



FERRAMENTAS PARA O ESTUDO DE GENÔMICA COMPARATIVA

Fenícia Brito

BIOINFORMÁTICA





“Bioinformática
porque existe
informação nas
entidades biológicas”

J. Miguel Ortega



Bases de datos

Uniprot

GEO

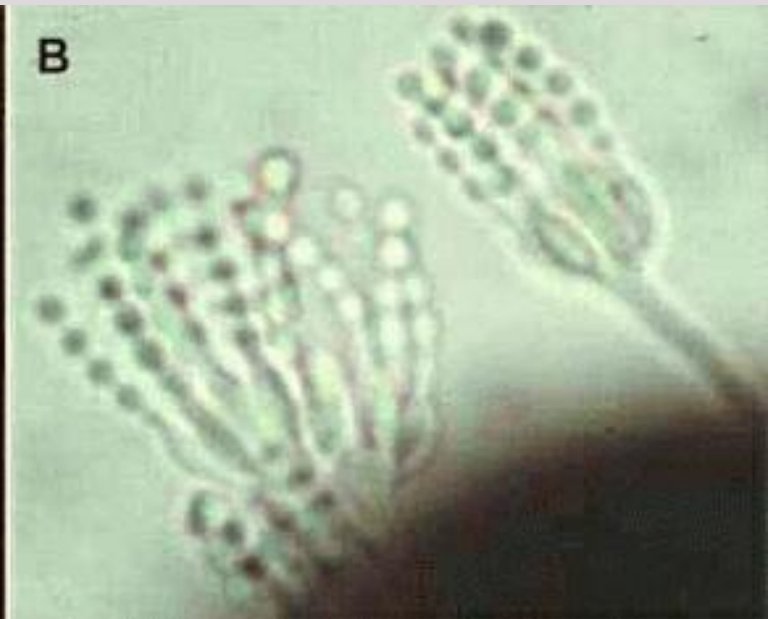
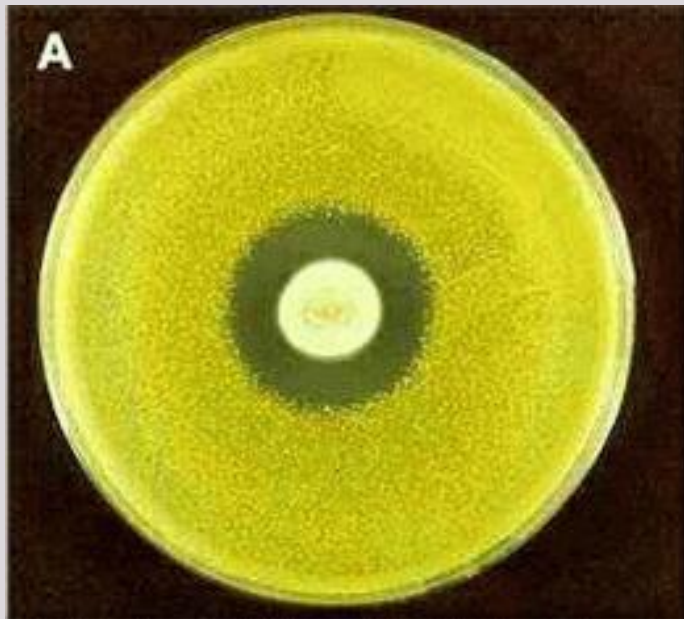
Taxonomy

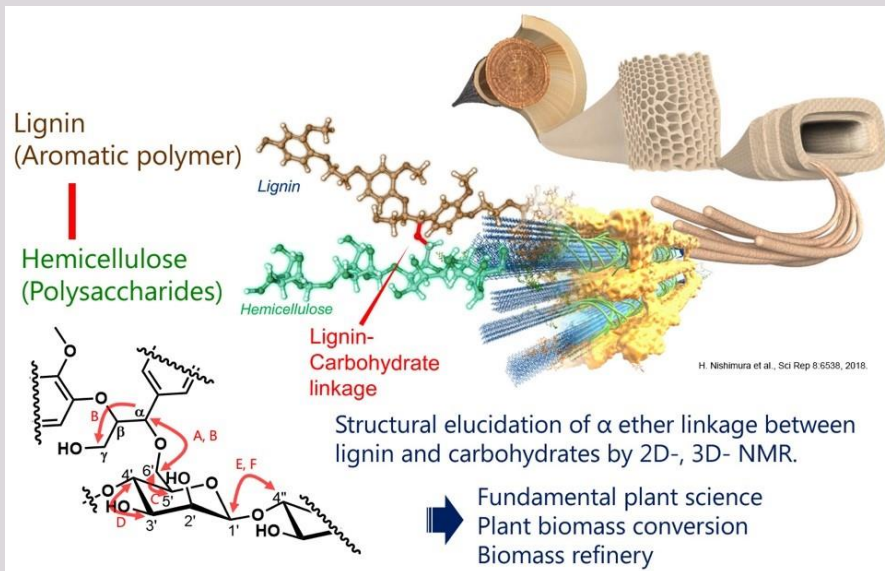
CAZy

...



Exemplo:





DEGRADAÇÃO DE RESÍDUOS LIGNOCELULÓSICOS

Origem da síntese de lignina

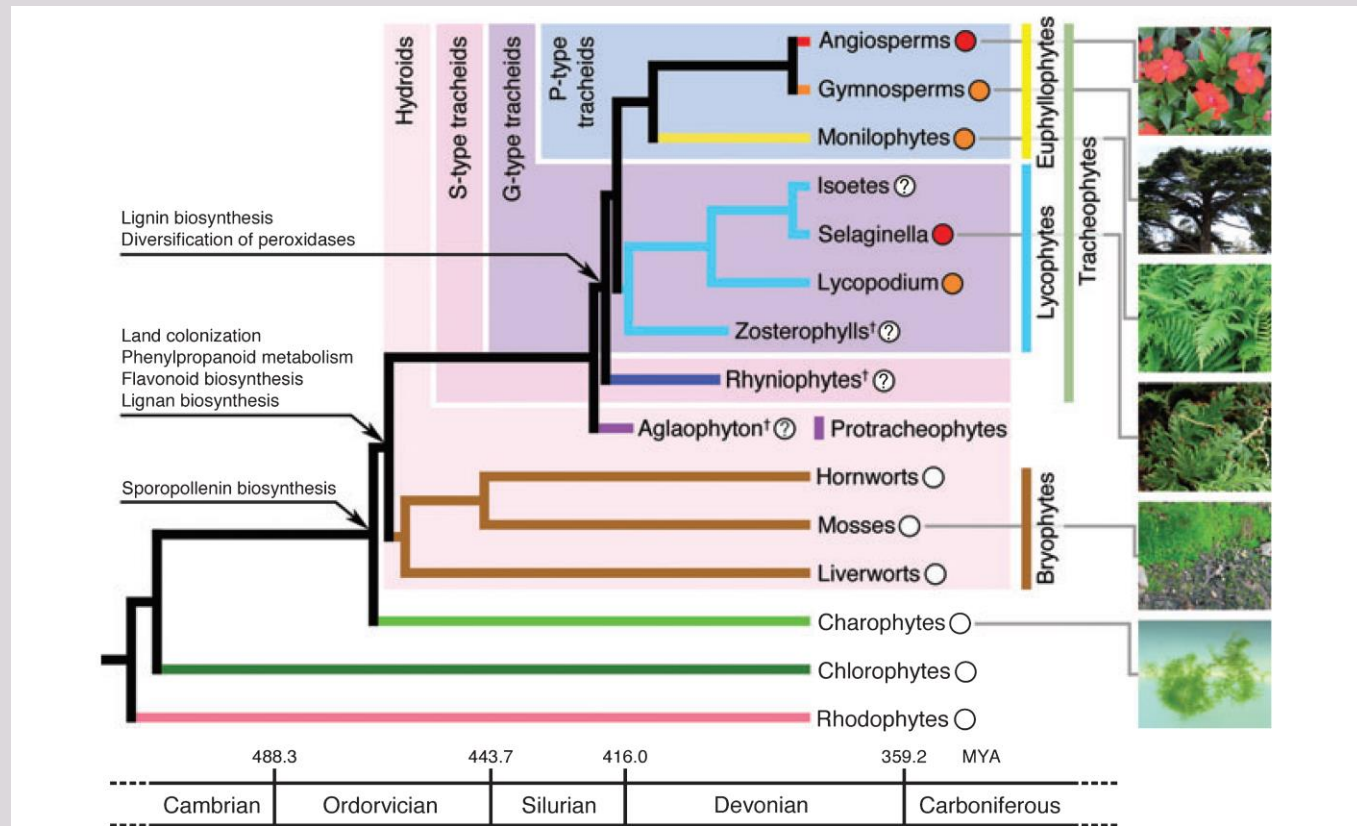


Fig. 2 A plant phylogenetic tree marked with the major milestones of evolution of lignin biosynthesis. The distribution of lignin and its monomeric composition across major plant lineages are denoted by a circle at each branch. Open circle, no lignin; orange circle, presence of H and G lignin; red circle, presence of S lignin in addition to H and G lignin; circle with question mark, unknown. Note that, within several groups with G lignin, S lignin-containing exceptions are known. †Extinct lineage.



PERÍODO
CARBONÍFERO

The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes

Dimitrios Floudas,¹ Manfred Binder,¹ Robert Riley,² Kerrie Barry,² Robert A. Blanchette,³

To gain access to cellulose, wood-decaying fungi must overcome or circumvent lignin; thus, we focus on fungal class II peroxidases (PODs), which degrade lignin in *P. chrysosporium* and other species (11) (figs. S7 to S19). We classified PODs into four major groups, including three ligninolytic forms—lignin peroxidase (LiP), manganese peroxidase (MnP), and versatile peroxidase (VP)—and a fourth POD type, defined here as “generic peroxidase” (GP), which is expected to include nonligninolytic low-redox potential peroxidases with catalytic properties similar to those of the peroxidase of *Coprinopsis cinerea* or the product of the *nopA* gene in *P. chrysosporium* (5, 12). LiPs possess a tryptophan residue on the surface of the enzyme corresponding to Trp¹⁷¹ in *P. chrysosporium* LiP-H8 that enables direct oxidation of lignin compounds via long-range electron transfer; MnPs possess two or three residues corresponding to Glu³⁵, Glu³⁹, and Asp¹⁷⁵

mycota, with parallel losses in lineages leading to the Pucciniomycotina, Ustilaginomycotina, Tremellomycetes, and *Dacryopinax* sp. (Fig. 1A). Diversification of PODs occurred in the lineage leading to the most recent common ancestor of the Agaricomycetes (node “A” in Fig. 1A), which is reconstructed as having two to seven POD gene copies in the various analyses. In addition, reconciliation analyses suggest that the ancestor of the Agaricomycetes possessed one or two genes encoding dye-decolorizing peroxidases (DyP), which are heme peroxidases that have been shown to degrade lignin model compounds (22), as well five to eight genes encoding oxidases (including glyoxal oxidase) involved in peroxide generation (5, 23). Collectively, these results suggest that the ancestor of Agaricomycetes was a white rot species that possessed a ligninolytic system with PODs, DyPs, and multiple pathways for H₂O₂ production.

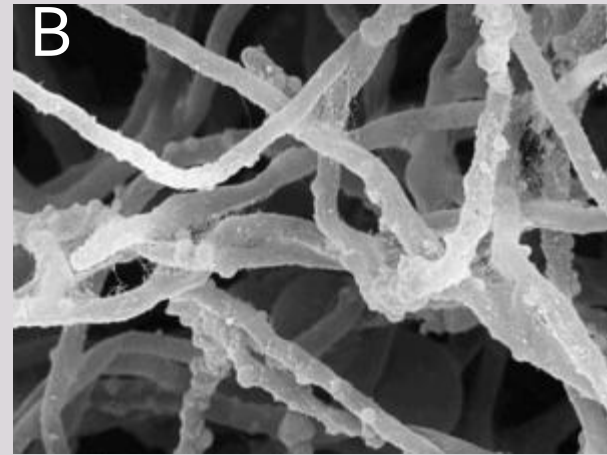
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- Espécie modelo: *Phanerochaete chrysosporium*



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Linhagem taxonômica

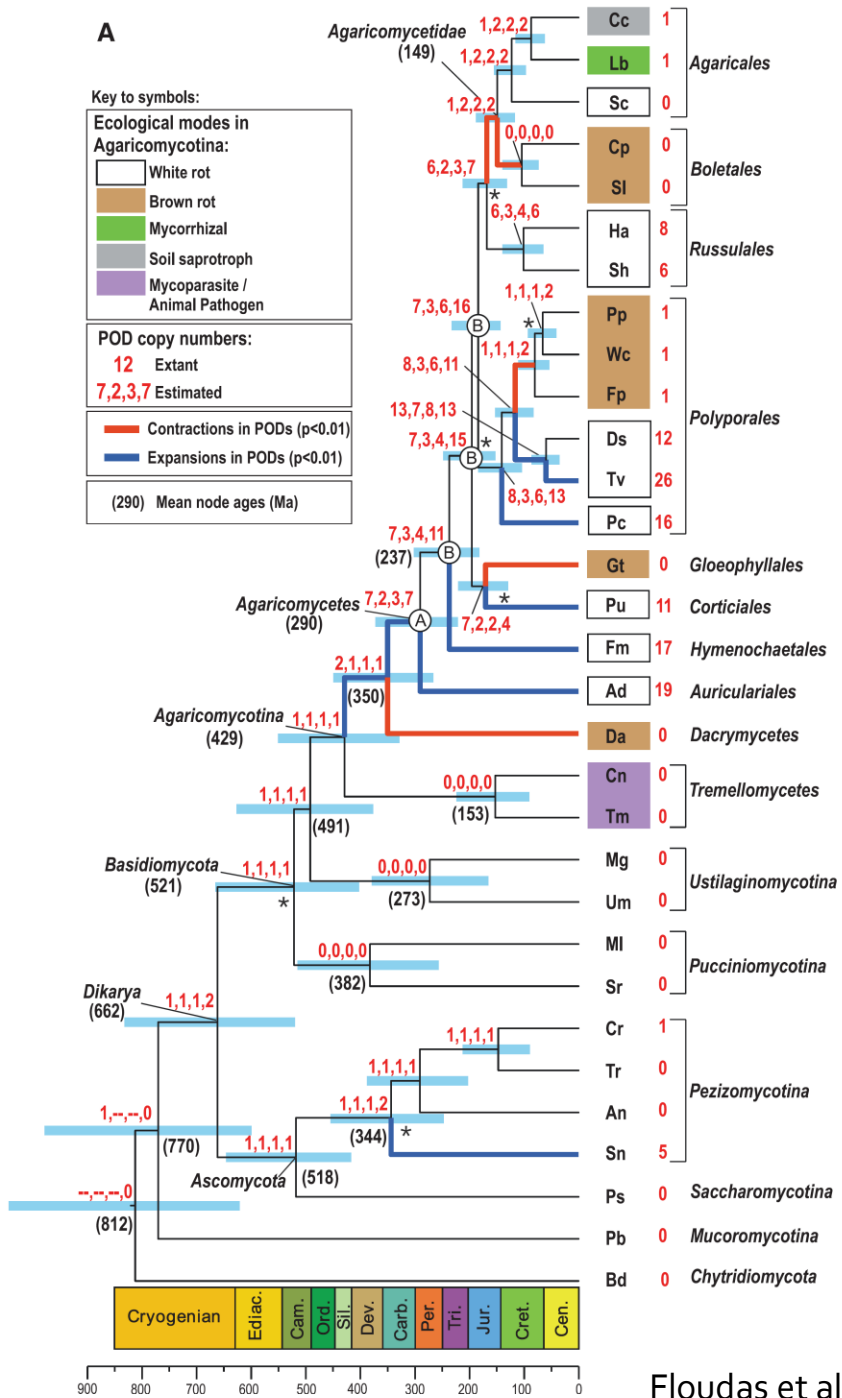
- › cellular organisms
- › Eukaryota
- › Opisthokonta
- › Fungi
- › Dikarya
- › Basidiomycota
- › Agaricomycotina
- › Agaricomycetes
- › Agaricomycetes incertae sedis
- › Polyporales
- › Phanerochaetaceae

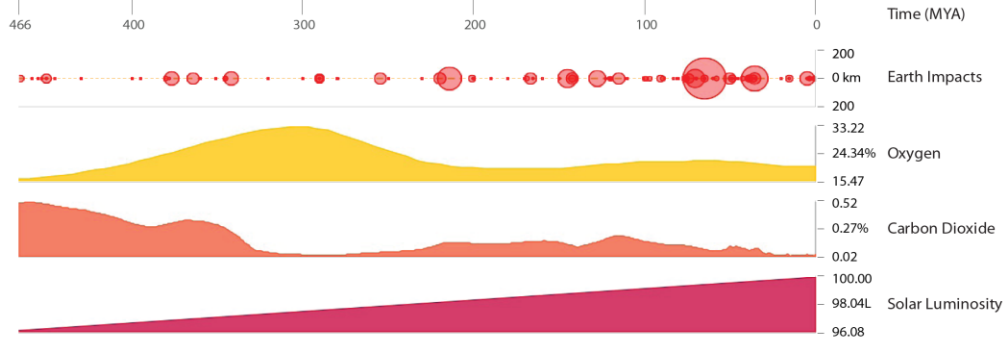
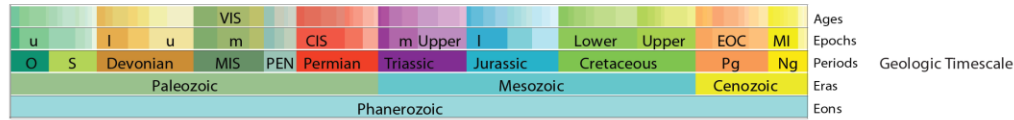
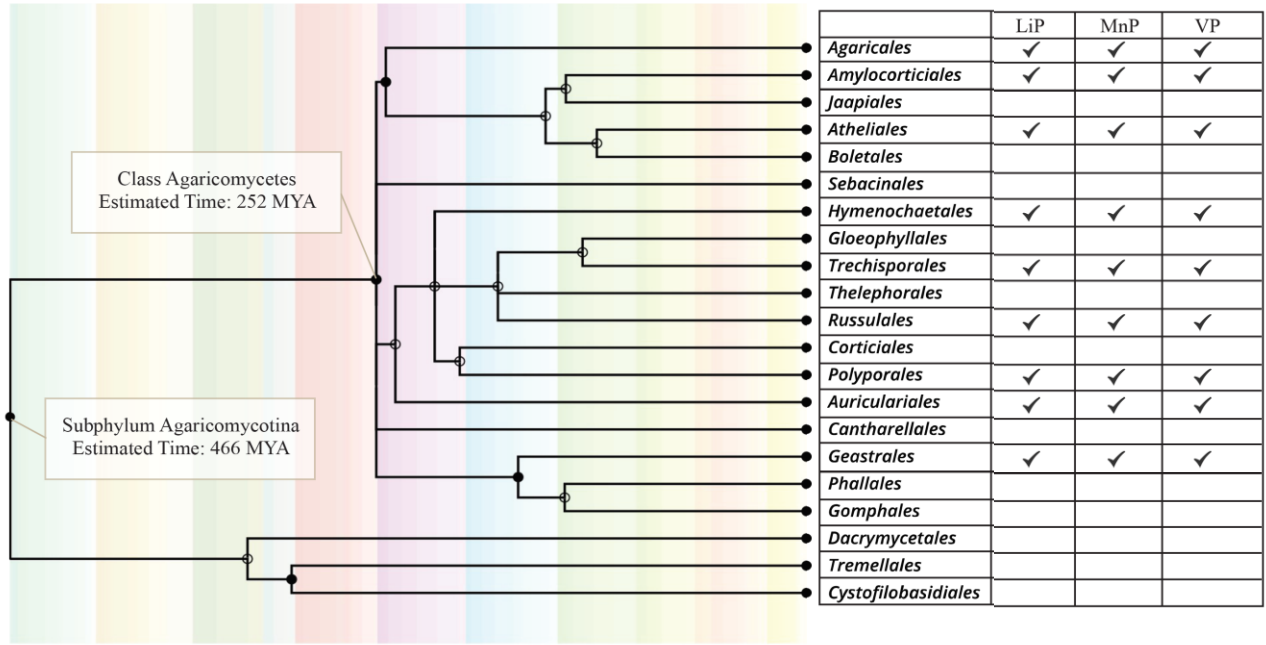
- Class II peroxidases

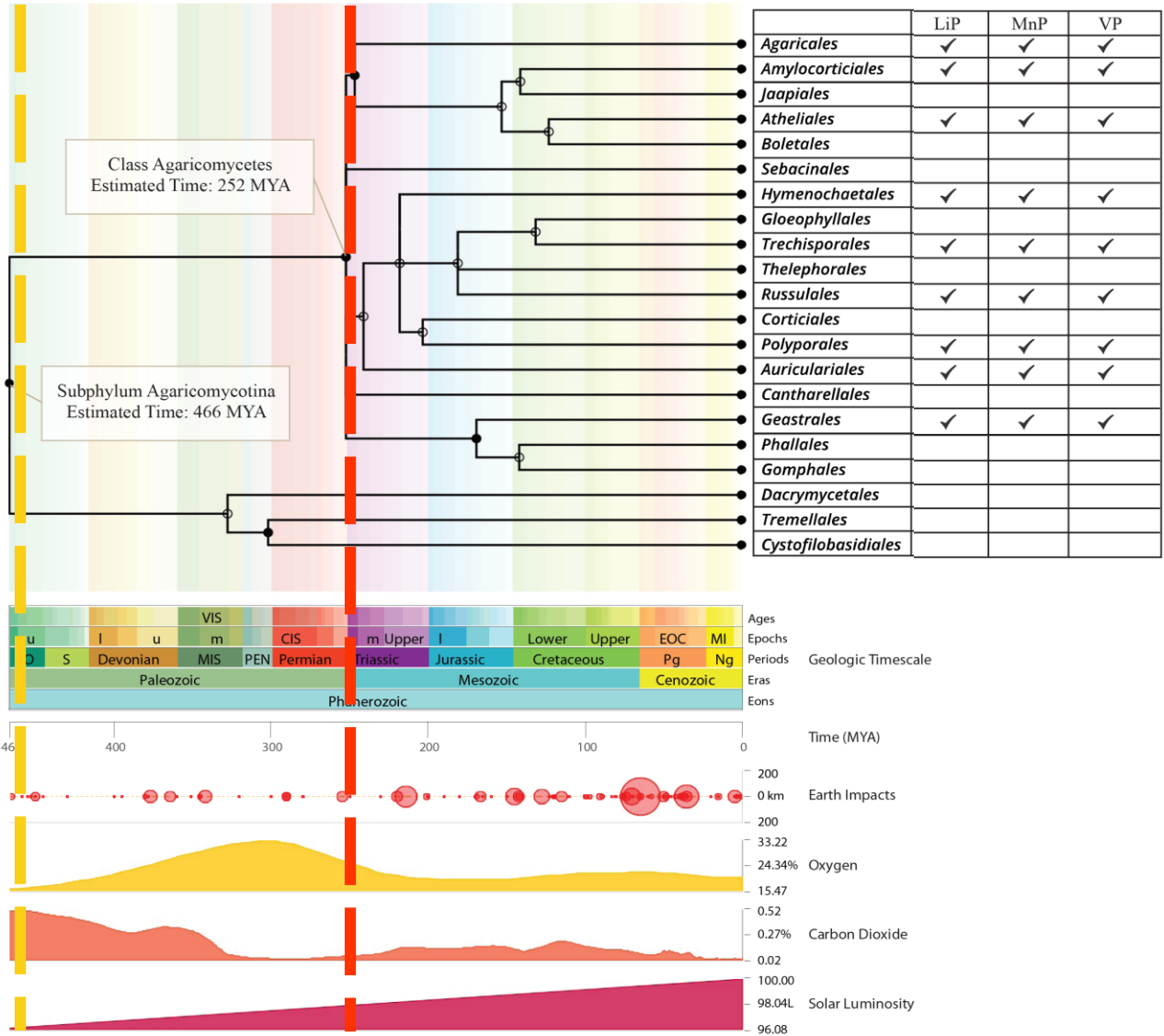
- LiP = lignin peroxidase
- *MnP* = manganese peroxidase
- Vp = *versatile peroxidase*

PRÁTICA











Resultado da busca na base uniprot

<input type="checkbox"/>	Entry	Entry name	Protein names	EC number	Gene names	Organism	Proteomes	Length	Taxonomic lineage (KINGDOM)
<input checked="" type="checkbox"/>	P31837	LIGA_PHACH	 Ligninase A	1.11.1.14	LIPA LPOB	Phanerochaete chrysosporium (White-rot fungus) (Sporotrichum pruinosum)		372	Fungi
<input type="checkbox"/>	P20011	LIGA_TRAVE	 Ligninase A	1.11.1.14		Trametes versicolor (White-rot fungus) (Coriolus versicolor)		13	Fungi
<input checked="" type="checkbox"/>	P31838	LIGB_PHACH	 Ligninase B	1.11.1.14	LIPB	Phanerochaete chrysosporium (White-rot fungus) (Sporotrichum pruinosum)		372	Fungi
<input type="checkbox"/>	P20012	LIGB_TRAVE	 Ligninase B	1.11.1.14		Trametes versicolor (White-rot fungus) (Coriolus versicolor)		13	Fungi
<input type="checkbox"/>	P20013	LIGC_TRAVE	 Ligninase C	1.11.1.14		Trametes versicolor (White-rot fungus) (Coriolus versicolor)		372	Fungi
<input checked="" type="checkbox"/>	P11542	LIG4_PHACH	 Ligninase H2	1.11.1.14	GLG4 LIP2	Phanerochaete chrysosporium (White-rot fungus) (Sporotrichum pruinosum)		372	Fungi
<input checked="" type="checkbox"/>	P06181	LIG8_PHACH	 Ligninase H8	1.11.1.14	LPOA	Phanerochaete chrysosporium (White-rot fungus) (Sporotrichum pruinosum)		372	Fungi
<input checked="" type="checkbox"/>	P49012	LIG2_PHACH	 Ligninase LG2	1.11.1.14	GLG2 LIP2	Phanerochaete chrysosporium (White-rot fungus) (Sporotrichum pruinosum)		371	Fungi
<input checked="" type="checkbox"/>	P21764	LIG3_PHACH	 Ligninase LG3	1.11.1.14	GLG3 LIP	Phanerochaete chrysosporium (White-rot fungus) (Sporotrichum pruinosum)		372	Fungi
<input checked="" type="checkbox"/>	P11543	LIG5_PHACH	 Ligninase LG5	1.11.1.14	GLG5 LIP6	Phanerochaete chrysosporium (White-rot fungus) (Sporotrichum pruinosum)		371	Fungi
<input checked="" type="checkbox"/>	P50622	LIG6_PHACH	 Ligninase LG6	1.11.1.14	GLG6	Phanerochaete chrysosporium (White-rot fungus) (Sporotrichum pruinosum)		372	Fungi

TaxOnTree

Including taxonomic information on your tree



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Run TaxOnTree

Input

Select the type of your input

- query identifier [?] Examples: [#1 #2](#)
- Amino acid sequence [?] Examples: [#1 #2](#)
- List of identifiers [?] Examples: [#1 #2](#)
- Tree in Newick [?] Examples: [#1 #2](#)

Enter your input here:

e.g. 4757876 or Q10589

Or upload a file:

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No file selected.

Job description

Write here a small description of your job

Your job will be saved in a guest account.

Options

BLAST options

Sequence Database:

Threshold (%): [?] Evalue: [?]

Maximum targets number: [?]

Alignment options

Analyze alignment with TrimAl. [?]

Alignment software

Filter options

Exclude protein isoforms. [?]

Limit the number of taxa in clades of a taxonomic category: Show taxa per

Show only samples from organisms in which the LCA level is equal or higher than [?]

Tree options

Tree rooting method: [?] [More](#)

Leaf name format:

Get your result

Enter a jobID and a file type

TaxOnTree generates a phylogenetic tree in NEXUS format designed to be opened in **FigTree**. Blast result and sequence alignment are also available for download.

FigTree is available for download [here](#) or at [FigTree's website](#).

Here are some NEXUS file generated by TaxOnTree: Sample [#1](#) [#2](#) [#3](#)

Instructions for visualizing your tree on FigTree can be found [here](#)

Getting error?

Check out the **log file** to have some clues on what is causing the error.