Survey of fungal lignocellulose-acting enzymes for improved plant biomass degradation capacities

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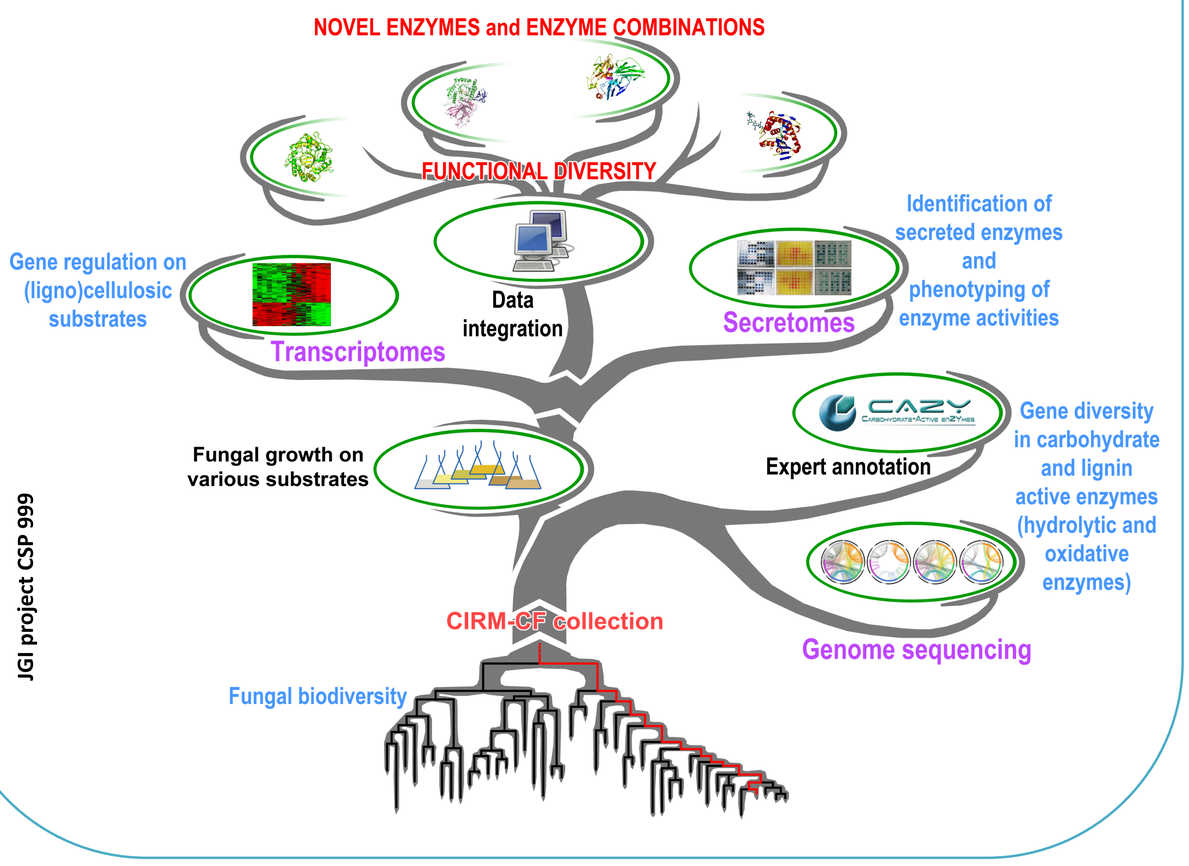
Comparative genomics of fungal enzyme machinery

- Filamentous fungi are the most potent degraders of lignocellulosic biomass
- They secrete high number and a broad variety of carbohydrates-active enzymes and lignin-active enzymes (CAZymes) **Levasseur et al. 2013. Lombard et al. 2013.**

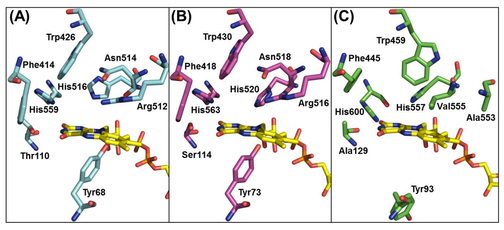


Genome sequencing and enzyme characterization

- CIRM a Biological Resource Center dedicated to the preservation of filamentous fungi of interest to agro-industries and their utilization (http://www6.inra.fr/cirm/Champignons-Filamenteux)
- The first genome sequence : *Pycnoporus cinnabarinus* : fungal model to study the enzyme mechanism to degrade lignin **Levasseur et al. 2014.**

Family	Total gene number
AA1 (multi-copper oxidases)	**5 laccases** *sensu stricto*, 1 Mco, 1 ferroxydase
AA2 (class II peroxidases)	**12** (4 LiP, 1 VP, 1 atypical-VP, 3 short-MnP, 2 chloroP, and 1 partial protein)
AA3_1 (cellobiose dehydrogenase)	1
AA3_2 (AAO, glucose oxidase/dehydrogenase)	19
AA3_3 (alcohol oxidase/dehydrogenase)	2
AA3_4 (pyranose oxidase)	2
AA5_1 (copper radical oxidases)	**7** (3 Glyoxal oxidases *sensu stricto*, 4 Cro)
AA6 (benzoquinone reductase)	1
AA8	1
AA9 (LMPO)	15
Total	60

- Enzyme characterization, structure/function studies, chimerical enzymes (bi-functional), enzyme synergy
- Applications of enzymes for lignin valorization (Indox project)

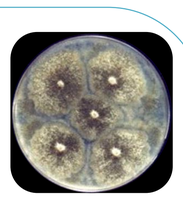


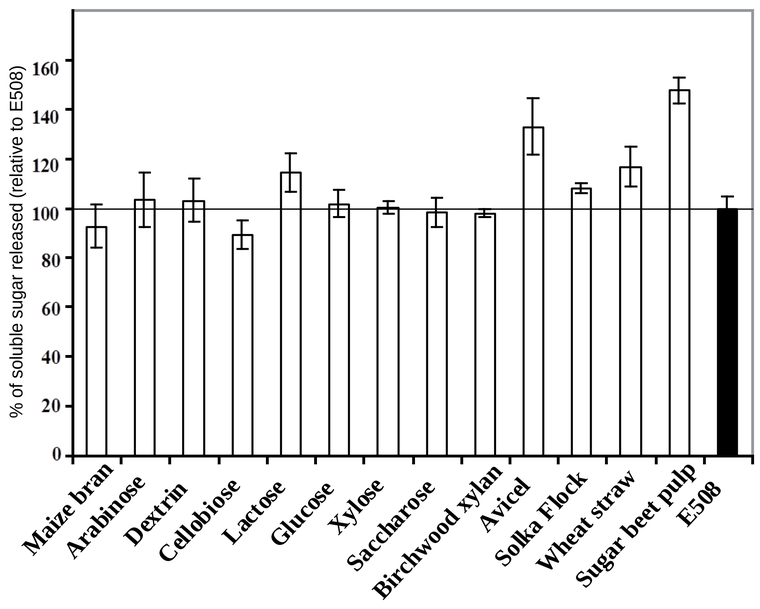
Fungal secretome analysis

- *Podospora anserina* : coprophilous fungus model adapted to complex biomass conversion
- *Pestalotiopsis sp* : mangrove fungal model to study salt-adapted enzymes

Podospora anserina

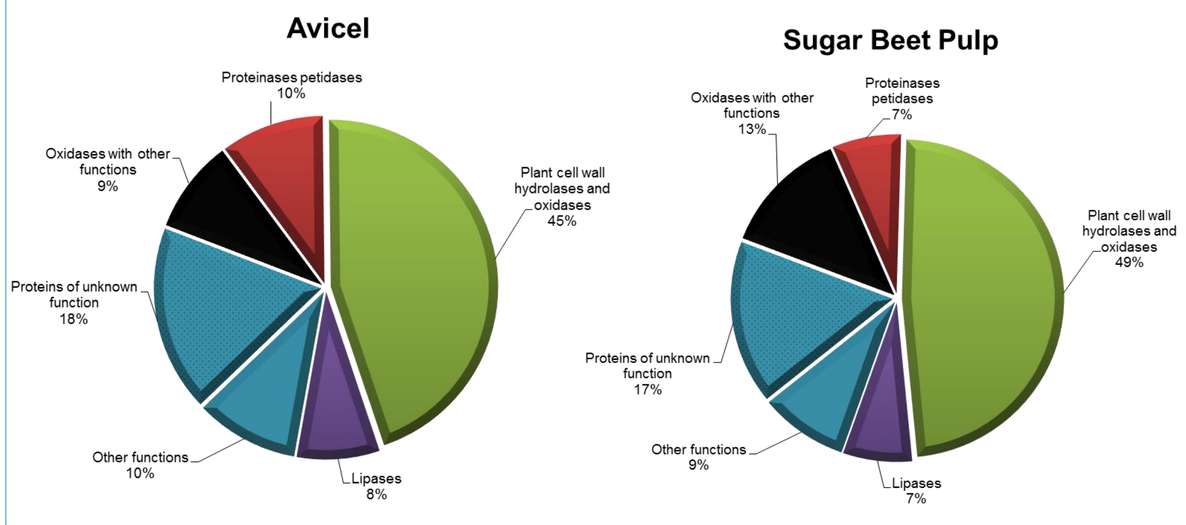
Poidevin et al. 2014





Wheat straw hydrolysis by *T. reesei* cellulases (E508) supplemented by *P. anserina* secretomes

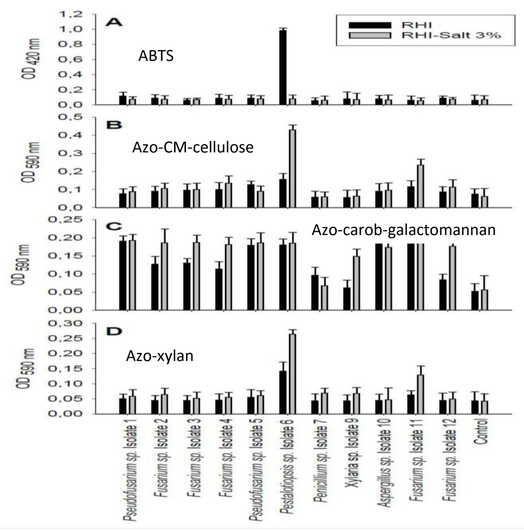
Proteomic analyses



Functional category analysis of the 142 proteins detected in *P. anserina* secretomes grown on Avicel and Sugar Beet Pulp.

Pestalotiopsis sp.

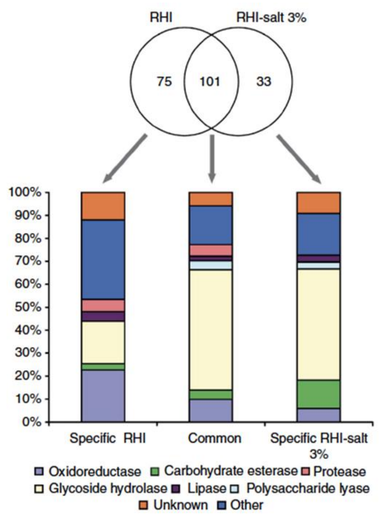
Arfi et al. 2013.

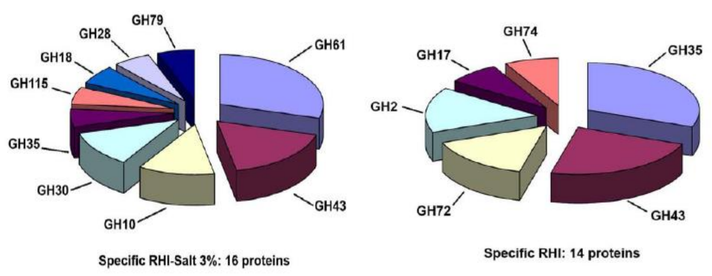


Rhizophora stylosa

Identification of salt tolerant enzymes : lignocellulolytic activity screening of isolated mangrove fungi after 8 days cultivation on non-saline or 3% saline conditions

Proteomic analyses





Salinity => Xylanases (GH43, GH10, GH30)
=> Cellulases (GH61, AA9 LPMO)

209 identified proteins with differential secretion : secretion of oxidoreductases found to be limited under saline conditions while cellulase and hemicellulase secretion were increased.

Arfi et al, 2013, Adaptation to salt of the lignocellulolytic arsenal of the mangrove fungus Pestalotiopsis sp. Nature Communications, 4:1810.
Lombard et al. 2013. "The Carbohydrate-active enzymes database (CAZy) in 2013" Nucleic Acids Res 42:D490–D495
Levasseur et al. 2013, Expansion of the enzymatic repertoire of the CAZy database to integrate auxiliary redox enzymes. Biotechnol Biofuels. 6(1):41.
Levasseur et al. 2014, The genome of the white-rot fungus Pycnoporus cinnabarinus: a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. BMC Genomics, 15(1):486.
Poidevin et al. 2014. "Comparative Analyses of *Podospora anserina* Secretomes Reveal a Large Array of Lignocellulose-Active Enzymes." Applied microbiology and biotechnology In Press.