Genetics shape microbial makeup in gilthead sea bream

M. Carla Piazzon
Fernando Naya-Català
Erick Perera
Oswaldo Palenzuela
Ariadna Sitjà-Bobadilla
Jaume Pérez-Sánchez

Video Byte

Keywords: Microbiome, Sparus aurata, selective breeding, growth, plant-based diets, genome-diet interactions, intestinal bacteria, Enteromyxum leei, domestication, plasticity, gilthead sea bream, microbiota, disease resistance, alpha diversity, parasitic infection, metabolism, metagenomics, aquaculture, nutrition, heritability

Posted Date: February 25th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-275924/v1>

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
[Read Full License](#)

Abstract

The gilthead sea bream is one of the most important fish farmed in the Mediterranean. Selecting for economically valuable genetic traits has helped improve bream farming efficiency. But little is known about the role played by intestinal microbes in selective breeding practices. To find out, researchers examined how genetic selection for different growth rates and diet affect intestinal bacteria in the gilthead sea bream. Bream were divided into three groups according to genetically selected growth rate: slow, intermediate, and fast, and were fed a plant-based diet, a sustainable alternative for the normally carnivorous gilthead sea bream. The plant-based diet significantly changed the microbial makeup of the slow- and intermediate-growth groups, with a much weaker effect observed for the fast-growth group. And when exposed to an intestinal parasite common to the gilthead sea bream, the fast-growth group showed significantly lower parasite intensity and abundance than the slow-growth group. Altogether, the results suggest that genetics strongly influence the microbiota of the gilthead sea bream, with fast-growth fish harboring microbes that are flexible to changes in diet and better able to cope with intestinal infection.