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Intraspecific diversity of recombination in *S. cerevisiae*

Matthieu Falque

GQE– Le Moulon, INRA, Univ. Paris-Sud & Université Paris-Saclay, France

Allelic recombination due to meiotic crossovers is a major driver of genome evolution, as well as a key player for the selection of high-performing genotypes in economically important species. To get more insights into crossover regulation, we developed a high-throughput method to measure recombination rate and crossover interference in 26 *S. cerevisiae* strains representing a large part of the diversity of the species. 15 intervals were monitored, covering chromosomes VI and XI entirely, and part of chromosome I. Average recombination rates and recombination landscapes varied significantly across strains, and some regions showed up to 9.5-fold variation. We observed interference which varied across strains and was positively correlated with crossover number. Recombination rate was strongly and negatively correlated with whole-genome sequence divergence between homologs, but less so when using solely

the sequences of the intervals probed for recombination and even less so when using the sequences in the DSB rich regions within these intervals, indicating that the negative correlations are not explained by cis-effects only. Finally, to investigate the genetic architecture of crossover rate, we built an incomplete diallel design from five parental strains and measured recombination in one region of chromosome XI for 10 different hybrids. The results suggest that recombination rate across hybrids may be mainly controlled by the level of sequence divergence between parental strains and by inbreeding effects, while additive effects of parental alleles were hardly significant. These results open the way to a better understanding of the genetic control of crossover formation, as well as building more efficient designs for yeast selection in industrial applications.

e: matthieu.falque@inra.fr