

Differentiation of the production method in turbot (*Scophthalmus maximus*) through the associated microbiota

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Background

- Indicate the production method on the label, wild or farmed, is mandatory to meet with the European normative for seafood labeling. However, mislabeling of the production method is one of the most common frauds in seafood products, with potential economic, environmental and health consequences.
- One of the species susceptible to suffer this fraud is the turbot, *Scophthalmus maximus*, one of the cultivated species in Europe with higher commercial value, being its price even higher for wild specimens.
- To fight against this fraud, new validated and standardized tools are necessary that allow the identification of the production method. In recent years, the study of microbial communities associated with organisms has been proposed as a traceability tool able to reflect the production method of the product, such as a fingerprint of its origin.

Objective

To investigate the possibilities of using the microbiome associated with different fish tissues, through next-generation sequencing, to characterize microbial communities present in wild and farmed individuals and determine the existence (or not) of bioindicator species for the production method in turbot (*S. maximus*).



Workflow and Expected results

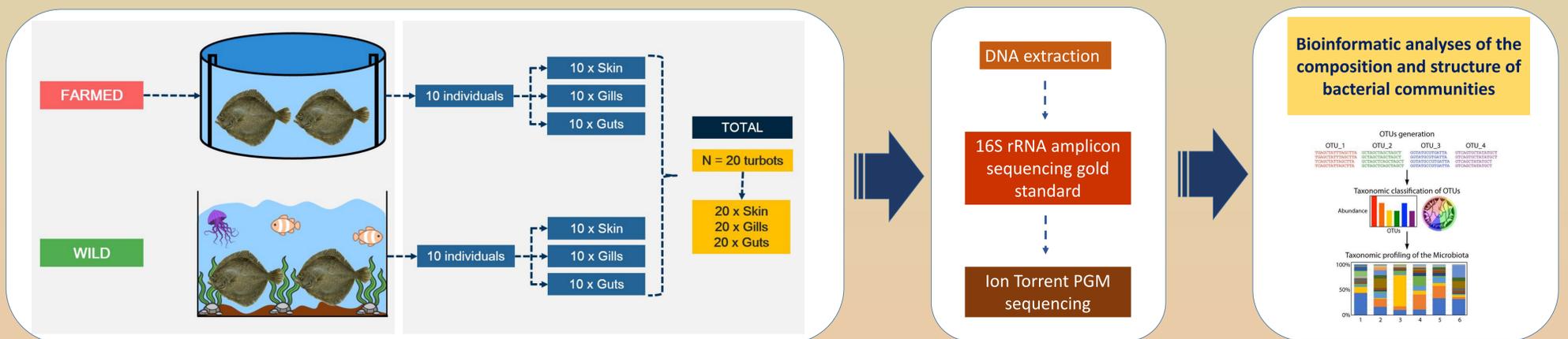


Fig. 1: experimental design and workflow

- All three sample types are good candidates to show important differences between wild and farmed organisms, but the **microbial community expected will be different depending on the tissue**:
 - The skin mucus and gills samples offer information about the microbiological conditions of the water in which the organisms grown. Additionally, skin mucus is a non-invasive sample compared with the other two.
 - The samples of gut microbiome offer information about the type of diet and health status of the individuals. The lowest diversity is expected for this sample type.
- For the **gut microbiome, lower diversity is expected in wild individuals. The opposite trend is expected for skin mucus and gills**, with expected lower diversity in farmed individuals.

Preliminary results and pursued objective

Worse bacterial amplification was detected for farmed individuals during the libraries preparation. Confirmed different bacterial community in each sample type and clear differences noticed between farmed and wild individuals.

More analysis with all samples are needed to determinate the structure and diversity of the bacterial community for the individuals with different production method, in each sample type, in order to find the microbiome more informative and establish a panel of biomarkers to trace the production method in turbot.

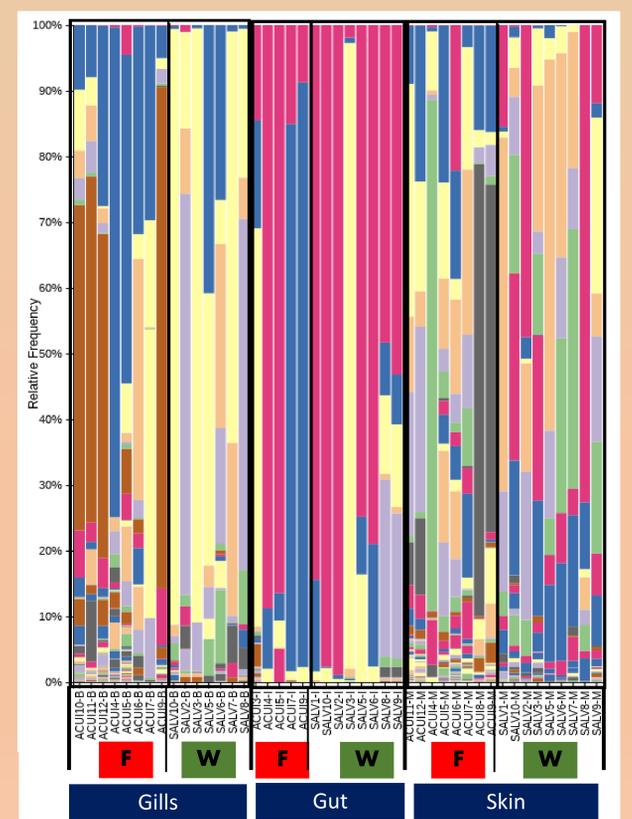


Fig. 2: preliminary results (not all samples) of the microbial community (family level) recovered from gills, gut and skin mucus, from the farmed and wild turbot.