



Figure S2. Phylogenetic analysis of mealybugs collected from sisal in South China. The 28S gene sequence of the mealybugs was amplified by PCR, and a phylogenetic tree was constructed using MEGA 6. The phylogenetic tree constructed by the neighbor-joining method. Numbers on branches are the bootstrap values (1000 replicates). The bold represented the 28S gene sequence amplified from *Dysmicoccus neobrevipes* in this study.