Bioprospection of D-xylose fermenting yeasts and discovery of a new efficient species - *Spathaspora* sp. nov.

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Plant biomass is one of the cheapest and most abundant renewable feedstock for sustainable development and is a promising source for biofuel production. Bioethanol produced from lignocellulose, known as second generation ethanol, have a promising potential as a biofuel. The polysaccharides components of the lignocellulosic material, such as cellulose and hemicellulose, can be converted (by hydrolysis) into simple sugars like xylose and glucose, which can be used as substrate for fermentation. Some yeasts not belonging to the genus *Saccharomyces* spp. have the ability to convert the components of the hemicellulosic fraction (xylose an arabinose) to ethanol. In this context, the aim of the present study was the isolation and identification of yeasts from tree trunk in decomposition, in order to assess their ability in the bioconversion of xylose to ethanol. For that, it was used for bioprospection a naturally enriched environment in hemicellulose degradation, the decaying wood. The samples were collected from a Purple Quaresmeira (*Tibouchina granulosa*) located at the ESALQ campus in Piracicaba, Sao Paulo. Eighty-three colonies were isolated with YNBX media, which after were inoculated in a media containing D-xylose as a sole carbon source. Only 11 strains did not showed the ability of ethanol production from xylose. The strains that exhibited this ability varied from 0.60 to 6.58 g L^{-1} of ethanol. Among all isolated strains, I38 and I54 were the highest ethanol producers. The I38 strain showed significantly higher results than the standard strains *Spathaspora arborariae* HM19.1A and *Sheffersomyces stipitis* NRRLY7124, while the I54 strain did not differed from HM19.1A, but was higher than the NRRLY7124. Based on the sequencing results (Sanger platform) of the D1/D2 domains of the large subunit of rRNA gene and of the ITS-5.8S region of rRNA gene, both strains (I38 and I54) were identified as a new species of the *Spathaspora* genus (*Spathaspora* sp. 1). Regarding the sequences of the D1/D2 domains, Spathaspora sp. 1 differs in 6 and 10 bp from the most related species *Spathaspora brasiliensis* (GenBank accession JN099271) and *Candida materiae* (GenBank accession FJ154790), respectively. According to the ITS region, this new species differs by 24 bp and one gap from the species *Sp. brasiliensis* (GenBank accession JN099271), and 24 bp and 14 gaps from *Candida jeffriesii* (GenBank accession NR111398). Currently, we are performing the description of this new species.