

**MORPHOLOGICAL AND MOLECULAR TAXONOMIC
STUDIES ON SOME MEALYBUG SPECIES
(HEMIPTERA: PSEUDOCOCCIDAE) THEIR
DISTRIBUTION AND HOST PLANTS IN DIFFERENT
GOVERNORATES IN EGYPT**

By

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ABSTRACT

Mealybugs (Hemiptera: Coccoidea: Pseudococcidae) are phloem – sucking insects, most of them are important and serious agricultural pests in Egypt and the world. Our study revealed the presence of seven mealybug species belonging to two subfamilies. Subfamily Pseudococcinae including (*Ferrisia virgata*, *Planococcus citri*, *Planococcus ficus*, *Saccharicoccus sacchari*, *Dysmicoccus brevipes*) and subfamily Phenacoccinae including (*Phenacoccus solenopsis*, *Phenacoccus parvus*), on different host plants at different governorates in Egypt. They were identified morphologically based on light & scanning microscope; a taxonomic key was constructed for these species. Synonyms, host plants, and geographical distributions are given for each species.

In the present study two molecular techniques were carried out to confirm morphological identification and to detect phylogeny among five mealybug species belonging to five genera. The first technique was by amplification of 28S rDNA gene using specific primers, the second technique was by using bacterial 16S rDNA gene of the examined mealybug species. Partial nucleotide sequences of the amplified products obtained were determined (by Macrogen Korea). The nucleotide sequences for EMM1, EMM2, EMM3, EMM4, EMM5, and EMM6 genes were blasted into Basic Local Alignment Search Tool (BLAST) at National Center for Biotechnology Information website (NCBI), and compared with those deposited in GenBank DNA database. The results represented the homology percentage between the partial sequences of 28S rRNA gene from each species and related species obtained from the Multiple Sequence Alignment (MSA) performed by Clustal W2 algorithm on Geneious Software Version (R8) default parameters. The data revealed a higher percentage of similarities between each other's species belonging to the same subfamily. The phylogenetic tree was constructed using the MEGA 7 and neighbor-joining method.

Key words: Pseudococcidae, Morphology, mealybug, taxonomic keys, synonyms, geographic distribution, 28S rDNA gene, bacterial 16S rDNA gene, phylogenetic tree.

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