



**Additional file 2: Figure S2.** The phylogenetic tree generated using from 64 mosquito sequences of CO1 was inferred by the Maximum Likelihood method and Tamura-Nei model with 1000 bootstrap replicates. Numbers next to branches indicate the branch percentage support. Samples which were part of this study are denoted by the start (\*) symbol. Branch support percentages > 70% are shown. GenBank accession numbers and countries of origin are indicated for all sequences. South Africa = ZAR, Malawi = MWI, Madagascar = MDG, Mozambique = MOZ, Mali = MLI, Kenya = KEN, Senegal = SEN, Sudan = SDN