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HOW *S. CEREVISIAE* YEAST HAS SHAPED ITS GENOME TO ADAPT TO ANTHROPOGENIC ENVIRONMENTS

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The yeast *Saccharomyces cerevisiae* plays an important role in food and beverage fermentations. In order to know how environmental constraints imposed by anthropogenic niches have shaped *S. cerevisiae* genomes and phenotypes, we sequenced the genome of 82 *S. cerevisiae* strains from various ecological origins. Using these genomic data, we found additional genetic elements acquired by introgression or by horizontal transfer. Here, we present two remarkable examples of divergent adaptation associated to yeast domestication for wine and milk fermentation. Firstly, we demonstrated the role of oligopeptide transporters encoded by *FOT* genes, which are recently acquired by wine yeasts from *Torulaspora microellipsoides*. These transporters with a broader specificity than *S. cerevisiae* dipeptides transporters, confer a strong competitive advantage during grape must fermentation and thus play a key role in the adaptation of wine yeasts to the nitrogen-limited wine fermentation environment. The genome of cheese strains, secondly, present some particular features. Genes of the *GAL* locus were replaced by their orthologues from a species apparently basal to the *Saccharomyces* clade. Allelic exchange of this locus in a wine strain enables improves growth speed in a media containing the two hexoses such as when released from the hydrolysis of lactose. In addition, a highly divergent high affinity transporter *GAL2* and a specific allele of the regulator *GAL80* were found. This work highlights the remarkable plasticity of yeast genomes as a mechanism of their adaptation to their environments.