Table 1: Estimates of divergence time among eukaryotes

Node[a]	Comparison	Proteins[b]			Amino acids (MG)	Divergence time estimates (Ma) from different methods[c]						
		Total	MG	SG		MGG_{LS}	MGL_{LS}	SGG_{LS}	SGL_{LS}	SGL_{DT}	SGL_{PL}	Summary
5	Arthropoda vs. Vertebrata	151	120	82	49,644	1,070 ± 101	964 ± 132	942 ± 101	908 ± 132	975 ± 86	994 ± 21	976 ± 97 (786–1166)
6	Cnidaria vs. Bilateria	26	19	17	6,790	1,288 ± 71	1,136 ± 76	1,314 ± 71	1,243 ± 76	1,339 ± 210	1,468 ± 74	1,298 ± 74 (1153–1443)
7	Porifera vs. Eumetazoa	22	19	17	7,090	1,382 ± 151	1,282 ± 122	1,341 ± 151	1,285 ± 122	1,361 ± 211	1,457 ± 54	1,351 ± 120 (1116–1586)
9	Pyrenomycetes vs Plectomycetes	29	18	12	8,952	591 ± 75	559 ± 67	435 ± 75	564 ± 67	654 ± 62	500 ± 19	551 ± 61 (431–671)
10	Candida vs. Saccharomyces	29	21	18	8,918	718 ± 108	714 ± 95	834 ± 108	743 ± 95	725 ± 65	604 ± 14	723 ± 84 (558–888)
11	Hemiascomycetes vs. filamentous Ascomycota	51	33	31	11,683	1,071 ± 125	1,031 ± 103	1,066 ± 125	981 ± 103	915 ± 54	826 ± 16	982 ± 94 (798–1166)
12	Archiascomycetes vs. other Ascomycota	72	56	45	24,348	1,119 ± 83	956 ± 93	1,056 ± 83	994 ± 93	1,011 ± 37	920 ± 12	1,009 ± 73 (866–1152)
13	Basidiomycota vs. Ascomycota	41	27	19	8,504	1,056 ± 165	1,021 ± 112	969 ± 165	927 ± 112	975 ± 48	862 ± 25	968 ± 116 (741–1195)
14	Mucorales/ Blastocladiales vs. Basidiomycota/ Ascomycota	24	16	15	5,202	1,056 ± 61	1,022 ± 54	921 ± 61	901 ± 54	935 ± 50	845 ± 24	947 ± 51 (847–1047)
15	Fungi vs. animals	188	92	69	31,362	1,594 ± 106	1,492 ± 46	1,511 ± 106	1,449 ± 46	1,435 ± 225	1,594 ± 24	1,513 ± 66 (1384–1642)
17	Mosses vs. vascular plants	51	47	46	4,898	777 ± 103	702 ± 127	677 ± 103	638 ± 127	*1,006 ± 62*	742 ± 28	707 ± 98 (515–899)
18	Chlorophytan green algae vs. higher plants	74	63	58	14,333	1,055 ± 76	946 ± 145	921 ± 76	901 ± 145	1,138 ± 45	845 ± 22	968 ± 93 (786–1150)
19	Rhodophyta vs. Chlorophyta+Embryophyta	50	46	43	8,673	1,465 ± 109	1,449 ± 71	1,507 ± 109	1,382 ± 71	1,445 ± 34	1,319 ± 27	1,428 ± 77 (1277–1579)
20	Plants vs. animals	188	143	99	60,274	1,554 ± 67	1,524 ± 53	1,486 ± 67	1,502 ± 53	1,708 ± 283	1,878 ± 26	1,609 ± 60 (1491–1727)
21	Alveolates vs. plants+animals+fungi	76	60	44	21,031	2,086 ± 83	1,807 ± 95	2,011 ± 83	1,903 ± 95	1,972 ± 49	2,057 ± 35	1,973 ± 78 (1820–2126)
22	Euglenozoans vs. plants+animals+fungi	99	80	52	27,759	1,968 ± 56	1,887 ± 68	2,018 ± 56	1,863 ± 68	2,010 ± 61	2,020 ± 35	1,961 ± 57 (1849–2073)
23	Giardia vs. plants+animals+fungi	45	32	28	11,251	2,276 ± 202	2,421 ± 258	2,424 ± 202	2,287 ± 258	2,153 ± 69	2,295 ± 51	2,309 ± 194 (1929–2689)

a-nodes correspond to the eukaryote phylogenetic tree (Fig. 2). Nodes 1–4 are fossil times and nodes 8 and 16 are phylogenetically constrained (see legend to Fig. 2) and are not shown. b-MG, constant rate proteins used in multigene analyses; SG, proteins used in supergene (concatenated) analyses. c-all error terms, except those for SGL_{DT}, are standard errors of the mean. For SGL_{DT}, the standard deviation is presented, and "credibility intervals" (asymmetric) for that method are presented in Supplemental Table 1 (see Additional file 1). Averages of all times and standard errors, excluding one outlier (italics), are shown in the column labeled "Summary," along with the 95% confidence interval.