شبكة المعلومات الجامعية
التوثيق الإلكتروني والميكروفيلم

بسم الله الرحمن الرحيم

MONA MAGHRABY

شبكة المعلومات الجامعية

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TAXONOMICAL AND ECOLOGICAL STUDIES ON SOME MEALYBUG SPECIES INFESTING FRUIT TREES AND ORNAMENTAL PLANTS IN EGYPT [Hemiptera: Sternorrhyncha Pseudococcidae]

By

DALIA NABIL ZAKI

B.Sc. Agri. Sc., Fac. of Agric. (Entomology), Cairo Univ., 1992
M.Sc. Agri. Sc., Fac. of Agric. (Entomology), Ain Shams Univ., 2013

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ABSTRACT

Dalia Nabil: "Taxonomical and Ecological Studies on Some Mealybug species Infesting Fruit Trees and Ornamental Plants in Egypt". Unpublished Ph.D. Dissertation, Ain Shams University, Faculty of Agriculture, Department of Plant Protection, Egypt, 2020.

Survey of mealybug species was carried throughout three successive years (2014-2016) in Egypt. Identification and confirmation procedures recorded 13 pseudococcid species which belonging to 8 genera in addition to one eriococcid species. Four species were recorded for the first time during the present work.

These species with their host plants were tabulated. Synonymy list for each species was provided. Bracket and pictorial identification keys for different categories of Pseudococcidae were constructed.

Two molecular techniques were applied to confirm identification, fingerprinting the surveyed species and investigated phylogenetic relationships between these species. These techniques are:

A. Inter Simple Sequences Repeats (ISSRs):

Three specific primers were used to amplify by PCR. These primers produced polymorphic fragments. Five fragments were considered as species-specific markers for four species out of the13 recorded species. This technique could be investigated for genetic-variations among populations from different localities and hosts. Results revealed that geographical distribution has role while host plants had no effect.

B. Small Subunit Ribosomal 18S rDNA gene:

This technique was used to investigate the nucleotide sequences for 14 surveyed species. Data obtained for each species were compared with those previously registered in GenBank with percentage of identity (97-100%).

One species *Trabotina serpentina* was registered for the first time worldwide, while four species from Egyptian materials were registered with new accession numbers.

Phylogenetic relationships between the 14 species were investigated using three criteria. First one based on 48 morphological characters of adult females, while the other two based on molecular techniques (ISSRs and 18S rDNA gene). Dendrograms were calculated using special programs. Results revealed that these criteria are closely related to each other. There is a gap between Pseudococcidae and Eriococcidae. While species belonging to the same genus are situated in the same cluster.

Ecological studies in *Ferrisia virgata* on acalypha shrubs and guava trees were carried out throughout two successive years in Qalyubiya and Giza governorates. Results showed that this species had main period of seasonal activity extended from June to January of the next year. Afterwards, population of all developments stages were disappeared from leaves and overwintered under back, root and soil. The population density reached it maximum activity in mid-October on acalypha shrubs and mid-November on guava trees.

This mealybug species found to have two overlapping annual generations during active period on the two hosts during the both years.

The effects of four climatic factors on the changes in population density during activity period was investigated. Results showed that the combined effects of (means, minimum, maximum, average temperature and percentage of relative humidity, two weeks earlier , as a group were effected on the changes of population density ,while each single factor had no effects.

Population density of *F. virgata* was more abundant on acalypha shrubs than guava trees, which means that mealybug species found to prefer acalypha than guava. Factors responsible for this phenomenon was also investigated.

Keywords: Pseudococcidae, *Ferrisia virgate*, Molecular genetic, Identification key, ISSRs, 18S rDNA, Polygenetic relationships, Seasonal fluctuation, Number of generations.

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