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Characterization of mealybug species associated with different host plants using morphological and molecular methods

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Mealybugs are significant pests with a wider host range, such as okra, tomato, turkey berry, coffee, brinjal, guava, papaya, pineapple, soursop, cassava, croton, and shoe flower. The aim of the research was to study the variation in mealybug species associated with different host plants. Mealybug samples (n = 180) were collected from selected fields in Kilinochchi, Jaffna, and Monaragala districts. They were morphologically identified based on published taxonomic keys. PCR was performed to confirm the species by amplifying the D3 region of the 28s rDNA. The sequences were analyzed for variation, and the phylogenetic tree was constructed using maximum-likelihood method. The field study revealed that mealybugs exist as a complex associated with ant species such as *Oecophylla smaragdina* and *Technomyrmex albipes*, mealybug destroyers, and sooty mold, which itself caused enormous damage to plants in terms of quantity and quality. Ten mealybug species belonging to seven genera were identified. Those were; *Phenacoccus solenopsis*, *Phenacoccus solani*, *Phenacoccus manihoti*, *Planococcus minor*, *Planococcus lilacinus*, *Ferrisia virgate*, *Coccidohystrix insolita*, *Paracoccus marginatus*, *Pseudococcus vibruni*, and *Rastrococcus mangiferae*. Among them, *P. solenopsis* was the most abundant species recorded in okra, tomato, turkey berry, and hibiscus crops, while *F. virgate* was the second most abundant mealybug species recorded in guava, brinjal, and croton crops. *P. solenopsis*, *F. virgate*, *P. minor*, and *P. lilacinus* were found in more than one host plant, confirming their preference for multiple host plant species. DNA sequence data were consistent with morphological identification. Phylogenetic tree analysis revealed that one *P. solenopsis* (Accession no. ON787841) was clustered separately from the rest of the same species identified (ON787838, ON787840, and ON787844), which were clustered with sequences from China and the USA. This might be a unique genetic variant belonging to Sri Lanka. This study contributes to understanding the species variation, host preference and other insects associated with mealybug species, which might be important in designing management strategies.