

Additional File 2

Bayesian and Maximum Parsimony (MP) trees generated using alternative partitioning strategies to analyze the multilocus dataset. Bayesian topologies are 50% majority rule consensus trees with posterior probabilities indicating node support. MP trees represent a strict consensus from equally parsimonious topologies with node support assessed through 1000 standard bootstrap pseudoreplicates. When phylogenetic resolution was sufficient, clades corresponding to lineages A to C are indicated. Posterior probabilities below 0.90 were omitted for simplicity. (a) Bayesian topology obtained by placing mitochondrial and nuclear data in different partitions. Bayesian trees produced partitioning mitochondrial (b) or nuclear (c) data alone by gene. MP topologies obtained using the entire multilocus dataset (d). MP trees built with mitochondrial (e) or nuclear (f) data alone.

