Comparative analysis of 35 basidiomycete genomes reveals diversity and uniqueness of the phylum

Robert Riley[1*], Asaf Salamov[1], Robert Otillar[1], Kirsten Fagnan[1], Bastien Boussau[2], Daren Brown[3], Bernard Henrissat[4], Anthony Levasseur[4], Benjamin Held[5], Laszlo Nagy[6], Dimitris Floudas[6], Emmanuelle Morin[7], Gerard Manning[8], Scott Baker[3], Francis Martin[6], Robert Blanchette[9], David Hibbett[6], Igor V. Grigoriev

[1]DOE Joint Genome Institute, Walnut Creek, CA, USA; [2]University of California, Berkeley, CA, USA; [3]Pacific Northwest National Laboratory, Richland, WA, USA; [4]Aix-Marseille Université, Marseille, France, [5]University of Minnesota, St. Paul, MN, USA; [6]Clark University, Worcester, MA, USA; [7]INRA, Champenoux, France; [8]Salk Institute for Biological Sciences, San Diego, CA, USA; [9]University of Minnesota, St. Paul, MN, USA

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Comparative analysis of 35 basidiomycete genomes reveals diversity and uniqueness of the phylum

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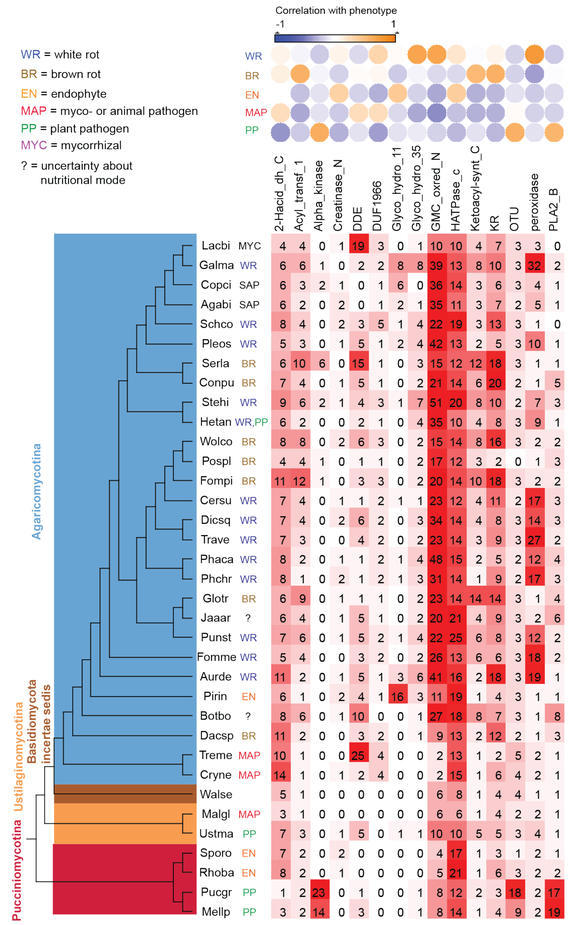
Abstract

Fungi of the phylum Basidiomycota (basidiomycetes), make up some 37% of the described fungi, and are important in forestry, agriculture, medicine, and bioenergy. This diverse phylum includes symbionts, pathogens, and saprobes including wood decaying fungi. To better understand the diversity of this phylum we compared the genomes of 35 basidiomycete fungi including 6 newly sequenced genomes. The genomes of basidiomycetes span extremes of genome size, gene number, and repeat content. A phylogenetic tree of Basidiomycota was generated using the Phyldog software, which uses all available protein sequence data to simultaneously infer gene and species trees. Analysis of core genes reveals that some 48% of basidiomycete proteins are unique to the phylum with nearly half of those (22%) comprising proteins found in only one organism. Phylogenetic patterns of plant biomass-degrading genes suggest a continuum rather than a sharp dichotomy between the white rot and brown rot modes of wood decay among the members of Agaricomycotina subphylum. There is a correlation of the profile of certain gene families to nutritional mode in Agaricomycotina. Based on phylogenetically-informed PCA analysis of such profiles, we predict that that *Botryobasidium botryosum* and *Jaapia argillacea* have properties similar to white rot species, although neither has liginolytic class II fungal peroxidases. Furthermore, we find that both fungi exhibit wood decay with white rot-like characteristics in growth assays. Analysis of the rate of discovery of proteins with no or few homologs suggests the high value of continued sequencing of basidiomycete fungi.

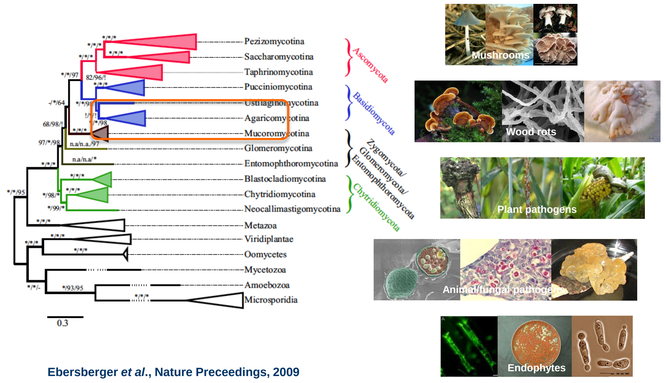
Basidiomycete genomes used in this study

Subphylum	Order	Organism	Genome size (Mb)	Gene number
Agaricomycotina	Agaricales	*Agaricus bisporus*	30.2	10438
		Coprinopsis cinerea	36.3	13393
		Galerina marginata	59.4	21461
		Laccaria bicolor	64.9	19036
		Pleurotus ostreatus	34.3	12330
		Schizophyllum commune	38.5	13210
	Auriculariales	*Auricularia delicata*	74.9	23577
	Boletales	*Serpula lacrymans*	42.8	12917
		Coniophora puteana	43.0	13761
	Cantharellales	*Botryobasidion botryosum*	46.7	16526
	Corticiales	*Punctularia strigosozonata*	34.2	11538
	Dacrymycetales	*Dacryopinax sp.*	29.5	10242
	Gloeophyllales	*Gloeophyllum trabeum*	37.2	11846
	Hymenochaetales	*Fomitiporia mediterranea*	63.4	11333
	Jaapiales	*Jaapia argillacea*	45.1	16419
	Polyporales	*Dichomitus squalens*	42.7	12290
		Ceriporiopsis subvermispora	39.0	12125
		Fomitopsis pinicola	46.3	14724
		Phanerochaete carnosa	46.3	13937
		Phanerochaete chrysosporium	35.1	10048
		Postia placenta	90.9	9113
		Trametes versicolor	44.8	14296
		Wolfiporia cocos	50.5	12746
	Russulales	*Heterobasidion annosum*	33.6	13405
		Stereum hirsutum	46.5	14072
	Sebacinales	*Piriformospora indica*	25.0	11767
	Tremellales	*Cryptococcus neoformans*	18.9	6967
		Tremella mesenterica	28.6	8313
Pucciniomycotina	Pucciniales	*Puccinia graminis*	88.6	20534
		Melampsora laricis-populina	101.1	16831
	Sporidiobolales	*Rhodotorula graminis*	21.0	7283
		Sporobolomyces roseus	21.2	5536
Ustilaginomycotina	Ustilaginales	*Ustilago maydis*	19.7	6522
	Malasseziales	*Malassezia globosa*	9.0	4286
Incertae sedis	Wallemiales	*Wallemia sebi*	9.8	5284

Correlation of protein family copy number with phenotype

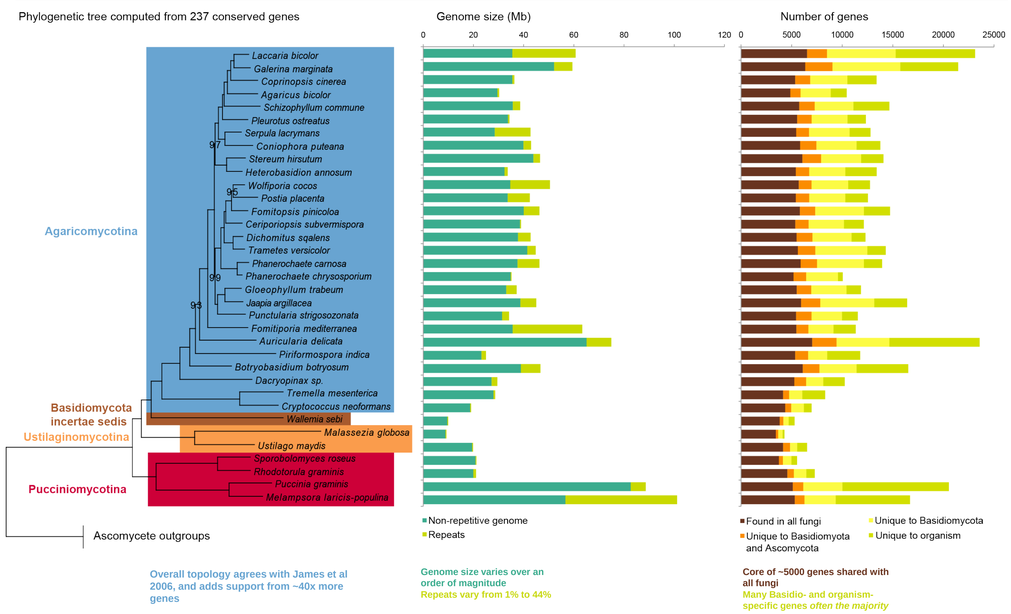


What are the basidiomycetes?



Ebersberger *et al.*, Nature Preceedings, 2009

Genomes overview – phylogeny, genome size, repeat content, number of genes, conservation across fungi

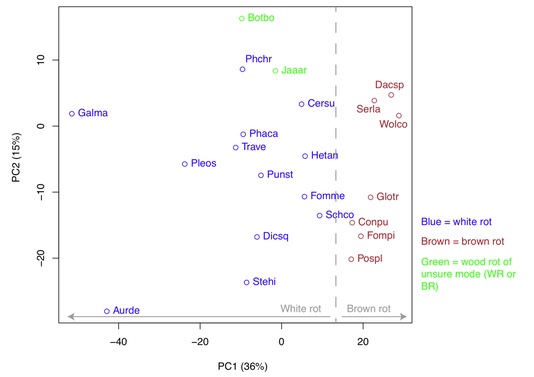


Overall topology agrees with James et al 2006, and adds support from ~40x more genes

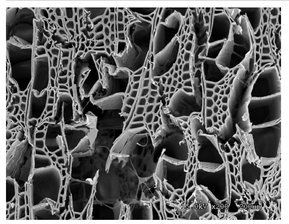
Genome size varies over an order of magnitude
Repeats vary from 1% to 44%

Core of ~5000 genes shared with all fungi
Many Basidio- and organism-specific genes *often the majority*

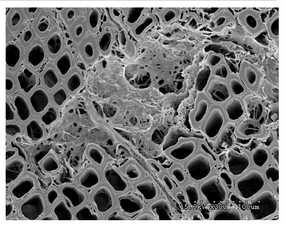
Phylogenetically-informed PCA of wood rotting fungi and their proteins related to carbohydrate/lignin-degradation shows separation of white/brown rots anduggests that *Botryobasidium botryosum and Jaapia argillacea* are white rots, despite both lacking class II lignin peroxidases



Growth assays on wood indicate that *Botryobasidium botryosum and Jaapia argillacea* are indeed white rots – complete degradation of cell walls with mycelia filling voids

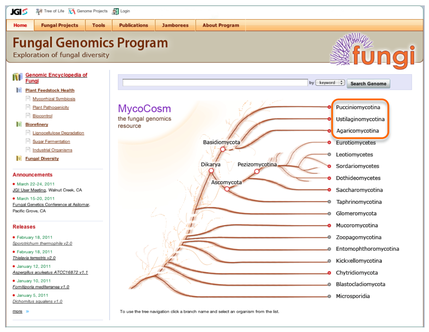


Botryobasidium botryosum on aspen

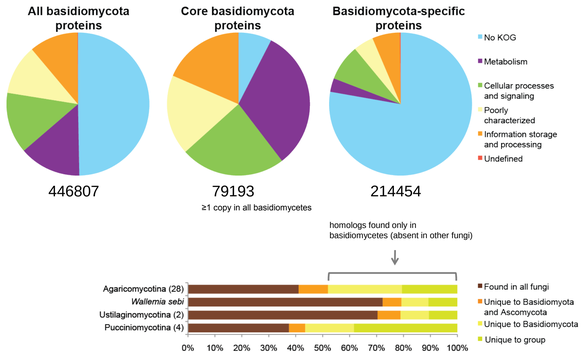


Jaapia argillacea on pine

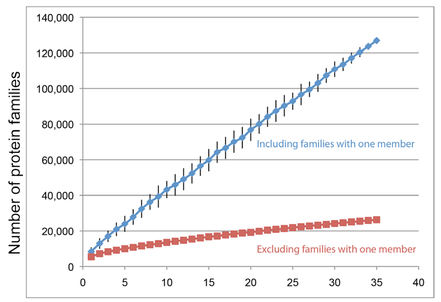
http://jgi.doe.gov/fungi



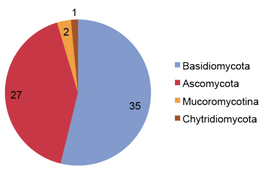
Basidiomycota core genes



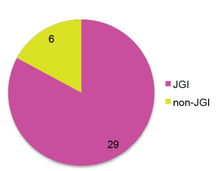
New protein families are discovered with each newly sequenced basidiomycete genome – nowhere near saturation



Number of genomes



Number of basidiomycetes



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