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Phylogenomics and Ecogenomics of the Mycorrhizal Symbiosis

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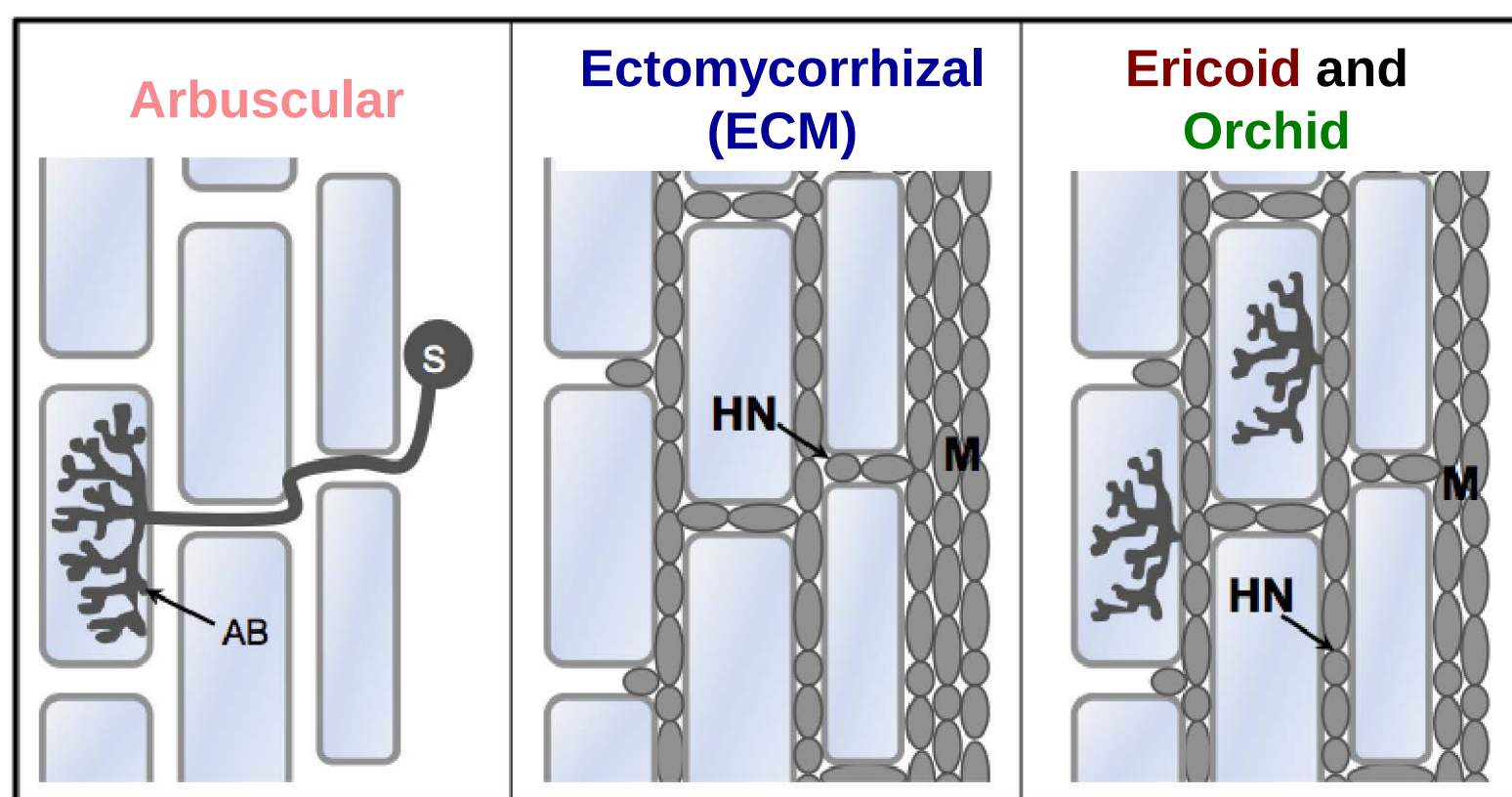


I. Abstract

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 2 dozen mycorrhizal genomes of numerous known mycorrhizal orders and several ecological types (ectomycorrhizal [ECM], ericoid, orchid, and arbuscular). JGI has developed and deployed high-throughput pipelines for genomic, transcriptomic, and re-sequencing, and platforms for assembly, annotation, and analysis. In the last 2 years we have sequenced 21 genomes of mycorrhizal fungi, and resequenced 6 additional strains of *L. bicolor*. Most of this data is publicly available on JGI MycoCosm's Mycorrhizal Fungi Portal (http://jgi.doe.gov/Mycorrhizal_fungi/), which provides access to both the genome data and tools with which to analyze the data. These data allow us to address long-standing issues in mycorrhizal evolution and ecology. For example, a major observation of mycorrhizal evolution is that each of the major ecological types appears to have evolved independently in multiple fungal clades. Using an ecogenomic approach we provide preliminary evidence that 2 clades (Cantharellales and Sebaciales) of a single symbiotic ecotype (orchid) utilize some common regulatory (protein tyrosine kinase) and metabolic (lipase) paths, the latter of which may be the product of HGT. Using a phylogenomic approach we provide preliminary evidence that a particular ecotype (ericoid) may have evolved more than once within a major clade (Leotiomyces).

IV. Ecogenomics of mycorrhizal fungi

IV.A. 4 major types of mycorrhizal symbioses



IV.B. Orchid symbioses of Cantharellales and Sebaciales are convergent. Does orchid symbiosis require specific genes?

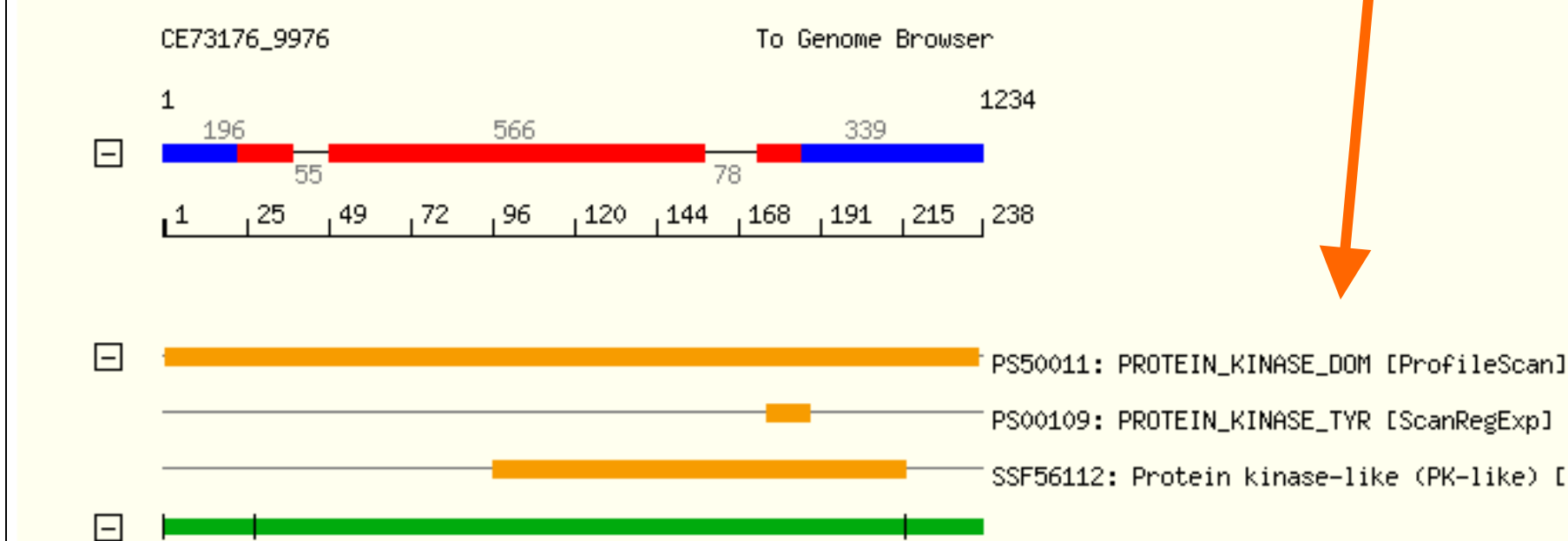
1. Do Blastp-MCL clustering of all 397639 mycorrhizal proteins in 21 genomes.
2. Filter for genes found in both *Tulasnella* and *Sebacia*, and nowhere else.
3. Found 344 genes in 50 families.

50 clusters, MCL inflation parameter: 2.0, page: 1	GO	GO	GO	GO	GO	GO
Cluster	T. calospora v1.0 FilteredModels1	T. melanosporum from Genoscope Genoscope_genes	T. matsutake FilteredModels2	S. luteus v1.0 FilteredModels1	S. brevipes FilteredModels1	S. vernifera v1.0 FilteredModels1
Totals: 183	Totals: 0	Totals: 0	Totals: 0	Totals: 0	Totals: 161	Totals: 0
1628	7	0	0	0	0	24
2786	23	0	0	0	0	1
3123	22	0	0	0	0	1
5831	4	0	0	0	0	13
6442	1	0	0	0	0	15
6449	15	0	0	0	0	1
7378	12	0	0	0	0	1
7651	4	0	0	0	0	8
8454	9	0	0	0	0	1
8470	6	0	0	0	0	4

Example of a *Tulasnella* member of a protein tyrosine kinase family

ASPECT	GO Id	GO Desc	Interpro Id	Interpro Desc
Molecular Function	0004672	protein kinase activity	IPR000719	Protein kinase, core
	0004713	protein-tyrosine kinase activity	IPR008266	Tyrosine protein kinase, active site
	0005524	ATP binding	IPR000719	Protein kinase, core
Biological Process	0006468	protein amino acid phosphorylation	IPR008266	Tyrosine protein kinase, active site

View/modify manual annotation
View nucleotide and 3-frame translation
NCBI blasto
Predicted number of transmembrane domains: 0

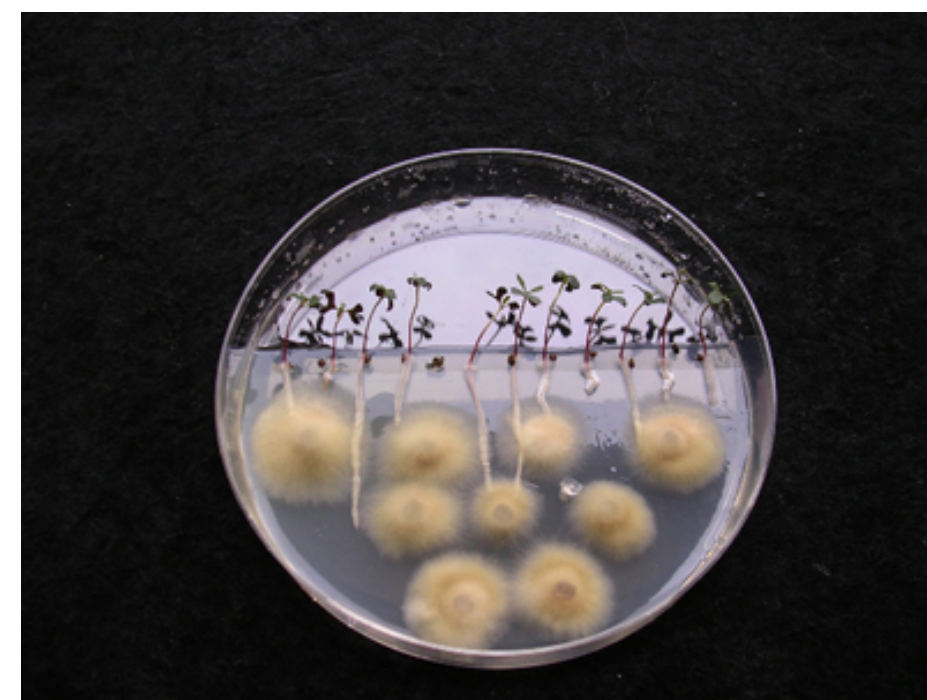


Orchid symbiosis-specific signal transduction?

II. Mycorrhizae are symbioses between fungi and plants



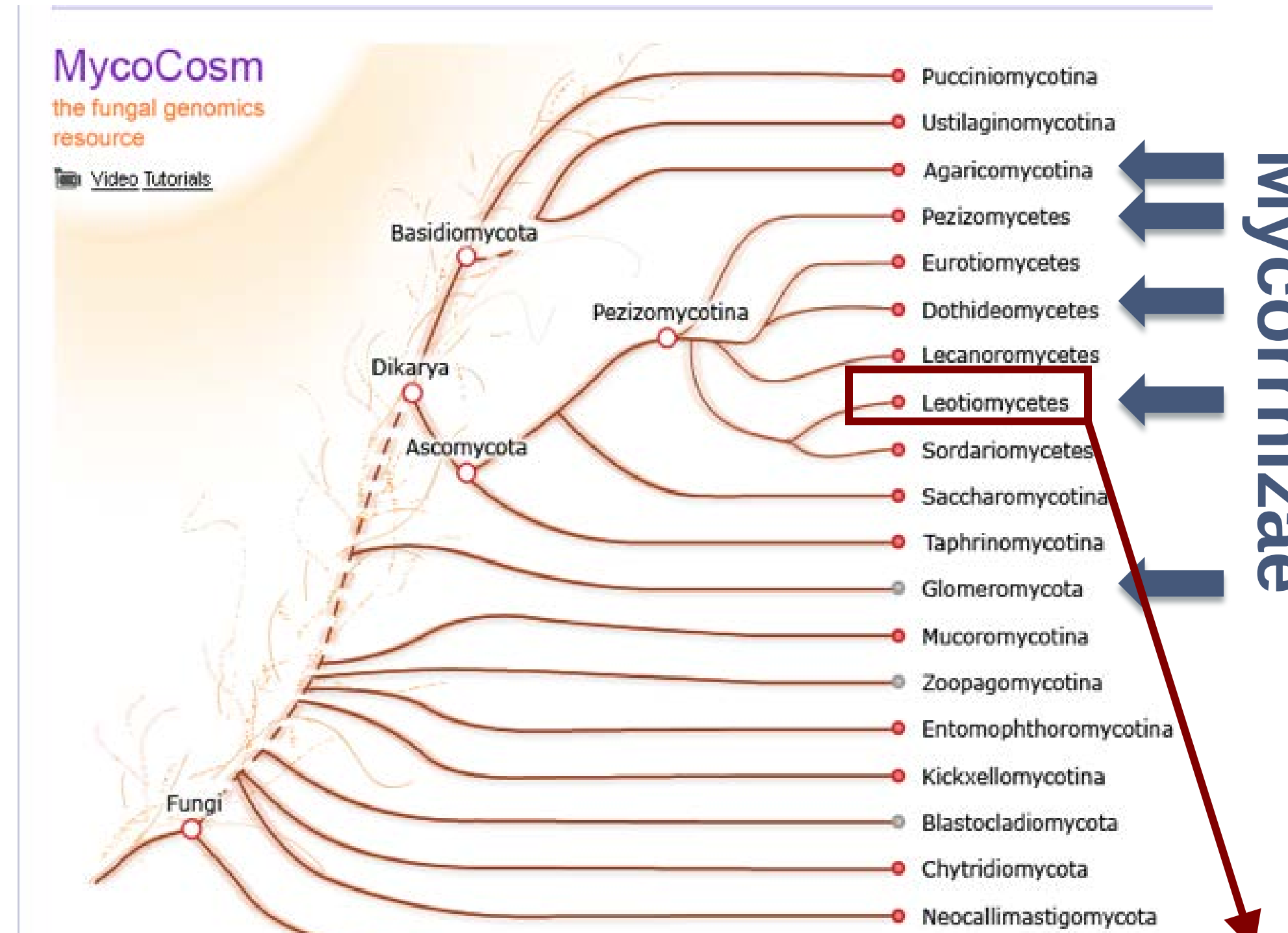
Simple model is that plant contributes photosynthate and fungus contributes soil nutrients, but can be much more complex.



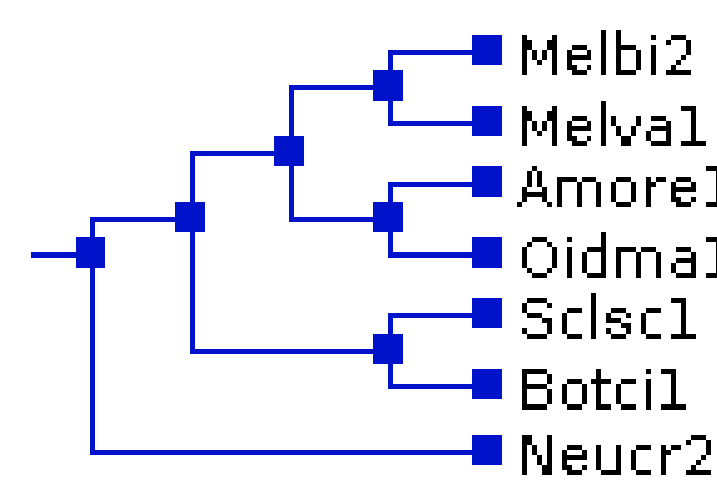
- 80% of land plants do it.
- Many and diverse fungi do it.
- Including familiar edible mushrooms such as porcini, matsutake, chanterelles.
- Oh, and truffles too.

V. Phylogenomics of mycorrhizal fungi

V.A. Mycorrhizal symbiosis arose in multiple clades



Leotiomyces species tree



Amorpha and *Oidiodendron* branch together

V.B. Leotiomyces clade has both ericoid symbionts and non-symbionts. Did ericoid symbiosis arise once?

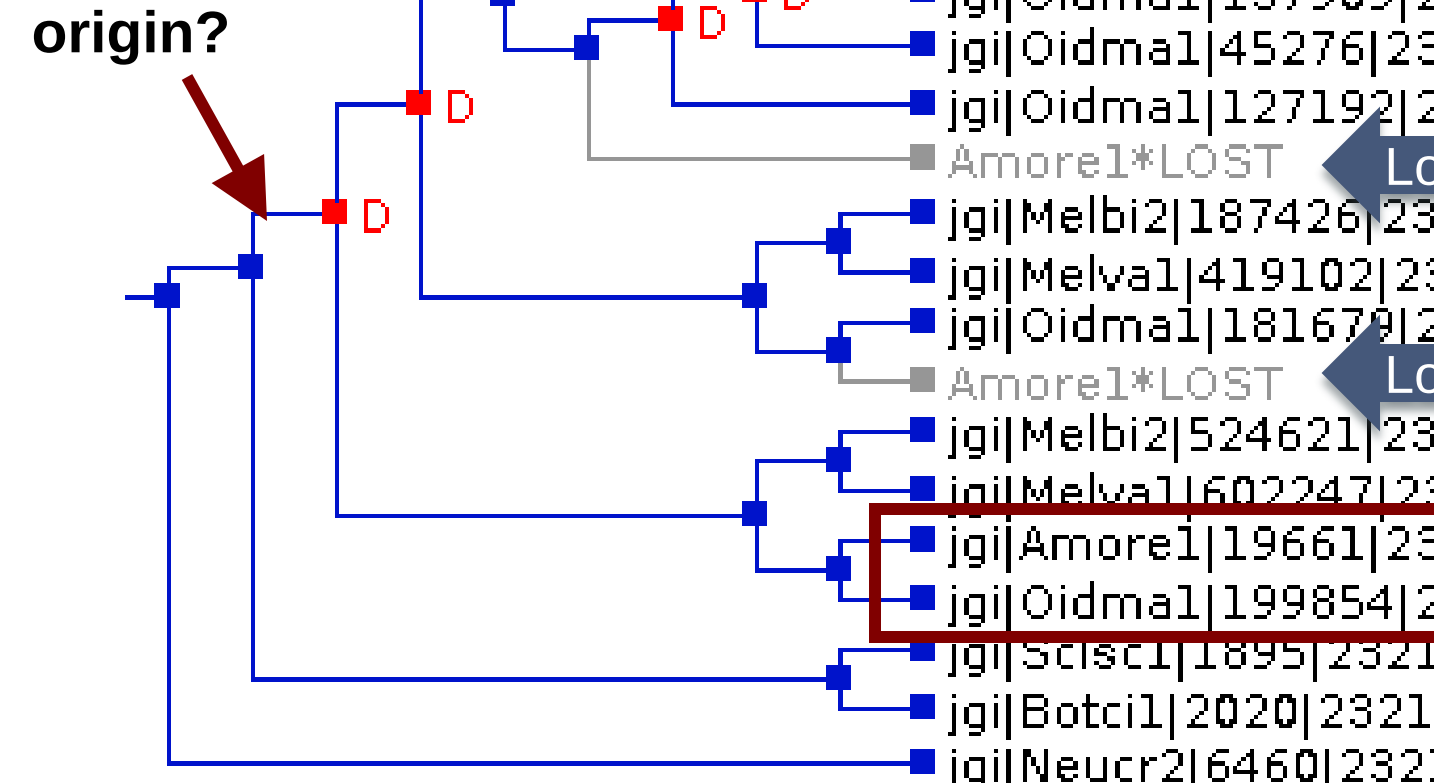
1. Do Blastp-MCL clustering of all 2156 Leotiomyces proteins in 3 ericoid (*Oidiodendron*, *Meliniomyces*), 2 pathogen, and 1 hydrocarbon-phagic (*Amorpha*) genomes.
2. Find orthologs and build clustalW-RaxML species tree, and then build gene trees.
3. Browse for ericoid-enriched gene family expansions.

Cluster	S. sclerotiorum ExternalModels	O. maius FilteredModels1	M. variabilis FilteredModels1	M. bicolor FilteredModels2	Neurospora crassa BroadModels	B. cinerea ExternalModels	A. resinosa FilteredModels1
	Totals: 14503	Totals: 16703	Totals: 20389	Totals: 18619	Totals: 10785	Totals: 16447	Totals: 9642
 594	0	2	10	5	0	0	0
 595	1	6	3	3	1	1	1
 596	1	7	2	1	1	2	2

Example of an ericoid-enriched gene family:

Serial duplications of a transcription factor in the *Amorpha*-*Oidiodendron* common ancestor were followed by multiple losses in *Amorpha*.

Ericoid origin?



Locus synteny



Exons and introns

Transcription factor Pfams