

of EF1 α F2, 18S, and 28S). Convergence of Bayesian analyses was assessed with the program MrConverge (34). Choices for sequence evolution models (all GTR + I + Γ) were taken from Brady *et al.* (20) for accuracy of comparison with their results and because our taxon-sampling schemes are nearly identical. Adequacy of the model of sequence evolution was evaluated with Bayesian posterior predictive simulation (51) using PuMA v0.903 (see Fig. S3) (52). Phylogenies were also estimated, using identical methods, when excluding *Martialis*, the Leptanillinae, the outgroups, both *Martialis* and outgroups, or both the Leptanillinae and outgroups. Alternative rootings were evaluated using Bayesian bipartition posterior probabilities, Bayes factors (32–34), and the Shimodaira-Hasegawa test (35, 36). For more detail on phylogenetic analyses and results, see *SI Materials and Methods*.

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