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OliveFMBN: an extensively annotated database of the microbiota of table olives.

ADVANCES IN MICROBIOLOGY OF TABLE OLIVES
International Congress

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Background

Table olives are among the most ancient and important fermented foods of the Mediterranean basin. Their production is strongly related to traditional practices, and the lack of thermal treatments of raw material, reliance on natural contamination and selective factors determine the dynamics of the microbial community. The microbiota of table olives has been reviewed (10.3390/foods12203783) but there is a need for a well annotated repository of existing data which might be useful for both meta-studies and for the design of microbiome-based starters.

Methods

We have used metataxonomic data extracted from FoodMicrobionet database, together with those obtained from the METAOlive project to provide quantitative insights on bacterial and fungal microbial communities of table olives and to identify core genera in different trade preparations. The data were supplemented with an extended metadata structure on table olive properties.

Results

Metataxonomic data and metadata are publicly available on GitHub. Version 0.3.2 of the repository includes data for 18 studies, with 533 samples for bacteria and 453 samples for fungi. Version 0.3.3, in preparation, will include other 350 additional samples from the METAOlive project. The data have been recently used to write a data driven review on table olive microbiota (10.1016/j.ijfoodmicro.2025.111344). An example of the output, the core bacterial microbiota of table olives, is shown in Figure 1.

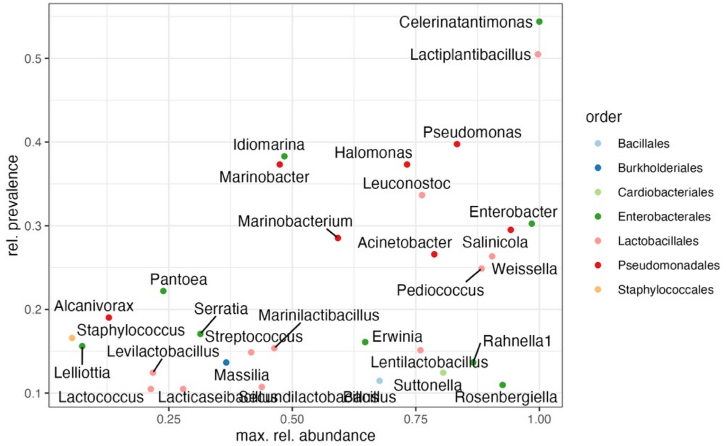

Fig. 1. The core bacterial microbiota of table olives. Data obtained from OliveFMBN v 0.3.2

Scan this QR code to access the full repository

Conclusions

OliveFMBN is an open access resource than can be easily used by researchers with minimum proficiency in R (it is available as phyloseq objects which can be processed with interactive apps available on the web, like MicrobiomeAnalyst or ShinyPhyloseq). Its potential uses include support for the writing of meta-studies and for the design of new studies, inference of microbial association networks, inferences on core and accessory microbiota of different types of olives. Given the size of the dataset, it can also be used in training machine learning algorithms for evaluating typicality or specificity of the microbiota.

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