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Phylogeny and comparative genome analysis of Basidiomycete fungi

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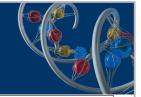
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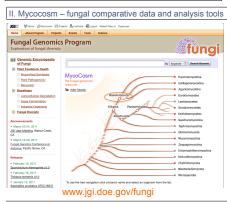
Phylogeny and comparative genome analysis of Basidiomycete fungi

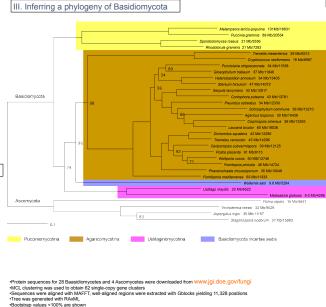
Robert Riley¹, Asaf Salamov¹, David Hibbett², and Igor Grigoriev¹ ¹DOE-Joint Genome Institute and ²Clark University rwriley@lbl.gov





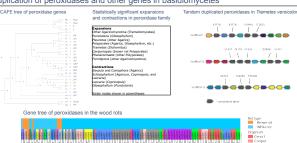
Fungi of the phylum Basidiomycota, make up some 37% of the described fungi and are important from the perspectives of forestry, agriculture, medicine, and bioenergy. This diverse phylum includes the mushrooms, wood rots, plant pathogenic rusts and smuts, and some human pathogens. To better understand 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.

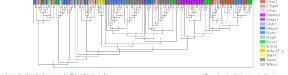




Pucciniomycotina is sister group to the rest of Basidiomycota
 Also notice sister group relationship of Wallemia sebi and Agaricomycotina – phylogenetic position previously unclear

VI. Duplication of peroxidases and other genes in basidiomycetes





Tandem duplicated genes in Basidiomycetes

	Number of		
Pfam	genes in tandems	f_{obs}/f_{exp}	Description
UDPGT	22	16.2	CAZy GT1, UDP glycosyltransferases
CoA_trans	22	15.1	Coenzyme A transferase
KR	81	10.3	Polyketide synthase
DUF465	7	9.0	Myosin/kinesin-associated domain
OsmC	12	8.3	Osmotically inducible stress protein
Ricin_B_lectin	14	7.2	CAZy CBM13, Ricin-type lectin domain
F-box	197	6.6	Protein interaction domain
ВТВ	72	6.5	BTB/POZ domain, protein binding
WSC	25	6.5	Putative carbohydrate binding domain
DUF124	5	6.5	Unknown
Arrestin_N	7	6.0	Arrestin, signal transduction
Ribonuc_red_sm	12	5.6	Ribonuclease reductase
STE3	23	5.3	Pheromone A receptor
Glyco_hydro_20b	5	5.2	CAZy GH20, glycosyl hydrolase
Hydrophobin	81	5.0	Fungal hydrophobin

Genes involved in tandem duplications

_	2500	
	2000	
	1500	
	1000	
	500	+
_	0	
		Ab Cc Lb Po Sc Cp St Ps Gt Fm Cs Ds Fp Pc Pp Tv WcHa Sh Cn TmMp Pg Rg Sr MgUmWs

	Clusters of tandem duplicated genes																					
600																						
500	t							_								\neg	Т					-
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	Ab Cc Lb Po Sc Cp Si Ps Gt Fm Cs Ds Fp Pc Pp Tv Wc Ha Sh Cn TmMp Pg Rg Sr MgUmWa																					

Largest cluster of tandem genes									
	villa								

Ab Cc Lb Po Sc Co St Pa Gt Fm Ca Da Fo Pc Po Tv WcHa Sh Cn TmMo Po Ro Sv MotumWi

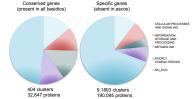
IV. Core Basidiomycete genes



of Basidomycota.

*Unique carbohydrate metabolism mechanisms appear to have evolved in each subphylum.

MCL clustering of Basidiomycete genes



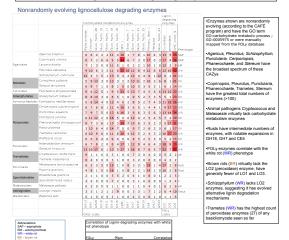
MCL clustering: Enright et al., NAR 2002 30(7):1575-84

MAFFT: Katoh et al., NAR 30(14):3059-66 Gblocks: Castresana, Mol Biol Evol. 2000 17(4):540-52 RAxML: Stamatakis & Alachiotis, Bioinformatics 2010 26(12):132-9

Approximately 76% of Basidio-specific genes have no known function -

Pfam domains in largest conserved Basidiomycete clusters								
Cluster size	Pfam domain	Probable function						
1066	adh_short	Alcohol dehydrogenase						
1023	WD40	Protein interaction domain						
1006	MFS_1	Major Facilitor Superfamily transporter						
1003	Sugar_tr	Sugar (and other solute) transporter						
778	MFS_1	Major Facilitor Superfamily transporter						
763	Ras	Ras GTPase - signal transduction						
697	Mito_carr	Mitochondrial carrier protein						
689	Pkinase	Protein kinase						
669	Aldo_ket_red	Aldo-keto reductase						
633	GMC_oxred_C	Oxidoreductase, possible cellobiose dehydrogenase						

V. Gain and loss of lignocellulose degrading enzymes



VII. Conclusions

·Phylogeny of 28 Basidiomycete fungi has been inferred, shedding light on previously unclear position of Wallemia

*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

 Tandem duplications appear to have played a role in peroxidase expansions in the white rot fungi

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