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# Morphometric and meristic differentiations of *Garra turcica* (Karaman, 1971) from the various branch of the Ceyhan River System, Türkiye

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**A B S T R A C T**

This study was conducted to determine metric and meristic differentiations of *Garra turcica* (Karaman, 1971) inhabiting different branches of the Ceyhan River System. Individuals sampled from 13 branches of the Ceyhan River System were examined for 11 metric and 8 meristic traits. Principal Component Analysis (PCA) and Linear Discriminant Function Analysis (LDFA) identified both for metric and meristic traits among the different branches of Ceyhan River system. SIMPER (Similarity Percentage) test showed that the most important contributions to this differentiation from metric measurements were caudal peduncle length (71.50%), dorsal fin height (8.04%) and body depth (5.23%), and from meristic traits were scales on lateral line (41.65%), scales above lateral line (20.09%) and pectoral fin rays (8.55%). It is known that, in inland waters, compared to marine areas, the rate of genetic and morphological differentiation is higher for closer geographical areas, especially due to the inability to migrate and environmental factors. However, it remains a question that needs to be answered as to why the metric and meristic features determined for this species are the ones that are the most influential in the differentiation. In addition, it should be investigated whether the morphological differentiation detected in the current study also occurs at the genetic level. In this case, it may be possible to define a subspecies for this species.

## INTRODUCTION

According to Menon (1964) and Goren and Ortal (1999), the *Garra* genus is reported to have spread from the Himalayas to the west and east. *Garra rufa*, on the other hand, is of Asian origin and is distributed throughout all of south western Asia, Africa, and Southeast Asia (Goren and Ortal, 1999). Geldiay and Balık (2009) report that there are two species of *Garra* genus in Türkiye: *G. rufa* and *Garra variabilis*. Recent studies in Türkiye have indicated that *G. caudomaculata* is an endemic species of the Asi River, *Garra culiciphaga* is found in the Seyhan, Ceyhan, and Asi River systems, and *G. turcica* is a synonym for *G. rufa* (Bayçelebi, 2020; Kara, 2023). In addition, the presence of endemic species such as *Garra kemali* and *Garra menderesensis* has been reported in Türkiye (Çiçek et al., 2018). *G. rufa* is distributed in the Aras River, Tigris-Euphrates system, Ceyhan and Seyhan river basins and Iran (Geldiay and Balık, 2009; Koyun, 2011; Kara and Can, 2023). It is reported that *G. rufa* individuals are found in the Ceyhan River system and they have a wide range of habitats from 126 m to 1233 m altitude (Kara and Alp, 2005; Kara et al., 2010). These fish are used for the treatment of some skin diseases (Psoriasis) in the "Balıklı Kaplıca" in Kangal district of Sivas (Demirci at al., 2016). Moreover, they are also demanded in the aquarium fish sector because they eat the algae that form in the aquarium environment (Aydın and Akman, 2020). *G. turcica* was reported by Karaman (1971) as a subspecies of *G. rufa* from the Ceyhan River due to its morphological differences.

Later, it was evaluated as a synonim of *G. rufa* by various researchers (Krupp, 1985; Bostancı, 2006; Ergüden and Göksu, 2012). Bayçelebi et al. (2018) redefined *G. turcica*, stating that it differs not only morphologically but also at the molecular level. According to this definition, it is distinguished from *G. rufa* by having a thinner body, a blunt snout and a generally short rostral head (Bayçelebi et al., 2018). *G. turcica* is found in benthopleagic, non-migratory, slow-flowing rivers, small pools and lakes, and in ecosystems with stony, gravelly, sandy and muddy bottoms (Krupp and Schneider, 1989). This species has a high tolerance to environmental conditions, capable of thriving in a wide temperature range and easily adapting to anthropogenically modified habitats (Çiçek et al., 2021). This environmental resilience of *G. turcica* is an important characteristic, both ecologically and for biodiversity studies. However, the variations of this species in different river systems and the underlying causes of these variations have not yet been sufficiently researched.

Morphometric and meristic variations, when the same species displays different characteristics in different river branches, are crucial for understanding these variations and evaluating the taxonomic and ecological relationships of the species. These variations can arise due to various factors such as genetic drift, natural selection, environmental factors, migration, and hybridization (Sing et al., 2021). Identifying these variations is an important step in understanding the status of the species' populations in local ecosystems, and such knowledge plays a critical role in the conservation of local biodiversity. In this context, studying the differences in the morphometric and meristic characteristics of *G. turcica* populations across different branches of the Ceyhan River system will provide important data for the development of conservation strategies for this species.

The aim of this study is to identify the morphometric and meristic differences among *G. turcica* populations in the different river branches of the Ceyhan River System. The methodological approaches used in this study will facilitate a better understanding of the taxonomic relationships and ecological differences between species. This research includes statistical analyses, particularly Principal Component Analysis (PCA) and Linear Discriminant Function Analysis (LDFA), to better understand the differences between river populations. These methods aim to deeply analyze the data and reveal the morphological and genetic differences of the species. Furthermore, this methodological approach is of great importance for regional biodiversity studies, as it will help in understanding the effects of environmental and genetic factors on variations between species.

## MATERIAL AND METHODS

### Sample Collections

This study was conducted on *G. turcica* (Figure 1) found in 13 streams (Figure 2, Table 1) located in the middle and upper Ceyhan River basin between April 2014 and May 2016. The body of *G. turcica* individuals is roundish and covered with large scales. The snout is blunt and the mouth is ventrally positioned and crescent-shaped. There are two pairs of very short barbels around the mouth. The dorsal fin starts in front of the ventral fin and has a straight free margin. There is a well-developed sucker attached to the lower lip. The color is usually brown with irregular light black markings (Figure 1). A total of 90 specimen were caught by electroshocking were brought to the laboratory in plastic containers containing 4% formaldehyde. The sampled fish number and total fish length ranges were given by river branches in Table 1. As explained in statistical analysis section, to enhance sample size and to explain variability more reasonable, a principal component analysis-PCA was applied to data, resulting to grouping of river branches.

**Figure 1.** An original photograph of *G. turcica* from studied area, Hemite Stream (Total length: 10.60 cm).

**Table 1.** River branches where samples were taken and their grouping according to PCA.

| River branch | Code | No. | Total length range (mm) | Sample Groups |
|---|---|---|---|---|
| Körsulu Stream | KO | 13 | (70.80-130.40) | Group-1 N= 23 |
| Pörnek Stream | PO | 10 | (70.80-120.80) | |
| Fırnız Stream | FI | 6 | (99.41-126.24) | Group-2 N=18 |
| Zeytin Stream | ZE | 6 | (66.43-122.26) | |
| Hemite Stream | HE | 6 | (45.65-120.80) | |
| Aksu Stream | AK | 8 | (98.57-125.85) | Group-3 N= 22 |
| Karasu Stream | KA | 5 | (63.85-113.75) | |
| Yarpuz Stream | YA | 4 | (99.11-123.93) | |
| İmalı Stream | IM | 5 | (84.79-109.36) | |
| Sabun Stream | SA | 5 | (92.55-108.32) | Group-4 N=27 |
| Savrun Stream | SAV | 8 | (95.31-126.25) | |
| Afşin-Yazıdere Stream | AFYD | 7 | (64.46-95.90) | |
| Homzan Stream | HO | 7 | (66.25-92.83) | |

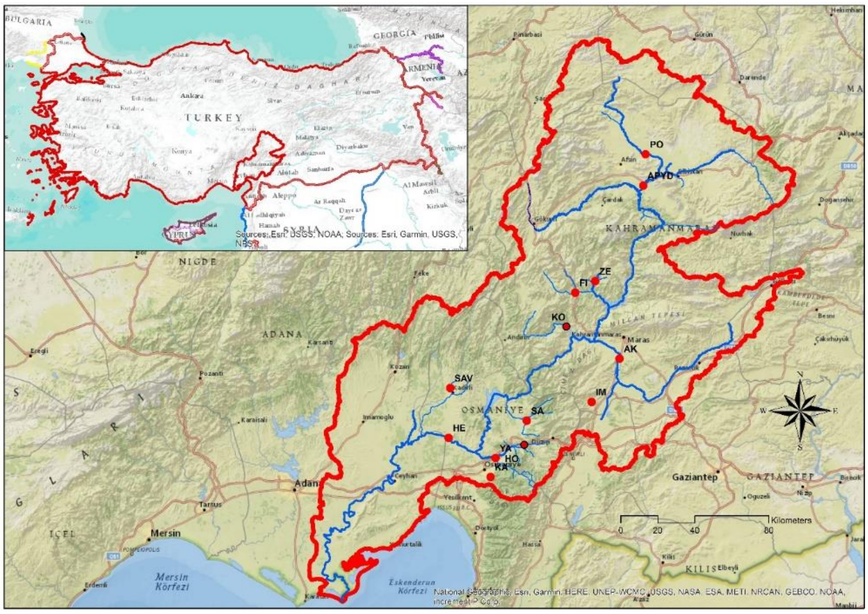


**Figure 2.** Sample sites with coodinates [Körsulu Stream (KO: 36° 38' 35.34'' E, 37° 37' 47.72'' N), Pörnek (PO: 37° 01' 55.62'' E, 38° 17' 37.92'' N), Fırnız Stream (FI: 36° 41' 18.48''E, 37° 45' 19.55''N), Zeytin Stream (ZE: 36° 46' 44.75''E, 37° 48' 22.20''N), Hemite Stream (HE: 36° 04' 22.50''E, 37° 11' 52.81''N), Aksu Stream (AK: 36° 54' 24''E, 37° 30 15''N), Karasu Stream (KA: 36° 16' 37''E, 37° 02' 50.82''N), Yarpuz Stream (YA: 36° 17' 45''E, 37° 07' 11''N), İmalı Stream (IM: 36° 17' 45''E, 37° 07' 11''N), Sabun Stream (SA: 36° 27' 29''E, 37° 15' 40''N), Afşin-Yazıdere Stream (AFYD: 37° 00' 34.04''E, 38° 10' 9.40''N), Homzan Stream (HO: 37° 26' 21.21''E, 37° 10' 26.17''N)].

**Morphometric and Meristic Traits**

In the laboratory, a total of 11 morphometric measurements and 8 meristic counts were recorded for each fish (Table 2). Morphometric measurements were taken from the left lateral aspect, and measured to the nearest 0.1 mm using a digital caliper. All meristic characters were counted twice on the same day by the same observer.

**Statistical Analysis**

Because fish have allometric growth, a common problem with morphometric data is that all measurements are highly correlated with length. In order to analyze the shape of the fish regardless of size, the size factor must be removed from the data. One of the most accurate ways to do this is to use Burnaby's (1966) method (Klingenberg, 1996). In this study total length (TL) was considered as size factor to be transformation base to other morphometric characters. Prior to transformation, almost all of the morphometric characters showed high correlations with total length (TL), whereas after transformation all the characters showed non-significant relationship with TL (Table 3).

**Table 2.** Morphometric and meristic traits of *G. turcica* used in this study.

| Traits | Description | Acronym |
|---|---|---|
| **Morphometric measurements:** | | |
| Total length | Tip of the upper jaw to the caudal end of the caudal fin | TL |
| Snout length | From symphysis of premaxilla to osseous orbit margin | SL |
| Caudal peduncle length | From end of anal fin to middle base of caudal fin | CPL |
| Dorsal fin height | From base to tip of longest ray | DFH |
| Orbital horizontal diameter | Between osseous orbital margin | OHD |
| Dorsal fin length | From base to tip of longest ray | DFL |
| Head length | From upper jaw symphysis to posterior tip of operculum | HL |
| Head depth | Just posterior to orbit | HD |
| Caudal peduncle depth | The minimum depth of the caudal peduncle | CPD |
| Predorsal length | Front of the upper lip to the origin of the dorsal fin | Pre-DL |
| Body depth | The maximal depth of the body | BD |
| **Meristic counts:** | | |
| Pectoral fin rays | Number of thorns in the pectoral fin | PcFR |
| Radius pectoral fin | Number of cartilages found in the space between thorns in the pectoral fin | RPcF |
| Radius anal fin | Number of cartilages found in the space between thorns in the anal fin | RAF |
| Radius dorsal fin | Number of cartilages found in the space between thorns in the dorsal fin | RDF |
| Radius ventral fin | Number of cartilages found in the space between thorns in the ventral fin | RVF |
| Scales on lateral line | Number of scales on the lateral line | SLL |
| Scales above lateral line | Number of scales above the lateral line | SALL |
| Scales below lateral line | Number of scales below the lateral line | SBLL |

**Table 3.** Correlation coefficients between total length (TL) and each of the other morphometric characters, r(TL~), prior and after transformation.

| Morphometric character | Prior to transformation r(TL~) | After transformation r(TL~) |
|---|---|---|
| BD | 0.909 | 0.000 |
| HL | 0.970 | 0.000 |
| OHD | 0.869 | 0.000 |
| SL | 0.752 | 0.000 |
| DFL | 0.923 | 0.000 |
| DFH | 0.882 | 0.000 |
| Pre-DL | 0.978 | 0.000 |
| CPL | 0.745 | 0.000 |
| HD | 0.955 | 0.000 |
| CPD | 0.959 | 0.000 |

Morphometric traits are continuous and more susceptible to the environmentally induced variability, while meristic traits are discrete and fixed early in development. Therefore, separate statistical analyses were conducted on morphometric (continuous) and meristic (discrete) data. All statistical analyses were performed for combined sexes since all morphometric measurements were transformed and the effect of size removed (Simon et al., 2010). Cross-correlations between transformed meristic and non-transformed metric traits, and also, each of distribution of individual trait were given in Figure 3.

Although 13 streams tributaries were sampled in the research, as can be seen in Table 1, the sample size does not seem to be sufficient for statistical evaluation at each river branches. Therefore, with the PCA analysis based on metric and meristic properties, the sample points were brought together into 4 groups (Figure 4) based on a combination of explained variance, Scree plot, and Eigenvalue approaches (Larose, 2015) (Table 4)

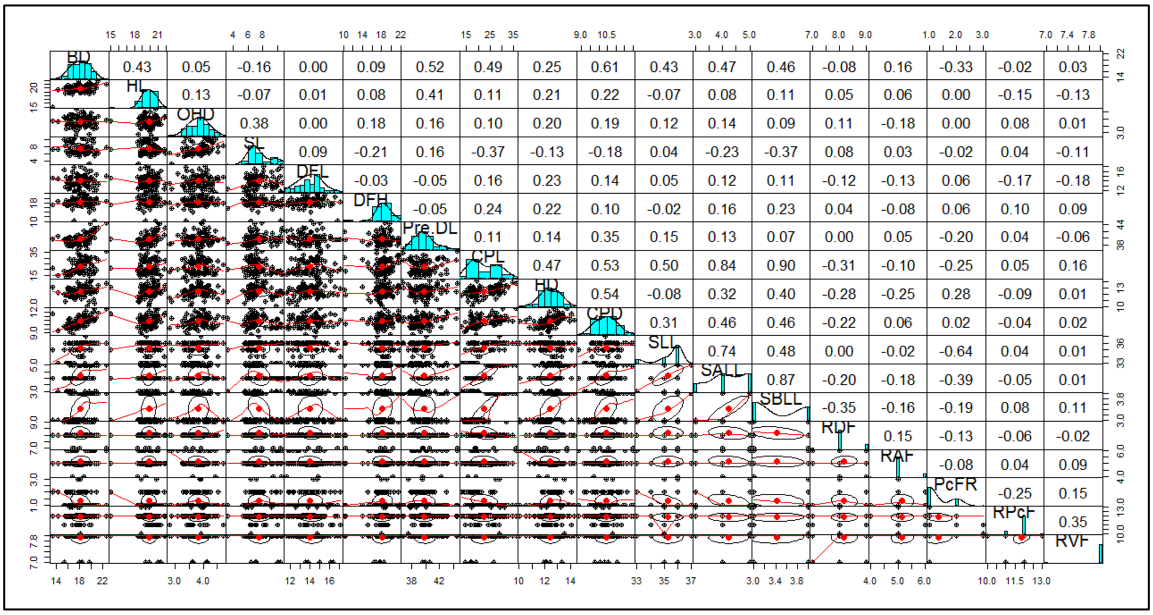


**Figure 3.** Distribution of each trait and cross-correlations between transformed meristic and non-transformed metric traits

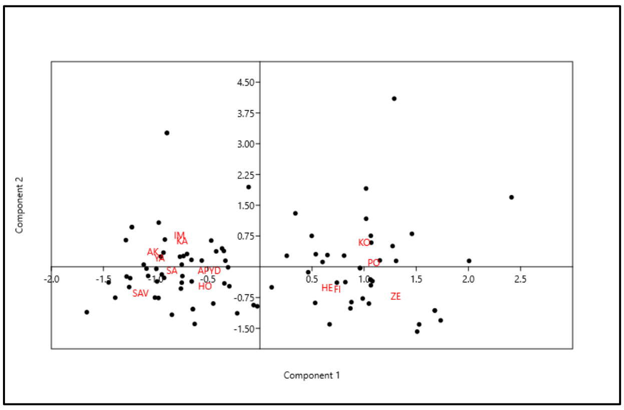


**Figure 4**. Allocation of river branches based on the PCA

**Table 4.** Eigenvalues, explained variances, and cumulative variance by each component resulted from PCA.

| PC | Eigenvalue | Variance, % | Cumulative variance, % |
|---|---|---|---|
| 1 | 33.70 | 71.11 | 71.11 |
| 2 | 4.33 | 9.13 | 80.23 |
| 3 | 3.63 | 7.65 | 87.89 |
| 4 | 2.05 | 4.33 | 92.21 |
| 5 | 1.38 | 2.91 | 95.13 |
| 6 | 0.95 | 2.01 | 97.14 |
| 7 | 0.63 | 1.32 | 98.46 |
| 8 | 0.49 | 1.03 | 99.49 |
| 9 | 0.15 | 0.33 | 99.82 |
| 10 | 0.08 | 0.18 | 100.00 |

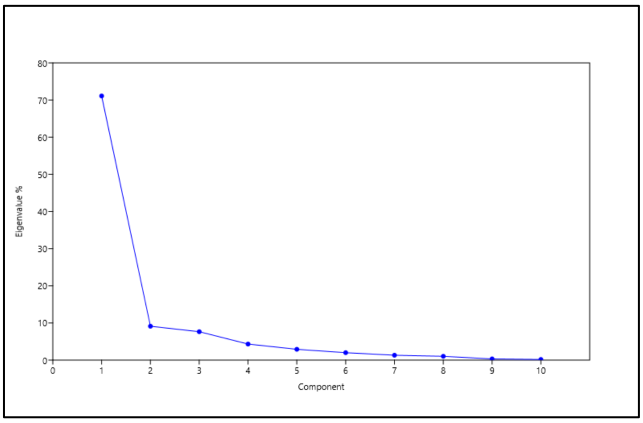


**Figure 5.** Scree plot from Principal Component Analysis

After the transformation (only for morphometric characters) and PCA, Discriminant Function Analysis (DFA) and SIMPER (Similarity Percentage) and were carried out on the data, respectively. Discriminant analysis is a statistical tool that is specifically designed to detect differences between two or more groups (Xanthopoulos et al., 2013). Therefore, it was applied to compute the classification success the grouping of river branches by PCA, based on confusion matrix. SIMPER (Similarity Percentage) was used for assessing which characters are primarily responsible for an observed difference between groups of samples quantitatively (Clarke, 1993).

All calculations and statistical analysis were conducted using MS Excel, PAST software (Hammer et al. 2001) and R (R Core Team, 2021).

## RESULTS

### Morphometric Traits

Percentage separations of four groups achieved by the first discriminant function (ld1) was 79.30%, second (ld2) was 18.74%, and third (ld3) was 1.96%. Stacked histograms of morphometric traits for ld1 discriminant function by groups were given in Figure 6. It's clearly evident that no overlaps between second and third, and between second and fourth, and between first and third groups. But some overlap observed between the first and fourth groups. In general, supporting to the PCA results, four groups can be identified from DFA. But histogram based on lda2 showed almost overlapping of each of groups with other (Figure 7).

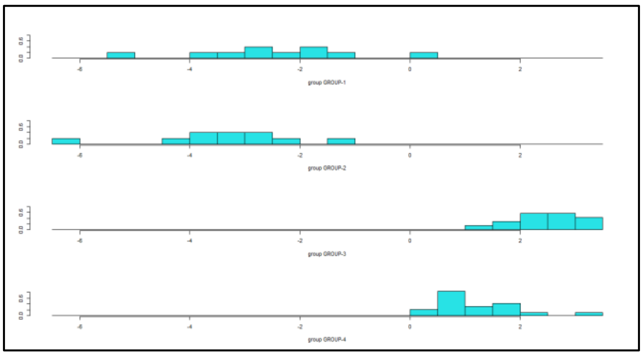

**Figure 6.** Stacked histograms based on ld1discriminant function

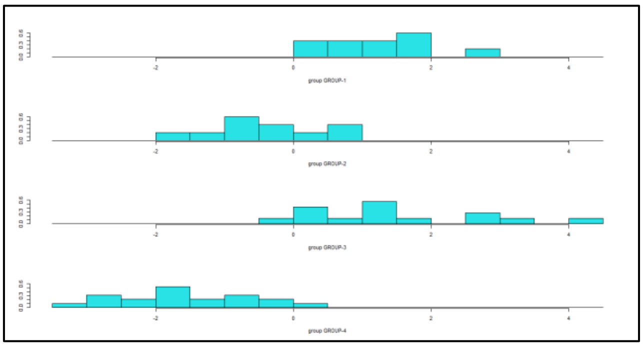

**Figure 7.** Stacked histograms based on ld2 discriminant function

In Figure 8, the placement of the groups according to the first and second discriminate functions based on linear DFA and the most morphometric features that affect the differentiation of the groups from each other were given as biplot vector vectors. The most important three traits leading to differentiation were caudal peduncle length-CPL (71.50%), dorsal fin height-DFH (8.04%) and body depth-BD (5.23%) (Figure 8 and Table 5).

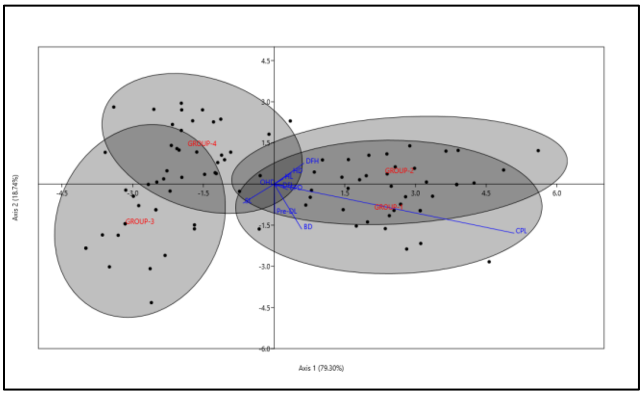

**Figure 8.** Four groups with 95 % confidence limits in ellipse form. Axis-1(ld1) and Axis-2 (ld2) explained 98.04 % of total variation based on the DFA for metric traits.

**Table 5.** Detailed SIMPER analysis results (Average dissimilarity, individual contribution, and cumulative contribution), based on Euclidean distance measure, of each morphometric traits to differentiation among groups.

| Morphometric trait | Av. dissim | Contrib. % | Cumulative % |
|---|---|---|---|
| CPL | 81.17 | 71.50 | 71.50 |
| DFH | 9.12 | 8.04 | 79.54 |
| BD | 5.94 | 5.23 | 84.77 |
| Pre-DL | 5.14 | 4.52 | 89.30 |
| SL | 4.79 | 4.21 | 93.51 |
| DFL | 3.10 | 2.73 | 96.24 |
| HL | 1.76 | 1.55 | 97.79 |
| HD | 1.40 | 1.23 | 99.02 |
| CPD | 0.84 | 0.74 | 99.76 |
| OHD | 0.27 | 0.24 | 100.00 |

For meristic traits, the DFA managed to assign correctly 87.78% of the fish to the groups after cross-validation. The high classification success provides support for the metric traits differences between the groups (Table 6).

**Table 6.** Classification results (confusion matrix) of discriminant function with 87.78 % success for metric traits

| | Group-2 | Group-1 | Group-3 | Group-4 | Total |
|---|---|---|---|---|---|
| Group-2 | 17 | 1 | 0 | 0 | 18 |
| Group-1 | 6 | 16 | 1 | 0 | 23 |
| Group-3 | 0 | 0 | 20 | 2 | 22 |
| Group-4 | 0 | 0 | 1 | 26 | 27 |
| **Total** | **23** | **17** | **22** | **28** | **90** |

**Meristic traits**

The first (ld1), second (ld2), and third (ld3) discriminant functions explained the separations between groups as 91.18%, 6.75%, and 2.07%, respectively. Stacked histograms based on ld1 and ld2 for groups were given in Figure 9 and Figure 10. Considering the ld1 discriminant function, there were exact differentiation between first and third, and between first and fourth groups, and in some degree but not clear between second and fourth groups. However, the histograms of each group based on lda2 overlapped on each other.

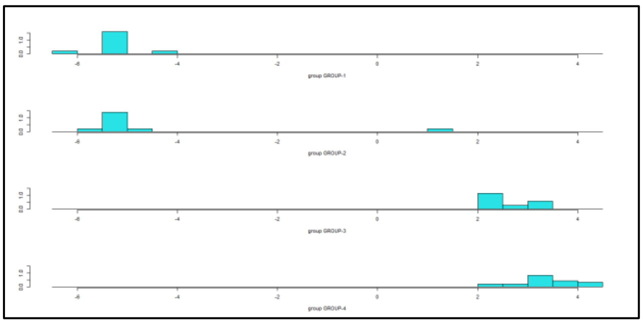

**Figure 9.** Stacked histograms for meristic traits based on ld1 discriminant function with 91.18 % explanation power

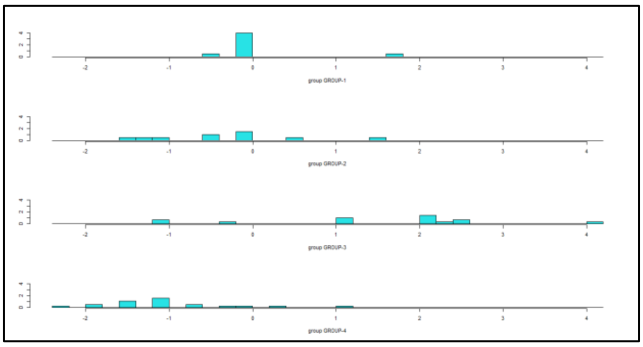

**Figure 10.** Stacked histograms for meristic traits based on ld1 discriminant function with 6.75% explanation power

The explanation percentages of the first and second discriminant functions on the differentiation of the groups and the biplot vector representation of the meristic features affecting the differentiation are given in Figure 11. After cross-validation, samples were correctly assigned to their group with an 80% classification success (Table 7). The most important four meristic traits leading to differentiation were scales on lateral line-SLL (41.65%), Scales above lateral line-SALL (20.09%), Number of scales below the lateral line-SBLL (9.39%), and Number of thorns in the pectoral fin-PcFR (8.55%) (Table 8).

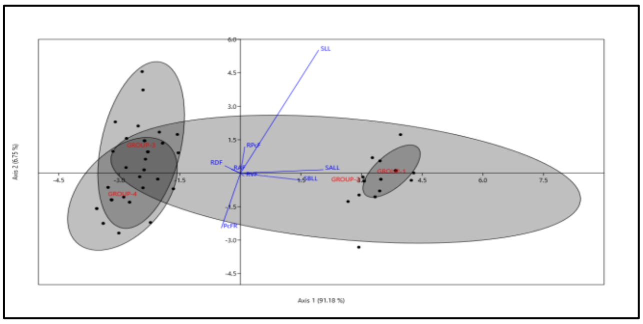

**Figure 11.** Graphical representation of DFA results for meristic traits. Axis-1(ld1) and Axis-2 (ld2) explained 97.93% of total variation.

**Table 7.** Classification results (confusion matrix) of discriminant function with 80% success for morphometric traits

| | Group-2 | Group-1 | Group-3 | Group-4 | Total |
|---|---|---|---|---|---|
| Group-2 | 7 | 8 | 2 | 1 | 18 |
| Group-1 | 0 | 23 | 0 | 0 | 23 |
| Group-3 | 0 | 0 | 19 | 3 | 22 |
| Group-4 | 0 | 0 | 4 | 23 | 27 |
| **Total** | **7** | **31** | **25** | **27** | **90** |

**Table 8.** Average dissimilarity, individual contribution, and cumulative contribution of each meristic traits to differentiation among groups by SIMPER analysis, based on Euclidean distance measure

| Morphometric Traits | Av. dissim | Contrib. % | Cumulative % |
|---|---|---|---|
| SLL | 2.84 | 41.65 | 41.65 |
| SALL | 1.37 | 20.09 | 61.74 |
| SBLL | 0.64 | 9.39 | 71.13 |
| PcFR | 058 | 8.55 | 79.68 |
| RDF | 0.47 | 6.94 | 86.62 |
| RPcF | 0.46 | 6.68 | 93.30 |
| RAF | 0.35 | 5.18 | 98.48 |
| RVF | 0.10 | 1.52 | 100.00 |

## DISCUSSION

Morphometric and meristic variations within the same fish species across different branches of a river may arise due to various factors such as genetic drift, natural selection, environmental influences, migration, and hybridization. These factors are often interrelated and tend to operate in conjunction, generating complex dynamics within fish populations, particularly in fragmented or geographically isolated ecosystems (Liam et al., 2022).

Genetic drift refers to the random fluctuation of allele frequencies over time within a population, and it becomes particularly pronounced in small and isolated populations. Over successive generations, genetic drift can lead to significant divergence in traits, even when those traits do not confer any adaptive advantage (Frankham, 2005). This phenomenon is of particular importance in populations inhabiting isolated habitats, such as river branches separated by natural or anthropogenic barriers. In such environments, reduced or absent gene flow e.g., due to dams can accelerate genetic drift and contribute to the emergence of morphometric and meristic differences (Liam et al., 2022). Over time, these changes in allele frequencies may lead to distinct sets of physical traits within each population, even in the absence of direct selective pressures (Sing et al., 2021).

Natural selection, on the other hand, acts on heritable traits that confer a survival or reproductive advantage. In fish populations, characteristics such as body shape, fin morphology, and behavioral traits may be shaped by natural selection, as individuals better adapted to their environment tend to survive and reproduce more successfully (Monk et al., 2021). In the case of *G. turcica*, it is likely that morphometric differences such as caudal peduncle length (CPL), dorsal fin height (DFH), and body depth (BD) are influenced by environmental conditions specific to each river branch. These traits can play critical roles in vital functions such as swimming efficiency, predator avoidance, and foraging success.

Environmental factors, including temperature, water quality, and food availability, also significantly influence morphological and meristic traits in fish populations. For example, variations in water flow and habitat structure across different branches of a river can impose differential selective pressures, resulting in pronounced adaptations in body shape and fin morphology. Populations in slow-flowing waters may evolve different body forms compared to those in fast-flowing streams, as body depth and fin configuration influence a fish's ability to maneuver against currents. Furthermore, changes in water temperature can affect metabolic rates and growth patterns, thereby contributing to interpopulation differentiation (Franssen et al., 2013). In this study, the observed differences in body shape and fin structure across branches of the Ceyhan River system are likely driven by such environmental factors.

Migration or its absence also plays a critical role in the development of morphometric and meristic variation. Migration introduces new genetic material into a population, enhancing genetic diversity and altering trait distributions. However, when migration is limited, as is often the case in river systems fragmented by dams, populations become more isolated, leading to faster local adaptation. This isolation reduces gene flow and fosters both genetic and morphological differentiation. The observed differences among *G. turcica* populations may therefore result from both isolation and adaptive responses to local environmental conditions, as migration between these fragmented habitats is likely infrequent.

Hybridization, the interbreeding between distinct species or populations, may give rise to novel combinations of morphometric and meristic traits. This phenomenon is more likely in systems where multiple fish species or populations share the same habitat. In the context of the Ceyhan River, hybridization may have contributed to the observed differentiation in *G. turcica*; however, verifying this hypothesis would require genetic analyses.

In this study, the morphometric traits contributing most to differentiation among river branches were identified as caudal peduncle length (CPL) (71.50%), dorsal fin height (DFH) (8.04%), and body depth (BD) (5.23%). These traits are crucial in assessing the fish's adaptation to its environment and its overall functional capacity. For instance, CPL plays a central role in swimming efficiency, as a longer caudal peduncle is associated with stronger propulsive force, which is essential in river systems with variable current regimes. DFH and BD may influence maneuverability and stability against currents. The pronounced differences in these morphometric traits across groups suggest that local selective pressures such as water flow, habitat structure, and predator-prey dynamics are shaping *G. turcica* populations in distinct ways. Seçer et al. (2025) stated that phenotypic flexibility increases in body shape variations in species belonging to the *Garra* genus in geographically distant populations, which is similar to our research findings.

Regarding meristic traits, the most significant contributors were the number of scales along the lateral line (SLL) (41.65), scales above the lateral line (SALL) (20.09%), and scales below the lateral line (SBLL) (9.39%). Meristic traits are generally more stable over time and less influenced by environmental factors, which makes them valuable indicators of genetic differentiation. For example, the number of scales along the lateral line is associated with the overall health and development of fish populations, as it relates to sensory function and habitat suitability. Differences in these meristic features may reflect unique adaptations of fish populations to local environmental conditions such as water temperature, current velocity, or food availability within different branches of the river.

Statistical analyses based on mean, standard deviation, and coefficient of variation support the existence of significant differences among river branches. In particular, the coefficient of variation within groups was low for key morphometric traits such as CPL, DFH, and BD, indicating limited variation within each group. However, statistically significant differences were observed between groups for these traits ($p < 0.05$). The difference in CPL was particularly pronounced, contributing the most to observed differentiation. This finding highlights the crucial role of swimming efficiency and body shape in the divergence of *G. turcica* populations within the Ceyhan River system. To fully understand the causes of these morphological differences and to determine whether they result from local adaptation, genetic drift, or other evolutionary processes further research, particularly incorporating genetic analyses, is necessary.

The mean, standard deviation, and coefficient of variation values for the most significant metric and meristic features responsible for the differentiation between river branches are presented in Table 9, and Figures 12-14. These values are categorized by river branch groups, and box plots and graphs displaying pairwise comparisons are also provided.

**Table 9.** Mean, standard deviation (SD) and coefficient of variation (cv, %) values of CPL, DFH and BD metric traits according to groups

| | CPL | | | DFH | | | BD | | |
|---|---|---|---|---|---|---|---|---|---|
| | **Mean** | **SD** | **cv** | **Mean** | **SD** | **cv, %** | **Mean** | **SD** | **cv** |
| GROUP-1 | 28.30[a] | 2.68 | 9.47 | 18.61[ab] | 1.60 | 8.60 | 19.55[a] | 1.02 | 5.22 |
| GROUP-2 | 27.70[a] | 3.41 | 12.32 | 19.47[a] | 1.81 | 9.30 | 18.11[b] | 0.92 | 5.07 |
| GROUP-3 | 17.46[b] | 1.92 | 11.01 | 17.49[b] | 2.10 | 12.01 | 18.33[b] | 1.74 | 9.47 |
| GROUP-4 | 18.15[b] | 1.94 | 10.67 | 18.15[b] | 0.91 | 5.04 | 17.05[c] | 1.21 | 7.07 |

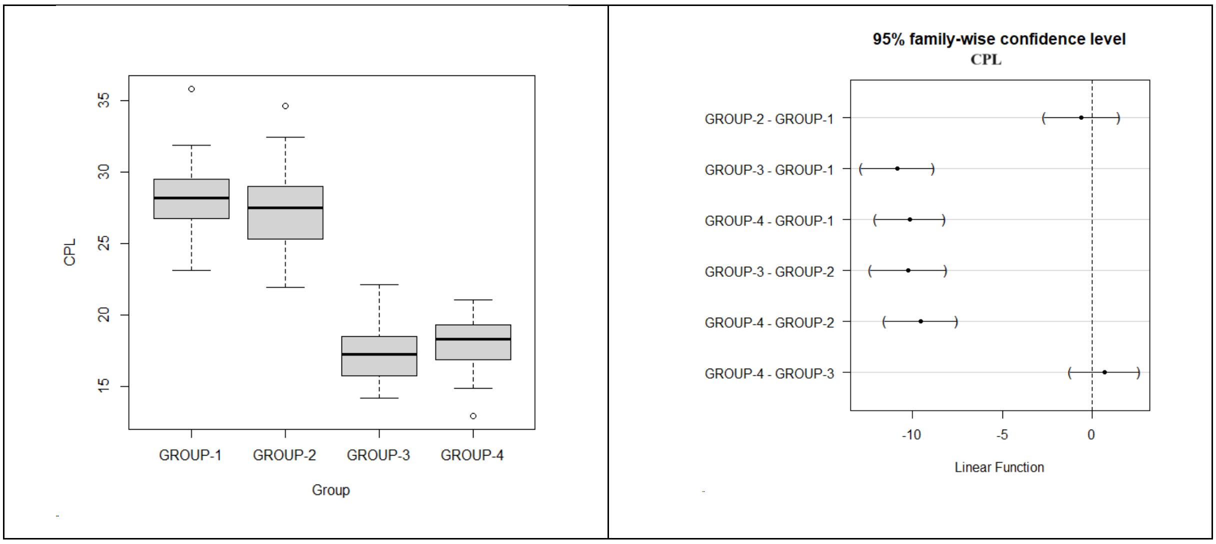


**Figure 12**. Box plots and pairwise comparison of means for caudal peduncle length-CPL (mm) of the groups. Based on the one-way ANOVA, pairwise comparisons in accordance to top to bottom of the right side of graphs were: GROUP-2 and GROUP-1 ($p>0.05$), GROUP-3 and GROUP-1 ($p<0.05$), GROUP-4 and GROUP-1 ($p<0.05$), GROUP-3 and GROUP-2 ($p<0.05$), GROUP-4 and GROUP-2 ($p<0.05$), and GROUP-4 and GROUP-3 ($p<0.05$).

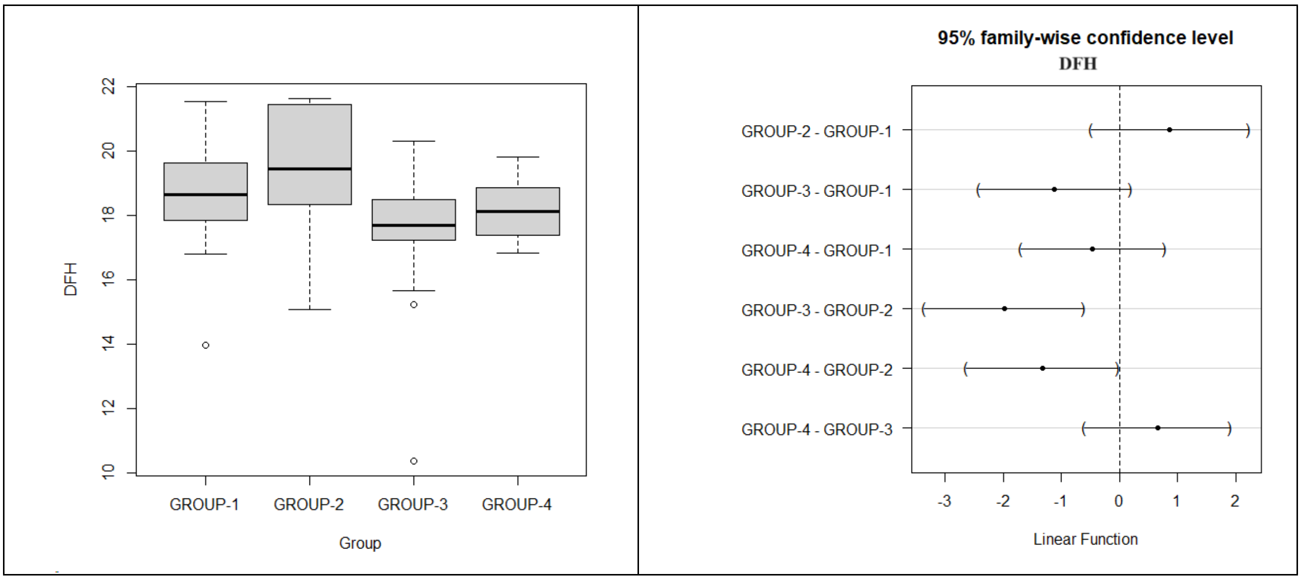


**Figure 13**. Box plots and pairwise comparison of means for dorsal fin height-DFH (mm)of the groups. Based on the one-way ANOVA, pairwise comparisons in accordance to top to bottom of the right side of graphs were: GROUP-2 and GROUP-1 (p>0.05), GROUP-3 and GROUP-1 (p>0.05), GROUP-4 and GROUP-1 (p>0.05), GROUP-3 and GROUP-2 (p<0.05), GROUP-4 and GROUP-2 (p<0.05), and GROUP-4 and GROUP-3 (p>0.05).

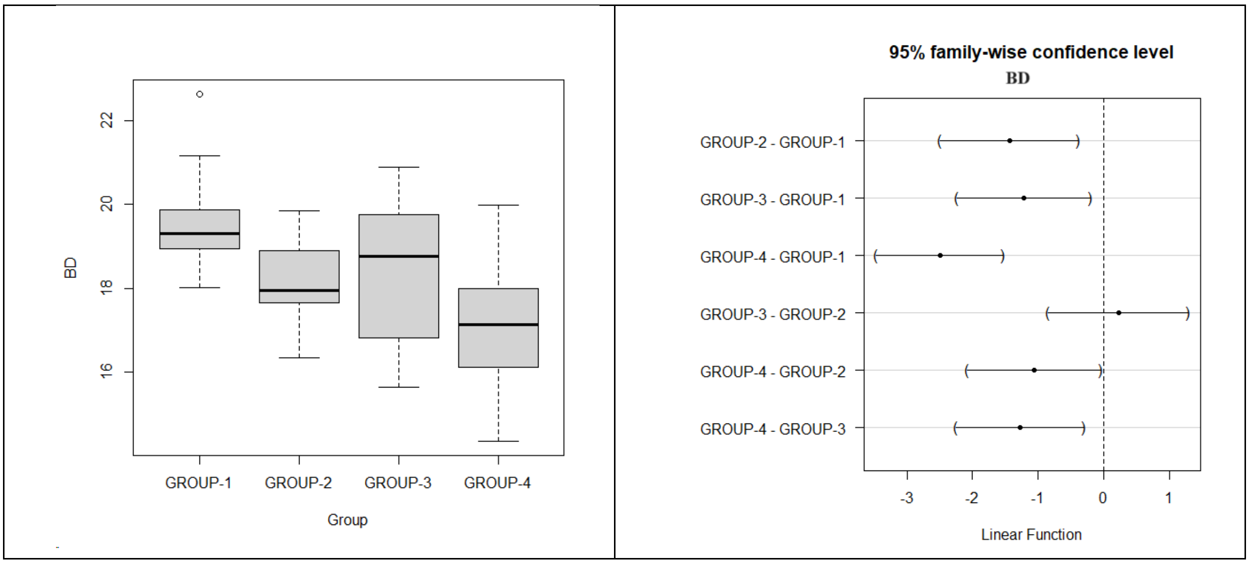


**Figure 14.** Box plots and pairwise comparison of means for body depth-BD (mm) of the groups. Based on the one-way ANOVA, pairwise comparisons in accordance to top to bottom of the right side of graphs were: GROUP-2 and GROUP-1 (p<0.05), GROUP-3 and GROUP-1 (p<0.05), GROUP-4 and GROUP-1 (p<0.05), GROUP-3 and GROUP-2 (p>0.05), GROUP-4 and GROUP-2 (p<0.05), and GROUP-4 and GROUP-3 (p<0.05).

Considering the SLL, SALL and SBLL traits that have the most impact on differentiation in terms of meristic traits, it is seen that there was a lot of variability among the intra-group variation coefficients, especially in the SALL and SBLL traits (Table 10). When the average values were compared, it was seen that there are differences between the groups (Table 10, Figure 15-17).

**Table 10**. Mean, standard deviation (SD) and coefficient of variation (cv, %) values of CPL, DFH and BD metric traits according to groups

| | SLL | | | SALL | | | SBLL | | |
|---|---|---|---|---|---|---|---|---|---|
| | **Mean** | **SD** | **cv** | **Mean** | **SD** | **cv** | **Mean** | **SD** | **cv** |
| GROUP-1 | 36.00 | 0.30 | 0.84 | 5.00 | 0.00 | 0.00 | 4.00 | 0.00 | 0.00 |
| GROUP-2 | 35.72 | 0.46 | 1.29 | 4.78 | 0.43 | 8.95 | 3.83 | 0.38 | 10.00 |
| GROUP-3 | 35.50 | 1.06 | 2.98 | 3.73 | 0.46 | 12.23 | 3.00 | 0.00 | 0.00 |
| GROUP-4 | 34.15 | 1.10 | 3.22 | 3.59 | 0.50 | 13.94 | 3.00 | 0.00 | 0.00 |

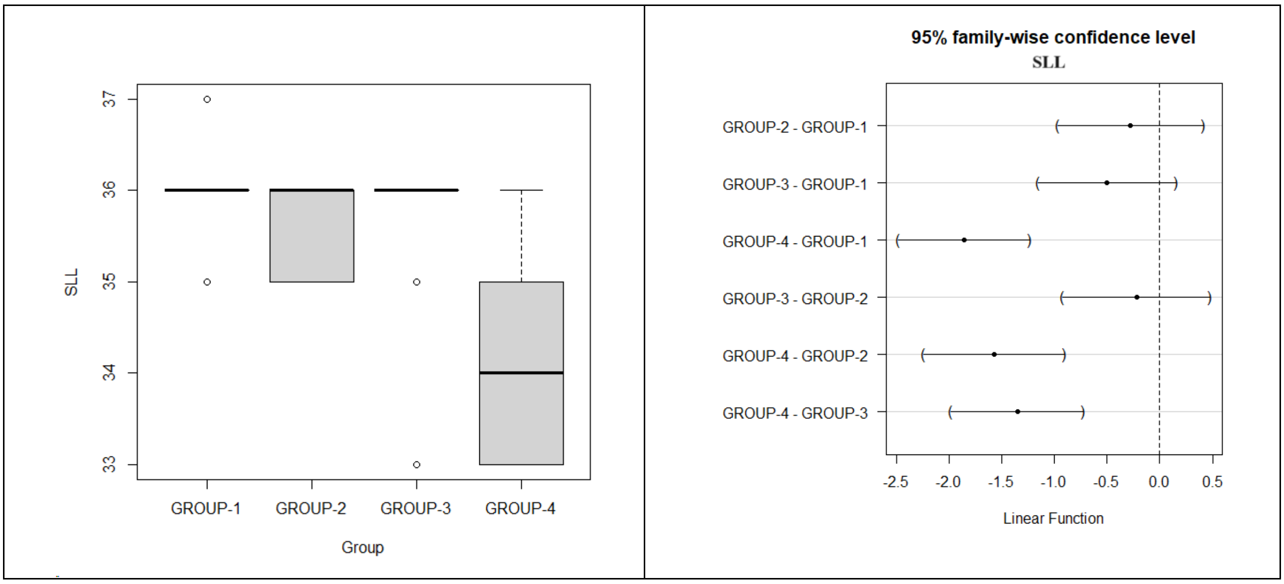


**Figure 15**. Box plots and pairwise comparison of means for scales on lateral line-SLL (mm)of the groups. Based on the one-way ANOVA, pairwise comparisons in accordance to top to bottom of the right side of graphs were: GROUP-2 and GROUP-1 ($p>0.05$), GROUP-3 and GROUP-1 ($p>0.05$), GROUP-4 and GROUP-1 ($p<0.05$), GROUP-3 and GROUP-2 ($p>0.05$), GROUP-4 and GROUP-2 ($p<0.05$), and GROUP-4 and GROUP-3 ($p<0.05$).

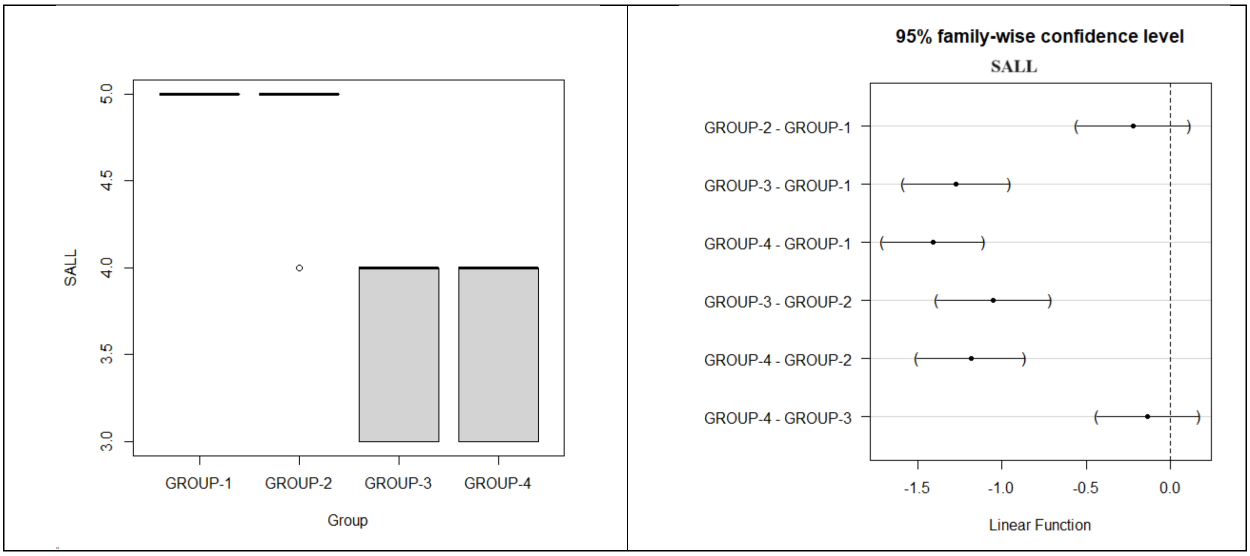


**Figure 16**. Box plots and pairwise comparison of means for scales above lateral line-SALL (mm) of the groups. Based on the one-way ANOVA, pairwise comparisons in accordance to top to bottom of the right side of graphs were: GROUP-2 and GROUP-1 ($p>0.05$), GROUP-3 and GROUP-1 ($p<0.05$), GROUP-4 and GROUP-1 ($p<0.05$), GROUP-3 and GROUP-2 ($p<0.05$), GROUP-4 and GROUP-2 ($p<0.05$), and GROUP-4 and GROUP-3 ($p>0.05$).

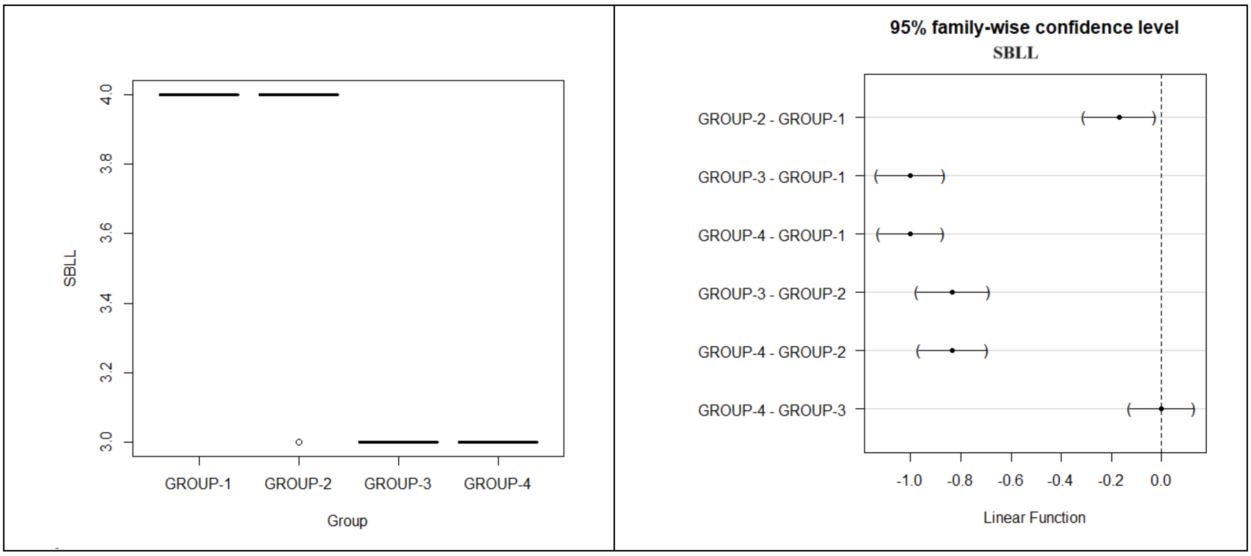


**Figure 17**. Box plots and pairwise comparison of means for scales below the lateral line -SBLL (mm) of the groups. Based on the one-way ANOVA, pairwise comparisons in accordance to top to bottom of the right side of graphs were: GROUP-2 and GROUP-1 ($p<0.05$), GROUP-3 and GROUP-1 ($p<0.05$), GROUP-4 and GROUP-1 ($p<0.05$), GROUP-3 and GROUP-2 ($p<0.05$), GROUP-4 and GROUP-2 ($p<0.05$), and GROUP-4 and GROUP-3 ($p>0.05$)

## CONCLUSION

As shown in Figure 2, the study area spans a relatively large region within the geographical context of Türkiye. It is generally observed that, particularly in inland waters, the rate of genetic and morphological differentiation tends to be higher in geographically closer areas compared to marine environments, primarily due to the limitations on migration and the influence of environmental factors. A similar pattern is evident in the present study. However, the underlying reasons for the prominence of certain traits such as caudal peduncle length (CPL) (71.50%) among metric traits and scales on the lateral line (SLL) (41.65%) among meristic traits as the primary contributors to differentiation, remain unclear. Furthermore, it is important to explore whether this morphological differentiation is also reflected at the genetic level. Genetic evidence could potentially support the classification of this species as a subspecies.

In conclusion, the differentiation observed in *G. turcica* populations across the Ceyhan River system is likely a result of a combination of genetic drift, natural selection, environmental factors, and limited migration. These findings highlight the importance of considering both genetic and environmental factors when studying the evolution and conservation of fish populations in fragmented river systems. Future studies incorporating genetic data will provide valuable insights into the underlying causes of these morphological differences and contribute to a better understanding of the evolutionary processes shaping *G. turcica* in the Ceyhan River system.


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## Compliance with Ethical Standards

### Authors' Contributions

All authors contributed to the study equal. All authors read and approved the final version.

### Conflict of Interest

The authors declare that there is no conflict of interest.

### Ethical Approval

The authors declare that formal consent is not required for this type of study. The study was carried out with the legal consent of the Ministry of Agriculture, and Forestry, General Directorate of Fisheries and Aquaculture (permission date 03.04.2014; permission number: 01334).

### Data Availability

The data supporting the findings of this study are available from the corresponding author upon request.


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