

Assembly, Annotation, and Analysis of Multiple Mycorrhizal Fungal Genomes

Alan Kuo¹, Igor Grigoriev¹, Annegret Kohler², Francis Martin², Mycorrhizal Genomics Initiative Consortium

¹DOE Joint Genome Institute, USA

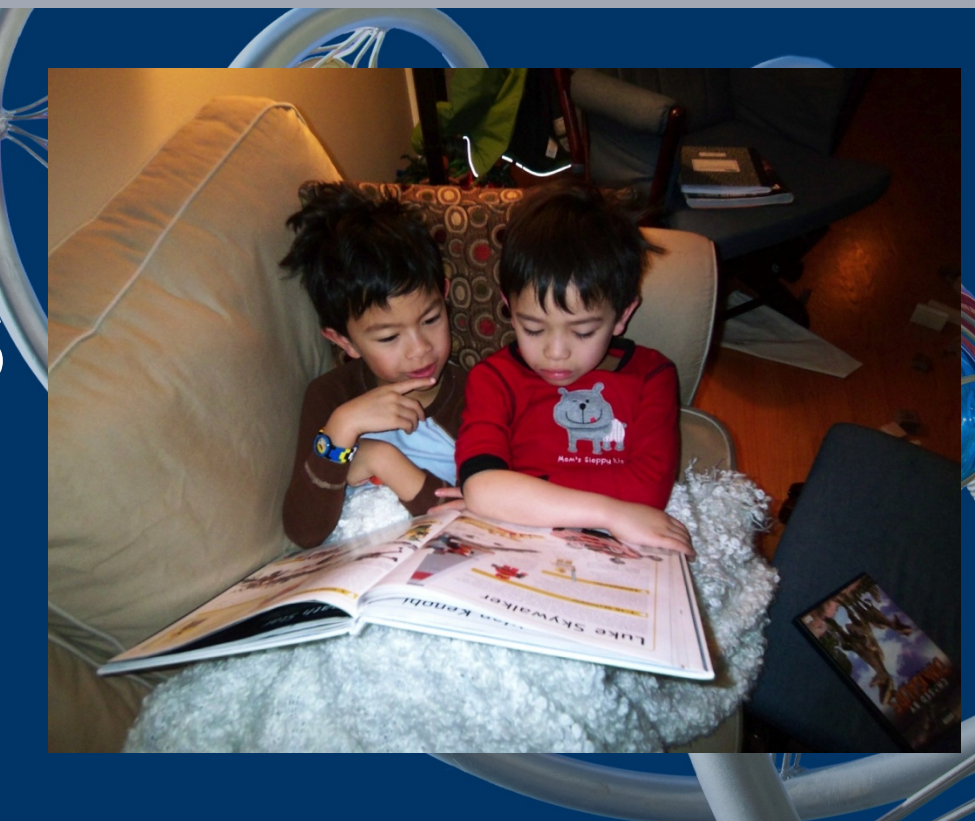
²INRA-Nancy, France

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Abstract

Mycorrhizal fungi play critical roles in host plant health, soil community structure and chemistry, and carbon and nutrient cycling, all areas of intense interest to the US Dept. of Energy (DOE) Joint Genome Institute (JGI). To this end we are building on our earlier sequencing of the *Laccaria bicolor* genome by partnering with INRA-Nancy and the mycorrhizal research community in the MGI to sequence and analyze dozens of mycorrhizal genomes of all Basidiomycota and Ascomycota orders and multiple ecological types (ericoid, orchid, and ectomycorrhizal). JGI has developed and deployed high-throughput sequencing techniques, and Assembly, RNASeq, and Annotation Pipelines. In 2012 alone we sequenced, assembled, and annotated 12 draft or improved genomes of mycorrhizae, and predicted ~232831 genes and ~15011 multigene families. All of this data is publicly available on JGI MycoCosm (<http://jgi.doe.gov/fungi/>), which provides access to both the genome data and tools with which to analyze the data. Preliminary comparisons of the current total of 14 public mycorrhizal genomes suggest that 1) short secreted proteins potentially involved in symbiosis are more enriched in some orders than in others amongst the mycorrhizal Agaricomycetes, 2) there are wide ranges of numbers of genes involved in certain functional categories, such as signal transduction and post-translational modification, and 3) novel gene families are specific to some ecological types.

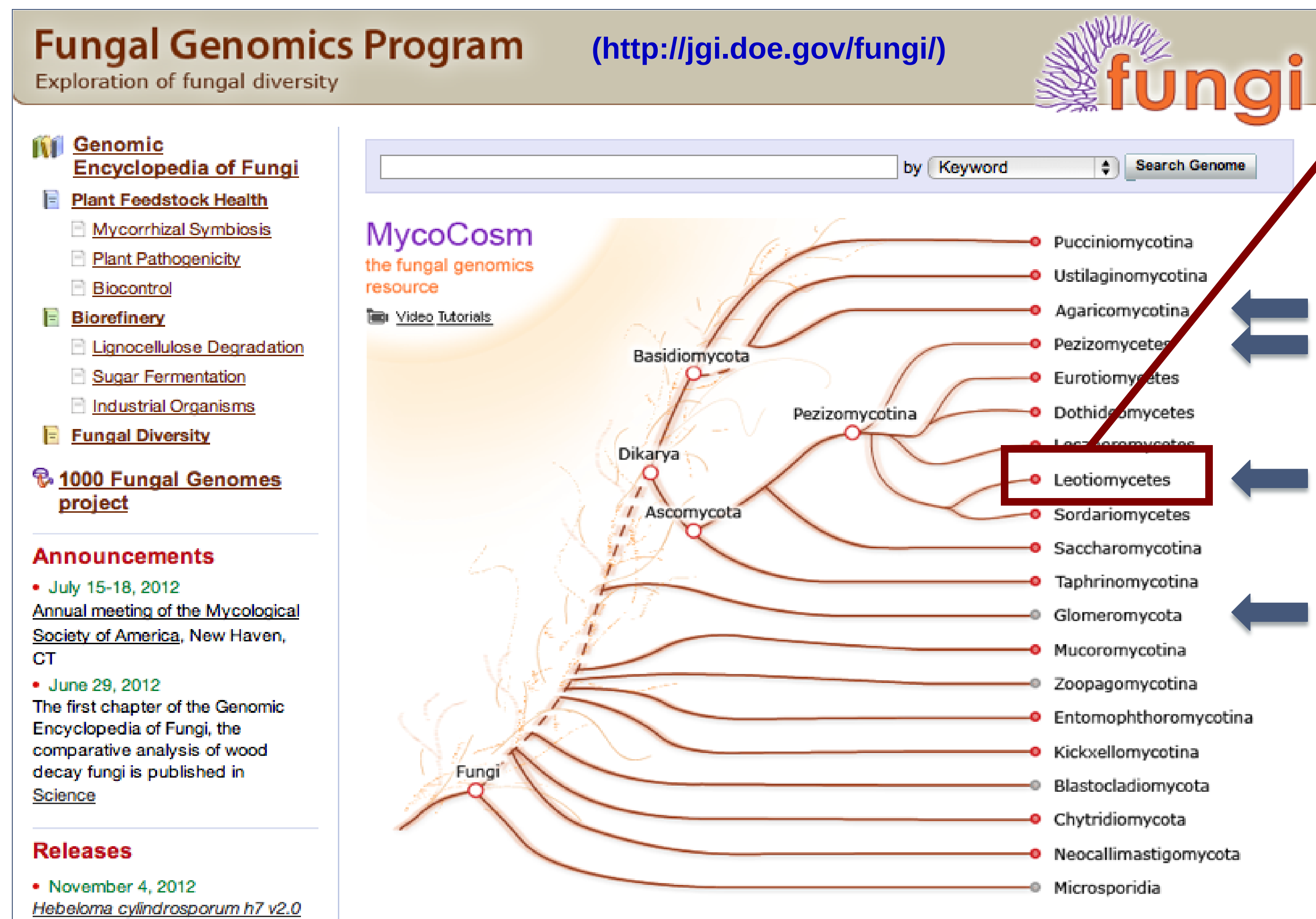
Mycorrhizal Fungi Eco-Group Portal (http://jgi.doe.gov/Mycorrhizal_fungi/)

JGI Home MycoCosm Project List Login

SEARCH BLAST DOWNLOAD INFO HELP!

Within the framework of the JGI Mycorrhizal Genomics Initiative, we are sequencing a phylogenetically and ecologically diverse suite of mycorrhizal fungi (Basidiomycota and Ascomycota), which include the major clades of symbiotic species associating with trees and woody shrubs. Analyses of these genomes will provide insight into the diversity of mechanisms for the mycorrhizal symbiosis, including endo- and ectomycorrhiza.

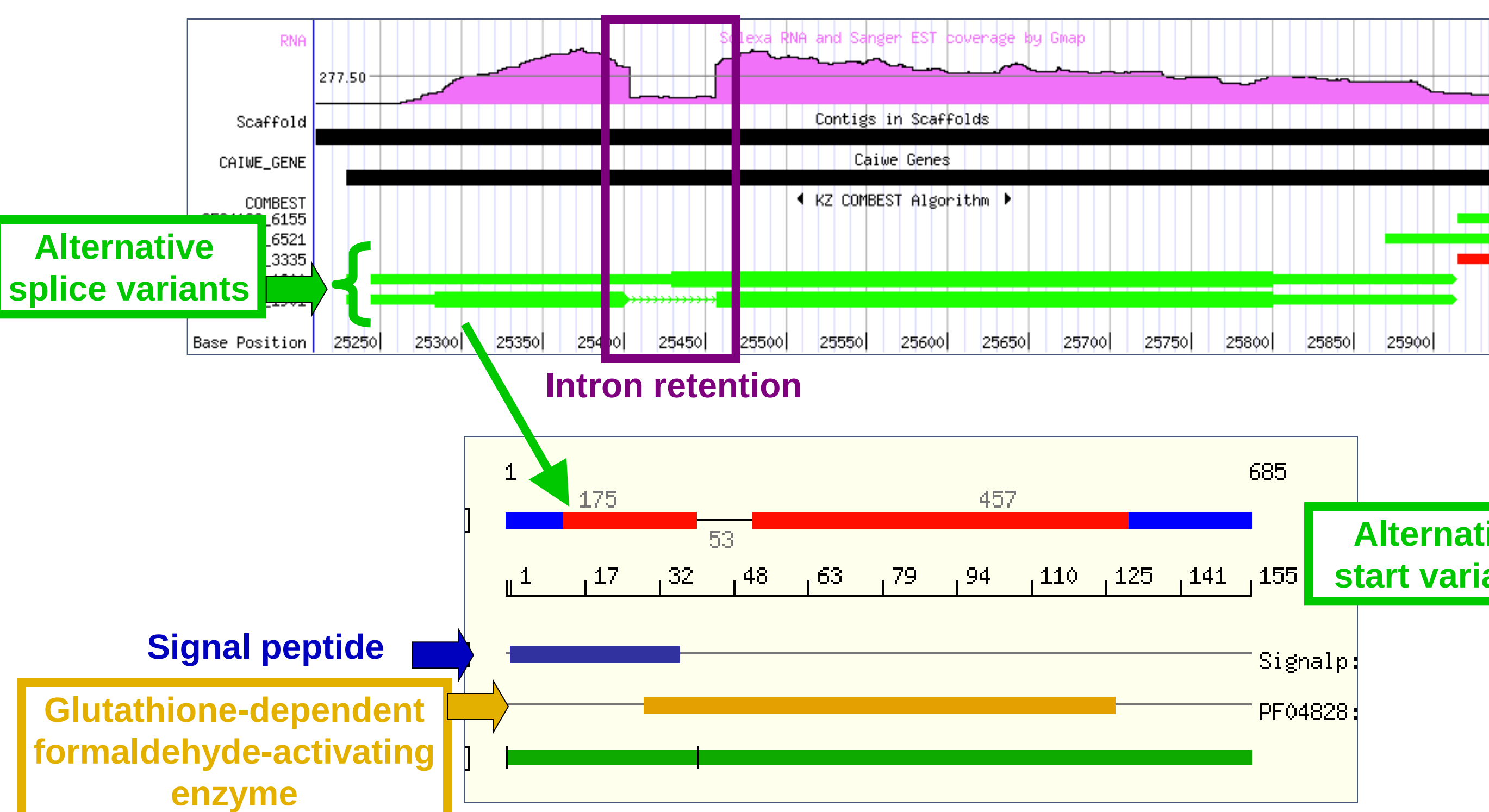
##	Organism	Name	Assembly length	# genes	Phylogeny	Ecology	transcripts per gene	genes per family
1	Amamu1	Amanita muscaria Koide v1.0	40,699,759	18,153	Agaricales	ECM	ND	2.05
2	Hebcy2	Hebeloma cylindrosporum h7	38,226,047	15,382	Agaricales	ECM	3.22	1.82
3	Lacam1	Laccaria amethystina LaAM-08-1 v1.0	52,197,432	21,066	Agaricales	ECM	2.99	2.09
4	Lacbi2	Laccaria bicolor v2.0	60,707,050	23,132	Agaricales	ECM	ND	2.58
5	Oidma1	Oidiodendron maius	46,426,256	16,703	Leotiomycetes	ericoid	ND	2.15
6	Paxin1	Paxillus involutus ATCC 200175	58,301,126	17,968	Boletales	ECM	ND	2.78
7	Paxnu1	Paxillus rubicundulus Ve08.2h10 v1.0	53,011,005	22,065	Boletales	ECM	3.05	2.38
8	Pilcr1	Piloderma croceum F 1598	59,326,866	21,583	Atheliales	ECM	ND	2.01
9	Pismi1	Pisolithus microcarpus 441 v1.0	53,027,657	21,064	Boletales	ECM	ND	2.24
10	Pisti1	Pisolithus tinctorius Marx 270 v1.0	71,007,534	22,701	Boletales	ECM	2.92	2.38
11	Sclici1	Scleroderma citrinum Foug A	56,144,862	21,012	Boletales	ECM	3.23	2.20
12	Sebve1	Sebacina vermifera MAFF 305830	38,094,242	15,312	Sebacinales	orchid	2.73	2.15
13	Suilu1	Suillus luteus UH-Slu-Lm8-n1	37,014,302	18,316	Boletales	ECM	3.82	2.00
14	Tubme1	Tuber melanosporum from Genoscope	124,945,702	7,496	Pezizomycetes	ECM	ND	1.42
15	Tulca1	Tulasnella calospora AL13/4D	62,392,858	19,659	Cantharellales	orchid	1.94	2.35



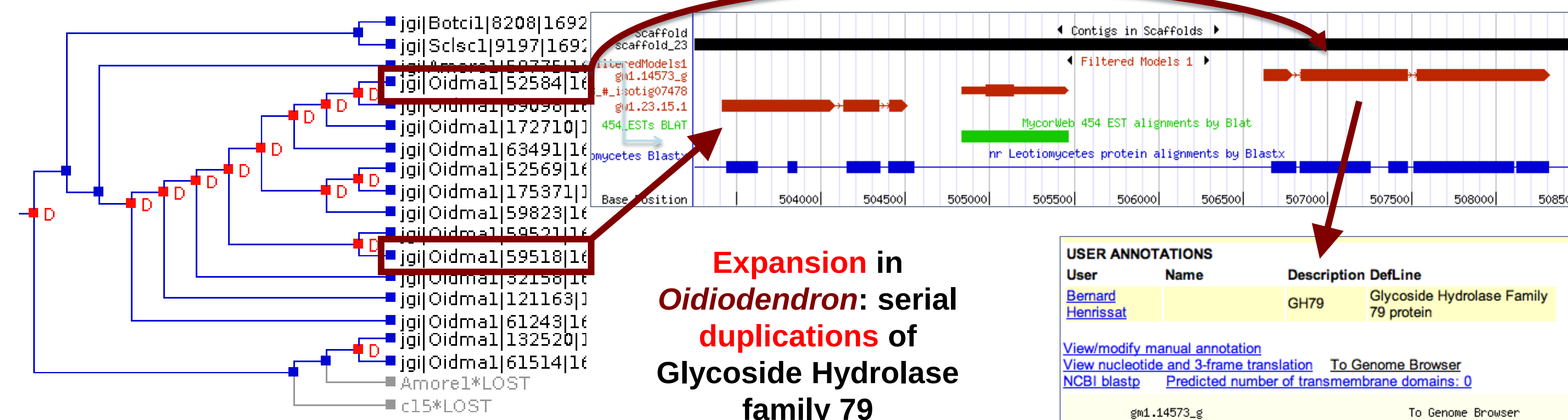
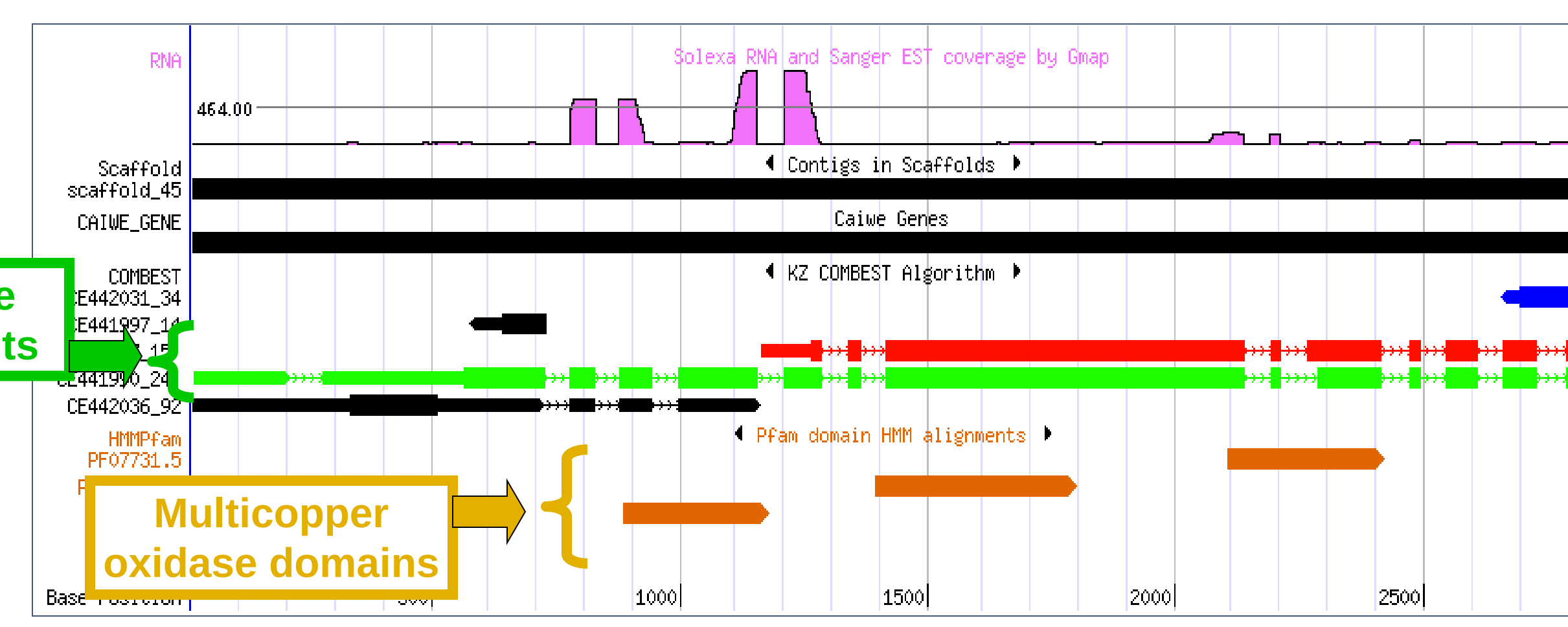
Gene families of Leotiomycetes: mycorrhizal *Oidiodendron* with hydrocarbon-phagic *Amorphotheca*, and pathogenic *Botrytis* and *Sclerotinia*

Cluster	A. resiniae FilteredModels1	B. cinerea ExternalModels	S. sclerotiorum ExternalModels	O. maius FilteredModels1
Totals: 9642	Totals: 16447	Totals: 14503	Totals: 16703	
176	5	3	2	7
177	3	7	6	1
178	3	3	3	Contraction
179	3	4	3	
180	1	4	4	8
181	2	6	4	5
182	3	5	4	5
183	4	3	3	7
184	2	3	3	9
185	1	5	3	8
186	1	5	2	9
187	3	5	5	4
188	3	5	2	7
189	2	3	3	9
190	1	1	1	14
191	3	3	3	Expansion

Alternative splicing in *Suillus*: intron retention loses secretion signal and GFA activity



Alternative starts in *Suillus*: downstream initiation site loses multicopper oxidase domain



Contraction in *Oidiodendron*: multiple losses of histidine kinase response regulator

Remaining *Oidiodendron*: histidine kinase has *Amorphotheca* ortholog

