GENOMIC ADAPTATIONS OF INDUSTRIAL FUEL ETHANOL PRODUCING *SACCHAROMYCES CEREVISIAE* YEAST STRAINS

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Growing environmental concerns over the use and depletion of nonrenewable fuel sources have recently stimulated interest in optimizing fermentation processes for large-scale production of fuel ethanol. In Brazil over 17 billion liters per year of ethanol are produced using sucrose rich broths (cane juice and/or molasses) and selected *S. cerevisiae* industrial strains. Since genetic differences between yeast strains used in these industrial processes may account for their dominance and fermentation efficiency, we have determined genome copy number differences among several industrial yeasts used for fuel ethanol production by microarray karyotyping (array-CGH). The yeast strains analyzed showed significant genomic differences with respect to the laboratory strain S288C and other industrial yeast strains (baking, brewing, and wine yeasts). Most differences were observed at telomeric or subtelomeric chromosomal regions, and generally represented deleted or highly polymorphic loci. These included several genes encoding for sugar transporters, both for hexoses (*HXT*) and maltose and other sugars (*MAL* and *MPH*), as well as genes involved in flocculation (*FLO*). Among the few genes that are consistently amplified in the fuel ethanol yeast strains were genes involved in pyridoxine and thiamine biosynthesis (*SNO* and *SNZ*), indicating that these industrial yeast cells probably have a greater demand for these vitamins. Indeed, our results indicate that these amplifications allow the industrial fuel ethanol yeasts to grow efficiently in media containing any combination of these two vitamins, especially at high sugar concentrations. Other examples of genomic engineering strategies developed for improved ethanol production from sucrose will be also presented.

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