Text S3: Phylogenetic analyses

Protein sequences were aligned using MUSCLE v3.8 (PMID: 15034147 [1]). Different models of sequence evolution were then evaluated using ProtTest v3.2 (PMID: 21335321 [2]); based on the Bayesian information criterion, this found the WAG matrix combined with a gamma rate distribution and a calculation for the proportion of invariant sites to be the most appropriate evolutionary model. These settings were therefore used to generate a maximum likelihood distance matrix and phylogeny using RAxML v7.0 (PMID: 16928733 [3]), with 100 bootstrap replicates produced to measure support for internal branches. The distance matrix was analysed using SplitsTree v4 (PMID: 9520503 [4]) as a further measure of uncertainty in the phylogeny.

References


