



Fig. S2. Phylogenetic tree based on *wsp* gene sequence data generated by UPGMA algorithm under nucleotide maximum composite likelihood model in MEGA 4.1. Each *wsp* sequence is labeled with the host species from which the *Wolbachia* strain was isolated (GenBank Accession No. is indicated in parentheses). Bootstrap values detected above 50% for 1000 replicates are shown before the branch. Size bar reflects phylogenetic divergence in genetic distance units. The *wsp* sequences isolated from *O. furnacalis*, *M. cingulum* and *L. grisescens* were labeled with “●”, “▼” and “▲” respectively.