

Molecular phylogeny and taxonomy of roaches (*Rutilus*, Leuciscidae) in the southern part of the Caspian Sea

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ABSTRACT

The aims of this study were to testify a phylogenetic hypothesis for the genus *Rutilus* in the Southern Caspian Sea using sequence variation of mitochondrial and nuclear genes and to define the taxonomic status of phylogenetic clades represented in this region. Phylogenetic analysis was based on the variability of mitochondrial genes cytochrome *b* and cytochrome *c* oxidase subunit I and nuclear recombination activating gene 1 and inter-photoreceptor retinoid-binding protein. Compared to previous studies, this phylogenetic analysis included significant material from the South Caspian, both from the collected samples and from GenBank data. As a result, only two species of *Rutilus* were confirmed in the ichthyofauna of the studied region. The first of them corresponds to *R. lacustris*, therefore, materials from the South Caspian can be included in genetically identified vouchers of this species to determine its morphological diagnostic features. The second species represented separate sister phylogenetic lineage for the Pontic populations of *R. frisii* sensu lato. Due to the low genetic distance between the Caspian and Pontic lineages and the strong overlap of their morphological features, but previously proven divergence in separate Pleistocene refugia, the Caspian populations are classified in this study as a subspecies *R. frisii kutum*.

Keywords: Ponto-Caspian region, Leuciscinae, *Rutilus lacustris*, *Rutilus frisii kutum*, Mitochondrial and Nuclear genes.

Article type: Research Article.

INTRODUCTION

Fish species of the genus *Rutilus* Rafinesque, 1820 belong to the phylogenetic Leuciscine lineage, which is widespread across Eurasia and diverged from other leuciscine lineages approximately 21 MYA, according to the molecular clock (Perea *et al.* 2010). A total of 12 nominal taxa (species, subspecies and varieties) currently included in this genus have been historically described from the Caspian basin (see Fricke *et al.* 2022). Six of them were accepted as valid species or subspecies by Berg (1949): *Rutilus atropatenus* Derjavin, 1937, *R. rutilus schelkovnikovi* Derjavin, 1926, *R. rutilus fluviatilis* Yakovlev, 1873, *R. rutilus caspicus* Yakovlev, 1870 and *R. frisii kutum* (Kamensky, 1901). The latter author considered these populations from the Upper Volga drainage as nominotypical *R. rutilus rutilus* (Linnaeus, 1758),

concept, according to which populations from the Caspian Sea have been classified as a separate subspecies, *R. frisii kutum* (Berg 1949; Bogutskaya & Naseka 2004; Vasil'eva & Luzhnyak 2013; Parin *et al.* 2014), in order to reflect stable (but low) morphological differences and geographic separation from the Black Sea population.

CONCLUSION

Phylogenetic analysis of *Rutilus* samples from the South Caspian based on mitochondrial and nuclear genes proves the presence of only two species in this area. The first corresponds to *R. lacustris*, and the second is classified as the Caspian subspecies of *R. frisii*, i.e., *R. frisii kutum*. The populations of *R. lacustris* from the South Caspian should be used as genetically identified vouchers of this species to develop its morphological key features.

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