Supplemental Material 1 – Additional descriptions on the phylogenetic methods and the support value thresholds used in this study

This study utilised five different phylogenetic methods to define the nodal support for class level groupings. Bootstrap analyses were performed using neighbour-joining (NJ) and maximum likelihood (ML) methods. NJ was performed using ARB (1) with Jukes-Cantor and Olsen substitution models and with 2,000 bootstrap replicates. ML was performed using PhyML v2.4.5 (2) using a general time reversible (GTR) model with gamma-distributed rate heterogeneity and an estimated proportion of invariable sites (assuming four substitution rate categories), and RAxML v7.0.3 (3) using the GTRMIX model with the rapid bootstrapping algorithm. Both ML methods were performed with 500 bootstrap replicates. PhyML and RAxML were interfaced using the ARB software environment. The GTR model was selected as the best-fit ML model based on the results of jModelTest (4) with the ingroup dataset. Bayesian Inference (BI) was performed using MrBayes v3.2.1 (5) with GTR model with gamma-distributed variation with six gamma categories. BI was performed using Metropolis-Coupled Markov Chain Monte Carlo (MC^3) for 3,100,000 generations with four chains (three chains were heated at chain temperature = 0.2 with a subsampling frequency of 400. Posterior probabilities were calculated from the last 1000 trees from each analysis (last 400,000 iterations), which is an effective relative burn-in of 87 %. RAxML trees of the corresponding datasets were used as the starting tree for BI analysis. The starting trees were scrambled with random perturbations (nperts = 10). For each given dataset, two simultaneous independent analyses were performed with two differently perturbed starting trees to improve statistical confidence. Maximum parsimony (MP) method was not selected for use in this study as MP is known to suffer from long branch attraction, which becomes prominent in large and highly divergent datasets such as this one (6-8).

Monophyly of clades represented in Figure 1 were called using ≥70 % ML nonparametric bootstrap proportion as the threshold (9). While Bayesian posterior probabilities (PP) are usually strongly correlated with ML bootstrap proportions (10), it is generally recognised that PP values tend to be higher than that of ML nonparametric bootstrap proportion ((11, 12) and references therein). Here we used ≥95 %, as a commonly suggested PP threshold (13, 14). Where branch nodes were not supported by confidence values of greater or equal to the threshold, the branches were multifurcated (15).

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