LEGENDS FOR SUPPLEMENTARY DATA

Additional file 1: Neighbor-Joining analyses based on 64 ITS2 sequences from individuals of the different species of Albitarsis Complex. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches, retaining only groups with frequency ≥60%. Outgroups are *An. darlingi* and *An. braziliensis*.

Additional file 2: Neighbor-Joining analyses based on 17 nuclear protein-coding white gene sequences. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches, retaining only groups with frequency ≥60%. Outgroups are *An. darlingi* and *An. braziliensis*.

Additional file 3: Maximum parsimony tree based on *COI* sequences. Numbers above branches indicate the percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1,000 replicates). DQ076234, *An. albitarsis* E (?) specimen from Portuguesa, Venezuela; DQ076231 - DQ076233, *An. albitarsis* E (*An. janconnae*) from the type locality in Roraima, Brazil. Bootstrap values >70% are shown. Outgroup comprises *An. darlingi* and *An. braziliensis*.

Additional file 4: Maximum likelihood tree based on *COI* sequences. Numbers above branches indicate ML bootstrap proportions (662 replicates). DQ076234, *An. albitarsis* E

(?) specimen from Portuguesa, Venezuela; DQ076231 - DQ076233, *An. albitarsis* E (*An. janconnae*) from the type locality in Roraima, Brazil. Bootstrap values >70% are shown. Outgroup comprises *An. darlingi* and *An. braziliensis*.