PNAS
www.pnas.org

Supplementary Information for

Fruiting body form, not nutritional mode, is the major driver of diversification in mushroom-forming fungi

Marisol Sánchez-García[a,b], Martin Ryberg[c], Faheema Kalsoom Khan[c], Torda Varga[d], László G. Nagy[d], and David S. Hibbett[a,1]

[a] Biology Department, Clark University, Worcester, MA 01610, USA
[b] Uppsala Biocentre, Department of Forest Mycology and Plant Pathology, Swedish University of Agricultural Sciences, SE-75005, Uppsala, Sweden
[c] Department of Organismal Biology, Evolutionary Biology Centre, Uppsala University, Uppsala, 752 36, Sweden
[d] Synthetic and Systems Biology Unit, Institute of Biochemistry, Biological Research Center, Szeged, 6726, Hungary

[1] David S. Hibbett
Email: dhibbett@clarku.edu

This PDF file includes:

Figures S1 to S14
Tables S2 to S19
SI References

Other supplementary information for this manuscript include the following:

Concatenated alignment
Phylogenetic tree
Character state coding (morphology and nutritional modes)
Table S1: Excel file with Genbank accession numbers of the sequences used to reconstruct the megaphylogeny

These files are available via the Open Science Framework (OSF) at: https://osf.io/y2vns/

www.pnas.org/cgi/doi/10.1073/pnas.1922539117

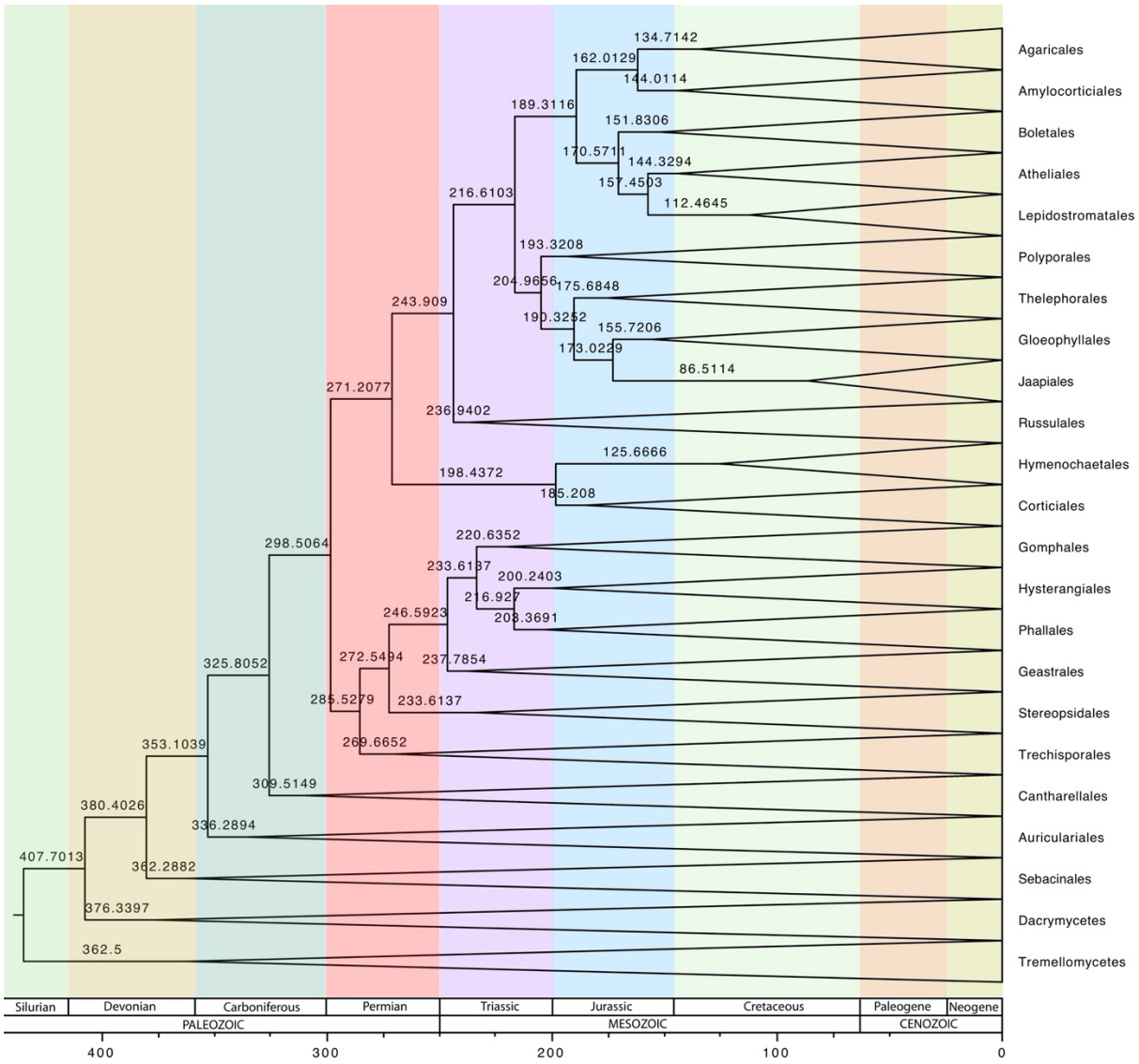

Figure S1. Ultrametric tree showing the origin of each order within the Agaricomycetes obtained with chronopl using 6 fossil calibrations. Numbers above branches indicate time in Mya.

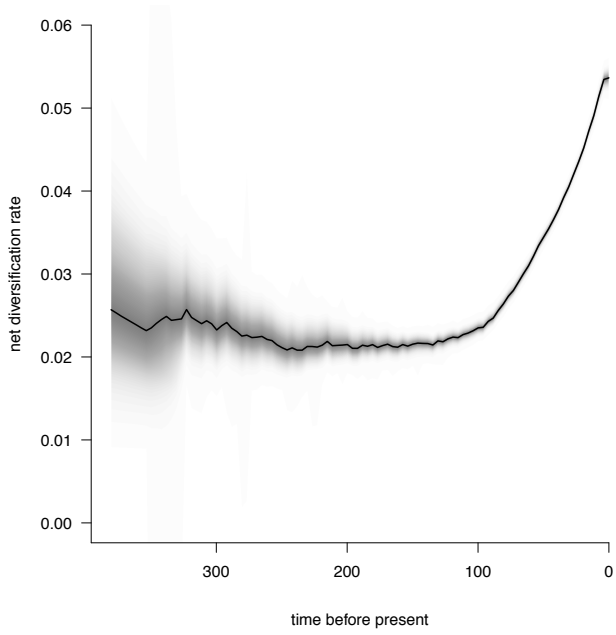

Figure S2. Rate through time plot of Agaricomycetes. Shading indicates confidence in the evolutionary rate reconstruction.

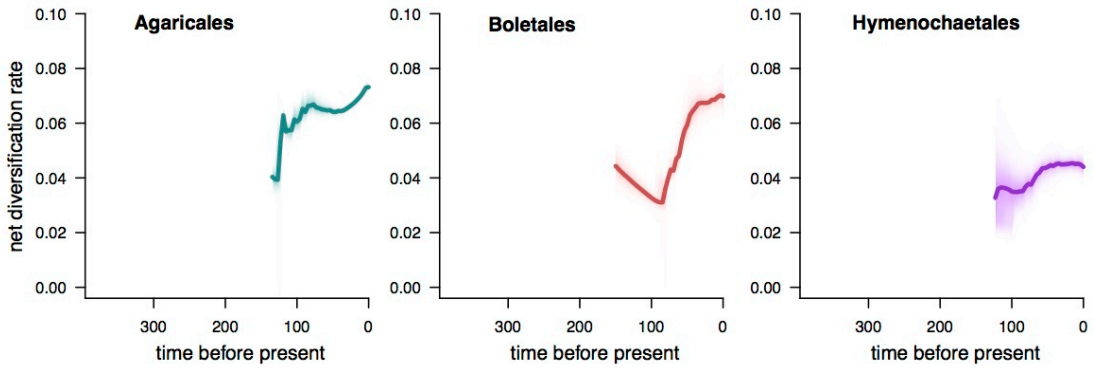

Figure S3. Rate through time plot showing three of the orders of Agaricomycetes with an increase of net diversification rate during the Cretaceous continuing into the Cenozoic. Shading indicates confidence in the evolutionary rate reconstruction.

Figure S4. Phylogenetic tree of the Agaricomycetes with ancestral state reconstruction of fruiting-body morphology types. The original PDF file can be found in the OSF repository: https://osf.io/y2vns/

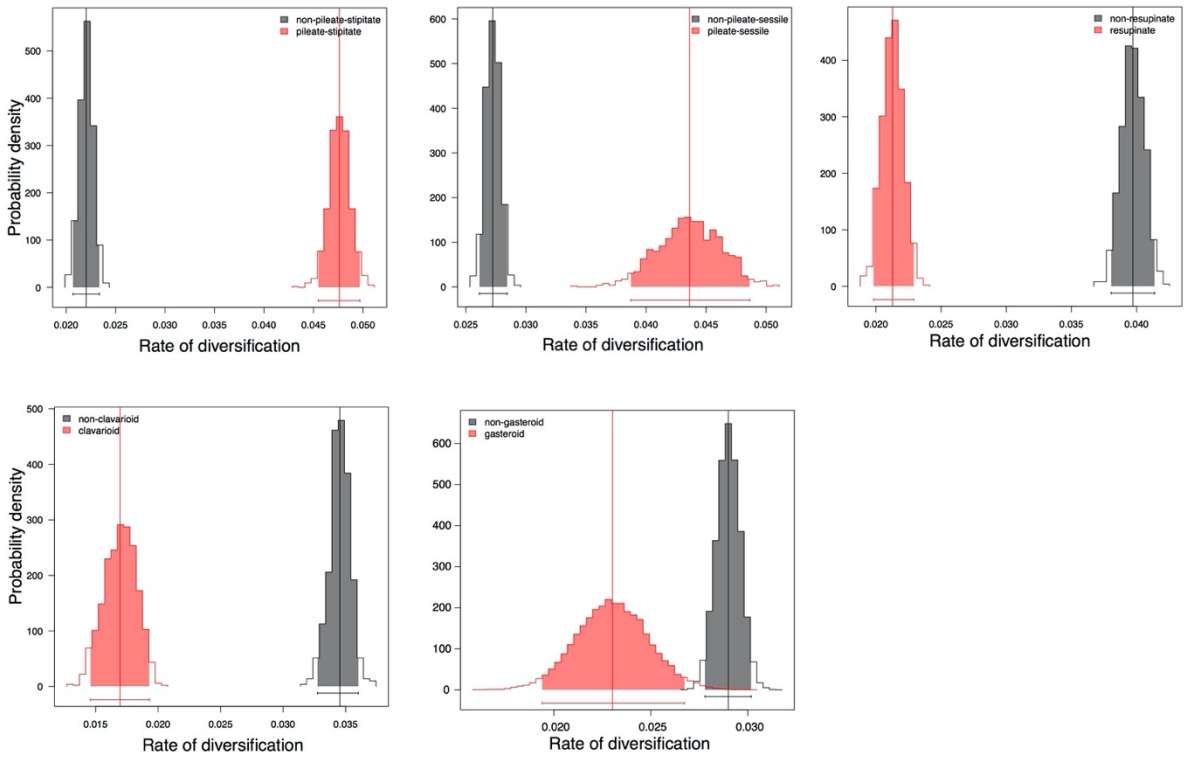

Figure S5. Posterior probability distributions of net diversification rates (speciation minus extinction) from the BiSSE model evaluating five types of morphology. The bar underneath each distribution represents the 95% credible interval obtained from the posterior distribution. The vertical lines represent the mean.

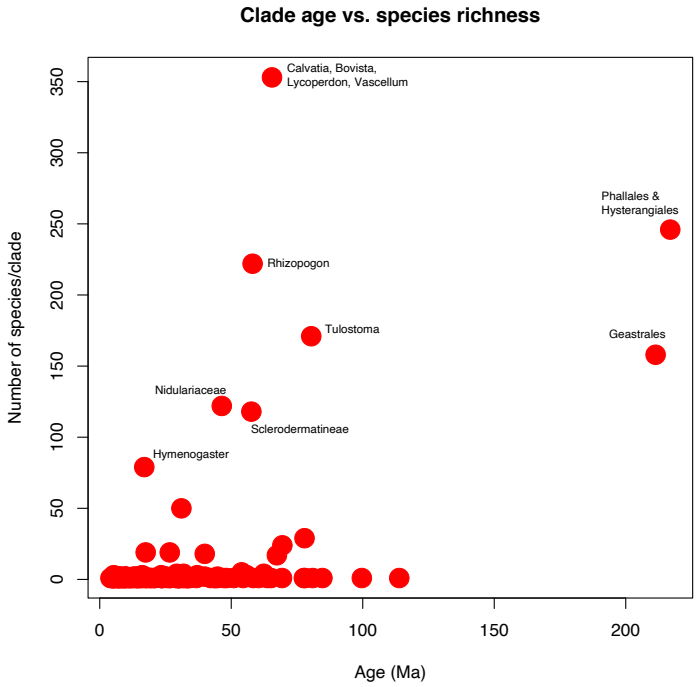

Figure S6. Clade age vs. estimated species richness, each dot represents a gasteroid clade.

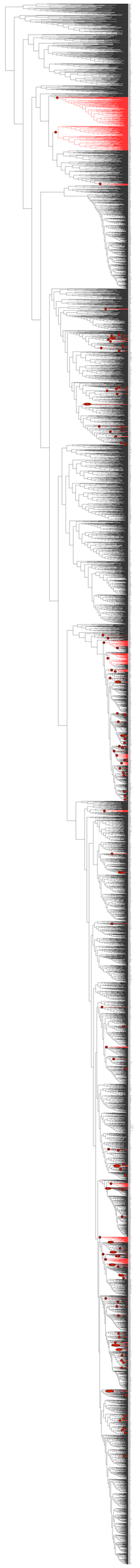

Figure S1: Phylogenetic tree of the Agaricomycetes showing origins of gasteroid forms. The original PDF file can be found in the PDF repository: https://doi.org/xxxxx

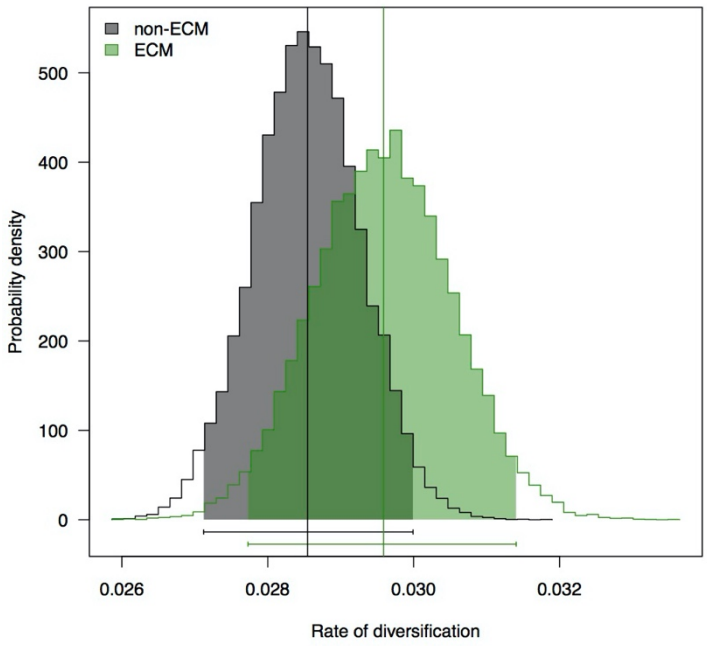

Figure S8. Posterior probability distributions of net diversification rates (speciation minus extinction) from the BiSSE model evaluating coding regime I. The bar underneath each distribution represents the 95% credible interval obtained from the posterior distribution. The vertical lines represent the mean.

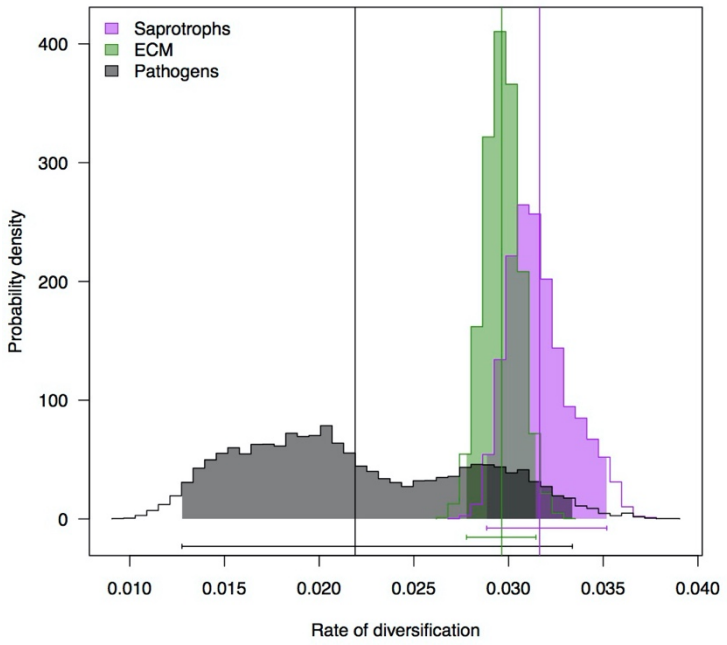

Figure S9. Posterior probability distributions of net diversification rates (speciation minus extinction) from the MuSSE model evaluating coding regime II. The bar underneath each distribution represents the 95% credible interval obtained from the posterior distribution. The vertical lines represent the mean.

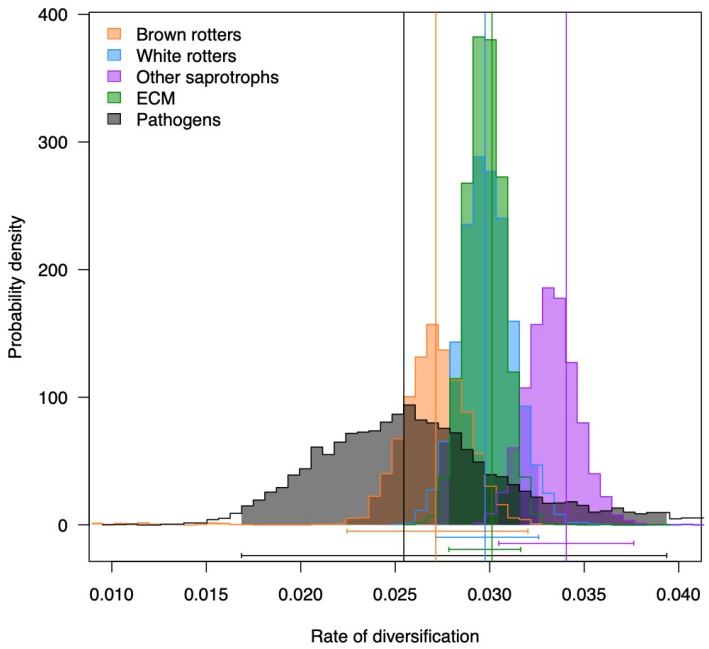

Figure S10. Posterior probability distributions of net diversification rates (speciation minus extinction) from the MuSSE model evaluating coding regime IV. The bar underneath each distribution represents the 95% credible interval obtained from the posterior distribution. The vertical lines represent the mean.

Figure S11. Phylogenetic tree of the Agaricomycetes with ancestral state reconstruction of nutritional modes using coding regime III. The original PDF file can be found in the OSF repository: https://osf.io/y2vns/

Figure S12. Phylogenetic tree of the Agaricomycetes with ancestral state reconstruction of nutritional modes using coding regime IV. The original PDF file can be found in the OSF repository: https://osf.io/y2vns/

Figure S13. Phylogenetic tree of the Agaricomycetes showing origins of the ECM mode. The original PDF file can be found in the OSF repository: https://osf.io/y2vns/

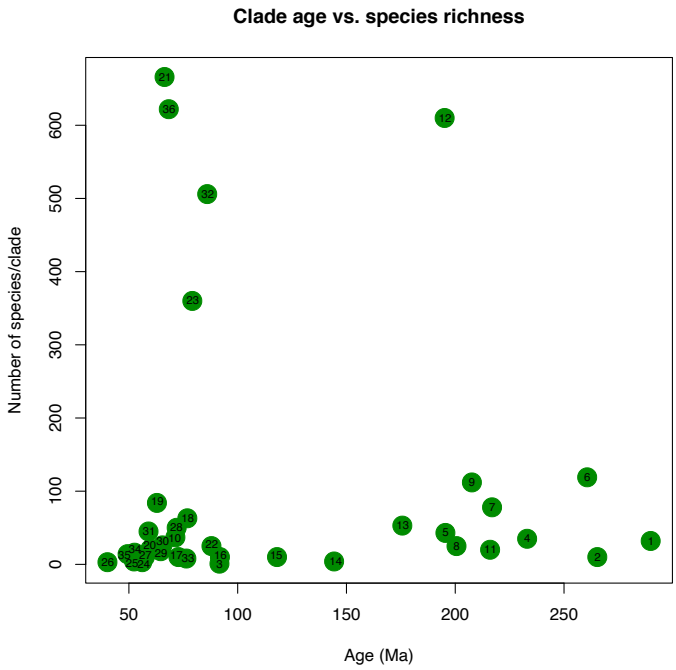

Figure S14. Clade age vs. estimated species richness, each dot represents an ECM clade. Numbers correspond to those in figure S13 and table S17.

Table S1. Genbank numbers of the sequences used to reconstruct the megaphylogeny.
The table can be found in the OSF repository: https://osf.io/y2vns/

Table S2. Parameter estimates from the MuSSE Maximum Likelihood (ML) analysis evaluating five types of morphology

	Pileate-stipitate	Pileate-sessile	Resupinate	Clavarioid	Gasteroid
Speciation rate	0.08878	0.06168	0.02490	0.02489	0.05916
Extinction rate	0.03883	0.02226	0.00520	0.00000	0.03295
Net diversification rate	0.04995	0.03942	0.0197	0.02489	0.02621

Table S3. Morphology MuSSE model testing. All models were compared against the unconstrained model (λ = speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate; AIC = Akaike information criterion). The best model is indicated in bold. ***P < 0.001.

Model	Df	Ln-likelihood	AIC	X^2	P(>|Chi|)
Unconstrained model	30	-41288	82637		
Equal speciation and extinction rate (r1=r2=r3=r4=r5)	22	-42326	84696	2075.67	< 2.2e-16 ***
Equal speciation rate (λ1=λ2=λ3=λ4=λ5)	26	-41582	83217	587.98	< 2.2e-16 ***
Equal extinction rate (μ1=μ2=μ3=μ4=μ5)	26	-41362	82776	2075.67	< 2.2e-16 ***
Equal diversification rate pileate-stipitate and pileate-sessile (r1=r2)	28	-41333	82722	89.057	< 2.2e-16 ***
Equal diversification rate resupinate, clavarioid and gasteroid (r3=r4=r5)	26	-41370	82792	163.54	< 2.2e-16 ***
Equal diversification rate clavarioid and gasteroid (r4=r5)	28	-41327	82710	76.839	< 2.2e-16 ***

Table S4. Parameter estimates from the BiSSE analyses evaluating morphology. State 1 always corresponds to the state of interest and state 0 corresponds to the absence of that state (λ = speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate).

Pileate - stipitate	λ0	λ1	μ0	μ1	r0	r1	q01	q10
Unconstrained model	0.03849	0.09676	0.01531	0.04909	0.02318	0.04767	0.0006	0.00096
Equal speciation rate (λ0=λ1)	0.06634	0.06634	0.04883	0.00955	0.01751	0.05679	0.00028	0.00155
Equal extinction rate (μ0=μ1)	0.0457	0.07942	0.02527	0.02527	0.02043	0.05415	0.00043	0.00122
Equal speciation and extinction rate (μ0=μ1, λ0= λ1)	0.08158	0.08158	0.05264	0.05264	0.02894	0.02894	0.00063	0.00094
Equal transition rate (q01=q10)	0.03758	0.10079	0.01379	0.0544	0.02379	0.04639	0.00081	0.00081
Transition rate 1→0 = 0 (q10=0) no reversal	0.03707	0.10459	0.00634	0.05943	0.03073	0.04516	0.00601	0
Transition rate 0→1 = 0 (q01=0)	0.03398	0.11117	0.0101	0.0702	0.02388	0.04097	0	0.00185
Pileate-sessile	**λ0**	**λ1**	**μ0**	**μ1**	**r0**	**r1**	**q01**	**q10**
Unconstrained model	0.06917	0.05498	0.04086	0.0113	0.02831	0.04368	0.00018	0.00842
Equal speciation rate (λ0=λ1)	0.06885	0.06885	0.04042	0.03075	0.02843	0.0381	0.00021	0.00747
Equal extinction rate (μ0=μ1)	0.06789	0.07345	0.03909	0.03909	0.0288	0.03436	0.00022	0.00712

Equal speciation and extinction rate (μ0=μ1, λ0= λ1)	0.06744	0.06744	0.0378	0.0378	0.02964	0.02964	0.00023	0.0068
Equal transition rate (q01=q10)	0.06685	0.08303	0.03722	0.05483	0.02963	0.0282	0.00067	0.00067
Transition rate 1→0 = 0 (q10=0) no reversal	0.06841	0.06539	0.03904	0.03588	0.02937	0.02951	0.00081	0
Transition rate 0→1 = 0 (q01=0)	0.06864	0.06882	0.04068	0.03136	0.02796	0.03746	0	0.01531
Resupinate	λ0	λ1	μ0	μ1	r0	r1	q01	q10
Unconstrained model	0.07117	0.02461	0.03139	0.00193	0.03978	0.02268	0.00028	0.00265
Equal speciation rate (λ0= λ1)	0.06013	0.06013	0.01716	0.04603	0.04297	0.0141	0.00047	0.00113
Equal extinction rate (μ0=μ1)	0.06223	0.03555	0.01831	0.01831	0.04392	0.01724	0.00039	0.00168
Equal speciation and extinction rate (μ0=μ1, λ0= λ1)	0.06944	0.06944	0.04016	0.04016	0.02928	0.02928	0.00022	0.00242
Equal transition rate (q01=q10)	0.06669	0.03248	0.025	0.01525	0.04169	0.01723	0.00083	0.00083
Transition rate 1→0 = 0 (q10=0) no reversal	0.07887	0.0214	0.04523	0.00005	0.03364	0.02135	0.00115	0
Transition rate 0→1 = 0 (q01=0)	0.07151	0.02586	0.03123	0.00002	0.04028	0.02584	0	0.00571
Clavarioid	λ0	λ1	μ0	μ1	r0	r1	q01	q10
Unconstrained model	0.06843	0.02129	0.03306	0.0025	0.03537	0.01879	0.00005	0.00522
Equal speciation rate (λ0= λ1)	0.0671	0.0671	0.03289	0.05677	0.03421	0.01033	0.00008	0.00179
Equal extinction rate (μ0=μ1)	0.06677	0.04338	0.03159	0.03159	0.03518	0.01179	0.00007	0.00259
Equal speciation and extinction rate (μ0=μ1, λ0= λ1)	0.07135	0.07135	0.04195	0.04195	0.0294	0.0294	0.00008	0.00094
Equal transition rate (q01=q10)	0.07393	0.02509	0.04344	0.00088	0.03049	0.02421	0.00009	0.00009
Transition rate 1→0 = 0 (q10=0) no reversal	0.07511	0.02414	0.04514	0	0.02997	0.02414	0.00014	0
Transition rate 0→1 = 0 (q01=0)	0.06696	0.02059	0.02934	0	0.03762	0.02059	0	0.00838
Gasteroid	λ0	λ1	μ0	μ1	r0	r1	q01	q10
Unconstrained model	0.08328	0.06796	0.05316	0.04553	0.03012	0.02243	0.00042	0.0001
Equal speciation rate (λ0= λ1)	0.08195	0.08195	0.05157	0.06138	0.03038	0.02057	0.00045	0.00008
Equal extinction rate (μ0=μ1)	0.0838	0.07483	0.05383	0.05383	0.02997	0.021	0.00043	0.00009
Equal speciation and extinction rate (μ0=μ1, λ0= λ1)	0.08221	0.08221	0.0528	0.0528	0.02941	0.02941	0.00038	0.00011
Equal transition rate (q01=q10)	0.08359	0.06408	0.05362	0.04004	0.02997	0.02404	0.00036	0.00036
Transition rate 1→0 = 0 (q10=0) no reversal	0.08347	0.06628	0.05338	0.04364	0.03009	0.02264	0.00041	0
Transition rate 0→1 = 0 (q01=0)	0.08529	0.05912	0.05863	0.00388	0.02666	0.05524	0	0.02793

Table S5. Morphology BiSSE model testing. All models were compared against the unconstrained model (λ = speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate; AIC = Akaike information criterion). The best model is indicated in bold. ***P < 0.001, **P < 0.01, *P < 0.05.

Model	Df	Ln-likelihood	AIC	X^2	P(>|Chi|)
Pileate-stipitate					
Unconstrained model	6	-40552	81116		
Equal speciation rate (λ0= λ1)	5	-40762	81535	420.89	< 2.2e-16 ***
Equal extinction rate (μ0=μ1)	5	-40594	81198	84	< 2.2e-16 ***
Equal speciation and extinction rate (μ0=μ1, λ0= λ1)	4	-41401	82811	1698.64	< 2.2e-16 ***
Equal transition rate (q01=q10)	5	-40556	81121	7.31	0.006865 **
Transition rate 1→0 = 0 (q10=0) no reversal	5	-42087	84183	3069.09	< 2.2e-16 ***
Transition rate 0→1 = 0 (q01=0)	5	-40958	81926	811.61	< 2.2e-16 ***
Pileate-sessile					
Unconstrained model	6	-40636	81283		
Equal speciation rate (λ0= λ1)	5	-40640	81289	8.41	0.003735 **
Equal extinction rate (μ0=μ1)	5	-40643	81296	15.25	9.44e-05 ***
Equal speciation and extinction rate (μ0=μ1, λ0= λ1)	4	-40650	81308	29.09	4.81e-07 ***
Equal transition rate (q01=q10)	5	-40780	81570	288.61	< 2.2e-16 ***
Transition rate 1→0 = 0 (q10=0) no reversal	5	-41082	82173	892.06	< 2.2e-16 ***
Transition rate 0→1 = 0 (q01=0)	4	-40775	81560	279.39	< 2.2e-16 ***
Resupinate					
Unconstrained model	6	-40423	80857		
Equal speciation rate (λ0= λ1)	5	-40569	81148	292.17	< 2.2e-16 ***
Equal extinction rate (μ0=μ1)	5	-40460	80930	74.38	< 2.2e-16 ***
Equal speciation and extinction rate (μ0=μ1, λ0= λ1)	4	-40905	81818	964.9	< 2.2e-16 ***
Equal transition rate (q01=q10)	5	-40498	81006	150.41	< 2.2e-16 ***
Transition rate 1→0 = 0 (q10=0) no reversal	5	-40983	81976	1120.53	< 2.2e-16 ***
Transition rate 0→1 = 0 (q01=0)	4	-40725	81460	604.74	< 2.2e-16 ***
Clavarioid/coralloid					
Unconstrained model	6	-39944	79901		
Equal speciation rate (λ0= λ1)	5	-39997	80004	104.94	< 2.2e-16 ***
Equal extinction rate (μ0=μ1)	5	-39964	79939	40.18	2.316e-10 ***
Equal speciation and extinction rate (μ0=μ1, λ0= λ1)	4	-40062	80132	235.9	< 2.2e-16 ***
Equal transition rate (q01=q10)	5	-39972	79955	56.36	6.040e-14 ***
Transition rate 1→0 = 0 (q10=0) no reversal	5	-40091	80193	293.99	< 2.2e-16 ***
Transition rate 0→1 = 0 (q01=0)	4	-40013	80036	137.48	< 2.2e-16 ***
Gasteroid					
Unconstrained model	6	-40504	81020		
Equal speciation rate (λ0= λ1)	5	-40508	81026	8.2	0.004185 **
Equal extinction rate (μ0=μ1)	5	-40505	81020	2.32	0.127609
Equal speciation and extinction rate (μ0=μ1, λ0= λ1)	4	-40524	81055	39.79	2.290e-09 ***
Equal transition rate (q01=q10)	5	-40507	81023	5.51	0.018865 *
Transition rate 1→0 = 0 (q10=0) no reversal	5	-40518	81046	28.09	1.156e-07 ***
Transition rate 0→1 = 0 (q01=0)	4	-41008	82026	1008.53	< 2.2e-16 ***

Table S6. Clades where the origin of a gasteroid form occurred, taxa included in each clade, estimated number of species and the age (Ma) of the clade. Numbers in the first column correspond to those in figure S7.

Clade	Taxa in each clade	Estimated number of species	Age (Ma)
1	Geastrales: Sphaerobolus, Schenella, Boninogster, Sclerogaster, Geastrum, Myriostoma	158	211
2	Phallales: Lycogalopsis, Gelopellis, Protubera, Ileodictyion, Clathrus, Laternea, Blumenavia, Pseudocolus, Abrachium Lysurus, Gastrosporium, Mutinus, Itajahya. Hysterangiales: Protubera, Phallogaster, Trappea, Hysterangium, Austrogautieria, Gallacea, Hallingea, Gummiglobus, castoreum, Nothocastoreum, Mesophellia, Andebbia, Malajczukia, Phlebogaster, Aroramyces	246	217
3	Gautieria	29	78
4	Leucogaster, Fevansia	24	69
5	Lactarius falcatus	1	24
6	Lactarius cressus	1	44
7	Lactarius pomiolens	1	33
8	Lactarius shoreae	1	29
9	Lactarius angiocarpus	1	19
10	Lactarius echinus	1	58
11	Lactarius	3	37
12	Arcangeliella daucina	1	13
13	Lactarius stephensii	1	85
14	Arcangeliella	2	14
15	Gymnomyces fallax	1	29
16	Russula	3	23
17	Macowanites	1	65
18	Macowanites/Russula	2	17
19	Gymnomyces sp	1	114
20	Russula pumicoidea	1	100
21	Gymnomyces	2	45
22	Cystangium	1	18
23	Russula	2	28
24	Russula	4	29
25	Macowanites americana	1	21
26	Macowanites sp	1	7
27	Sedecula pulvinata	1	78
28	Gymnopaxillus	4	62
29	Rhizopogon	222	58
30	Truncocolumella	1	33
31	Scleroderma, Diplocystis, Astraeus,Tremellogaster,Calostoma, Pisolithus	118	58
32	Melanogaster, Alpova	18	40
33	Melanogaster, Alpova	19	27
34	Mycoamaranthus	3	56
35	Royoungia coccineinana	1	21
36	Royoungia	2	7
37	Solioccasus	2	17
38	Kombocles	1	10
39	Gymnogaster	1	30
40	Gastroboletus turbinatus	1	5
41	Gastroboletus sp.	1	5
42	Gastroboletus sp.	1	5
43	Costatisporus cyanescens	1	9
44	Spongiforma thailandica	2	25
45	Royoungia	2	10
46	Castallanea pakaraimophila	1	44

47	Octaviania	50	31
48	Chamomixia	3	5
49	Roosbeevera	19	17
50	Heliogaster	2	13
51	Octaviania ??	2	8
52	Jimtrappea, Duraniella	2	7
53	Mackintoshia persica	1	12
54	Boletus semigastroideus	1	4
55	Boletus subalpinus	1	6
56	Stephanospora, Mayamontana	17	67
57	Guyanagaster	2	40
58	Cribbea gloriosa	1	9
59	Cribbea raphanipes	1	8
60	Nia vibrissa	2	25
61	Limnoperdon incarnatum	1	81
62	Amanita arenaria	1	55
63	Amanita	5	54
64	Amanita torrendi	1	45
65	Amanita sp H909	1	8
66	Entoloma prismaticum	1	60
67	Richoniella sp.	1	30
68	Entoloma asterosporum	1	14
69	Richoniella	1	32
70	Richoniella	3	16
71	Entoloma hypogaeum	1	8
72	Richoniella	1	24
73	Richoniella	1	6
74	Nidulariaceae: Nidula, Mycocalia, Crucibulum, Cyathus, Nidularia	122	46
75	Hydnangium	1	51
76	Hydnangium	1	48
77	Hydnangium	1	14
78	Psathyrella secotioides	1	18
79	Tulostoma	171	80
80	Montagnea	1	32
81	Montagnea	1	42
82	Galeropsis	1	19
83	Lepiota viridigleba	1	10
84	Lepiota geogenia	1	33
85	Gigasperma	1	5
86	Podaxis	1	78
87	Lycoperdaceae (name from GenBank)	1	20
88	Lycoperdaceae (name from GenBank)	1	12
89	Calvatia, Bovista, Lycoperdon, Vascellum	353	66
90	Macrolepiota gasteroidea	1	37
91	Mycenastrum corium	1	47
92	Macrolepiota turbinata	1	16
93	Chlorophyllum agaricoides	1	16
94	Agaricus	2	6
95	Barcheria	1	11
96	Agaricus deserticola	2	5
97	Gigasperma	1	69
98	Thaxterogaster	1	30
99	Cortinarius as Amarrendia	1	34
100	Thaxterogaster campbellae	1	30
101	Thaxterogaster ohauensis	1	24
102	Thaxterogaster	2	14

103	Thaxterogaster/Cortinarius	4	32
104	Thaxterogaster	1	27
105	Protoglossum	2	7
106	Thaxterogaster	1	27
107	Thaxterogaster	1	7
108	Cortinarius pavelekii	2	8
109	Cortinarius as Amarrendia	1	15
110	Cortinarius globuliformis	2	10
111	Cortinarius sejuctus	1	14
112	Protoglossum/Cortinarius	2	10
113	Setchelliogaster	1	64
114	Descomyces	1	17
115	Wakefieldia	1	25
116	Gastrocybe	1	7
117	Psilocybe weraroa	1	9
118	Galeropsis	1	12
119	Hymenogaster	79	17
120	Pholiota nubigena	1	8
121	Leratiomyces erythrocephalus	1	11
122	Clavogaster virescens	1	5
123	Auritella geoaustralis	1	7

Table S7. Morphology BiSSE model testing when pruning two clades that show transitions from a gasteroid to a non-gasteroid state. All models were compared against the unconstrained model (λ = speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate; AIC = Akaike information criterion). The best model is indicated in bold. ***P < 0.001.

Gasteroid test					
Unconstrained model	6	-40248	80509		
Equal speciation rate (λ0= λ1)	5	-40252	80515	7.22	0.007209**
Equal extinction rate (μ0=μ1)	5	-40249	80508	1.00	0.317031
Equal speciation and extinction rate (μ0=μ1, λ0= λ1)	4	-40268	80544	39.01	3.373e-09***
Equal transition rate (q01=q10)	5	-40256	80521	13.83	0.000199***
Transition rate 1→0 = 0 (q10=0) no reversal	5	-40248	80506	1.17	1
Transition rate 0→1 = 0 (q01=0)	4	-40767	81545	1037.2	< 2.2e-16 ***

Table S8. Parameter estimates from the BiSSE analysis evaluating nutritional modes using coding regime I. 0 = non-ECM, 1 = ECM (λ = speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate).

	λ0	λ1	μ0	μ1	r0	r1	q01	q10
Unconstrained model	0.03849	0.09676	0.01531	0.04909	0.02318	0.04767	0.0006	0.00096
Equal speciation rate (λ0= λ1)	0.06634	0.06634	0.04883	0.00955	0.01751	0.05679	0.00028	0.00155
Equal extinction rate (μ0=μ1)	0.0457	0.07942	0.02527	0.02527	0.02043	0.05415	0.00043	0.00122
Equal speciation and extinction rate (μ0=μ1, λ0= λ1)	0.08158	0.08158	0.05264	0.05264	0.02894	0.02894	0.00063	0.00094
Equal transition rate (q01=q10)	0.03758	0.10079	0.01379	0.0544	0.02379	0.04639	0.00081	0.00081
Transition rate 1→0 = 0 (q10=0) no reversal	0.03707	0.10459	0.00634	0.05943	0.03073	0.04516	0.00601	0
Transition rate 0→1 = 0 (q01=0)	0.03398	0.11117	0.0101	0.0702	0.02388	0.04097	0	0.00185

Table S9. Nutritional mode BiSEE model testing. All models were compared against the unconstrained model (λ = speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate; AIC = Akaike information criterion). The best models are indicated in bold. ***P < 0.001, **P < 0.01.

Model	Df	Ln-likelihood	AIC	X^2	P(>|Chi|)
Unconstrained model	6	-39913	79839		
Equal speciation rate (λ0= λ1)	5	-39913	79836	0.30	1.00000
Equal extinction rate (μ0=μ1)	5	-39913	79837	0.31	0.57940
Equal speciation and extinction rate (r0=r1)	4	-39914	79836	1.39	0.49957
Equal transition rate (q01=q10)	5	-39918	79847	10.05	0.00152 **
Transition rate 1→0 = 0 (q10=0) no reversal	5	-39957	79924	87.17	< 2e-16 ***
Transition rate 0→1 = 0 (q01=0)	5	-40205	80420	583.89	< 2e-16 ***

Table S10. Parameter estimates from the MuSSE analysis evaluating nutritional modes using coding regime II. saprotrophs, ECM, pathogens (λ = speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate). Note. saprotrophs that are also pathogens were included in the category of pathogens. Endophytes, lichen forming fungi or the ones with unknown status were coded as NA.

	Saprotrophs	ECM	Pathogens
Speciation rate	0.07485	0.07878	0.06892
Extinction rate	0.03997	0.0493	0.05429
Net diversification rate	0.03488	0.02948	0.01463

Table S11. Nutritional mode MuSSE model testing coding regime II. All models were compared against the unconstrained model (λ= speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate; AIC = Akaike information criterion). The best models are indicated in bold. *P < 0.05.

Model	Df	Ln-likelihood	AIC	X^2	P(>|Chi|)
Unconstrained model	12	-40391	80805		
Equal speciation and extinction rate (r1=r2=r3)	8	-40396	80808	11.3106	0.02329 *
Equal speciation rate (λ1=λ2=λ3)	10	-40391	80802	1.2288	0.54096
Equal extinction rate (μ1=μ2=μ3)	10	-40393	80807	5.6964	0.05795
Equal speciation and extinction (SAP and ECM)	10	-40392	80803	2.2509	0.32451

Table S12. Parameter estimates from the MuSSE analysis evaluating nutritional modes using coding regime III. wood decayers, saprotrophs, ECM, pathogens (λ = speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate). Note. saprotrophs that are also pathogens were included in the category of pathogens. Endophytes, lichen forming fungi or the ones with unknown status were coded as NA.

	Wood decayers	Other saprotrophs	ECM	Pathogens
Speciation rate	0.04333	0.11631	0.07812	0.07151
Extinction rate	0.01255	0.08246	0.04847	0.05109
Net diversification rate	0.03078	0.03385	0.02965	0.02042

Table S13. Nutritional mode MuSSE model testing coding regime III. All models were compared against the unconstrained model (λ = speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate; AIC = Akaike information criterion). The best models are indicated in bold. ***P < 0.001.

Model	Df	Ln-likelihood	AIC	X^2	P(>|Chi|)
Unconstrained model	20	-40667	81375		
Equal speciation and extinction rate (r1=r2=r3=r4)	14	-40877	81782	418.80	< 2.2e-16 ***
Equal speciation rate (λ1=λ2=λ3=λ4)	17	-40774	81582	212.81	< 2.2e-16 ***
Equal extinction rate (μ1=μ2=μ3=μ4)	17	-40731	81495	126.44	< 2.2e-16 ***
Equal speciation and extinction (Wood, SAP, ECM)	16	-40869	81769	402.33	< 2.2e-16 ***
Equal speciation and extinction (Wood, ECM)	18	-40736	81508	137.33	< 2.2e-16 ***

Table S14. Parameter estimates from the MuSSE analysis evaluating nutritional modes using coding regime IV. wood decayers, saprotrophs, ECM, pathogens (λ = speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate). Note. saprotrophs that are also pathogens were included in the category of pathogens. Endophytes, lichen forming fungi or the ones with unknown status were coded as NA.

	Brown rot	White rot	Other SAP	ECM	Pathogen
Speciation rate	0.02233	0.0461	0.10159	0.07535	0.06149
Extinction rate	0.0008	0.01537	0.06129	0.04481	0.03817
Net diversification rate	0.02153	0.03073	0.0403	0.03054	0.02332

Table S15. Nutritional mode MuSSE model testing coding regime IV. All models were compared against the unconstrained model (λ = speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate; AIC = Akaike information criterion). The best models are indicated in bold. ***P < 0.001.

Model	Df	Ln-likelihood	AIC	X^2	P(>|Chi|)
Unconstrained model	30	-40748	81557		
Equal speciation and extinction rate (r1=r2=r3=r4=r5)	22	-40957	81958	416.77	< 2.2e-16 ***
Equal speciation rate (λ1=λ2=λ3=λ4=λ5)	26	-40853	81759	209.88	< 2.2e-16 ***
Equal extinction rate (μ1=μ2=μ3=μ4=μ5)	26	-40796	81643	94.20	< 2.2e-16 ***

Table S16. Parameter estimates from the MuSSE analysis evaluating nutritional modes using coding regime II in which saprotrophs that are also pathogens were included in the category of saprotrophs. saprotrophs, ECM, pathogens (λ = speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate).

	Saprotrophs	ECM	Pathogens
Speciation rate	0.06595	0.07827	0.02169
Extinction rate	0.02327	0.0486	0
Net diversification rate	0.04268	0.02967	0.02169

Table S17. Nutritional mode MuSSE model testing coding regime II in which saprotrophs that are also pathogens are considered as saprotrophs. All models were compared against the unconstrained model (λ= speciation rate; μ = extinction rate; r = net diversification rate; q = transition rate; AIC = Akaike information criterion). The best models are indicated in bold. ***P < 0.001.

Model	Df	Ln-likelihood	AIC	X^2	P(>|Chi|)
Unconstrained model	12	-40067	80157		
Equal speciation and extinction rate (r1=r2=r3)	8	-40163	80342	192.951	< 2.2e-16 ***
Equal speciation rate (λ1=λ2=λ3)	10	-40102	80224	70.748	4.441e-16 ***
Equal extinction rate (μ1=μ2=μ3)	10	-40102	80224	70.743	4.441e-16 ***
Equal speciation and extinction (SAP and ECM)	10	40118	80255	102.034	< 2.2e-16 ***

Table S18. Clades where an origin of ECM occurred, genera included, estimated number of species, crown and stem age, mean diversification rates of the ECM clades and their non-ECM sister groups. Numbers in the first column correspond to those in figures S13 and S14. Asterisks (*) indicate clades where putative losses or transitions to pathogens have occurred.

Clade	Genera in each clade	Estimated number of species	Crown age (Mya)	Stem age (Mya)	ECM clade net diversification rate	Non-ECM sister clade diversification rate
1	Sebacina, Tremelloscypha, Helvellosebacina, Tremellodendron	32	271	289	0.008929594	0.009400322
2	Tulasnella	10	221	265	0.013318341	0
3	Ceratobasidium	1	91	91	0.04068652	0
4	Sistotrema1, Hydnum	35	218	233	0.012159663	0.014191934
5	Sistotrema2, Clavulina, Membranomyces	43	182	195	0.018619874	0.012239036
6	Cantharellus, Craterellus, Afrocantharellus	119	244	260	0.015427151	0
7	Hysterangiales. Protubera, Phallogaster, Trappea, Hysterangium, Gallaceae, Hallingea, Austrogautieria, Gummiglobus, Nothocastoreum, Andebbia, Mesophellia, Malajczukia, Phlebogaster, Aroramyces, Castoreum	78	200	216	0.017391061	0.020016643
8	Clavariadelphus, Ramaria_1	25	185	200	0.018394491	0.017450909
9	Ramaria (most), Gloeocantharellus, Turbinellus, Gomphus, Gautieria	112	194	207	0.018143223	0.018558556
10	Coltricia, Coltriciella	37	65	71	0.050677816	0
11	Neoalbatrellus, Polyporoletus, Laeticutis, Albatrellus, Xeroceps, Fevansia, Leucogaster, Byssoporia	20	185	216	0.013864007	0
12	Multifurca, Lactarius, Russula, Lactifluus	610	188	195	0.030948487	0.014383666
13*	Thelephora, Tomentella, Polyozellus, Pseudotomentella, Sarcodon, Hydnellum, Tomentellopsis, Phellodon, Boletopsis	53	161	175	0.027788577	0.02691748
14	Byssocorticium	4	96	144	0.025421164	0
15	Tylospora, Amphinema	10	104	118	0.023837319	0
16	Tretomyces, Piloderma	10	78	91	0.022512521	0
17	Gymnopaxillus, Austropaxillus	10	62	72	0.021840384	0
18*	Rhizopogon, Suillus, Truncocolumella	63	58	76	0.084447888	0
19	Scleroderma, Diplocystis, Astraeus, Tremellogaster, Calostoma, Gyroporus, Pisolithus, Corditurbera	84	57	62	0.066428038	0.067409965
20	Melanogaster, Alpova, Paragyrodon, Paxillus, Gyrodon	21	49	59	0.066431698	0.071039873
21*	Afroboletus, Alessioporus, Aureoboletus, Australopilus,Austroboletus, Baorangia, Boletellus, Boletus, Borofutus, Bothia, Butyriboletus,Caloboletus, Castellanea,Chamonixia,Chiua, Corneroboletus, Costatisporus, Crocinoboletus, Cupreoboletus, Cyanoboletus, Duraniella, Exsudoporus, Fistulinella, Gastroboletus, Guyanaporus, Gymnogaster, Harrya, Heimioporus, Heliogaster, Hemileccinum, Hortiboletus, Hourangia, Imleria, Imperator, Jimtrappea, Kombocles, Lanmaoa, Leccinellum,Leccinum, Mackintoshia,	666	62	66	0.075188315	0.067606279

	Mucilopilus, Mycoamaranthus, Neoboletus, Nigroboletus, Octaviania, Parvixerocomus, Phylloporus, Porphyrellus, Pseudoaustroboletus, Pulveroboletus,Retiboletus, Roosbeevera, Royoungia, Rubinoboletus, Rubroboletus, Rugiboletus, Singerocomus, Solioccasus, Spongiforma, Stobilomyces, Suillellus, Sutorius, Tylopilus, Veloporphyrellus, Veloporphyrellus, Xanthoconium, Xerocomellus, Xerocomus, Zangia,Phylloboletellus					
22	Hygrophorus	25	80	87	0.05458382	0.04839526
23	Amanita	360	75	79	0.053408364	0.054149675
24	Catathelasma	3	37	56	0.053202838	0.053778648
25	Guyanagarika	4	39	52	0.052403965	0
26	Albomagister	3	26	40	0.050889798	0
27	Porpoloma	10	47	57	0.051766076	0.05175836
28	Tricholoma	50	67	71	0.06808559	0.054038023
29	Lyophyllum	18	56	64	0.053051543	0.052869045
30*	Entoloma	26	58	65	0.09117641	0.090196146
31	Laccaria, Hydnangium	45	56	59	0.069617107	0.111167663
32	Cortinarius	506	83	85	0.093826141	0.061679851
33	Setchelliogaster, Descolea, Descomyces, Wakefieldia	8	63	76	0.058655341	0.068036751
34	Phaeocollybia	16	47	52	0.062074359	0
35	Hebeloma, Naucoria, Alnicola, Hymenogaster	14	42	49	0.112161144	0.111915803
36	Inocybe, Auritella, Tubariomyces, Mallocybe	622	65	68	0.071245432	0.08122333

Table S19. List of fossils to estimate divergence times in Agaricomycetes

Fossil	Node	Minimum age	Reference
Hymenochaetales			
Quatsinoporites cranhamii	MRCA Hymenochaetales	125-129	Smith et al., 2004
Agaricales			
Palaeoagaricites antiquus	MRCA Agaricales	100-110	Poinar and Buckley, 2007
Archaeomarasmius legetti	MRCA Marasmineae	90-94	Hibbet et al. 1997
Nidula baltica	MRCA Nidulariaceae	40	Poinar, 2014
Polyporales			
Ganodermites lybicus	MRCA Ganoderma	18	Fleischmann et al., 2007
Boletales			
Suillus/Rhizopogon ECM	MRCA Suillaceae	45	Lepage et al., 1997

SI References

1. Smith SY, Currah RS, Stockey RA (2004) Cretaceous and Eocene poroid hymenophores from Vancouver Island, British Columbia. Mycologia 96(1).180–186.
2. Poinar GO, Buckley R (2007) Evidence of mycoparasitism and hypermycoparasitism in Early Cretaceous amber. Mycol Res 111(4):503–506.
3. Hibbet DS, Grimaldi D, Donoghue MJ (1997) Fossil mushrooms from Miocene and Cretaceous ambers and the evolution of Homobasidiomycetes. Am J Bot 84(8):981–991.
4. Poinar G (2014) Bird's nest fungi (Nidulariales: Nidulariaceae) in Baltic and Dominican amber. Fungal Biol 118(3):325–329.
5. Fleischmann A, Krings M, Mayr H, Agerer R (2007) Structurally preserved polypores from the Neogene of North Africa: Ganodermites libycus gen. et sp. nov. (Polyporales, Ganodermataceae). Rev Palaeobot Palynol 145(1–2):159–172.
6. Lepage BA, Currah RS, Stockey RA, Rothwell GW (1997) Fossil ectomycorrhizae from the middle Eocene. Am J Bot 84(3):410–412.