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Dear Editor,

It is my pleasure to submit our manuscript "Predictability of the community-function landscape in wine yeast ecosystems" for your consideration as a *Research article* in *Nature Microbiology*.

Predictively linking taxonomic composition and quantitative ecosystem functions is a major aspiration in microbial ecology, which must be resolved if we wish to engineer microbial consortia. Here, we have addressed this critical goal by answering two of the main current questions in functional ecology: i) is there a phylogenetic signal in ecologically-relevant traits, which determine the individual contributions of a species to community functions? and ii) can we predict how the individual contributions of a species to a community function change in different community contexts, due to interactions with other community members? As a model system to address these two questions, here we have studied wine fermentations, a system of profound socio-economic significance and one of the first microbiomes ever domesticated and exploited by humans.

First, we characterized the phylo-functional relationships among wine yeast species, measuring a total of 43 ecological and enological traits in a collection of 60 wine yeast strains belonging to 30 different species (spanning the expectable phylogenetic diversity of most commonly found wine yeasts). We find that almost all traits measured exhibit strong phylogenetic signals and can be imputed from a standard, fungal genetic marker. Then, we assembled and assayed hundreds of synthetic yeast consortia, and we show that the contributions of individual wine yeasts to alcoholic fermentation can be predicted in different community contexts, as they follow simple quantitative rules that parallel the global epistasis concept in evolutionary genetics. Using methods that we have introduced in a recent work to infer the community-function landscape from a subset of observed consortia (Diaz-Colunga et al., 2022. <https://doi.org/10.1101/2022.06.21.496987>), we can quantitatively predict the wine fermentation function (sugar consumption) in complex wine yeast consortia, based on their community composition.

We believe that this work provides new and relevant results in the interface of microbial biotechnology and systems biology and, besides addressing fundamental open questions in functional ecology, our results and methodologies provide a blueprint for rationally managing microbial processes of biotechnological relevance.

As relevant researchers that may act as reviewers for this work, we suggest:

- Rachel Dutton (UCSD, California; [rjdutton@ucsd.edu](mailto:rjdutton@ucsd.edu))
- Primrose J. Boynton (Wheaton College, Massachusetts; [boynton\\_primrose@wheatoncollege.edu](mailto:boynton_primrose@wheatoncollege.edu))
- Isak S. Pretorius (Macquarie University, Australia; [sakkie.pretorius@mq.edu.au](mailto:sakkie.pretorius@mq.edu.au))

I submit this manuscript on behalf of my co-authors, and I declare that this manuscript is not under consideration elsewhere. However, please, note that the current version of this manuscript has been already posted in the preprint server BioRxiv (<https://www.biorxiv.org/content/10.1101/2022.12.15.520418v1?rss=1>).

All the funding and competing interest are declared in the manuscript.

Looking forward to hearing from you.

Best regards,

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