

**SUPPLEMENTARY MATERIAL FOR THE PAPER “A
nested phylogenetic reconstruction approach provides
scalable resolution in the eukaryotic Tree Of Life”**

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1 SUPPLEMENTARY FIGURES AND TABLES

1.1 Supplementary Figure S1

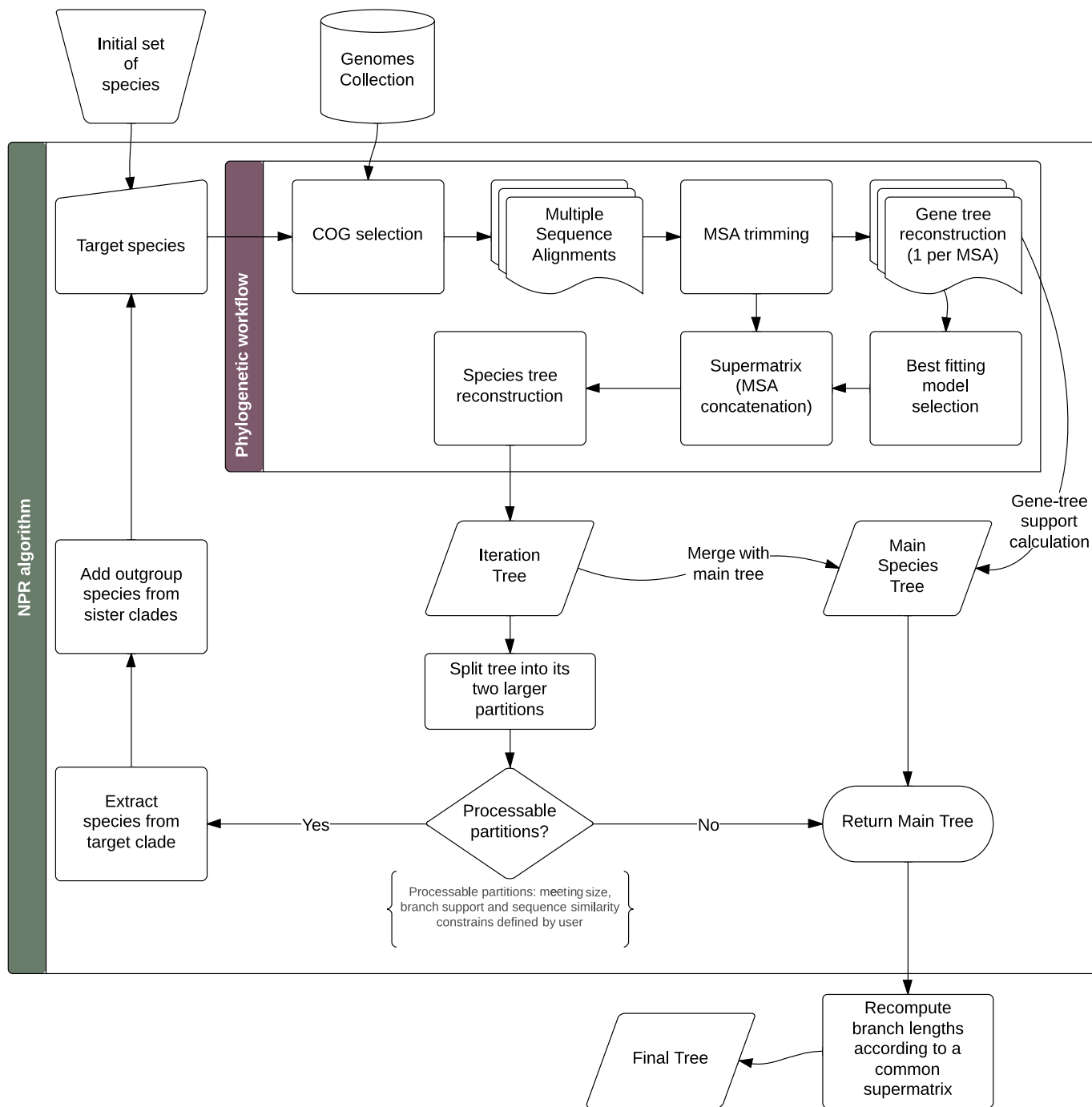


Fig. 1: **Schematic representation of the NPR algorithm.** Flowchart representing the NPR algorithm and the phylogenetic workflow used for the reconstruction of the eukaryotic tree of life presented along with this manuscript. Note that steps within the phylogenetic workflow box apply only for the RAxML-based phylogenetic pipeline described in the methods section.

1.2 Supplementary Figure S2

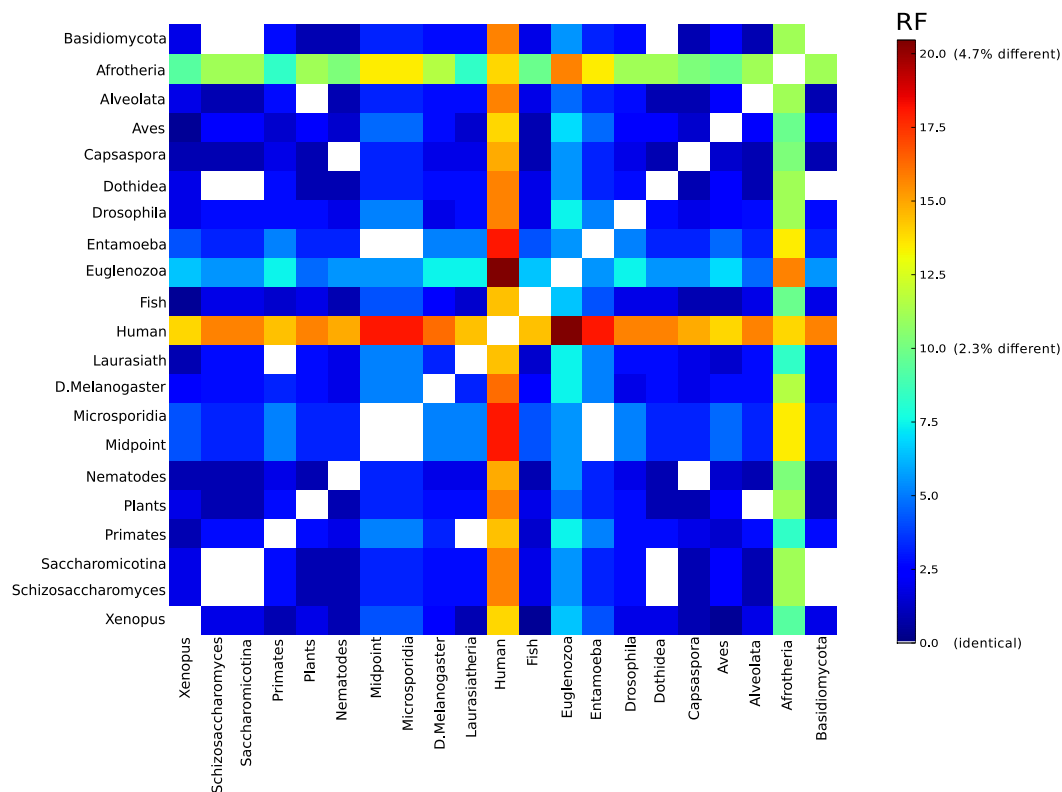


Fig. 2: **Topological distance among several NPR trees rooted to different clades.** Heatmap matrix represents the topological distance, in Robinson Foulds (RF) units, between 21 NPR executions. Each NPR execution used identical pipeline parameters and species set, differing only on the outgroup node used to root the first iteration tree. Normalized distances (RF/maxRF) are also shown in the scale bar as a percentage value. X and Y axes indicate the clade used to root the first iteration of each NPR thread.

1.3 Supplementary Figure S3

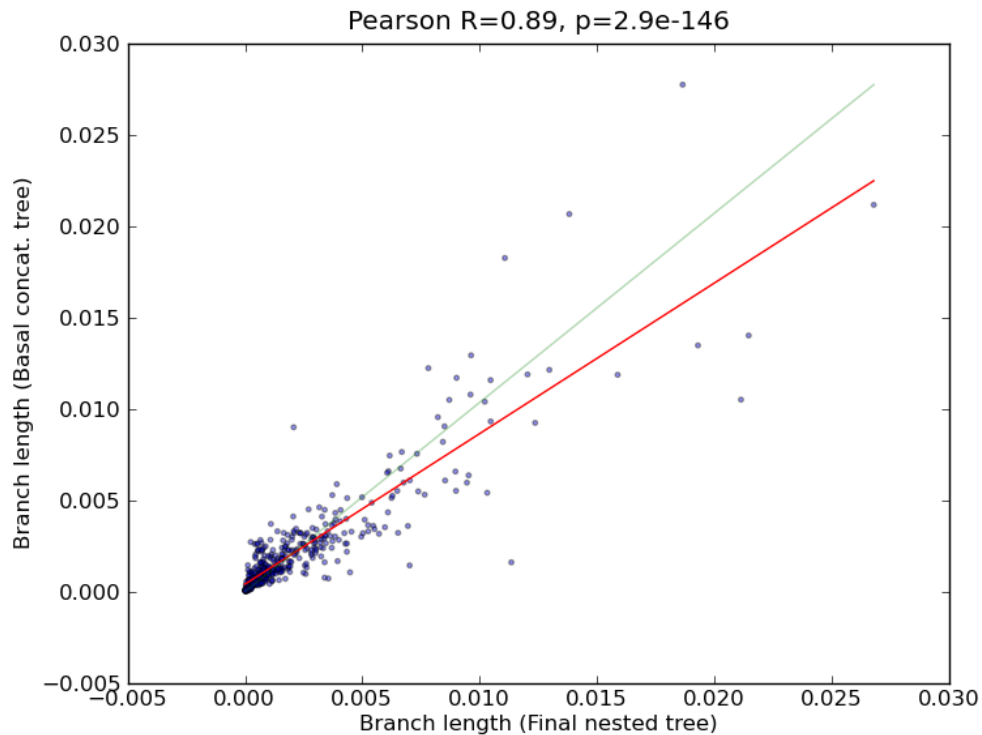


Fig. 3: **Pearson correlation and linear regression between nested and the basal concatenation tree.** Branch lengths in the nested tree (X axis) are optimized according to the refined concatenated alignment of each internal node. Branch lengths in the basal concatenation tree (Y axis) are optimized according to the original set of 131 OGs. Red line represents the linear correlation between the two measures. Bisector line is show in green. Note that branch lengths in the nested tree tend to be larger than in the classic concatenation tree.

1.4 Supplementary Figure S4

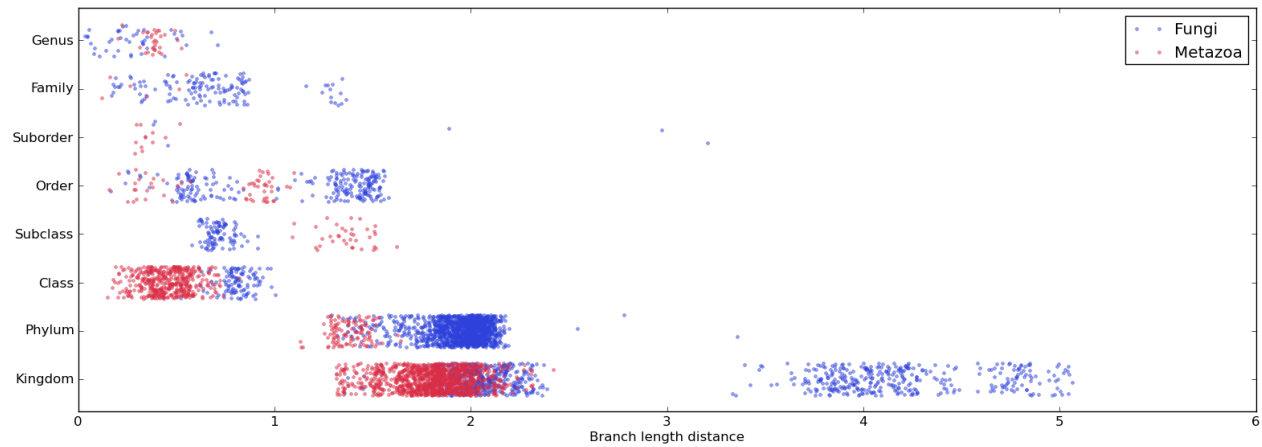


Fig. 4: Branch length distances between all pairs of species within the fungi (blue) and metazoa (red) clades, sorted by the rank of their first common taxonomic group. Note that, for all taxonomic divisions, except for “sub-class”, maximum distances in fungi are larger.

1.5 Supplementary Figure S5

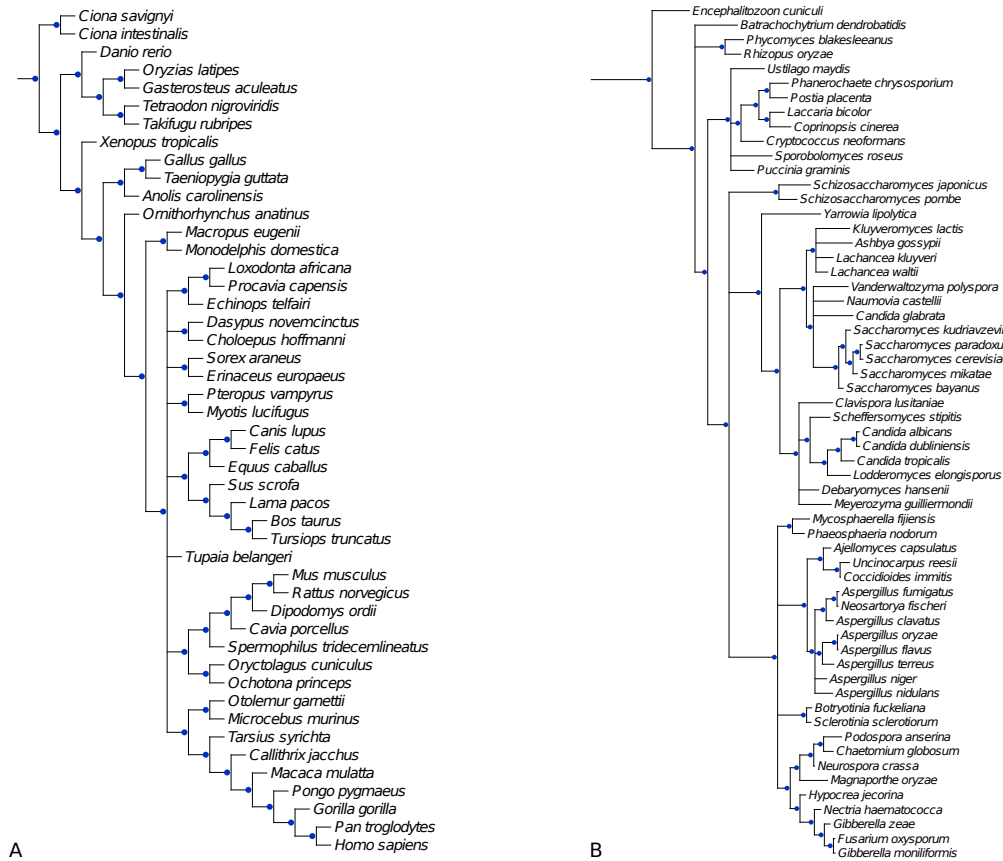


Fig. 5: Reference species tree for the chordates clade (A) and the fungal clade (B). Fungal reference tree adapted from Marcet-Houben et al. [Marcet-Houben and Gabaldón, 2009] where the nodes with a phylome support below 50% have been collapsed. In the chordate tree, nodes poorly supported in the literature have also been collapsed.

1.6 Supplementary Table S1.

TaxID	Proteome Source	Scientific Name	CommonName
3055	Phytozome	Chlamydomonas reinhardtii	
70448	Integr8	Ostreococcus tauri	
3218	Phytozome	Physcomitrella patens	
88036	Phytozome	Selaginella moellendorffii	
44056	JGI	Aureococcus anophagefferens	
4784	JGI	Phytophthora capsici	

TaxID	Proteome Source	Scientific Name	CommonName
436017	Integr8	Ostreococcus lucimarinus	
242159	Integr8	Ostreococcus 'lucimarinus'	
296543	JGI	Thalassiosira pseudonana	
4787	BI	Phytophthora infestans	Potato late blight fungus
5888	Integr8	Paramecium tetraurelia	
5911	KEGG	Tetrahymena thermophila	
4558	JGI	Sorghum bicolor	Milo
4577	maizesequence	Zea mays	Maize
15368	Phytozome	Brachypodium distachyon	
39947	Integr8	Oryza sativa	Japanese rice
3702	Integr8	Arabidopsis thaliana	Thale-cress
59689	Phytozome	Arabidopsis lyrata	Lyrate rockcress
3847	Phytozome	Glycine max	Soybeans
186039	JGI	Fragilariopsis cylindrus	
556484	JGI	Phaeodactylum tricornutum	
67593	JGI	Phytophthora sojae	
164328	JGI	Phytophthora ramorum	
353151	Integr8	Cryptosporidium hominis	
353152	Integr8	Cryptosporidium parvum	
507601	NCBI	Toxoplasma gondii	
5762	JGI	Naegleria gruberi	
5786	JGI	Dictyostelium purpureum	
352472	Integr8	Dictyostelium discoideum	
73824	JGI	Populus balsamifera	Balsam poplar

TaxID	Proteome Source	Scientific Name	CommonName
29760	Genoscope	Vitis vinifera	Wine grape
412133	KEGG	Trichomonas vaginalis	
184922	Integr8	Giardia lamblia	
294381	KEGG	Entamoeba histolytica	
370354	KEGG	Entamoeba dispar	
192875	BI	Capsaspora owczarzaki	
5865	Integr8	Babesia bovis	
5693	Integr8	Trypanosoma cruzi	
5691	KEGG	Trypanosoma brucei	
5660	Integr8	Leishmania braziliensis	
81824	Integr8	Monosiga brevicollis	
278021	AntonosporaDB	Antonospora locustae	
333668	Integr8	Theileria parva	
5874	Integr8	Theileria annulata	
36329	Integr8	Plasmodium falciparum	
31271	Integr8	Plasmodium chabaudi	
347515	Integr8	Leishmania major	
5671	Integr8	Leishmania infantum	
45351	Integr8	Nematostella vectensis	
481877	Integr8	Enterocytozoon bieneusi	
5855	Integr8	Plasmodium vivax	
5851	Integr8	Plasmodium knowlesi	
352914	Integr8	Plasmodium yoelii	
5823	Integr8	Plasmodium berghei	
284813	Integr8	Encephalitozoon cuniculi	
578460	NosemaRef	Nosema ceranae	
109760	BI	Spizellomyces punctatus	
109871	BI	Batrachochytrium dendrobatidis	
4837	JGI	Phycomyces blakesleeanus	

TaxID	Proteome Source	Scientific Name	CommonName
64495	BI	Rhizopus oryzae	
36080	JGI	Mucor circinelloides	
76773	Hyphal	Malassezia globosa	
237631	Integr8	Ustilago maydis	
402676	BI	Schizosaccharomyces japonicus	
6239	Ensembl	Caenorhabditis elegans	Nematode
6238	Integr8	Caenorhabditis briggsae	
6669	JGI	Daphnia pulex	
51511	Ensembl	Ciona savignyi	
7719	Ensembl	Ciona intestinalis	
40563	JGI	Sporobolomyces roseus	
284812	BI	Schizosaccharomyces pombe	
483514	BI	Schizosaccharomyces octosporus	
284591	Integr8	Yarrowia lipolytica	
7955	Ensembl	Danio rerio	Zebra fish
8364	Ensembl	Xenopus (Silurana)	
203908	JGI	Melampsora laricis-populina	
5297	BI	Puccinia graminis	
214684	Integr8	Cryptococcus neoformans	
5217	JGI	Tremella mesenterica	
121225	VECTORBASE	Pediculus humanus	Human lice
7029	NIH	Acyrtosiphon pisum	
7425	NCBI	Nasonia vitripennis	
8090	Ensembl	Oryzias latipes	Medaka
13563	JGI	Heterobasidion annosum	
5334	JGI	Schizophyllum commune	
4922	NCBI	Pichia pastoris	
332648	Integr8	Botryotinia fuckeliana	

TaxID	Proteome Source	Scientific Name	CommonName
325569	Integr8	Sclerotinia sclerotiorum	
7070	NCBI	Tribolium castaneum	Rust-red flour beetle
69293	Ensembl	Gasterosteus aculeatus	Three spined stickleback
28377	Ensembl	Anolis carolinensis	
9258	Ensembl	Ornithorhynchus anatinus	Duck-billed platypus
5306	JGI	Phanerochaete chrysosporium	
104341	JGI	Postia placenta	
5322	JGI	Pleurotus ostreatus	
36911	BI	Clavispora lusitaniae	
4956	Genolevures	Zygosaccharomyces rouxii	
54734	JGI	Mycosphaerella graminicola	
83344	JGI	Mycosphaerella fijiensis	
321614	Integr8	Phaeosphaeria nodorum	
500485	Integr8	Penicillium chrysogenum	
7091	SILKDB	Bombyx mori	Silk moth
99883	Ensembl	Tetraodon nigroviridis	
31033	Ensembl	Takifugu rubripes	Tiger puffer
9031	Ensembl	Gallus gallus	Bantam
59729	Ensembl	Taeniopygia guttata	Zebra finch
29883	JGI	Laccaria bicolor	
5346	BI	Coprinopsis cinerea	
284590	Integr8	Kluyveromyces lactis	
284811	YGOB	Ashbya gossypii	
4934	Genolevures	Lachancea kluyveri	
436907	YGOB	Vanderwaltozyma polyspora	
242507	Integr8	Magnaporthe oryzae	
5116	JGI	Cryphonectria parasitica	

TaxID	Proteome Source	Scientific Name	CommonName
27335	BI	Verticillium albo-atrum	
498257	BI	Verticillium dahliae	
5016	JGI	Cochliobolus heterostrophus	
502780	BI	Paracoccidioides brasiliensis	
9315	Ensembl	Macropus eugenii	
13616	Ensembl	Monodelphis domestica	
284592	Integr8	Debaryomyces hansenii	
294746	Integr8	Meyerozyma guilliermondii	
322104	Integr8	Scheffersomyces stipitis	
381046	Genolevures	Lachancea thermotolerans	
4914	Hyphal	Lachancea waltii	
27288	YGOB	Naumovia castelii	
29879	JGI	Neurospora discreta	
5145	PodosporaDB	Podospora anserina	
63577	JGI	Trichoderma atroviride	
140110	JGI	Nectria haematococca	
29001	JGI	Alternaria brassicicola	
45151	BI	Pyrenophora tritici-repentis	
559297	BI	Ajellomyces dermatitidis	
339724	BI	Ajellomyces capsulatus	
554155	BI	Arthroderma otae	
33188	BI	Uncinocarpus reesii	
344612	Integr8	Aspergillus clavatus	
180454	Integr8	Anopheles gambiae	
9371	Ensembl	Echinops telfairi	Lesser hedgehog tenrec
284593	Genolevures	Candida glabrata	

TaxID	Proteome Source	Scientific Name	CommonName
40127	JGI	Neurospora tetrasperma	
367110	Integr8	Neurospora crassa	
573728	JGI	Myceliophthora thermophila	
306901	Integr8	Chaetomium globosum	
51453	JGI	Hypocrea jecorina	
29875	JGI	Hypocrea virens	
5518	BI	Gibberella zeae	
489714	BI	Microsporum gypseum	
63418	BI	Trichophyton equinum	
246410	BI	Coccidioides immitis	
454284	BI	Coccidioides posadasii	
451804	Integr8	Aspergillus fumigatus	
331117	Integr8	Neosartorya fischeri	
425011	Integr8	Aspergillus niger	
227321	Integr8	Aspergillus nidulans	
341663	Integr8	Aspergillus terreus	
7175	VECTORBASE	Culex pipiens	
7159	Integr8	Aedes aegypti	
7222	flybase	Drosophila grimshawi	
7260	flybase	Drosophila willistoni	
9785	Ensembl	Loxodonta africana	African savannah elephant
9813	Ensembl	Procavia capensis	Rock dassie
9361	Ensembl	Dasyopus novemcinctus	
9358	Ensembl	Choloepus hoffmanni	Hoffmann's two-toed sloth
379508	Integr8	Lodderomyces elongisporus	
5480	BI	Candida parapsilosis	
5482	BI	Candida tropicalis	
4931	YGOB	Saccharomyces bayanus	
5507	BI	Fusarium oxysporum	
117187	BI	Gibberella moniliformis	

TaxID	Proteome Source	Scientific Name	CommonName
5062	BI	Aspergillus oryzae	
5059	BI	Aspergillus flavus	
7244	flybase	Drosophila virilis	
7230	flybase	Drosophila mojavensis	
237561	CGD	Candida albicans	
573826	Integr8	Candida dubliniensis	
114524	Hyphal	Saccharomyces kudriavzevii	
7234	flybase	Drosophila persimilis	
46245	flybase	Drosophila pseudoobscura	
7217	flybase	Drosophila ananassae	
42254	Ensembl	Sorex araneus	Eurasian shrew
9365	Ensembl	Erinaceus europaeus	
37347	Ensembl	Tupaia belangeri	Common tree shrew
114525	Hyphal	Saccharomyces mikatae	
9796	Ensembl	Equus caballus	Equine
30611	Ensembl	Otolemur garnettii	
30608	Ensembl	Microcebus murinus	Grey mouse lemur
9478	Ensembl	Tarsius syrichta	
27291	Hyphal	Saccharomyces paradoxus	
559292	SGD	Saccharomyces cerevisiae	
7245	flybase	Drosophila yakuba	
7220	flybase	Drosophila erecta	
7227	flybase	Drosophila melanogaster	
9615	Ensembl	Canis lupus	Dogs
9685	Ensembl	Felis catus	Cat
132908	Ensembl	Pteropus vampyrus	
59463	Ensembl	Myotis lucifugus	
30538	Ensembl	Lama pacos	
9986	Ensembl	Oryctolagus cuniculus	Domestic rabbit
9978	Ensembl	Ochotona princeps	Southern american pika

TaxID	Proteome Source	Scientific Name	CommonName
43179	Ensembl	Spermophilus tridecemlineatus	
9483	Ensembl	Callithrix jacchus	Common marmoset
7238	flybase	Drosophila sechellia	
7240	flybase	Drosophila simulans	
9823	Ensembl	Sus scrofa	Wild boar
10141	Ensembl	Cavia porcellus	Guinea pig
9544	Ensembl	Macaca mulatta	Rhesus macaque
9913	Ensembl	Bos taurus	Cow
9739	Ensembl	Tursiops truncatus	Bottle-nosed dolphin
10020	Ensembl	Dipodomys ordii	
9600	Ensembl	Pongo pygmaeus	Orang utan
10090	Ensembl	Mus musculus	Mouse
10116	Ensembl	Rattus norvegicus	Brown rat
9593	Ensembl	Gorilla gorilla	Gorilla
9606	Ensembl	Homo sapiens	Man
9598	Ensembl	Pan troglodytes	

Tab. 1: List of species present in the tree. Proteome source databases are encoded as follows: AntonosporaDB (<http://forest.mbl.edu/cgi-bin/site/antonospora01>), BI (www.broadinstitute.org), CGD (www.candidagenome.org/), Duke (www.genome.duke.edu/), Ensembl (<http://ensembl.org>), Flybase (<http://flybase.org/>), Genolevures (www.genolevures.org/), Genoscope (<http://www.genoscope.cns.fr/>), Hyphal (<http://fungalg genomes.org/blog/>), Integr8 (www.ebi.ac.uk/integr8), JGI (www.jgi.doe.gov), KEGG (www.genome.jp/kegg), Maizesequence, NCBI (www.ncbi.nlm.nih.gov), NIH (www.nih.gov), NosemaRef [Cornman et al., 2009], Phytozome (www.phytozome.net/), PodosporaDB (<http://podospora.igmors.u-psud.fr/>), SGD (www.yeastgenome.org/), SILKDB (www.silkdb.org), Vectorbase (<http://vectorbase.org>), YGOB (<http://wolfe.gen.tcd.ie/ygob/>).

1.7 Supplementary Table S2

NCBI group	Conflicting species	Supported alternative	Support aLRT/GT	Comments
Eimeriorina	Toxoplasma	Toxoplasma as sister group of Plasmodium/Theileria	1/0.41	NCBI classification is not in accordance with latest studies. Our topology is (see Kuo et al., 2008)
Eucoccidiorida	Toxoplasma	Toxoplasma as sister group of Plasmodium/Theileria	1/0.41	See above

NCBI group	Conflicting species	Supported alternative	Support aLRT/GT	Comments
Coccidia	Toxoplasma	Toxoplasma as sister group of Plasmodium/Theileria	1/0.41	See above
Fabids	Vitis vinifera	Vitis vinifera within Fabids	1/0.27	NCBI is more in accordance with latest studies. This species has also been problematic in other analyses (see Burleigh et al., 2010)
Tracheophyta	Physcomitrella patens	Physcomitrella sister to Selaginella	1/0.55	NCBI is more in accordance with latest studies.
Mitosporic Saccharomycetales	Lodderomyces elongisporum	Loderomyces within the Candida clade	1/0.92	NCBI classification is not in accordance with latest studies. (see James et al., 1994, Marcet-Houben and Gabaldón, 2009, James et al., 2006)
Candida	Lodderomyces elongisporum	Loderomyces within the Candida clade	1/0.92	See above
Saccharomycetaceae	Pichia pastoris	P.pastoris within the candida clade	1/0.97	See above
Debaryomycetaceae	Several Candida species	See tree	1/0.32	See above
Arthroderma	Trichophyton equinum	Trychophyton equinum as sister group of Microsporium gypseum	1./0.83	See above
Giberella	Fusarium oxysporum	See tree	1./0.89	See above and Ma et al., 2010
Nectriaceae	Fusarium oxysporum	See tree	1/0.92	See above and Ma et al., 2010
mitosporic Trichocomaceae	Aspergillus nidulans, A. fumigatus, Neosartoria fisherii	See tree	1/0.87	See above and Wang et al., 2009
Aspergillus	Aspergillus nidulans, A. fumigatus, Neosartoria fisherii	See tree	1/0.56	See above and Wang et al., 2009
mitosporic Onygenales	Ajellomyces capsulatus, Trichophyton equinum, Microsporium gypseum, Arthroderma otae, Uncinocarpus reesii	See tree	1/0.76	See above and Sharpton et al., 2009
Amoebozoa	Entamoeba histolytica, E. dispar	Entamoeba with Trichomonas/Giardia	1/0.29	NCBI is more in accordance with latest studies.

NCBI group	Conflicting species	Supported alternative	Support aLRT/GT	Comments
Coelomata	Nematodes, Arthropodes and Chordates	Ecdysozoa	1/0.33	A debated node, although most latest analyses tend to support Ecdysozoa
Smegmamorpha	Gasterosteus aculeatus	See tree	0.94/0.30	The monophyly of this group is based on morphological data, and molecular studies have not been conclusive (see Miya et al., 2003, MIYA et al., 2005)
Sciurognathi	Cavia procelus	Cavia sister to Dipodomys, Mus and Rattus.	xx/0.25	A debated classification (see D'Erchia et al., 1996 for instance)

Tab. 2: Inconsistencies found between the final TOL topology and NCBI taxonomy classification. Groups in blue indicate those that NCBI taxonomy is more in agreement with recent literature, suggesting errors in our topology. The rest of the groups are currently under debate or abandoned, relevant literature is cited.

1.8 Supplementary Table S3

TaxID	Proteome Source	Scientific Name
5325	JGI	Trametes versicolor
5341	JGI	Agaricus bisporus
28583	JGI	Allomyces macrogynus
29898	BI	Rhodotorula graminis
31870	BI	Glomerella graminicola
34387	JGI	Trichophyton tonsurans
35720	BI	Thielavia terrestris
39416	BI	Tuber melanosporum
40483	JGI	Fomitopsis pinicola
40492	KEGG	Stereum hirsutum
40993	JGI	Aspergillus carbonarius
42742	JGI	Gelatoporia subvermispora

TaxID	Proteome Source	Scientific Name
5551	BI	Trichophyton rubrum
58839	JGI	Encephalitozoon intestinalis
63400	JGI	Arthroderma benhamiae
63417	NCBI	Trichophyton verrucosum
64363	BI	Mycosphaerella pini
80637	BI	Coniophora puteana
80884	JGI	Colletotrichum higginsianum
81056	JGI	Wolfiporia cocos
85929	BI	Mycosphaerella populorum
104355	JGI	Gloeophyllum trabeum
114155	JGI	Dichomitus squalens
148960	JGI	Wallemia sebi
153609	JGI	Moniliophthora perniciosa
202698	JGI	Punctularia strigosozonata
208348	KEGG	Puccinia triticina
208960	JGI	Fomitiporia mediterranea
866546	BI	Schizosaccharomyces cryophilus

Tab. 3: List of the new species added in the second version of the Tree of Life. Proteome source databases are encoded as follows: BI (www.broadinstitute.org), JGI (www.jgi.doe.gov), KEGG (www.genome.jp/kegg), NCBI (www.ncbi.nlm.nih.gov).

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