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# Ecology and diversity of yeasts in fermented food ecosystems

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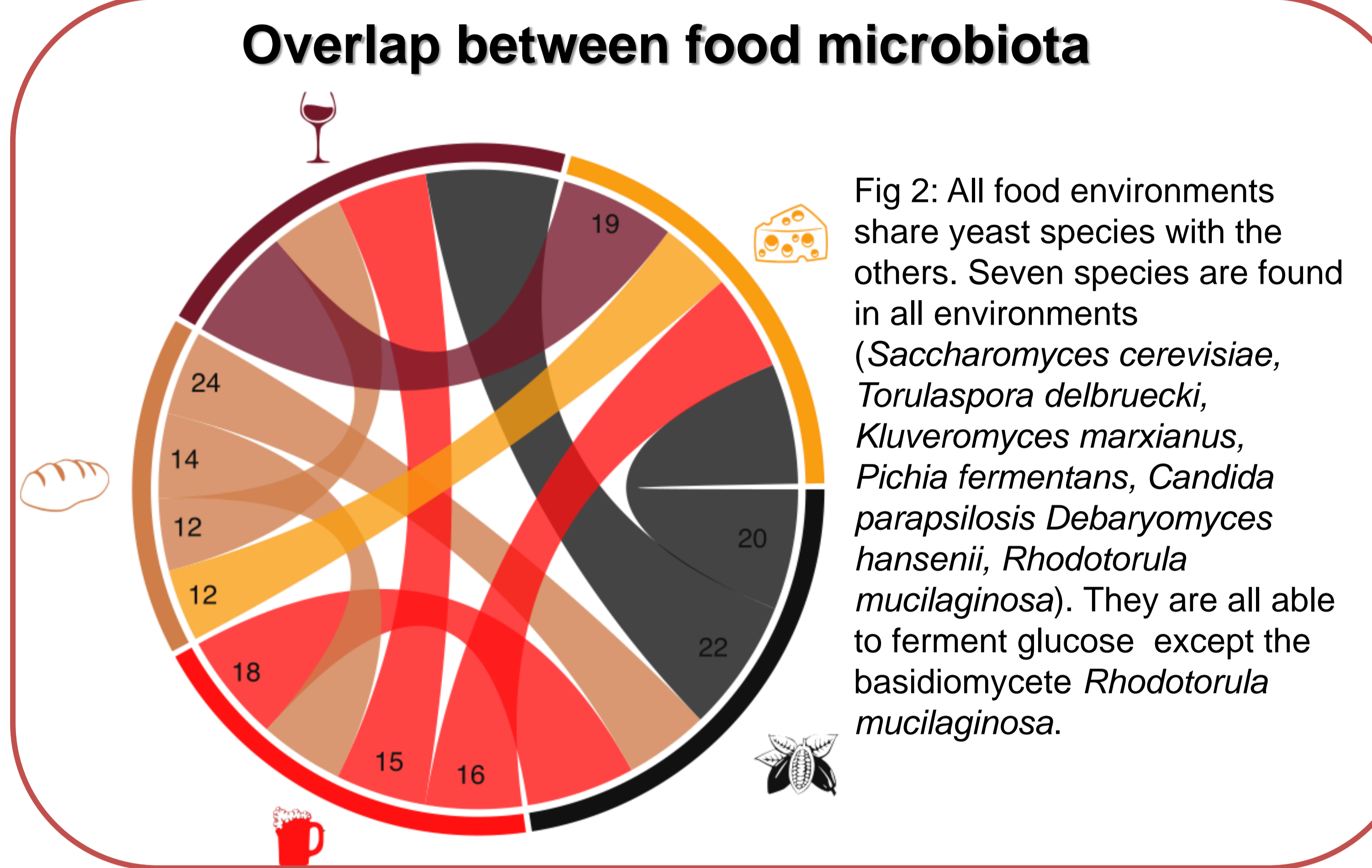
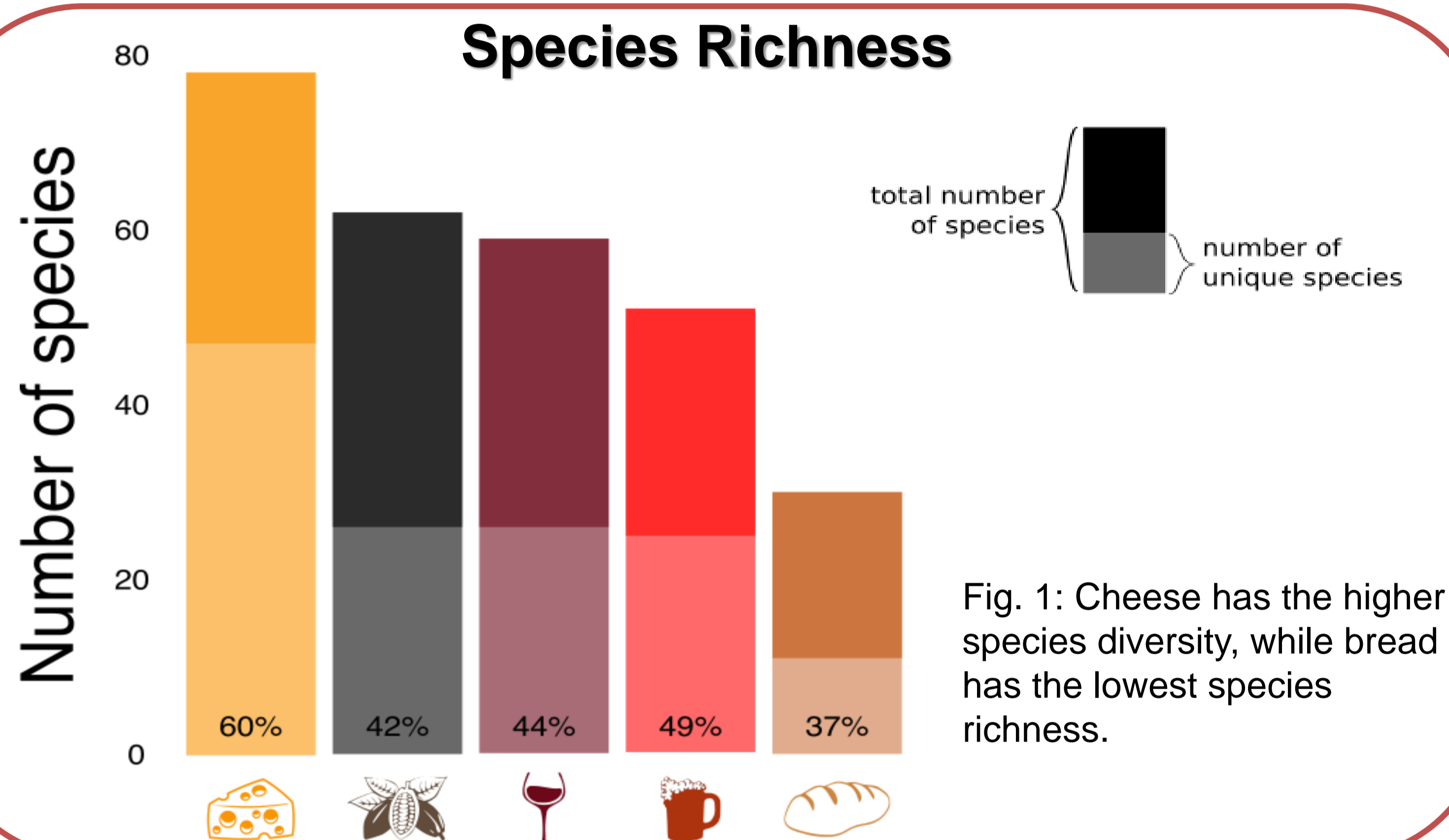


## Introduction:

Fermentation can be regarded as one of oldest food processing technologies. For centuries, the practical knowledge of fermentation processes has been transferred through generations. Some fermented food products have a global distribution, whilst others are restricted to particular human cultures. Here, we have chosen to compare microbial communities of global spread fermented products: bread, wine, beer, chocolate and cheese. These microbial communities are composed of both bacteria and yeasts, but we have focused on yeast diversity. We compared incidence and diversity between different food environments. We describe i) the diversity of each environment, ii) the ubiquity of each yeast species and iii) the overlap between food products and their neighbor environments.

## Methods

The species incidence data for this analysis came from 85 published papers investigating yeast diversity in food fermentations. Yeast named unambiguously using both genus and species name were used, and these names were checked against the online Yeast 2011 resource for synonyms and taxonomic reassignments. The consulted papers provided us with a dataset of 320 yeast species in 8 environments (5 fermented food products bread, wine, beer, chocolate and cheese; and 3 associated environments grapes, flies and raw milk). We based the analysis on presence/absence data within each environment. The R packages ggplot, plotly, vegan, circlize, plotrix, FactoMineR, dendextend were used for analysis and visualization. Phylogenetic trees were constructed using the ITS region sequences of type strains downloaded from the YeastIP database (<http://genome.jouy.inra.fr/yeastip/index.php>) or from the CBS database when not available in YeastIP (<http://www.cbs.knaw.nl/>). The phylogeny was inferred by using the Maximum Likelihood method based on the Tamura-Nei model. The tree with the highest log likelihood is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Phylogenetic analyses were conducted in MEGA6



## Beta diversity between food products

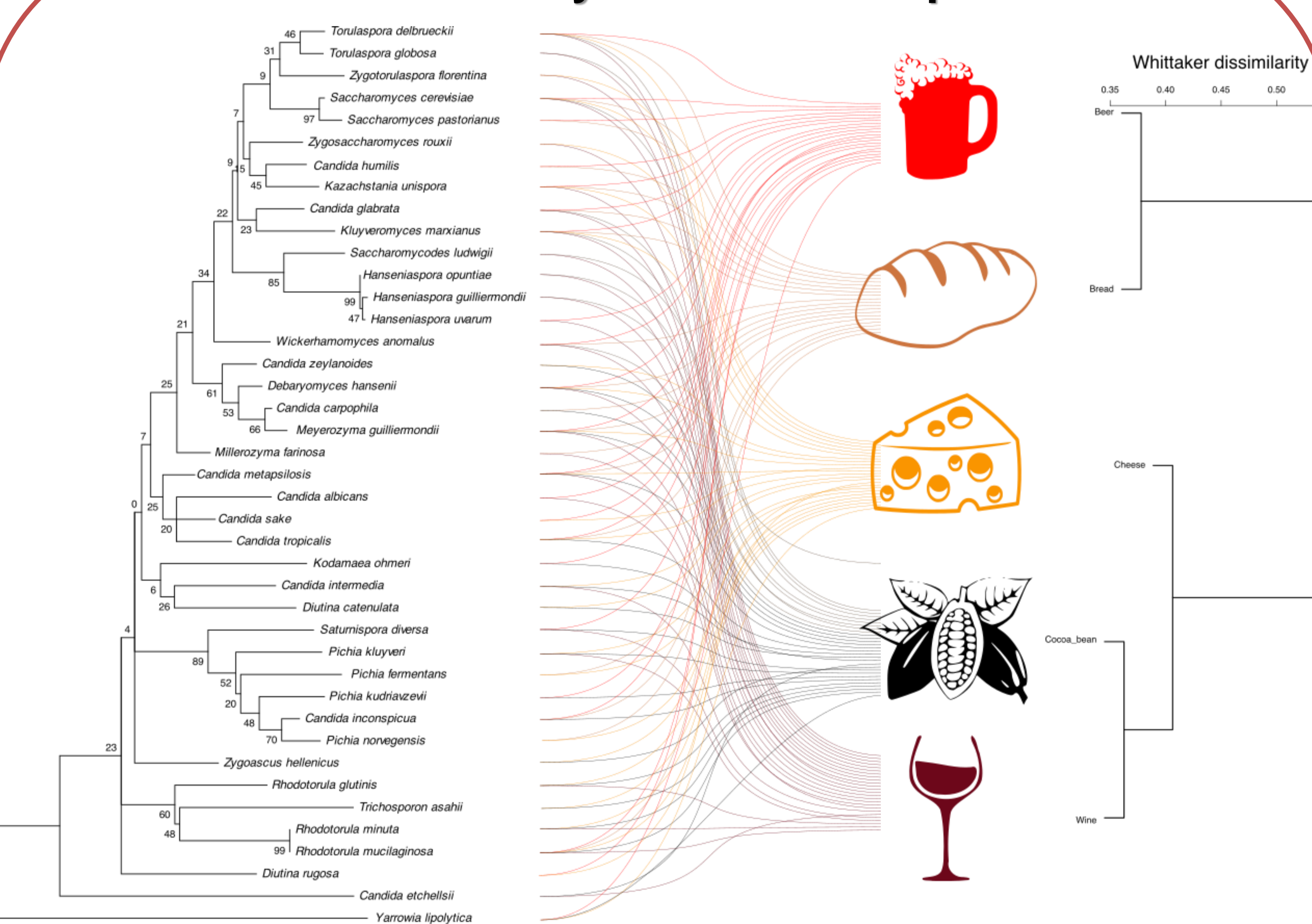


Fig. 3: The similarity between food environments based on shared species is not mirrored by their phylogeny.

## Conclusions

We performed an extensive literature survey and we were able to compare the yeast diversity and community composition in the five most important and world spread fermented food ecosystems. We observed that only seven out of 320 species detected are present in all the five environments. We showed that the grouping between environments based on species diversity is not related with phylogeny: There are not specific clades associated with specific environments. Moreover, we confirm that "fermentative" communities are not only dominated by *Saccharomyces* yeasts and that even non-fermentative species are ubiquitous in fermented food. Finally we highlighted the potential influence of vectors and origin of substrates in the contribution of yeast species diversity. The role of dispersion on the formation of fermentative microbial communities still needs to be studied in further depth.

## Species dispersion

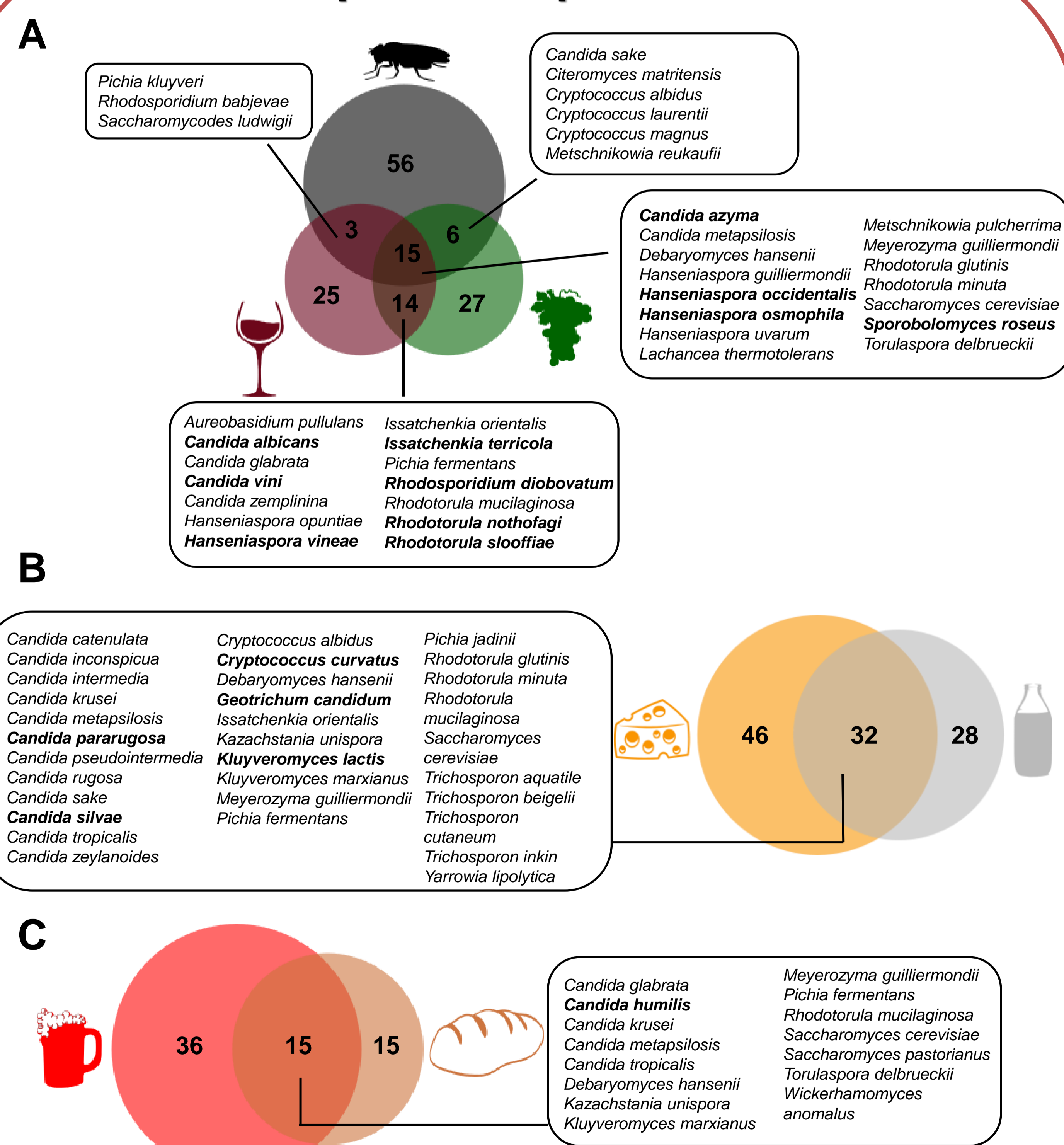


Fig. 4: A) Yeast may be dispersed by insects. Among the seven yeast species that were found in all the fermented products, four of them were also found in drosophila (*S. cerevisiae*, *T. delbrueckii*, *C. parapsilosis*, *D. hansenii*). Fly vectoring in the wine ecosystem may occur directly on must fermentation or on grapes. B) 32 species found in final cheese products may have been derived from raw milk. C) Beer and bread share 15 species which may have common origin in cereals. Unique species from each compared set of habitats are highlighted in bold.