S7 Figure. Phylogenetic analysis of *cytb* amino acid sequence does not recover the five distinct lineages identified by analysis of concatenated mitochondrial and 18S sequences. Statistical support for clades (bootstrap values from Maximum Likelihood analysis, 100 bootstrap replicates) are indicated below each node. Tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Analysis of 365 total characters produced a tree with poor statistical support for many nodes and a topology that does not reflect the results of analysis of concatenated mitochondrial and 18S sequences.