSEHİR**	**KOCAELİ**	**ADANA**	**AMASYA**
AFYON	1.00											
KONYA	0.44	1.00										
ISPARTA	0.96	0.48	1.00									
SAMSUN	0.92	0.52	0.96	1.00								
ANKARA	0.44	1.00	0.48	0.52	1.00							
İZMİR-TAH	0.88	0.48	0.84	0.80	0.48	1.00						
İZMİR-URK	0.88	0.48	0.84	0.80	0.48	1.00	1.00					
USAK	1.00	0.44	0.96	0.92	0.44	0.88	0.88	1.00				
KIRSEHİR	0.48	0.88	0.52	0.56	0.88	0.52	0.52	0.48	1.00			
KOCAELİ	0.88	0.48	0.92	0.96	0.48	0.76	0.76	0.88	0.52	1.00		
ADANA	0.40	0.88	0.44	0.48	0.88	0.44	0.44	0.40	0.76	0.52	1.00	
AMASYA	0.92	0.52	0.96	1.00	0.52	0.80	0.80	0.92	0.56	0.96	0.48	1.00

In this study, various molecular analyses were conducted to reveal the phylogenetic relationships and nucleotide compositions of the *mtDNA ATP6* gene region of the samples. For this purpose, considering the molecular characterization results, the sampling locations were grouped into four main regions, and one province was selected from each region. Sequences of the *mtDNA ATP6* gene region were obtained from these samples, and comparative gene sequences of different species were retrieved from NCBI to construct a phylogenetic tree. The aim was to elucidate the phylogenetic relationship between perch and other species. The process of obtaining and analyzing DNA sequences was carried out as follows:

First, the sequencing of DNA isolated from the samples was performed by a commercial service provider, Oligomer Biotechnology Inc. The obtained sequence data were analyzed using Sequencher 4.5 software, where forward and reverse primer sequences for each sample were assembled. Reading errors and low-quality regions were manually corrected based on chromatogram inspection, and contig sequences were generated. In this way, clean and reliable *ATP6* gene region sequences were obtained for each sample. The sequences were then converted into FASTA format using Microsoft Office Word and prepared for phylogenetic analyses.

Sequence alignment was performed with MEGA 6.0 software (Tamura 2013), and the aligned sequences were compared with the NCBI database using BLAST analysis to verify sequence accuracy and similarity levels. For phylogenetic inference, Neighbor-Joining (NJ) trees were constructed in MEGA 6.0, and genetic distance matrices among species were calculated. This approach enabled the identification of evolutionary relationships among the samples and the interpretation of intra- and interspecific genetic similarities. In addition, nucleotide compositions of the species were determined from the aligned sequences. According to the base composition analysis of the *ATP6* gene region, the average proportions were calculated as thymine (T) 24.2%, cytosine (C) 13.5%, adenine (A) 30.4%, and guanine (G) 31.9% (Table 4). Overall, a high degree of homogeneity in base composition was observed among the samples, indicating that the *ATP6* gene region is highly conserved structurally across the analyzed species.

Table 4 Nucleotide composition of the *mtDNA ATP6* gene

Samples	T(U)	C	A	G	Total
ADANA	24.2	13.6	30.4	31.8	727.0
İZMİR	24.5	13.5	29.8	32.2	621.0
AFYON	24.1	13.5	30.7	31.8	721.0
KONYA	24.1	13.5	30.6	31.7	725.0
Average	24.2	13.5	30.4	31.9	698.5

Furthermore, phylogenetic analyses were performed using *mtDNA ATP6* gene region sequences isolated from *Perca fluviatilis* individuals. The obtained sequences were analyzed in MEGA 6.0 software using the Maximum Likelihood (ML) algorithm, and both intraspecific variations and interspecific evolutionary relationships were examined. The results showed that the four samples included in this study (ADANA, İZMİR-TAH, KONYA, and AFYON) clustered within the same clade together with *P. fluviatilis* reference sequences retrieved from GenBank, displaying high levels of similarity. Notably, the ADANA, İZMİR-TAH, and KONYA samples clustered on the same branch with GenBank references *OQ676940.1, OQ676941.1*, and *OQ676945.1*, supported by bootstrap values ranging from 62% to 100%, strongly confirming that these samples belong genetically to the *P. fluviatilis* species.

The topology of the phylogenetic tree revealed that the examined individuals were highly similar to each other as well as to the database-derived *P. fluviatilis* sequences, indicating limited intraspecific genetic diversity. This finding highlights the effectiveness of the *ATP6* gene region in resolving phylogenetic relationships at the intraspecific level. Additionally, closely related species, *P. schrenkii* and *P. flavescens*, formed a distinct clade positioned in close proximity to each other, supported by a bootstrap value of 89%, suggesting that these species may have diverged from a common ancestor. *Sander lucioperca* was used as an outgroup and, as expected, was placed in a separate clade from the other species (Figure 3).

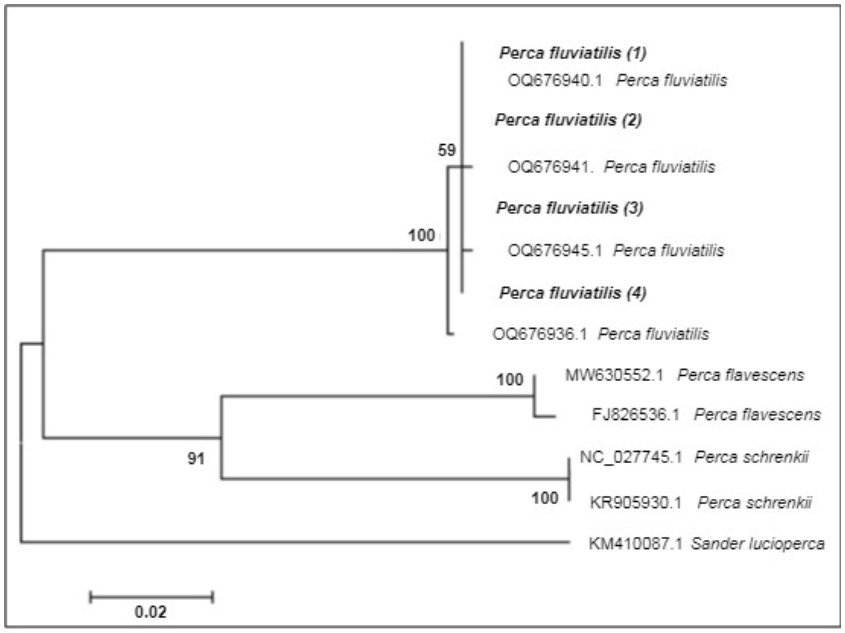

Figure 3 Phylogenetic tree of *mtDNA ATP6* gene sequences obtained from individuals of the perch species (1: Seyhan Dam- ADANA, 2: Tahtalı Dam- İZMİR, 3: Altınapa Dam- KONYA (Gene region sequence could not be obtained), 4: Şeyitler Dam- AFYON)

In this study, *mtDNA cytb* (cytochrome b) gene region sequences isolated from *P. fluviatilis* individuals were analyzed to determine the intraspecific base composition. The obtained sequence data were aligned using MEGA 6.0 software, and nucleotide frequencies were subsequently calculated. For three different samples (ADANA, İZMİR-TAH, and AFYON), the average nucleotide composition of the *cytb* gene region was determined as thymine (T) 30.9%, cytosine (C) 30.4%, adenine (A) 24.0%, and guanine (G) 14.8% (Table 5). This distribution indicates that thymine and cytosine are predominant in the *cytb* region, whereas guanine content is considerably low. These findings demonstrate that the *mtDNA cytb* gene region is characterized by A+T richness and a relatively low G+C ratio. Moreover, the overall consistency of base proportions among samples suggests that the level of intraspecific genetic variation is limited.

Table 5 Nucleotide composition of the *mtDNA cytb* gene

Samples	T(U)	C	A	G	Total
ADANA	31.0	29.7	24.0	15.2	938.0
İZMİR	30.6	30.1	24.5	14.8	1003.0
AFYON	31.2	31.9	22.9	14.0	520.0
Average	30.9	30.4	24.0	14.8	820.3

Phylogenetic analyses based on *mtDNA cytb* (cytochrome b) genes are widely recognized as an important tool for understanding evolutionary relationships among species and for conducting molecular-level taxonomic classification. In this context, *cytb* gene region sequences isolated from *P. fluviatilis* individuals were used to construct a phylogenetic tree (Figure 4). The analyses were performed using the Maximum Likelihood (ML) method under the Tamura-Nei model, which accounts for different rates of transition and transversion substitutions, thereby providing a more realistic modeling of nucleotide replacements.

In the ML tree, the three analyzed samples (ADANA, İZMİR-TAH, and AFYON) clustered within the same clade with high bootstrap support values, confirming their close genetic similarity and suggesting that they likely originate from the same or geographically related populations. Bootstrap values shown on the branches represent the statistical confidence levels of the inferred relationships; values above 70% indicate strong support, while those above 90% suggest highly reliable evolutionary relationships. Accordingly, the high bootstrap values observed for the *cytb* sequences analyzed here demonstrate the robustness of the phylogenetic structure and the accuracy of the classification.

The clustering pattern further indicates that genetic variation within *P. fluviatilis* is limited, implying that the *cytb* region may have restricted power for resolving intraspecific variation. However, it remains a highly reliable molecular marker for species identification. The observed homogeneity may also reflect the fact that the analyzed individuals originate from the same geographical population. When reference sequences from closely related taxa such as *P. schrenkii* and *P. flavescens* were included, *P. fluviatilis* samples were clearly separated into a distinct clade. This separation supports the ability of the *cytb* gene to resolve interspecific evolutionary differences while simultaneously confirming intraspecific homogeneity. The outgroup species (*Sander lucioperca*) was positioned in a clearly distinct clade, as expected, reflecting its more distant evolutionary lineage within Percidae.

Molecular markers are widely recognized as essential tools in fish population genetics for elucidating genetic diversity and evolutionary relationships. Okumuş and Çiftçi (2003) emphasized that each marker type, including allozymes, microsatellites, RAPD, AFLP, *mtDNA*, and nuclear DNA markers, possesses specific advantages and limitations, with varying resolution capacities in detecting genetic variation. In particular, microsatellites are considered highly effective in detecting intraspecific variation due to their high polymorphism, while ISSR markers have been demonstrated to be powerful for assessing both environmental adaptations and inter-population differentiation (Zhigileva et al. 2013; Zhigileva et al. 2022; Alyamkin et al. 2022).

The results of the present study based on ISSR markers revealed a high level of genetic diversity within *P. fluviatilis* populations in Türkiye. Of the 100 scorable bands obtained, 68 were polymorphic, corresponding to a polymorphism rate of 68%, thereby confirming the discriminative power of ISSR markers. Comparable findings were reported by Liu et al. (2006) in *Paralichthys olivaceus*, Maltagliati et al. (2006) in Cyprinodontiform fishes, and Mohammadabadi et al. (2017) in *Poecilia reticulata*, where ISSR markers successfully detected high levels of polymorphism and genetic variability. Thus, the findings of the present study align with previous reports and demonstrate the efficiency of ISSR markers in revealing genetic variation in perch populations.

The dendrogram and PCA analyses clearly indicated inter-population differentiation, with the Adana Seyhan Dam population being genetically distinct from the others. This divergence can likely be attributed to isolation and limited gene flow. Similar patterns have been documented by Wawrzyniak et al. (2020), who reported environmentally driven genetic differentiation among perch populations in Poland, and by Vanina et al. (2019), who identified significant genetic distinctiveness of the Polish population compared with others. Furthermore, Hai Sa et al. (2012) revealed low genetic diversity in wild populations from Xinjiang, China, while Ragauskas et al. (2023) found low-to-moderate variability in Baltic Sea perch populations, associating differentiation with geographic isolation, habitat changes, and anthropogenic impacts. The genetic separation of the Adana population observed in the present study is therefore consistent with these earlier findings.

Interestingly, the İzmir-Tahtalı and İzmir-Ürkmez populations exhibited 100% similarity, suggesting that environmental similarities in these habitats may be directly reflected in their genetic structure. Michel et al. (2009) previously identified habitat-based clustering in perch populations, a pattern also corroborated by our results, which indicate that habitat isolation plays a key role in shaping population genetic structure.

At the interspecific level, *mtDNA*-based studies within the Percidae family have provided important insights into phylogenetic relationships. Sloss et al. (2004), using *cytb* and 16S rRNA sequences, revealed phylogenetic patterns that partly conflicted with traditional morphological classifications, suggesting the need for taxonomic re-evaluation in certain groups. Similarly, Nesbo et al. (1999) reported high levels of genetic differentiation among populations sampled from Europe and Siberia. In our study, *cytb* sequence analyses confirmed the genetic homogeneity of *P. fluviatilis* populations, while clearly distinguishing them from closely related species. This supports the utility of the *cytb* gene as a robust molecular marker for resolving interspecific evolutionary relationships.

Overall, the combined evidence from ISSR and *mtDNA* analyses suggests that the genetic diversity of *P. fluviatilis* populations in Türkiye is shaped by habitat isolation, geographic distance, and environmental factors. These results are consistent with previous studies (Hai Sa et al. 2012; Vanina et al. 2019; Wawrzyniak et al. 2020; Ragauskas et al. 2023) and highlight the importance of genetic monitoring for the conservation and sustainable management of perch populations.

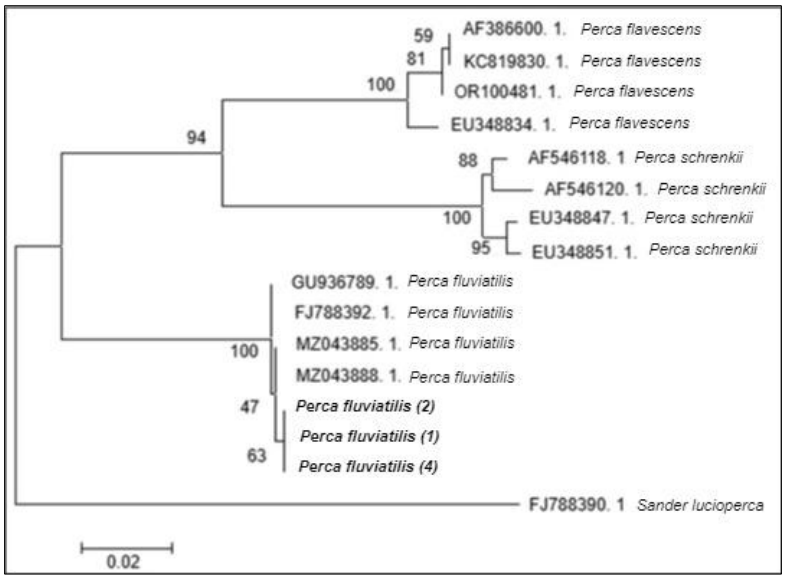

Figure 4 Phylogenetic tree of *mtDNA cytb* gene sequences obtained from individuals of the perch species (1: Seyhan Dam- ADANA, 2: Tahtalı Dam- İZMİR, 3: Altınapa Dam- KONYA (Gene region sequence could not be obtained), 4: Şeyitler Dam- AFYON)

4. Conclusion

The integrated analysis of molecular characterization, phylogenetic relationships in *P. fluviatilis* populations from different lakes and dams in Turkey reveals a clear link between genetic diversity, environmental conditions, and physiological responses. ISSR marker analyses demonstrated considerable genetic variation among populations, with the Adana population showing notable isolation and distinctiveness, corroborated by PCA and UPGMA clustering. *mtDNA* analyses (*ATP6* and *cytb*) confirmed species identity and indicated limited intra-species genetic variation, while also resolving inter-species relationships with close relatives such as *P. schrenkii* and *P. flavescens*. Collectively, these findings suggest that environmental factories not only shape the physiological structure but may also interact with genetic structure, highlighting the adaptive mechanisms of *P. fluviatilis* populations. This integrative approach underscores the importance of combining molecular assessment for the conservation, management, and ecological evaluation of perch populations.

Compliance with ethical standards

Disclosure of conflict of interest

The authors declare that they have no conflicts of interest.

Author contribution

KA and İD have obtained specimens. KA and İD performed the experiments and analysed the data. KA and İD drafted and revised the manuscript.

Data availability

The datasets generated during or analysed during the current study are available from the corresponding author upon reasonable request.

Declarations

The research was approved by the Local Ethics Committee for Aquatic Vertebrate Experiments of Isparta University of Applied Sciences with the decision number 003 dated 22 May 2025 and the number E-90006624-804 -18721.

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