

Comparative mitogenomics of *Sugiyamaella* species, yeasts of biotechnological importance

Paula Silva Matos, Heron Hilário, Rennan Garcias Moreira, Carlos Augusto Rosa,
Thiago Mafra Batista, Glória Regina Franco

Universidade Federal do Sul da Bahia

Abstract

Microorganisms are widely used in the industry to produce several compounds. In the bioethanol production the most commonly used yeast is *Saccharomyces cerevisiae*, which converts sugars, mainly from sugarcane, into ethanol. However, this yeast is unable to degrade some plant polymers such as lignin to fermentable sugars, which prevents full use of the raw material. Some yeasts, like *Sugiyamaella xylanicola*, are able to metabolize these polymers, being promising candidates for second-generation ethanol production. These capabilities are conferred by enzymes encoded in the nuclear genomes of these microorganisms. However, phylogenetical information about fermenting yeasts can be obtained by sequencing their mitochondrial genomes, since they are small, ease to assemble and contain informative gene sequences. In this study we sequenced, assembled and annotated the mitogenome of the yeast *S. xylanicola* UFMG-CM-Y1884T, collected from decaying woods in the Caraça Mountains of Minas Gerais. The complete mitogenome of *S. xylanicola* was characterized and compared with previously published *S. lignohabitans* CBS 10342 and *S. cerevisiae* mitogenomes. The *Sugiyamaella* mitogenomes are 28 and 48 Kb long, and shorter than the 85 Kb *S. cerevisiae* mitogenome. A total of 26 and 46 mitochondrial tRNAs were annotated for *S. xylanicola* and *S. lignohabitans*, respectively, which consist of more than the minimal set of 24 tRNAs required for translation, reported for *S. cerevisiae*. The *Sugiyamaella* mitochondrial genomes encode a complete respiration system, including NADH dehydrogenase complex I. In *S. cerevisiae* and several other yeasts, complex I is missing, which leads to a reduction of the respiratory energy yield. Further, we intend to investigate other aspects of mitochondrial genomes in order to discover additional possible *Sugiyamaella* advantages over the more commonly used yeasts for ethanol production.

Funding: Pronex/FAPEMIG