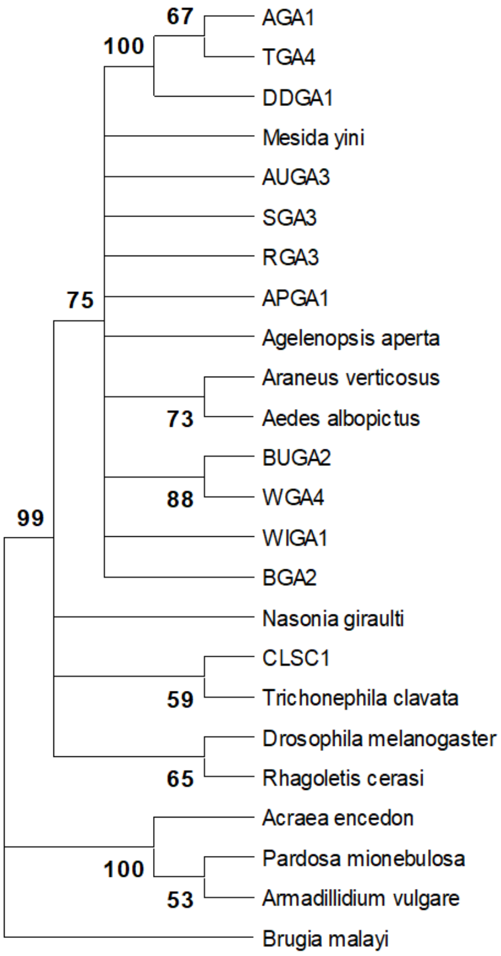

**Supp. Mat. 3**: The evolutionary history of the concatenation of Wolbachia MLST genes (*coxA*, *fbpA*, *gatB*, *hcpA*) was inferred by using the Maximum Likelihood method and Hasegawa-Kishino-Yano model [1]. The tree with the highest log likelihood (-4070.13) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 0.1716)). This analysis involved 24 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. There were a total of 1332 positions in the final dataset.