

Phylogeny and comparative genome analysis of Basidiomycete fungi

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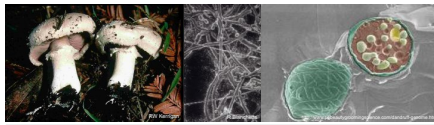
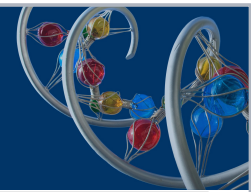
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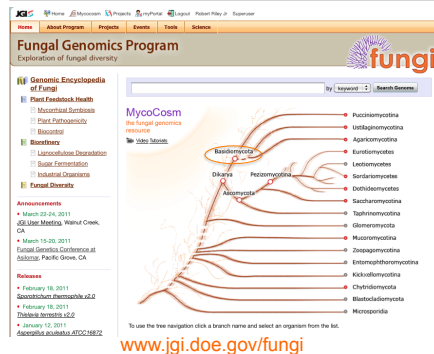
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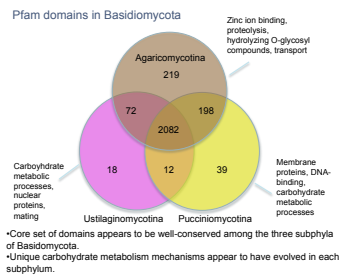
I. Abstract

Fungi of the phylum Basidiomycota, make up some 37% of the described fungi, and are important from the perspectives of forestry, agriculture, medicine, and bioenergy. This diverse phylum includes the mushrooms, wood rots, plant pathogenic rusts and smuts, and some human pathogens. To better understand these important fungi, we have undertaken a comparative genomic analysis of the Basidiomycetes with available sequenced genomes. We report a phylogeny that sheds light on previously unclear evolutionary relationships among the Basidiomycetes. We also define a 'core proteome' based on protein families conserved in all Basidiomycetes. We identify key expansions and contractions in protein families that may be responsible for the degradation of plant biomass such as cellulose, hemicellulose, and lignin. Finally, we speculate as to the genomic changes that drove such expansions and contractions.

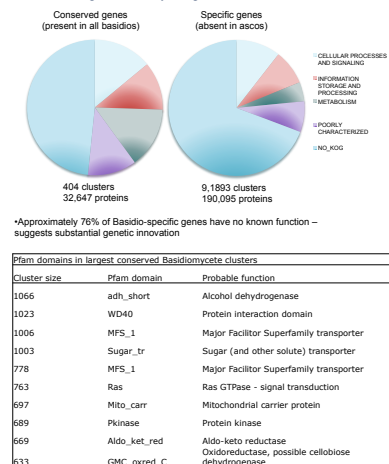
II. MycoCosm – fungal comparative data and analysis tools



IV. Core Basidiomycete genes



MCL clustering of Basidiomycete genes



V. Gain and loss of lignocellulose degrading enzymes

Nonrandomly evolving lignocellulose degrading enzymes

	Carbohydrate metabolism enzymes	Lignin degradation enzymes
Agaricomycota	Agaricus bisporus, Coprinopsis cinerea, Laccaria bicolor, Pleurotus ostreatus, Stereum hirsutum, Trichoderma reesei	Agaricus bisporus, Coprinopsis cinerea, Laccaria bicolor, Pleurotus ostreatus, Stereum hirsutum, Trichoderma reesei
Ustilaginomycota	Ustilago maydis, Ustilago horum, Ustilago violacea	Ustilago maydis, Ustilago horum, Ustilago violacea
Puccinimycota	Puccinia striiformis, Puccinia recondita, Puccinia blight, Puccinia graminis	Puccinia striiformis, Puccinia recondita, Puccinia blight, Puccinia graminis
Basidiomycota	Trametes versicolor, Phanerochaete chrysosporium, Rhizoglyphus cryophilus, Marasmius rotula, Marasmius proterus, Marasmius rotula, Marasmius proterus	Trametes versicolor, Phanerochaete chrysosporium, Rhizoglyphus cryophilus, Marasmius rotula, Marasmius proterus, Marasmius rotula, Marasmius proterus

VII. Conclusions

- Phylogeny of 28 Basidiomycete fungi has been inferred, shedding light on previously unclear position of *Wallemia sebi*
- Core genome analysis shows substantial conservation of Pfam domains between Basidiomycota and Ascomycota, and among the Basidiomycete subphyla, with some unique families of carbohydrate metabolism and proteolysis genes specific to subphyla
- Numerous families of lignocellulose-degrading enzymes are evolving in a nonrandom fashion in Basidiomycota. The white rot phenotype correlates with numbers of FOLY enzymes
- Tandem duplications appear to have played a role in peroxidase expansions in the white rot fungi

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