



6TH

INTERNATIONAL
SYMPOSIUM
ON GENOMICS IN
AQUACULTURE



GIA 2020

BOOK OF ABSTRACTS



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GENETIC SELECTION FOR GROWTH DRIVES DIFFERENCES IN INTESTINAL MICROBIOTA COMPOSITION AND PARASITE DISEASE RESISTANCE IN GILTHEAD SEA BREAM

Piazzon, M.C.¹, Naya-Català, F.², Perera, E.^{1,2}, Palenzuela, O.¹, Sitjà-Bobadilla, A.¹, Pérez-Sánchez, J.²

1. Fish Pathology Group, Institute of Aquaculture Torre de la Sal, CSIC, Spain.

2. Nutrigenomics and Fish Growth Endocrinology Group, Institute of Aquaculture Torre de la Sal, CSIC, Spain.

SUMMARY

The key effects of intestinal microbiota in animal health have led to an increasing interest in manipulating these bacterial populations to improve animal welfare. The aquaculture sector is no exception and in the later years many studies have described these populations in different fish species. However, this is not an easy task, as intestinal microbiota is composed of very dynamic populations that are influenced by different factors, such as diet, environment, host age and genetics. In the current study, we aimed to determine whether the genetic background of gilthead sea bream (*Sparus aurata*) influences the intestinal microbial composition, how these bacterial populations are modulated by dietary changes, and their effect on disease resistance.

To that aim, three different groups of families of gilthead sea bream that were selected during one-two generations for growth (fast, intermediate and slow)¹ were kept together in the same open-flow tanks and fed a control or a well-balanced plant-based diet during nine months. Twelve animals per group were sacrificed and the adherent bacteria from the anterior intestinal portion were collected and immediately used for DNA extraction. The V3-V4 region of the 16S rRNA of each individual sample was amplified and sequenced by Illumina MiSeq. After quality filtering, taxonomic assignment was performed with a custom-made pipeline using the RDP database. Alpha diversity was calculated using Phyloseq and beta diversity using PERMANOVA and PLS-DA models. Metagenome prediction and pathway analysis were performed using Piphillin. In parallel, 30 fish of the fast- and slow-growth groups were infected with the intestinal parasite *Enteromyxum leei* and the disease signs, prevalence, intensity and parasite abundance were evaluated.

No differences were detected in alpha diversity indexes among families, though the bacterial composition was significantly different. Of note, the plant-based diet significantly changed the microbiota in the intermediate- and slow-growth families, with a much lower effect on the fast-growing group. However, the small changes detected in this set of families potentially account for more changes at the metabolic level when compared to the other families. Upon parasitic infection, the fast-growing group showed significantly lower disease signs and parasite intensity and abundance than the slow-growing animals. These results show a clear genome-metagenome interaction indicating that the fast-growing families harbour a microbiota that is more flexible upon dietary changes and can help to cope with intestinal infections.

¹Perera *et al.*, 2019. *Aquaculture* 507: 349–360.