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### Title

Comparative Analysis of 35 Basidiomycete Genomes Reveals Diversity and Uniqueness of the Phylum

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### Publication Date

2013-03-12

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

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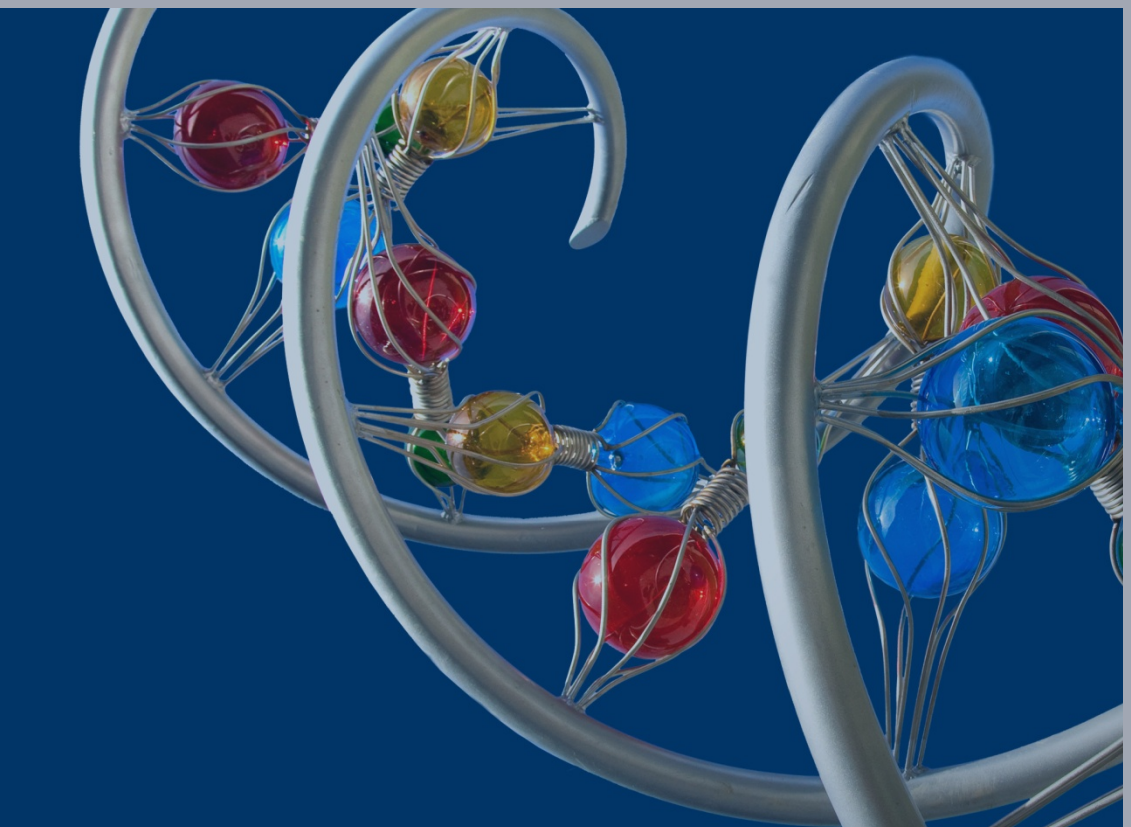
March 2013

The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231

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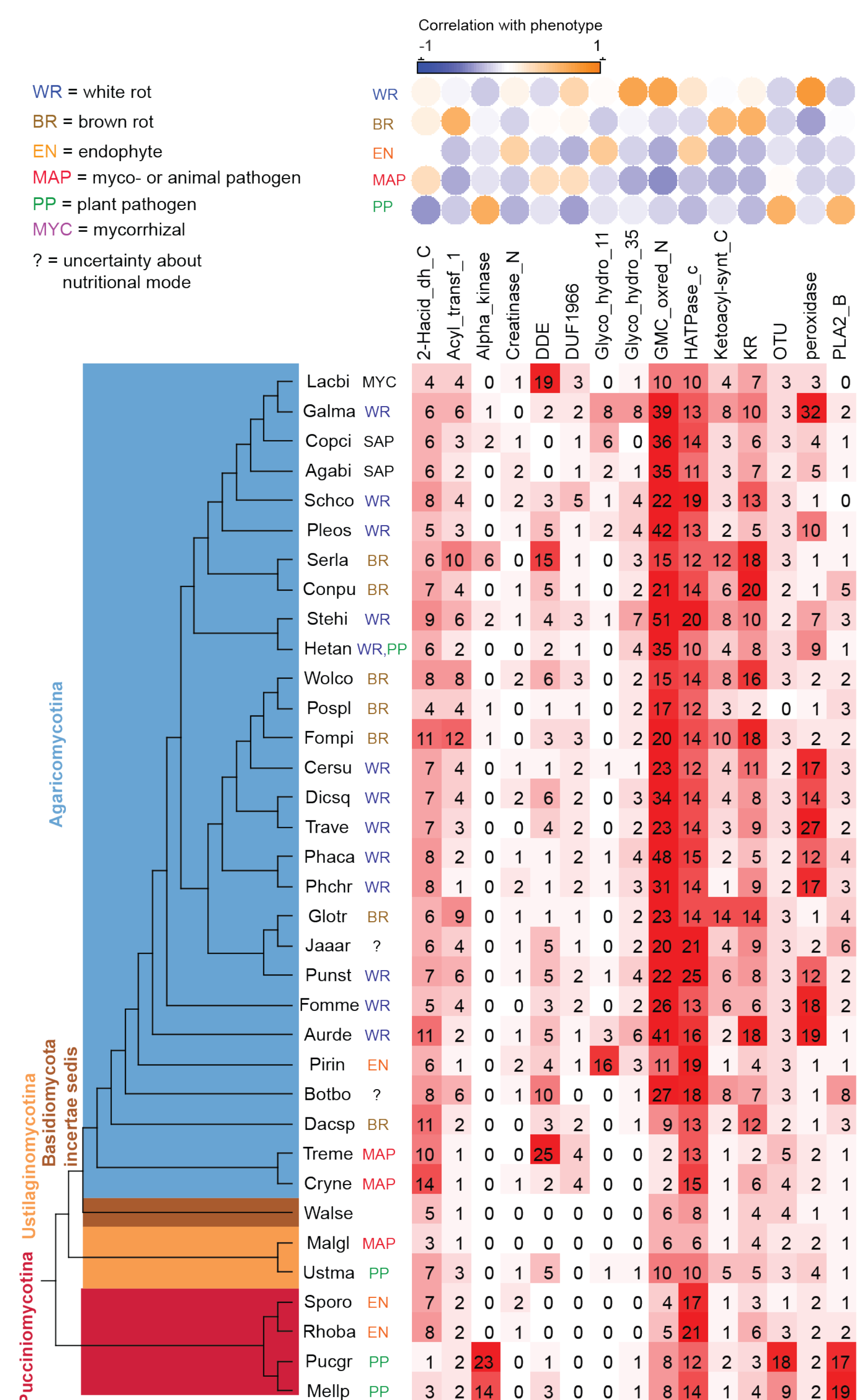




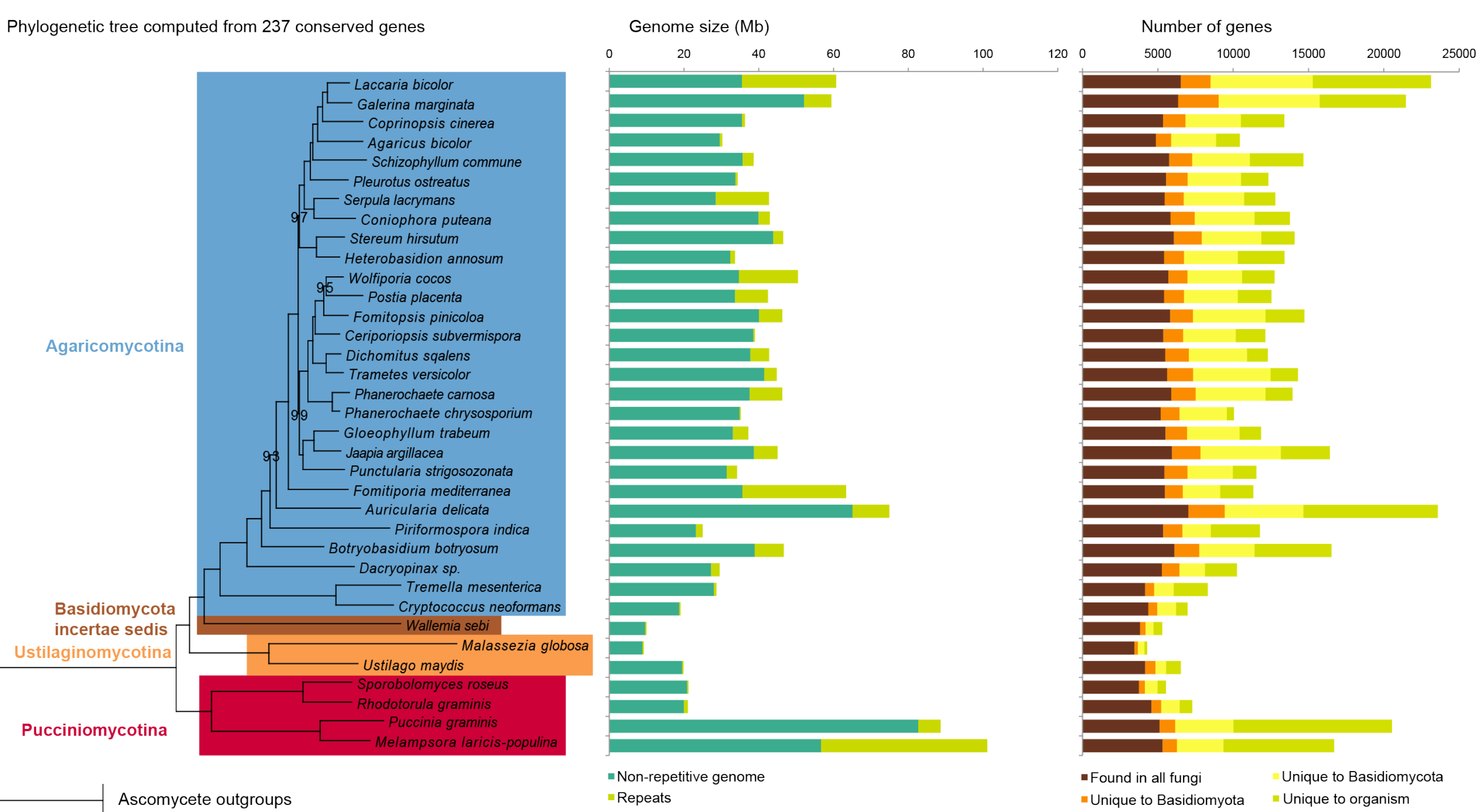
**Abstract**  
Fungi of the phylum Basidiomycota (basidiomycetes), make up some 37% of the described fungi, and are important in forestry, agriculture, medicine, and bioenergy. This diverse phylum includes symbionts, pathogens, and saprobes including wood decaying fungi. To better understand the diversity 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 Phylog 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 lignolytic 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.

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

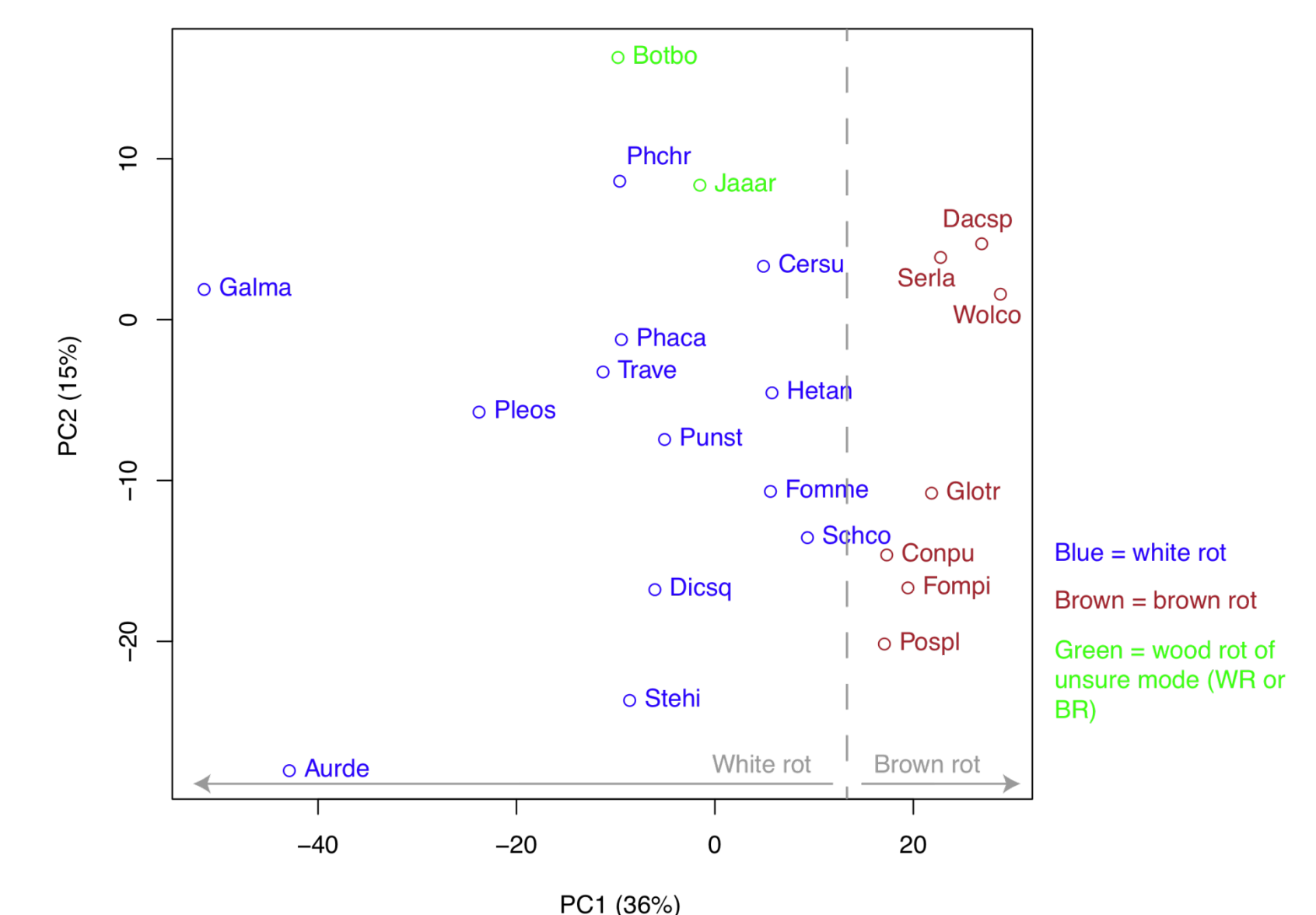
### Correlation of protein family copy number with phenotype



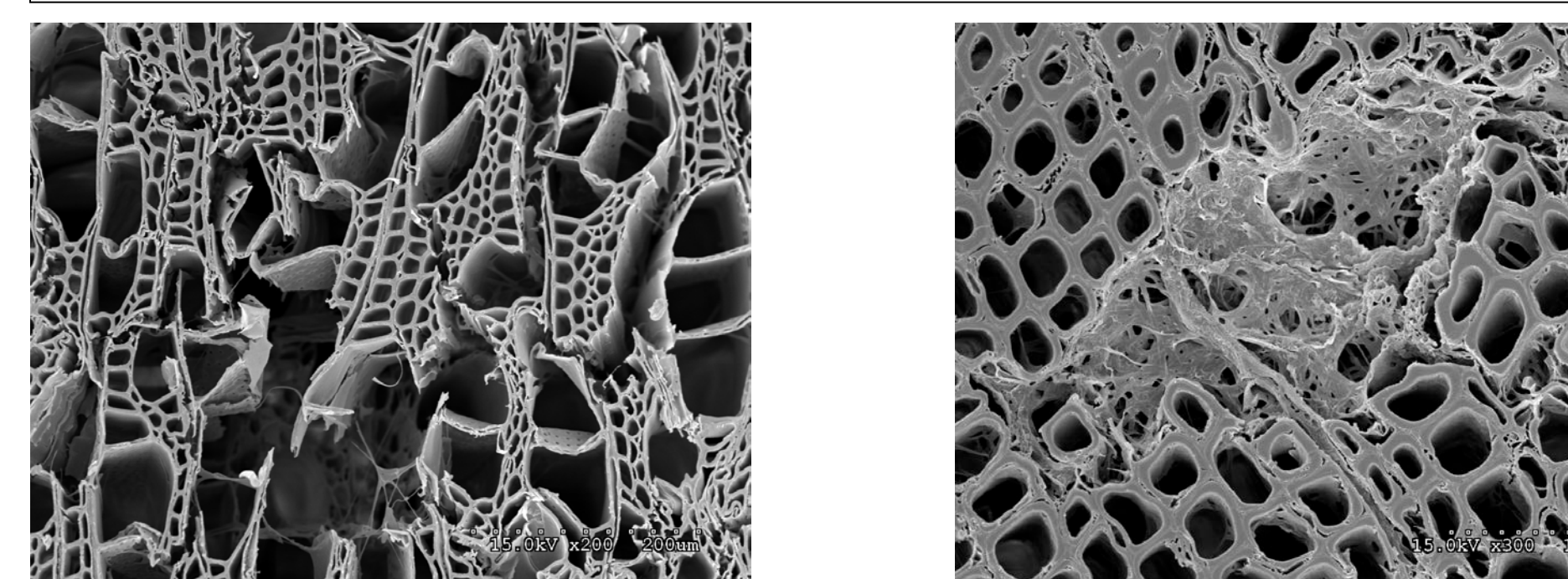
### Genomes overview – phylogeny, genome size, repeat content, number of genes, conservation across fungi



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



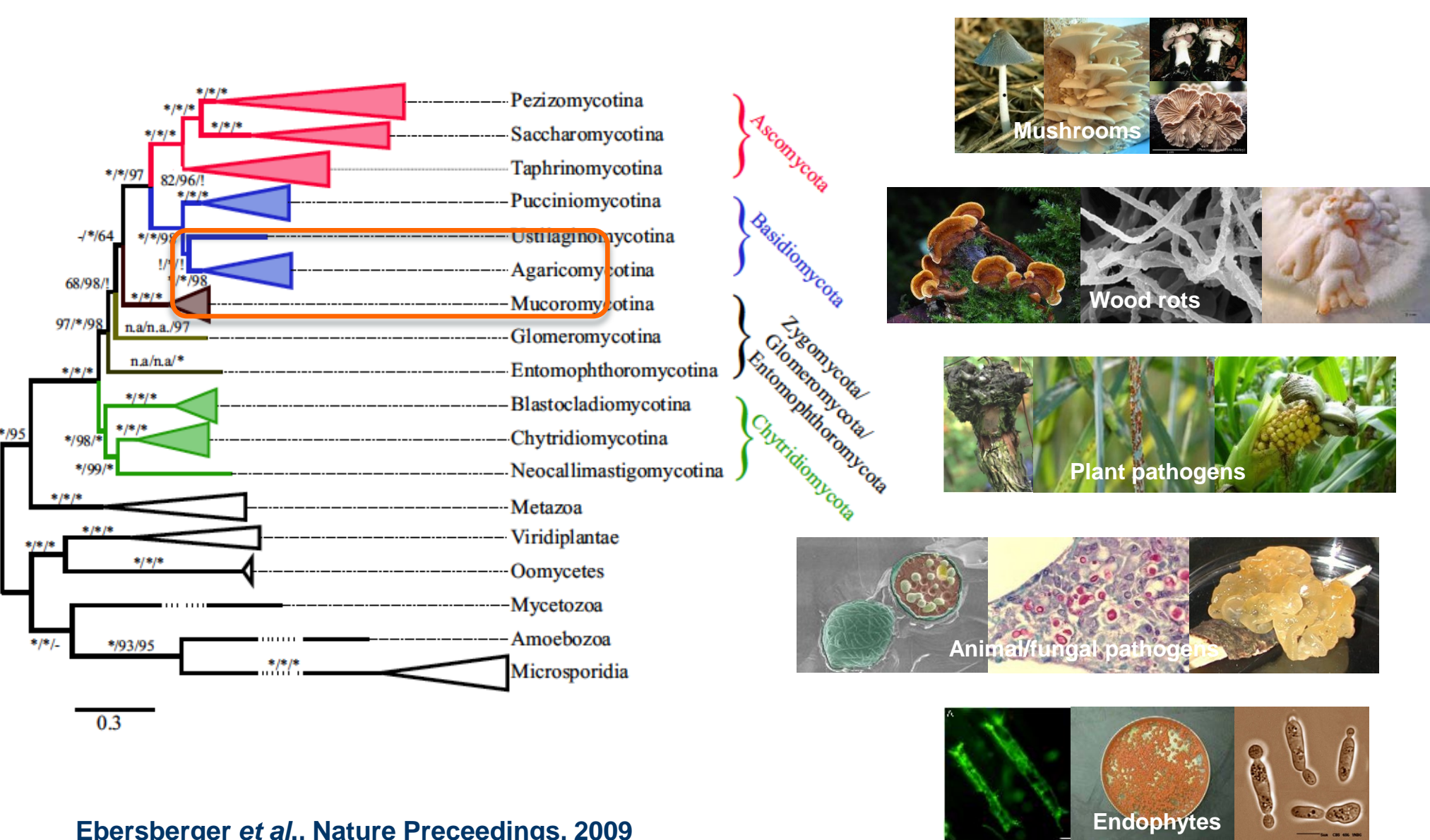
Growth assays on wood indicate that *Botryobasidium botryosum* and *Jaapia argillacea* are indeed white rots – complete degradation of cell walls with mycelia filling voids



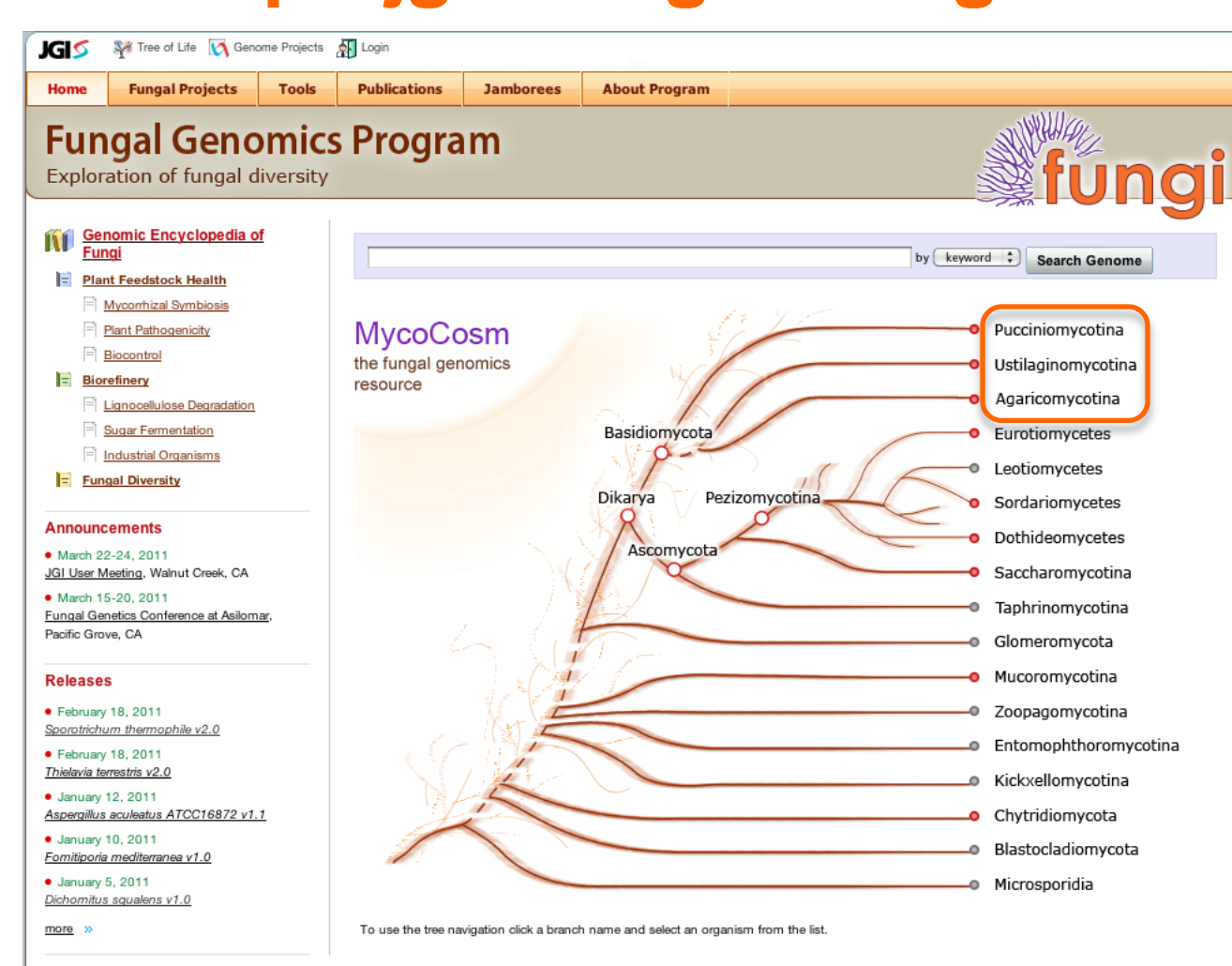
*Botryobasidium botryosum* on aspen

*Jaapia argillacea* on pine

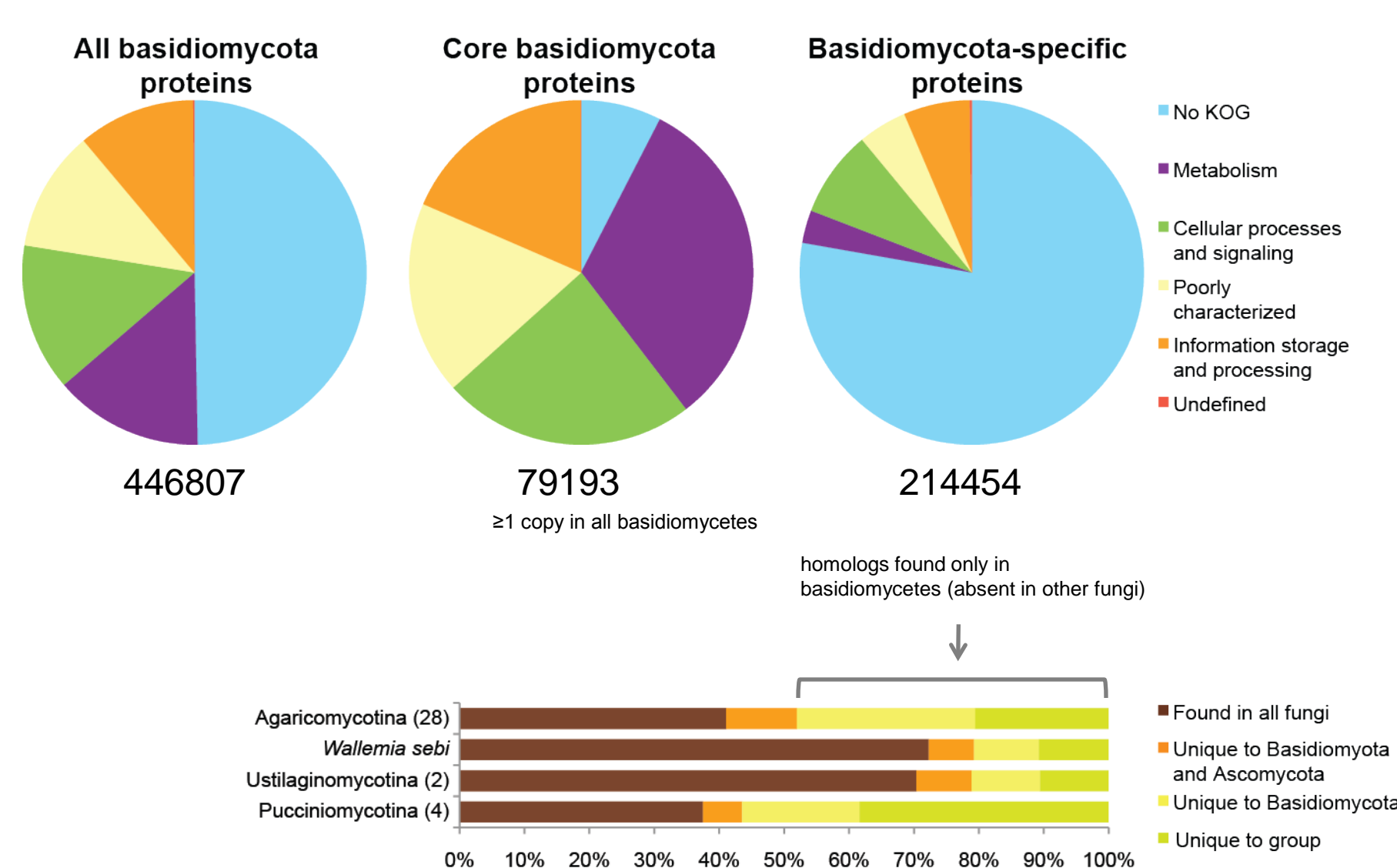
### What are the basidiomycetes?



<http://jgi.doe.gov/fungi>



### Basidiomycota core genes



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

