

Microsatellite loci and genetic structure of artificial populations of *Cotesia flavipes* (Hymenoptera, Braconidae)

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ABSTRACT. Cotesia flavipes (Cameron) is a parasitoid wasp used in the biological control of the sugarcane borer (Diatraea saccharalis) (Fabr., 1794). Studies on the genetic diversity of C. flavipes are hampered by the lack of highly polymorphic molecular markers. In this report, a set of 11 microsatellite loci were developed from an enriched library of C. flavipes. Four microsatellite loci were polymorphic and were screened in 212 C. flavipes individuals (183 females and 29 males) that were randomly sampled from seven rearing laboratory populations. The number of alleles ranged from two to three. The average inbreeding

coefficient ($F_{\rm IS}$) among all laboratory populations was 0.120, indicating an excess of homozygotes. The average genetic diversity within the laboratory populations was 0.292, which is lower than the values reported for wild *Cotesia* spp populations. Genetic diversity was most pronounced within laboratory populations (70 to 90%). Most of the observed alleles were fixed or close to fixation. This low overall genetic diversity may have originated from a founder effect, i.e., the contribution of a small number of individuals (genes and alleles) to the formation of these populations. To our knowledge, this study is the first to provide microsatellite loci and an analysis of the genetic structure of *C. flavipes*. Our results suggest that new introductions of *C. flavipes* may increase genetic diversity and improve the efficiency of the biological control of *D. saccharalis*. In addition, population structure data could be used to estimate the minimum number of wasps to be imported.

Key words: Molecular marker; SSR; Rearing laboratories; Population genetics; Biological control

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