

Transcriptional responses to priority effects in nectar yeast

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Abstract

Priority effects, where the order and timing of species arrival influence the assembly of ecological communities, have been observed in a variety of taxa and habitats. However, the genetic and molecular basis of priority effects remains unclear in most cases, hindering the mechanistic understanding of priority effects. We sought to gain such understanding for the common nectar yeast *Metschnikowia reukaufii*, which engages in strong priority effects with other species of nectar yeast, including *M. rancensis*, another species commonly found in the nectar of our study plant, the hummingbird-pollinated *Diplacus* (*Mimulus*) *aurantiacus*. After inoculation into two contrasting types of synthetic nectar simulating early arrival of *M. rancensis*, we conducted whole-transcriptome sequencing of 108 genetically diverse strains of *M. reukaufii*. We found that several genes were differentially expressed in *M. reukaufii* strains when the nectar had been conditioned by growth of *M. rancensis*. Many of these genes were associated with amino acid metabolism, consistent with our previous finding that early-arriving species limit late-arriving species' growth by reducing amino acid availability. Furthermore, investigation of expression quantitative trait loci (eQTLs) revealed that genes involved in amino acid transport and resistance to antifungal compounds were enriched in genetic variants, with differing effects on gene expression based on priority effects of *M. rancensis*. These results demonstrate that intraspecific variation in the ability of nectar yeasts to respond to nutrient limitation and direct fungal competition may underpin the molecular mechanisms of priority effects.

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