Microbial communities to assess the traceability and freshness of seafood: A metagenomic approach

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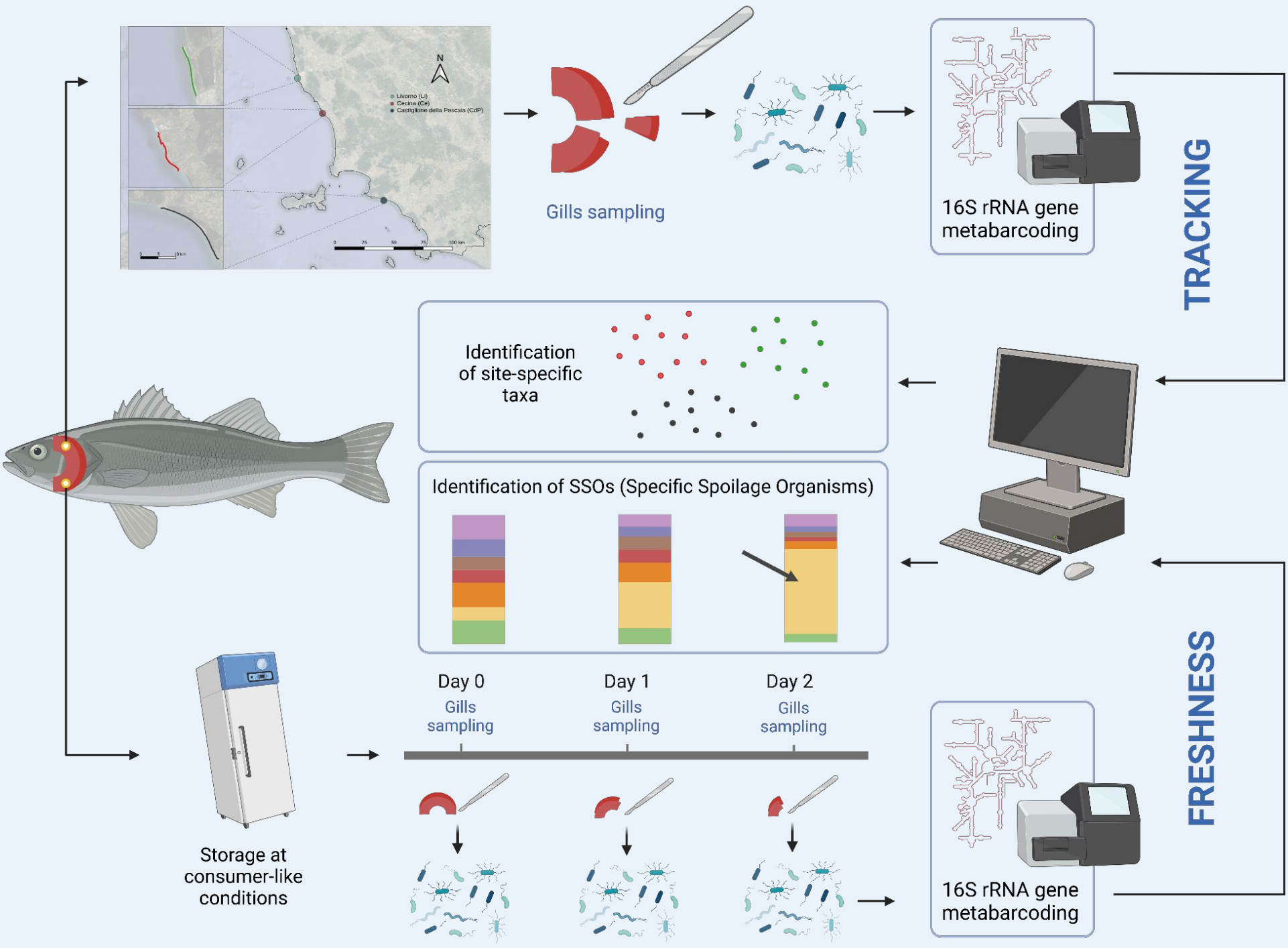


BACKGROUND

With the exponential growth of world population, also seafood consumption is constantly growing. In this context, the most difficult challenges the European Union and policy makers are facing are the **sustainability**, **transparency** and **safety** of fishery. **Microbial communities** associated with seafood have been already proposed and tested as markers for food tracking and safety.
This work aimed at the exploration of seafood **traceability** and **safety** through the analysis of its associated bacterial communities.
This study aimed at the creation of a pipeline for the analysis of fish microbiota to assess its provenance, but also at the production of new sensors capable of an *in loco* fish **freshness evaluation**, to be used to supervise the fish market.

MATERIALS & METHODS

Fish specimens were caught from three different sampling sites belonging to the Tuscany coast during the summer of 2022 (*S. aurata*, seabream) and autumn-winter 2023/2024 (*D. labrax*, seabass). Genomic DNA was extracted from 2 cm of gill tissue. Amplicons of the 16S V3-V4 hypervariable regions were sequenced on an Illumina MiSeq Platform, and obtained reads were analysed using software R (version 4.4.2).

Gills of seabasses individuals from Scotland were sampled using a swab. Extraction, amplification and sequencing were done following the protocol described in the previous paragraph.

RESULTS - TRACKING

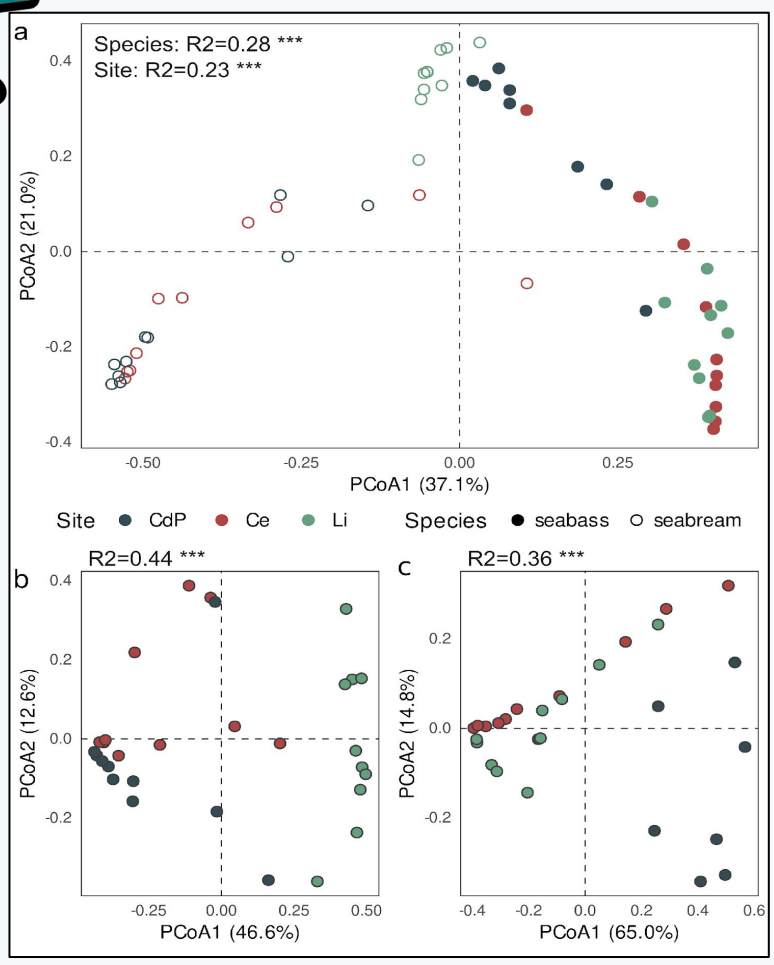
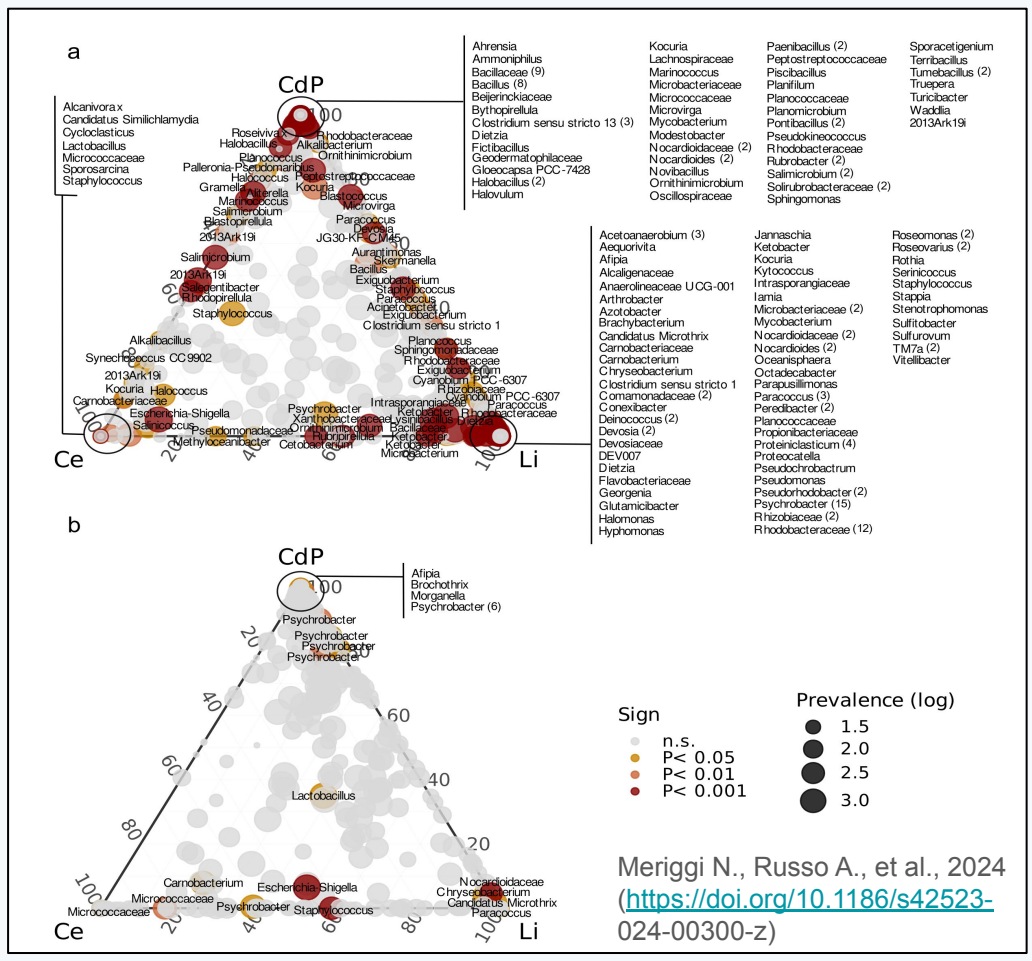


Figure 1. **Bacterial distribution among sites in *S. aurata* and *D. labrax* species.** PCoA based on Bray-curtis distance on the complete dataset (a) and after splitting it according to the fish species, i.e. seabream (b) and seabass (c).



Meriggi N., Russo A., et al., 2024 (https://doi.org/10.1186/s42523-024-00300-z)

Figure 2. **Bacterial profiles switch according to different sites.** Ternary plot reported the ASVs mean relative abundances distribution on ternary space. Likelihood ratio test (LRT) selected the ASVs significantly influenced by the sites (colored points) according to the seabream (a) and seabass (b) datasets.

RESULTS - FRESHNESS

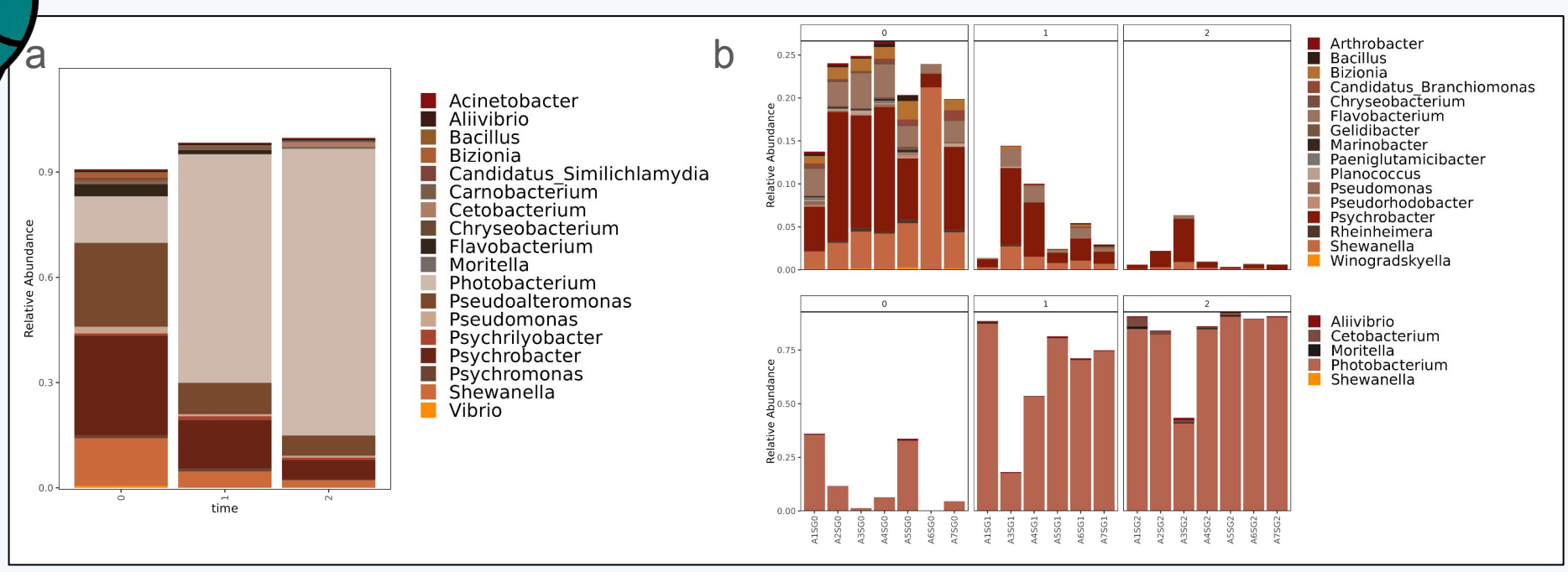
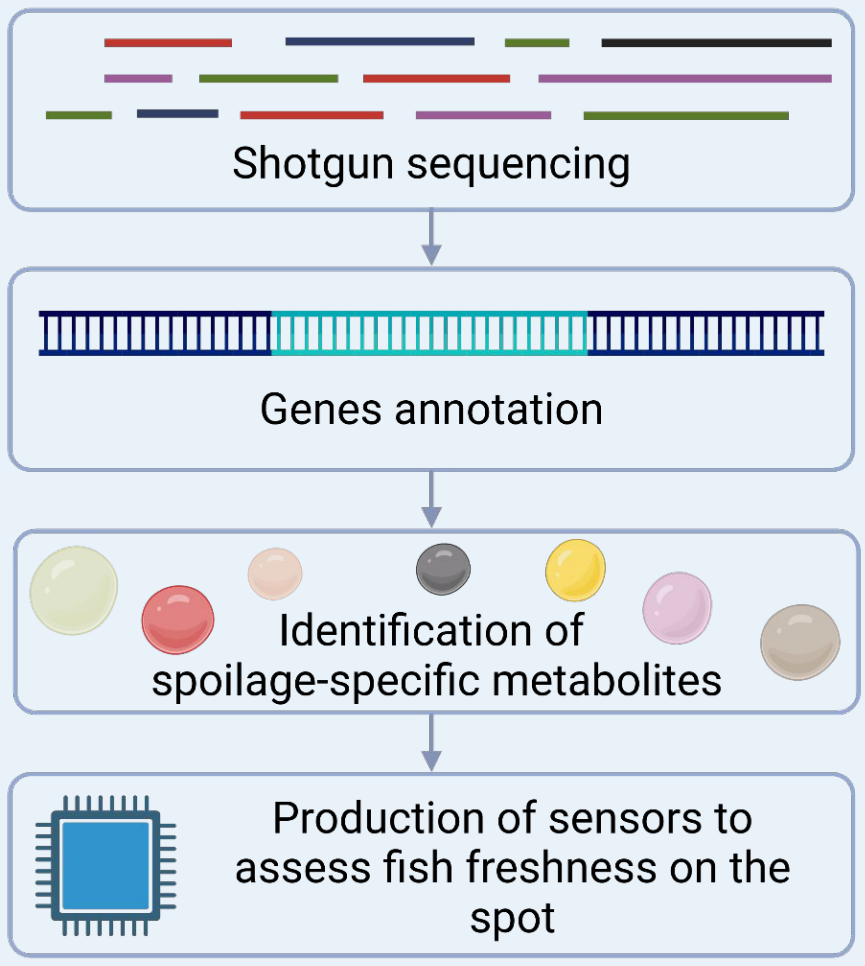


Figure 3. **Seabass necrobiota along time series.** Barplot of the mean relative abundance of the top 18 most abundant genera among samples (a); Barplots of the relative abundance of differentially abundant ASVs ($p < 0.05$) grouped by genus (b). On top the ASVs that decrease with spoilage, on the bottom the ones that increase over-time.

ONGOING ACTIVITIES

TRACKING

Collection of wild and farmed fishes from other countries to find site-specific and wild/farmed specific taxa

FRESHNESS