

MUGIL CEPHALUS: COSMOPOLITAN SPECIES OR SPECIES COMPLEX?

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Abstract

The cosmopolitan distribution of *Mugil cephalus* is under discussion at present. Morphometrics based on Landmark distances, meristics and 12S rRNA (domain 1 and 2), cytochrome c oxidase subunit I (COI) and cytochrome b (cytb) mitochondrial DNA markers data from several locations worldwide are presented. Combined results indicate a global species complex in need of taxonomic revision.

Keywords: *Biometrics, Genetics, Fishes, Systematics, Biogeography.*

Mugil cephalus, *Mugil platanus* and *Mugil liza* form species group with close morphological relationships. According to [1] grey mullet, *M. cephalus*, has a worldwide distribution (51N - 42 S) and *M. platanus* is considered as a synonymy in South American waters. Nevertheless, extreme conservative morphology of this species stands in contrast with the degree of allozymic differentiation detected at a global scale [2]. The aim of the present work is to compare the taxonomic relationships of *Mugil cephalus* with *M. platanus* and *M. liza*, based on a multidisciplinary approach, using meristic, morphometric and mitochondrial DNA sequencing techniques.

Tab. 1. Tamura-Nei genetic distance and standard error for each sample and gene.

	12S rRNA-1	12S rRNA-2	COI	Cytb
Med-USA	0.0170 ± 0.0059	0.0163 ± 0.0061	0.0414 ± 0.0077	0.0586 ± 0.0107
Med-Miya	0.0101 ± 0.0046	0.0201 ± 0.0070	0.0269 ± 0.0077	0.0574 ± 0.0100
USA-Miya	0.0274 ± 0.0079	0.0201 ± 0.0071	0.0420 ± 0.0082	0.0576 ± 0.0104
<i>M.pl/M.li</i> -Med	0.0139 ± 0.0052	0.0168 ± 0.0057	0.0229 ± 0.0053	0.0479 ± 0.0091
<i>M.pl/M.li</i> -US A	0.0289 ± 0.0082	0.0253 ± 0.0073	0.0325 ± 0.0066	0.0498 ± 0.0090
<i>M.pl/M.li</i> -Miya	0.0243 ± 0.0071	0.0269 ± 0.0077	0.0248 ± 0.0059	0.0406 ± 0.0079

Samples of *M. cephalus* were collected from the Mediterranean (Med), the western Atlantic (USA); *M. platanus* from South America, and *M. liza* from the Caribbean. Twenty-one morphometric variables were taken as interlandmark distances of involved species. Meristic data were also considered for each specimen following [3]. Genetic analysis of 12S rRNA (domain 1 and 2), cytochrome c oxidase subunit I (COI) and cytochrome b (cytb) were carried out following [4] and using GenBank *M. cephalus* sequences as reference. Phylogenetic relationships were inferred by neighbor-joining analysis based on Tamura-Nei model.

detected among *M. cephalus* samples overlapped with values shown between *M.pl/M.li* and *M. cephalus* (Table 1). Phylogenetic trees had similar topology for all molecular markers (Figure 1). Although a monophyletic group for *M.pl/M.li* was detected, it was included in *M. cephalus* lineage.

This evidence coupled with [2] suggest that the cosmopolitan distribution of *M. cephalus* should be reconsidered and new levels of species assignation are expected.

References

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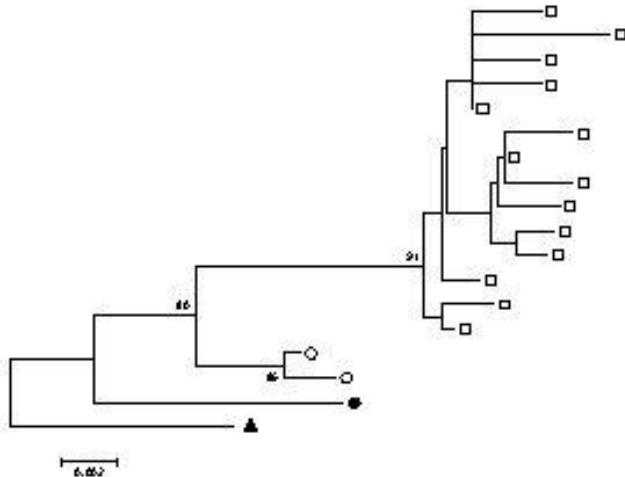


Fig. 1. Neighbor-Joining tree based on Tamura-Nei distance. *M. cephalus* from the Mediterranean (empty circle), USA (solid circle) and Genbank reference (triangle) and *M. platanus*/*M. liza* (square).

The interlandmark distances showed differentiation between the individuals of *M. platanus* and *M. cephalus* analysed. The number of lateral scales differentiated *M. liza*, *M. platanus* and *M. cephalus* being a diagnostic character in meristic analysis. However, the high genetic closeness detected between *M. platanus* and *M. liza* haplotypes and shared haplotypes did not support species level differentiation. Besides, the distances