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FIRST EVALUATION OF ASSOCIATED GUT MICROBIOTA IN WILD THICK-LIPPED GREY MULLETS (*Chelon labrosus*, RISSO 1827)

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Introduction

The need for species diversification in Mediterranean aquaculture has promoted the culture of omnivorous and herbivorous species. Within this context, it is worth noting the high potential presented by the species of the family Mugilidae (mullets), which is considered a priority within the current strategies of European aquaculture (Alexander et al. 2015). One of the mullets with potential for use in aquaculture is the thick-lipped grey mullet (*Chelon labrosus*), due to its great adaptability to different culture conditions, omnivorous profile, high osmoregulatory capacity, and resistance to environmental variations (Pujante et al., 2018). However, there is a lack of information regarding the composition and functions of its intestinal microbiota.

Documenting the bacteria present in healthy individuals is the first step to understanding the impacts of microbial manipulation in aquaculture systems (Tarnecki et al., 2016). In this sense, the knowledge of bacterial diversity from healthy wild fish in their natural environment is essential. Furthermore, the study of the functionality of the intestinal microbiota of wild fish provides information on its capacity to adapt to different culture conditions. Thus, this study aimed to characterize the intestinal microbiota of wild *C. labrosus* and explore its potential functionality on the host.

Material and methods

Eight wild thick-lipped grey mullets (average weight and length: 115.3 ± 5.0 g and 20.3 ± 0.6 cm, respectively) were caught in May 2021 with a net in the Port of Velez Malaga, (36°44’54.9”N 4°03’57.6”W, Malaga, Spain), kept alive and transported to the Centro de Experimentación de Ecología y Microbiología de Sistemas Acuáticos Controlados Grice-Hutchinson (CEMSAC) of the University of Malaga facilities within one hour. Animals were euthanized by immersion in water with a 2-phenoxyethanol overdose (1 mL L^{-1}). Specimens were then individually weighed, and intestinal samples were extracted. Then, each tract was divided into two major sections, anterior and posterior sections, and kept at −80 °C until the subsequent analysis.

Intestinal contents of anterior and posterior sections from wild fish were collected, and DNA was extracted. Subsequently, the V3-V4 regions of 16S rRNA were sequenced using the Illumina technology and results were analyzed by bioinformatics pipeline. The functional profile of the microbial community was analyzed using PICRUSt software.

Results and discussion

Shannon and Simpson diversity indices were significantly higher in the posterior section of wild specimens. The overall taxonomic composition suggests certain homogeneity in the anterior section of the intestine and heterogeneity in the posterior section (Figure 1). Due to this, no statistical differences were detected at any level among both intestinal sections. The intestinal microbiota of wild *C. labrosus* was dominated by the *phylum* Proteobacteria, whereas Tenericutes, Spirochaetes, and Cyanobacteria appeared in the posterior section with low relative abundance. This is consistent with previous studies on wild fish (Liu et al., 2016; Ramírez and Romero, 2017).

Predicted functions of intestinal microbiota showed the most abundant those related to amino acid metabolism, carbohydrate metabolism, energy metabolism, membrane transport, and cell replication and repair. Furthermore, the analysis revealed microbial functional genes related to the elimination of environmental toxins. These functions of intestinal microbiota might provide beneficial effects for the host.

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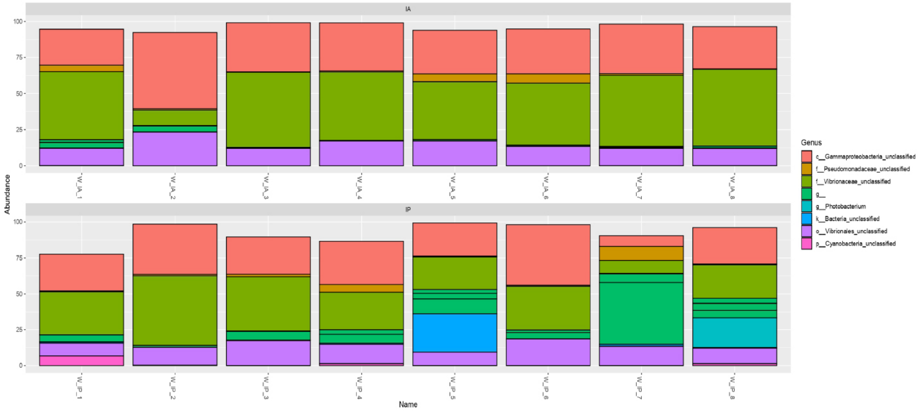

Figure 1. Relative abundance (percentage) of the top 10 genus level for each sample of intestinal microbiota from anterior and posterior section of wild *C. labrosus*. In the figure, W_IA corresponds to the anterior intestinal section of wild fish, and W_IP corresponds to the posterior intestinal section of wild fish.

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