Genomic Evolution of the Ascomycete Yeasts

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Galactose utilization. Galactose is a hexose sugar found in lignocellulose among other sources, which can be utilized by many yeasts, and in some cases, fermentation is achieved. The first three steps of galactose metabolism are catalyzed by GAL1 (galactokinase), GAL2 (galactokinase-1-phosphate uridylyl transferase), and GAL10 (UDP-glucose-4-epimerase). In general, galactose utilization is widespread in the yeasts, including Saccharomyces and Basidiomycota, and is accompanied by known galactose utilization genes. However, some strains of Ogataea polymorpha and Ascomycota rubescens are known to have sequenced lack known galactose utilization genes. Moreover, Nadsonia fulvescens and Schizosaccharomyces pombe possess galactose utilization genes, yet appear not to use galactose. These discrepancies can be explained by experimental error, misannotation, or differences among strains, but may also indicate our incomplete understanding of galactose utilization in the yeasts.

Methotrophy (methanol utilization). Several yeast species can metabolize methanol, including the newly-published Ogataea polymorpha and Candida arborescens. To investigate the evolution of methotrophy, we reanalyzed the yeast genomes for the methanol pathway genes described in Klenk et al. Methotrophy appears to have evolved once within the Saccharomyces, and only the known methotrophic species contain a complete set of methotrophy genes. Additionally, the distribution of methotrophy genes on the phylogenetic tree implies that losses of the AOX, DAS, and FDH genes led to the loss of methotrophy in Pichia manniicola and Debora trivialis.