



Brazilian Bioethanol Science and Technology Laboratory

In silico exploitation of the genome and transcriptome of *Pseudozyma brasiliensis* GHG001 for bioethanol production.

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IMPORTANCE OF THE WORK

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Second generation bioethanol using pentoses, that represent a large portion of the lignocellulosic biomass such as sugarcane bagasse, is currently not possible using industrial yeast strains (*Saccharomyces cerevisiae*) since they do not naturally ferment these sugars.

The genus *Pseudozyma* has members with biotechnological potential. *P. brasiliensis* GHG001, isolated from the intestinal tract of a *Chrysomelidae*, has shown great potential for biomass deconstruction, since it grows using xylose and xylan as sole carbon sources and produces high amount of an endoxylanase (GH11). We have assembled its genome for further analyses.

We have isolates of putative new species of the genus. Genome assembly and their improved annotation (using e.g. RNAseq) will help finding new genes coding for enzymes for biomass hydrolysis and pentose catabolism, regulatory regions, pentose transporters, that could be used in the transformation of *S. cerevisiae*. Future goals include Comparative Genomics with other members of *Ustilaginaceae*, and a Systems Biology approach using integrated annotation and transcriptomics data, that might improve our understanding of pentose assimilation and predict phenotypes for second generation bioethanol. **PREVIOUS WORK**





(A) Growth of *P. brasiliensis* in minimal medium with different carbon sources. (B) Endoxylanase activities of the supernatant from cultures grown for 120 h at 30°C in glucose (1%), xylose (2%) and xylan from beechwood (2%). (C) Endoxylanase activities of the supernatant from culture grown for 96 h at 30 °C in xylan from beechwood (2%).



Phylogenetic tree of *Pseudozyma spp.*, including other members of *Ustilaginaceae* (ITS1, ITS2 and D1/D2 of the LSU rRNA). The isolates in our laboratory: *Pseudozyma brasiliensis* GHG001, *Pseudozyma sp.* F16C1, *Pseudozyma sp.* F2C2, *Pseudozyma sp.* F5C1, and *Pseudozyma sp.* F8B2 (red arrows).







CURRENT WORK

Genome assembly and annotation of the isolates of the genus *Pseudozyma*.



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