



Genetic diversity and variability in populations of the white wax insect *Ericerus pela*, assessed by AFLP analysis

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ABSTRACT. The white wax insect *Ericerus pela* Chavannes (Hemiptera: Coccoidea) is an economically valuable insect species that has been used for over a thousand years in China. The present study focuses on assessing the genetic variability in different populations of *E. pela* collected from seven Chinese provinces. The amplified fragment length polymorphism technique was used to generate DNA fingerprints of individuals from each population using nine primer combinations (*EcoRI-MseI*). A total of 435 polymorphic loci were generated; fragment sizes ranged from 200 to 1000 bp. The percentage of polymorphic loci was 85.29%. Nei's genetic diversity and Shannon index indicated consistency in the results, which showed that the Sichuan population had the highest diversity, followed by Yunnan and Zhejiang populations. Dendrogram analysis showed the shortest genetic distance between the Sichuan and Yunnan populations, suggesting that they probably form sister groups. High genetic differentiation between

population values among all sampled populations indicated a low degree of genetic variability within each population (40.85%) and higher variation among populations (59.15%). Gene flow estimate values were low in all samples, suggesting low gene flow from events such as interbreeding and migration. Low gene flow values also suggested that populations among species of *E. pela* might become genetically heterogeneous, due to counteracting forces such as strong differential selection. Our data support the probability that *E. pela* will remain localized, and has a low potential to spread beyond current habitats.

Key words: White wax insect; Genetic diversity; Genetic variability; Gene flow