



Population genetic structure of *Myzus persicae nicotianae* (Hemiptera: Aphididae) in China by microsatellite analysis

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ABSTRACT. The tobacco aphid, *Myzus persicae nicotianae* (Hemiptera: Aphididae), is an important agricultural pest that feeds on host plants and transmits plant viruses in China. To effectively control this pest, we investigated the genetic variation and genetic structure of 54 populations of tobacco aphids collected in China, using five microsatellite loci. An average of 7 alleles with effective number ranging from 1.5 to 6.6 was detected using these five loci, and the average polymorphic information content (PIC) was 0.652, suggesting that the five selected microsatellite loci were polymorphic and suitable for the study of population genetics. The expected heterozygosities in the populations studied ranged from 0.128 and 0.653, with an average value of 0.464. However, the observed heterozygosities ranged from 0.250 and 0.942 (average = 0.735), revealing

a high genetic variability and heterozygosity excess in the Chinese tobacco aphid populations. The global fixation index (F_{ST}) and mean gene flow (N_m) were 0.34 ($P < 0.0001$) and 0.50, respectively, suggesting the high genetic differentiation among Chinese populations. The 54 populations of tobacco aphids were classified into two groups. The populations did not cluster geographically, as populations from the same provinces were usually present in different clusters. This was also confirmed by the Mantel test, which showed no significant correlation between the genetic distance and geographical distance or altitude. Long distance migration might be responsible for the lack of distance-related isolation.

Key words: *Myzus persicae nicotianae*; Genetic diversity; Genetic differentiation; Parthenogenesis; Genetic structure