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## Wheat sourdoughs: a new model to link ecology and evolution

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We are studying wheat sourdough as a new ecosystem model for linking ecology and evolution. The sourdough consists of a mixture of flour and water that is fermented by yeasts and lactic acid bacteria (LAB). The baker can make it in a natural way by mixing flour and water in its bakehouse (natural sourdough) or on the opposite can purchase it from outside. Like in batch culture, bakers refresh natural sourdough along and between bread-making process by adding fresh flour and water. The microbial dynamic and the microbial genetic and phenotypic evolution of these semi-opened sink/source ecosystem can be studied, when including bakers in participatory research action. The species diversity of wheat sourdough has been intensively described in European artisan bakers. Most sourdough contains *S. cerevisiae* as dominant yeast species or a species belonging to the *Saccharomyces* most-closely related clade, *Kazachstania*. Using metabarcoding analysis (pyrosequencing and Illumina) and identification of over 1000 yeast isolated strains, we have analyzed the species composition of sourdoughs coming from 36 French bakers with diverse socio-cultural practices (farmer-bakers, artisan bakers, companies). We found that geography did not explain the sourdough species composition but bakery practices did. While companies mostly carry *S. cerevisiae* as dominant sourdough species, farmer-bakers harbor much higher species diversity with new yeast species of the *Kazachstania* clade. The analysis of the metabolic phenotype (i.e. fermentation kinetics, glucose, maltose, acetate, lactate, glycerol and ethanol consumption/production) and population size of sourdough isolated strains and type strains of six *Kazachstania* species and *Saccharomyces cerevisiae* revealed phenotypic convergence of sourdoughs strains

belonging to different yeast species. The genome of the *Kazachstania* species are currently sequenced and annotated and will be used to identify the genes that might be associated to the phenotypic convergence, using RNAseq analysis.