

Poster 1

Species richness of *Myxobolus* (Cnidaria, Myxozoa) parasites infecting thicklip grey mullet *Chelon labrosus* in the Douro River, Portugal

J. Guimarães¹, **G. Casal**^{1,2}, **A. Alves**¹, **C. Araújo**^{3,4} and **S. Rocha**^{1,4,*}

¹ School of Medicine and Biomedical Sciences (ICBAS), University of Porto, Rua Jorge Viterbo Ferreira no. 228, 4050-313 Porto, Portugal

² TOXRUN – Toxicology Research Unit, University Institute of Health Sciences, CESPU, CRL, 4585-116 Gandra, Portugal

³ Faculty of Sciences (FCUP), University of Porto, Rua do Campo Alegre, s/n, FC4, 4169-007 Porto, Portugal

⁴ Instituto de Investigação e Inovação em Saúde (i3S), University of Porto, Rua Alfredo Allen no. 208, 4200-135 Porto, Portugal

* Correspondence: srrocha@icbas.up.pt

Abstract

Background: Myxozoans are widespread cnidarian parasites that mostly infect fish and annelids as temporary and definitive hosts, respectively [1]. Mulletts are a diverse fish group, which ubiquitous nature leaves vulnerable to parasitic infections [2]. **Objective:** This study aimed to acknowledge the myxozoan diversity infecting thicklip grey mullet *Chelon labrosus* in the Douro River estuary in northern Portugal. **Methods:** The internal and external organs of 13 specimens were macro- and microscopically examined. Cysts and infected tissues were individually photographed and processed for sequencing of the small subunit ribosomal gene (18S rDNA). Phylogenetic reconstructions were performed using maximum likelihood and Bayesian inference methodologies. **Results:** Eleven potentially new *Myxobolus spp.* were morphologically described and molecularly characterized. Additionally, a novel host, geographic region and morphometric profile was reported for *Myxobolus pupkoi* Gupta et al., 2022. Molecular comparisons further matched two of the novel *Myxobolus* sequences with sphaeractinomyxon types previously reported from marine oligochaetes in another Portuguese estuary. Phylogenetic analyses revealed the novel sequences clustering according to host affinity, with tree topologies resolving well-supported lineages of myxobolids infecting mullets from the genera *Chelon*, *Mugil*, *Crenimugil* and *Planiliza*. **Conclusions:** The elevated number of potentially novel *Myxobolus spp.* found in *C. labrosus* confirmed the successful hyperdiversification of these myxozoans in mullets [2], further reinforcing molecular-based comparisons as imperative for taxonomic descriptions. Morphometrical divergence between geographical isolates of *M. pupkoi* was hypothesized to correlate with adaptation to distinct abiotic factors and annelid communities. The formation of more than one *Chelon*-infecting lineage revealed that myxobolids entered this genus multiple times during their evolution. Lastly, the matching of two novel *Myxobolus* sequences with sphaeractinomyxon types reinforces the latter as specific life-cycle counterparts of mugiliform-infecting *Myxobolus* [3]. The large number of unmatched sphaeractinomyxon sequences positioned within the *Chelon* lineages suggests that *Myxobolus* diversity in Portuguese estuaries remains underestimated.

Keywords: 18S rDNA; diversity; life cycle

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