

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

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

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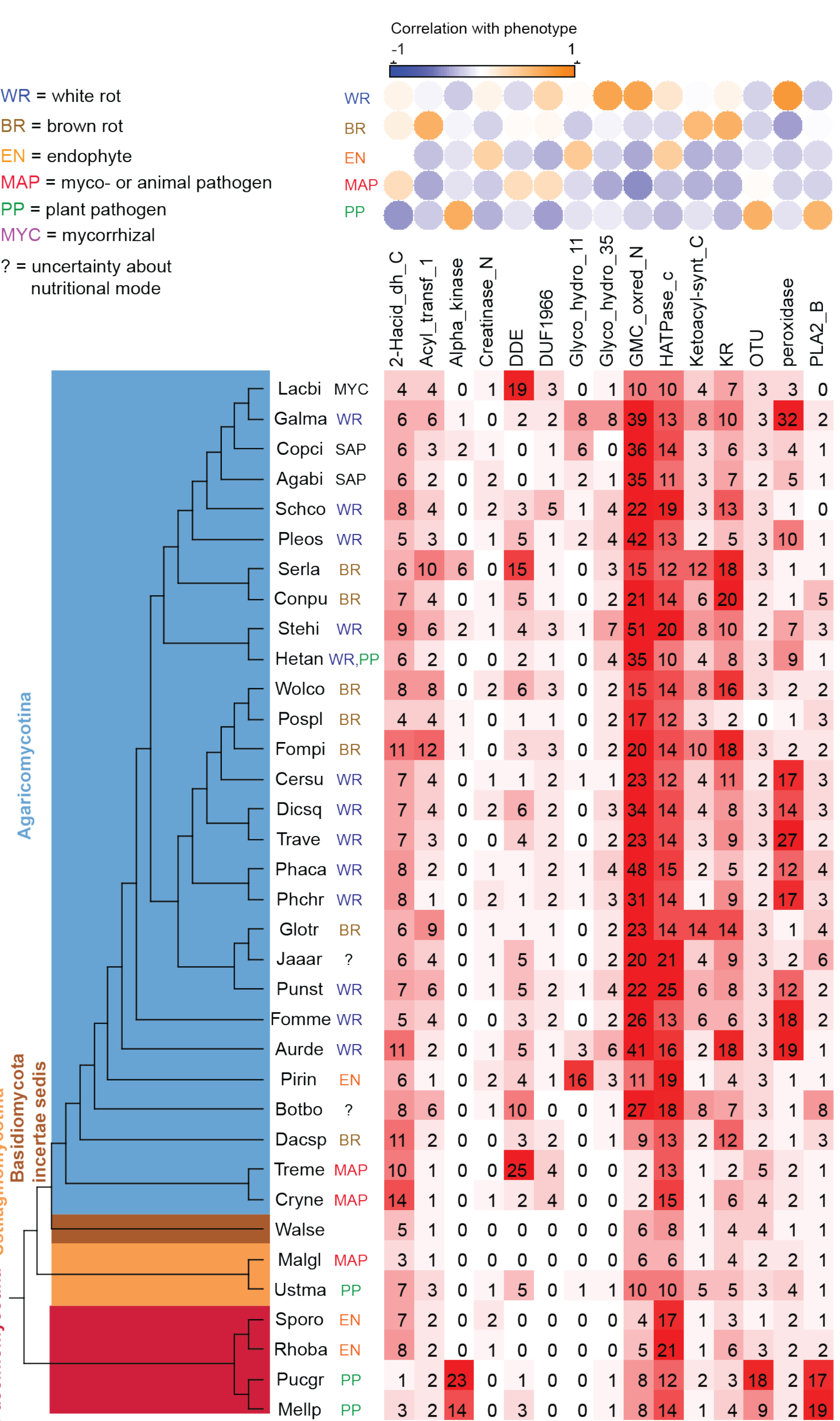
Abstract

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 Phydog 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 ligninolytic 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.

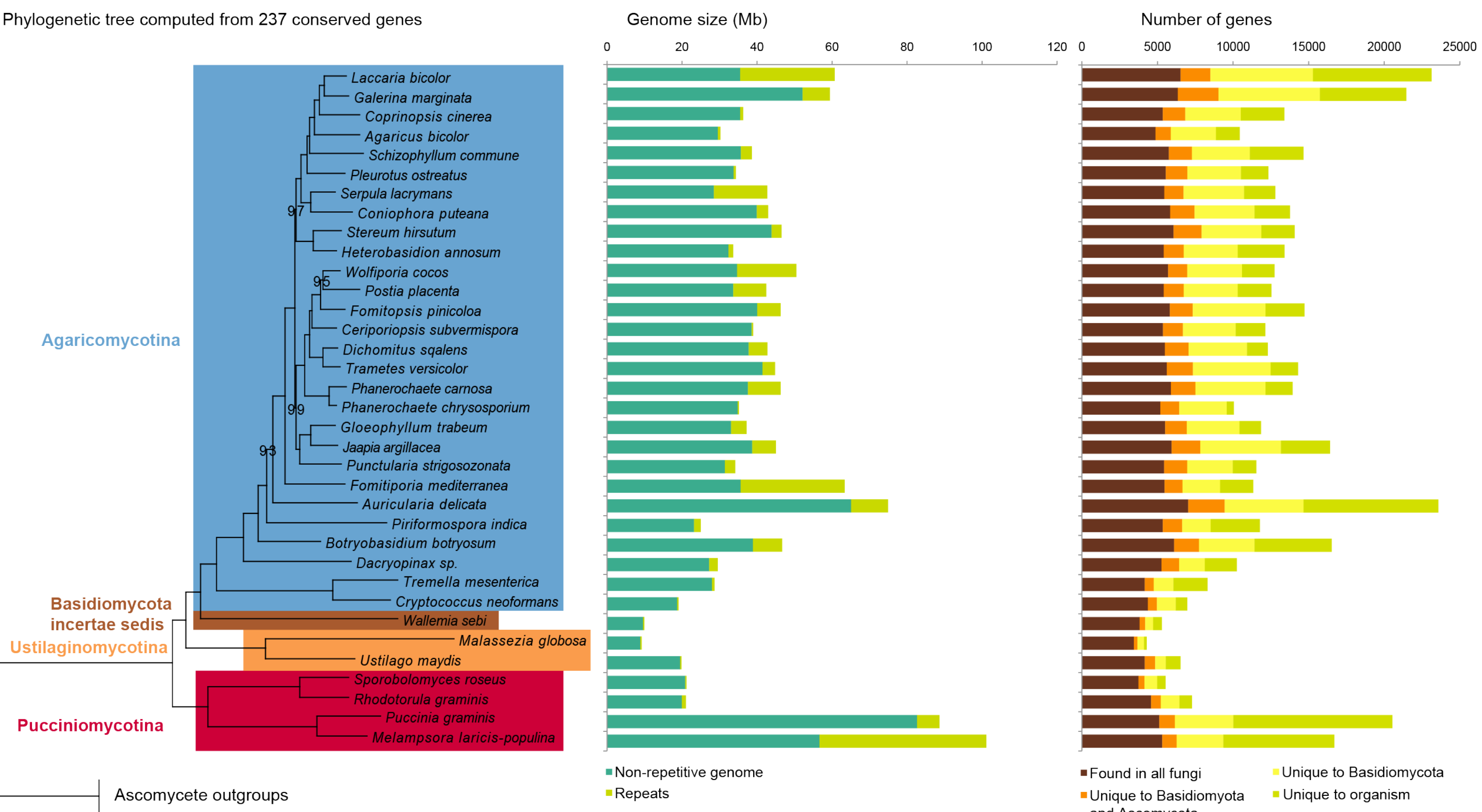
Basidiomycete genomes used in this study

Subphylum	Order	Organism	Genome size (Mb)	Gene number		
Agaricomycotina	Agaricales	<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		
		Auriculariales	<i>Auricularia delicata</i>	74.9	23577	
		Boletales	<i>Serpula lacrymans</i>	42.8	12917	
			<i>Coniophora puteana</i>	43.0	13761	
		Cantharellales	<i>Botryobasidium botryosum</i>	46.7	16526	
		Corticiales	<i>Punctularia strigosozonata</i>	34.2	11538	
		Dacrymycetales	<i>Dacryopinax</i> sp.	29.5	10242	
		Gloeophyllales	<i>Gloeophyllum trabeum</i>	37.2	11846	
		Hymenochaetales	<i>Fomitiporia mediterranea</i>	63.4	11333	
		Jaapiales	<i>Jaapia argillacea</i>	45.1	16419	
	Polyporales	<i>Dichomitus squalens</i>	42.7	12290		
		<i>Ceriporiopsis subvermispora</i>	39.0	12125		
		<i>Fomitopsis pinicola</i>	46.3	14724		
		<i>Phanerochaete carmosa</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		
		Russulales	<i>Heterobasidium annosum</i>	33.6	13405	
			<i>Stereum hirsutum</i>	46.5	14072	
		Sebacinales	<i>Piriformospora indica</i>	25.0	11767	
		Tremellales	<i>Cryptococcus neoformans</i>	18.9	6967	
			<i>Tremella mesenterica</i>	28.6	8313	
		Pucciniomycotina	Pucciniales	<i>Puccinia graminis</i>	88.6	20534
				<i>Melampsora laricis-populina</i>	101.1	16831
Sporidiobolales	<i>Rhodotorula graminis</i>		21.0	7283		
	<i>Sporobolomyces roseus</i>	21.2	5536			
Ustilaginomycotina	Ustilaginales	<i>Ustilago maydis</i>	19.7	6522		
	Malasseziales	<i>Malassezia globosa</i>	9.0	4286		
Incertae sedis	Wallemiales	<i>Wallemia sebi</i>	9.8	5284		

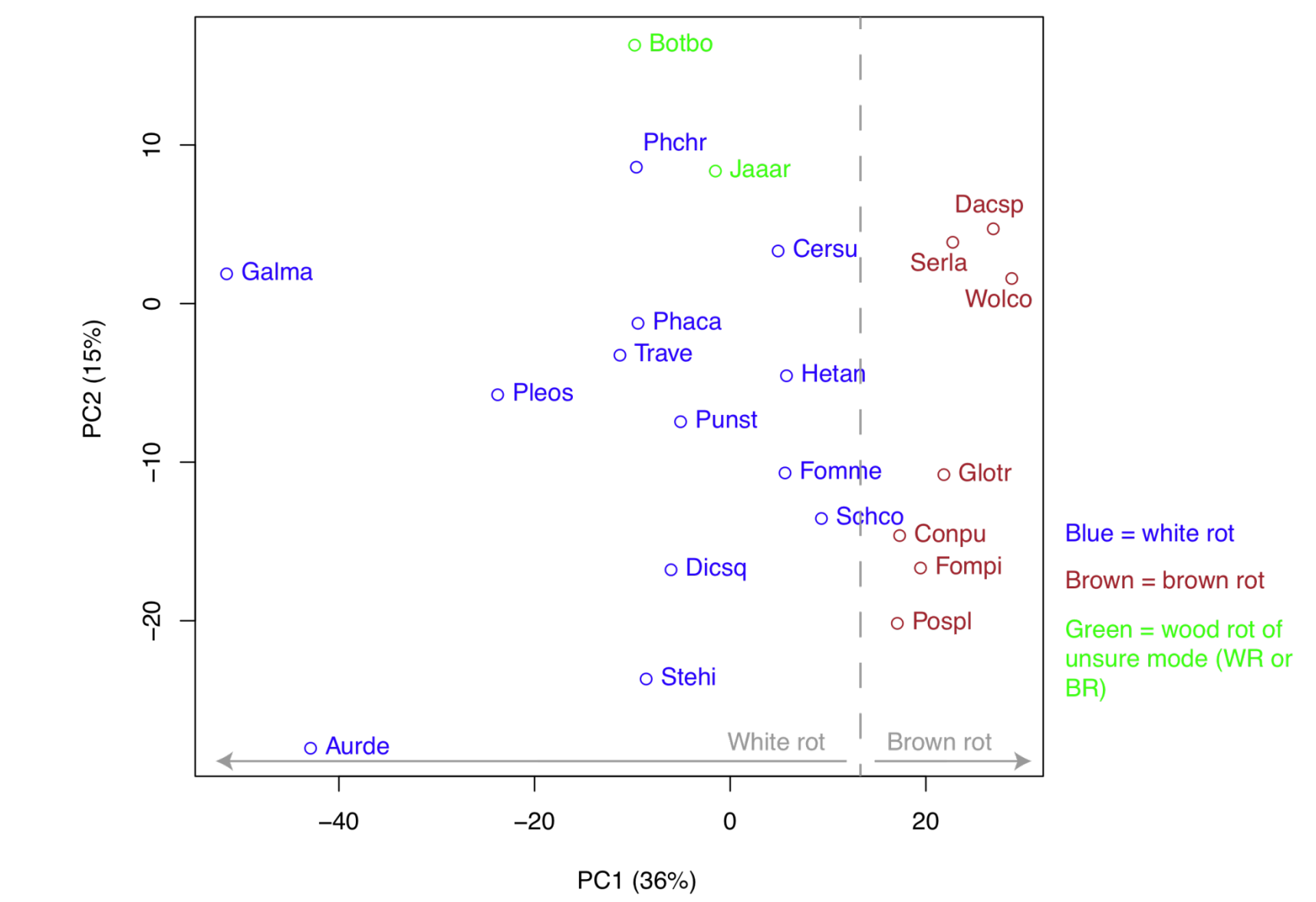
Correlation of protein family copy number with phenotype



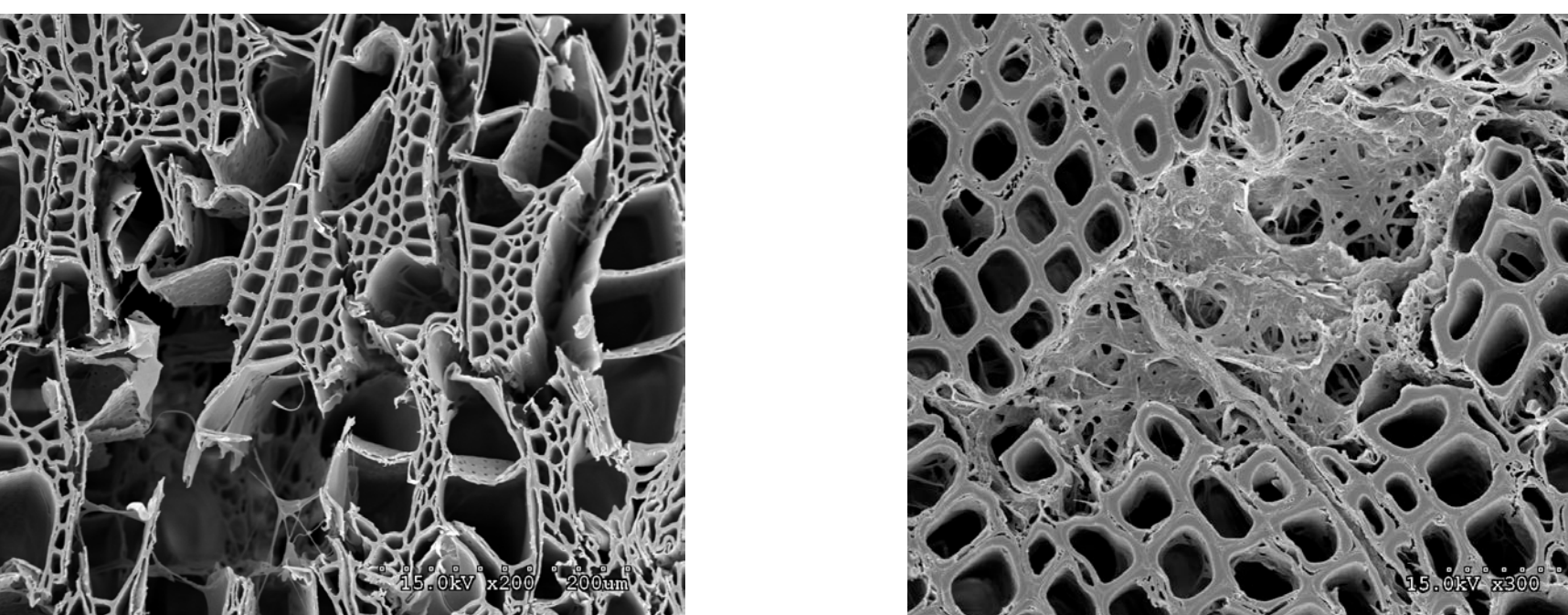
Genomes overview – phylogeny, genome size, repeat content, number of genes, conservation across fungi



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



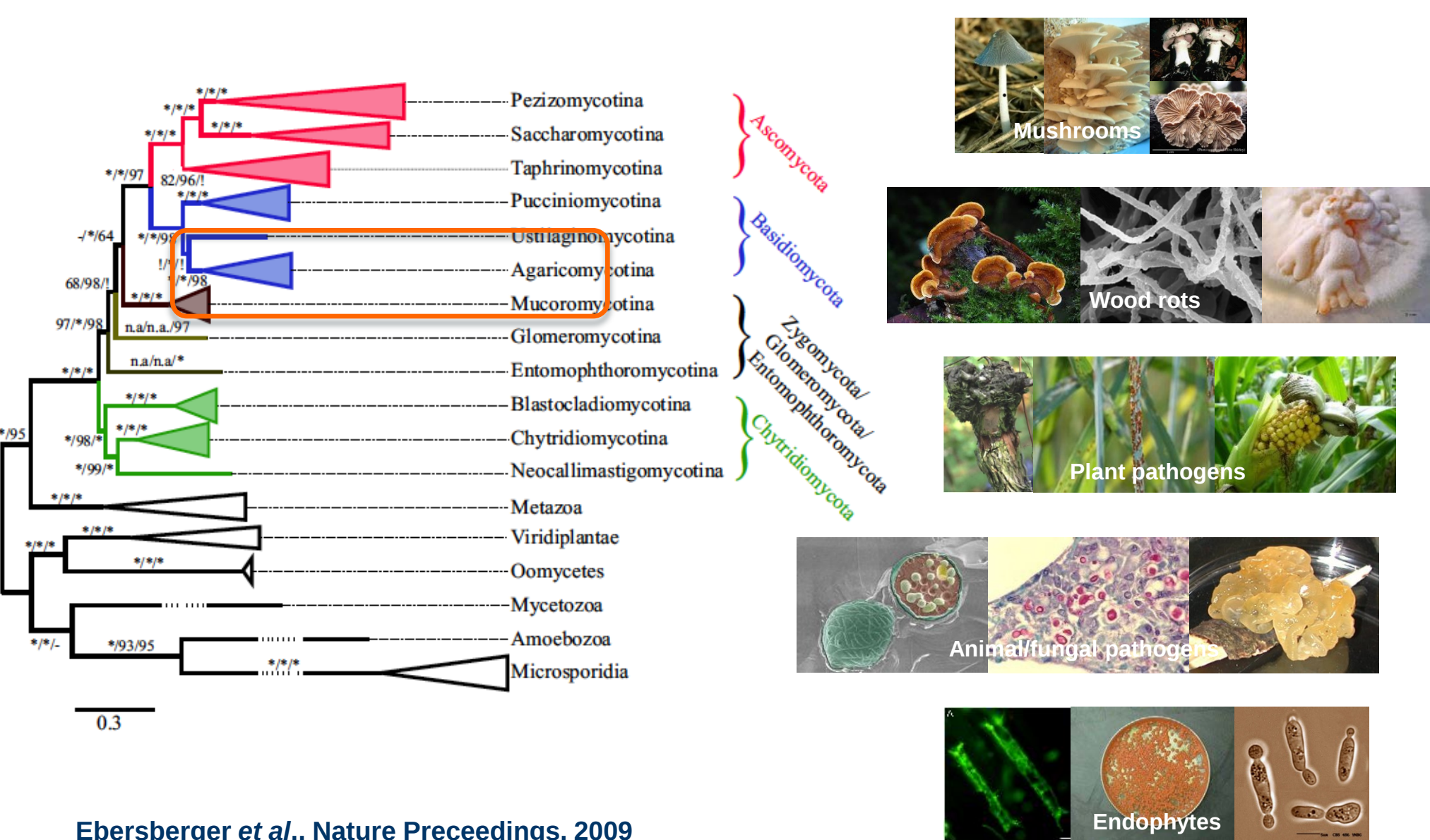
Growth assays on wood indicate that *Botryobasidium botryosum* and *Jaapia argillacea* are indeed white rots – complete degradation of cell walls with mycelia filling voids



Botryobasidium botryosum on aspen

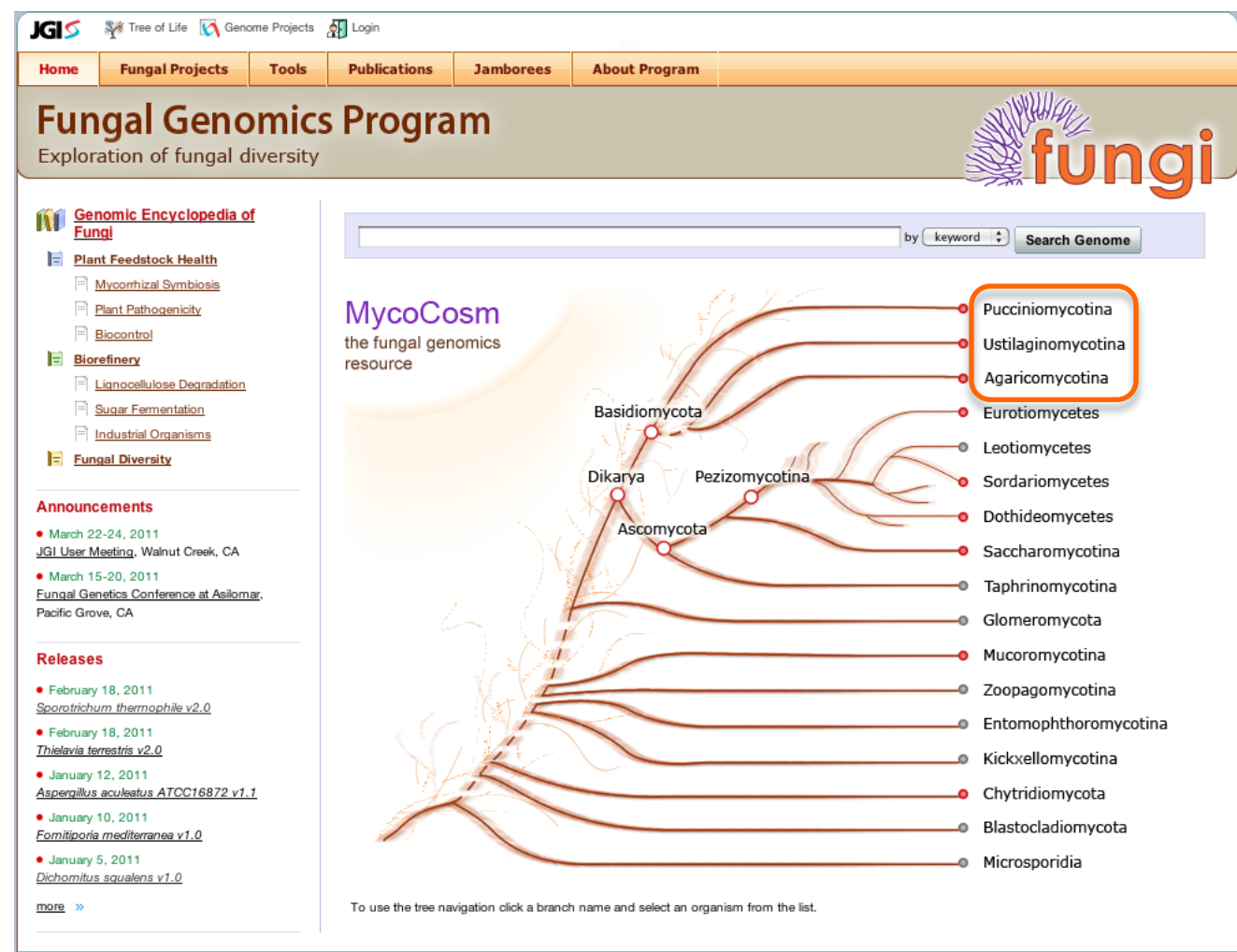
Jaapia argillacea on pine

What are the basidiomycetes?

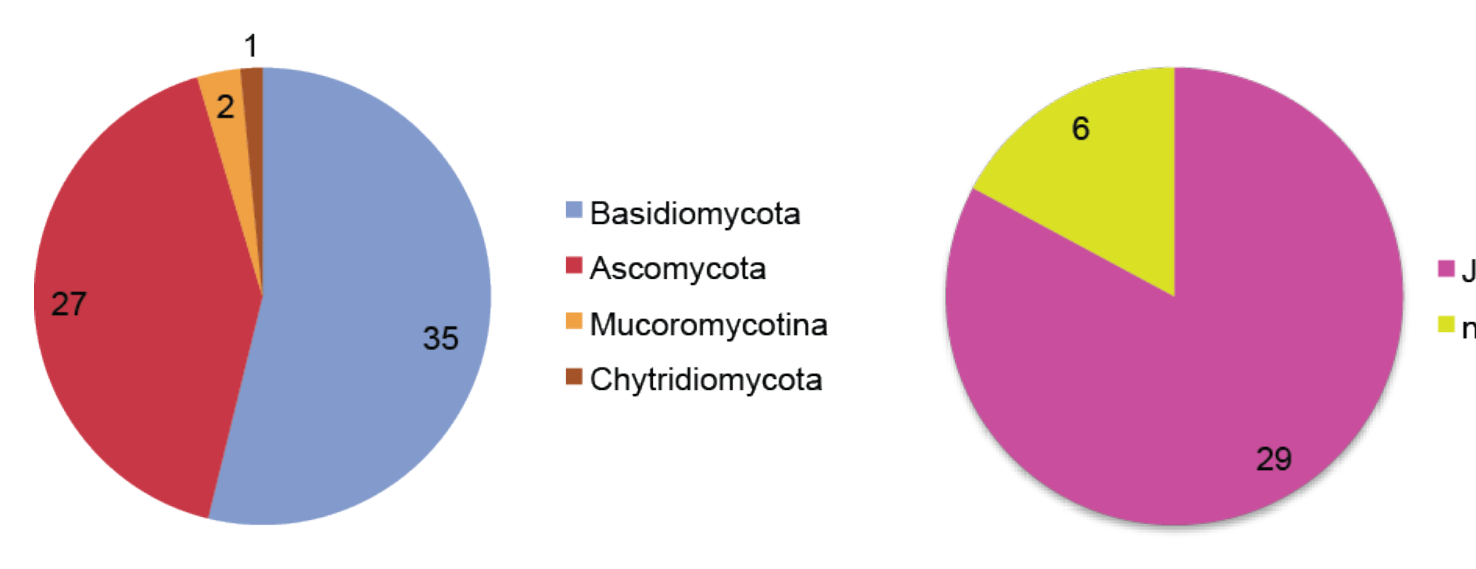


Ebersberger et al., Nature Preceedings, 2009

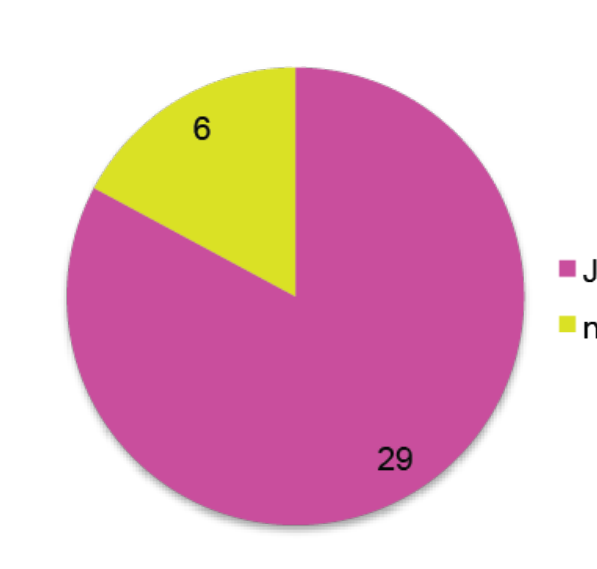
<http://jgi.doe.gov/fungi>



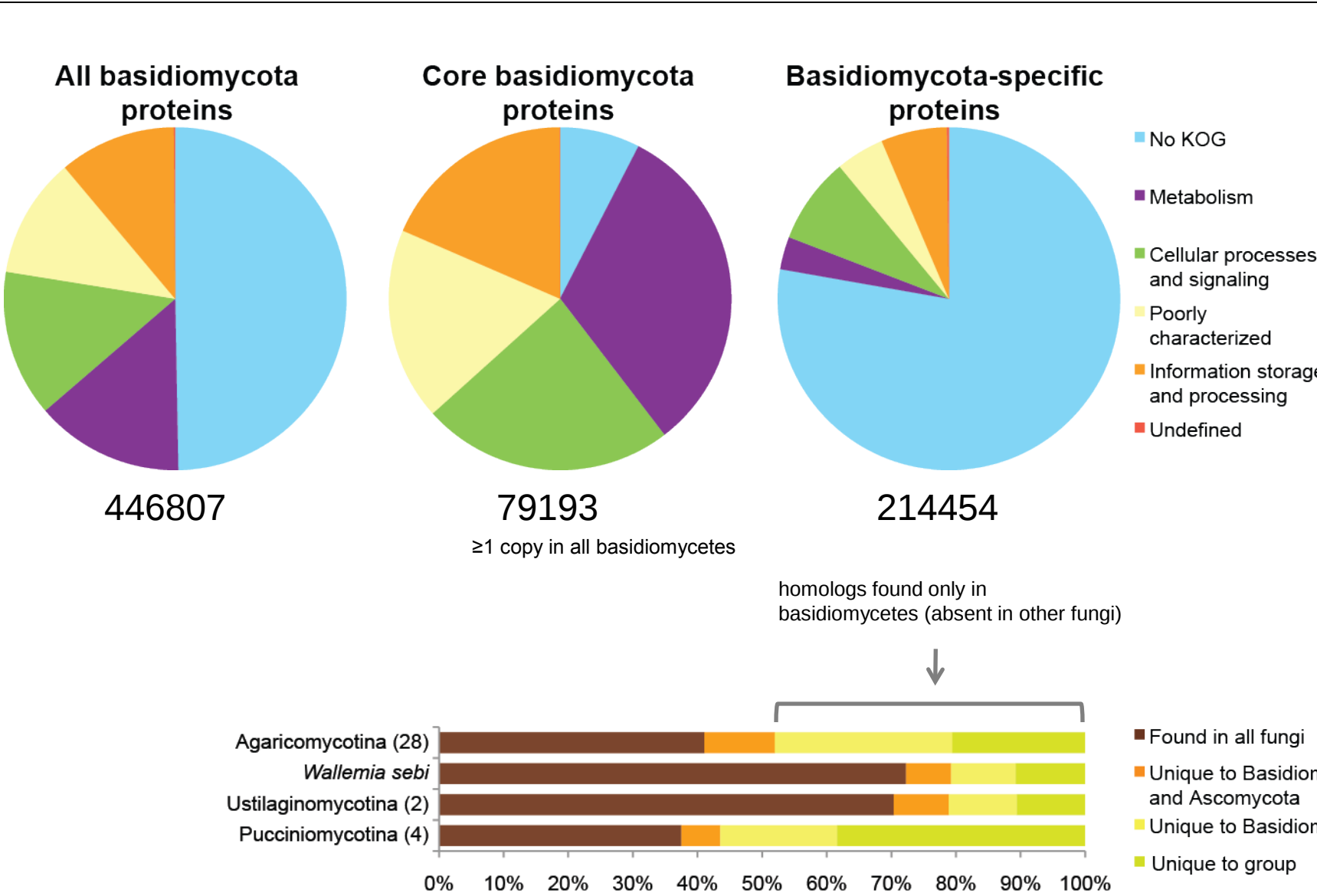
Number of genomes



Number of basidiomycetes



Basidiomycota core genes



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

