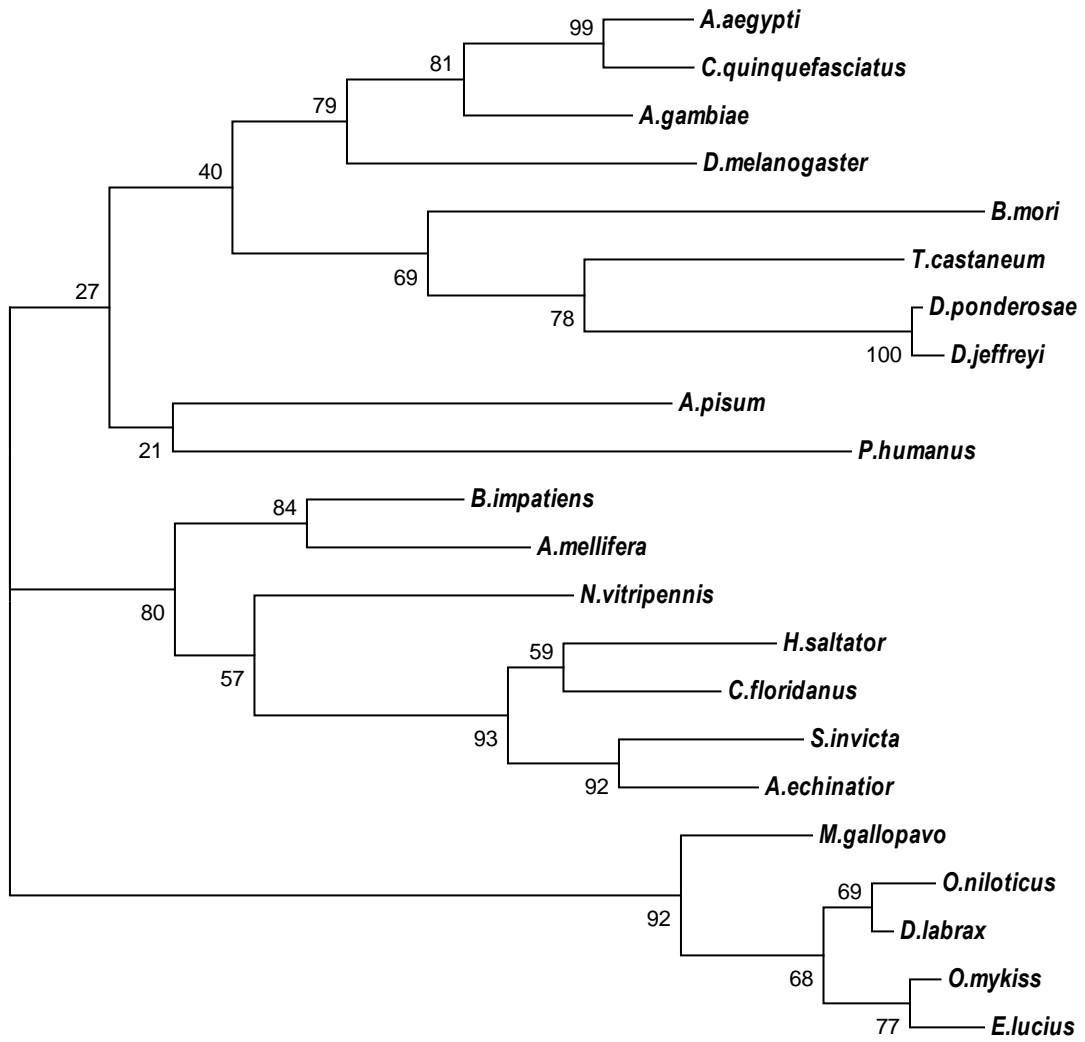


### Supplementary Figure 3

**Phylogenetic analysis:** IPPI sequences were obtained from NCBI and VectorBase (Lawson et al., 2009) databases and used for the alignments and phylogenetic analysis. IPPI sequences were aligned using ClustalW (Higgins et al., 1994). A Maximum Likelihood tree was built using MEGA software 5.1 (Tamura et al., 2011) with a bootstrapping of 1000 (Felsenstein, 1985). Pairwise deletion method was selected for the gaps/missing data in MEGA software.

**Accession numbers:** *Aedes aegypti*: AAEL006144; *Drosophila melanogaster*: CG5919; *Bombyx mori*: NP\_001040323.2; *Anopheles gambiae*: XP\_321388.4; *Culex quinquefasciatus*: XP\_001868438.1; *Apis mellifera*: XP\_001121223; *Tribolium castaneum*: XP\_971524.1; *Acyrtosiphon pisum*: BAH70865.1; *Pediculus humanus*: XP\_002430029; *Nasonia vitripennis*: XP\_001601348.2; *Dendroctonus jeffreyi*: AAX78437; *Camponotus floridanus*: EFN72628; *Solenopsis invicta*: EFZ09362; *Acromyrmex echinator*: EGI57379; *Dendroctonus ponderosae*: AFI45054.1; *Bombus impatiens*: XP\_003493342.1; *Harpegnathos saltator*: EFN89888.1; *Oreochromis niloticus*: XP\_003450277.1; *Oncorhynchus mykiss*: NP\_001154091.1; *Esox Lucius*: AC014500.1; *Dicentrarchus labrax*: CBN81762.1; *Meleagris gallopavo*: XP\_003207023.1.



0.1