

Heterosis between and within yeast species

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We are particularly interested in the performance of the first hybrid generation (F1 hybrids), especially when hybrids are viable and able to outperform one or both parents under different environmental conditions, a phenomenon known as heterosis. The aim of our work was to understand and identify mechanisms underlying heterosis. We used *Saccharomyces* yeasts as a model system due to their laboratory practicality, their ability to form viable hybrids and reliable fitness measurements. First, we competed a range of different F1 hybrids with their wild or domesticated parental populations; we identified prevalent heterosis for crosses between domesticated and wild populations of different yeast species but not for crosses between wild populations of the same yeast species. Thus the environment from where parental strains were isolated seems to affect heterosis, and F1 hybrids with a domesticated background display more extensive heterosis. By using monosporic clones as parental strains in heterosis studies we might be inflating heterosis measurements due to parental disadvantage and not the F1 hybrid advantage. Thus we set out to compare asexual fitness of heterozygous yeast isolates with homozygous monosporic clones for both domesticated and wild yeast populations; we found that the monosporic cloning might explain some, but not all, of the heterosis seen, potentially accounting for the difference in heterosis between domesticated and wild yeast strains. We then focused on heterosis at the transcriptome level and analysed the transcription of a representative heterotic F1 hybrid relative to its parents in environments that favoured one or the other parent. Hybrid transcription was varied and resembled the fitter parent in specific environments. For the first time to our knowledge, multigenic heterosis at a transcriptome level was identified, which render the F1 hybrid better adapted than its parents to different environmental conditions. Heterosis studies in *Saccharomyces* yeasts, due to their simplicity, can evidence characteristics with an impact on heterosis while also tracing the evolutionary history of divergent populations.

