

Genome Sequencing of the Yeast *Saccharomyces cerevisiae* Strain 202-3

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Abstract : In this work the sequencing and genome characterization of a natural isolate of *Saccharomyces cerevisiae* yeast (strain 202-3), identified with potential for the production of second generation ethanol from sugarcane bagasse hydrolysates is presented. This strain was selected because its capability to consume xylose during the fermentation of sugarcane bagasse hydrolysates, taking into account that many strains of *S. cerevisiae* are incapable of processing this sugar. This advantage and other prominent positive aspects during fermentation profiles evaluated in bagasse hydrolysates made the strain 202-3 a candidate strain to improve the production of second-generation ethanol, which was proposed as a first step to study the strain at the genomic level. The molecular characterization was carried out by genome sequencing with the Illumina HiSeq 2000 platform paired end; the assembly was performed with different programs, finally choosing the assembler ABYSS with kmer 89. Gene prediction was developed with the approach of hidden Markov models with Augustus. The genes identified were scored based on similarity with public databases of nucleotide and protein. Records were organized from ontological functions at different hierarchical levels, which identified central metabolic functions and roles of the *S. cerevisiae* strain 202-3, highlighting the presence of four possible new proteins, two of them probably associated with the positive consumption of xylose.

Keywords : cellulosic ethanol, *Saccharomyces cerevisiae*, genome sequencing, xylose consumption

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