

Methodology

Microsatellite markers for genetic studies of the fall armyworm, *Spodoptera frugiperda*

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ABSTRACT. We developed six microsatellite markers for the fall armyworm *Spodoptera frugiperda* (Lepidoptera: Noctuidae). The SSR loci were isolated with enriched genomic library protocol by using native individuals as a genome source for markers. These loci were characterized in 48 individuals and they were tested for the ability to identify candidate migrants exchanged among the samples. The number of alleles per locus ranged from 5 to 18 (10.8 on average). The observed polymorphism information content ranged from 0.172 to 0.891. Beside the lower efficiency to obtain SSR loci, the six microsatellites were polymorphic and sufficiently discriminant for the genetic studies of *S. frugiperda*; it allowed us to identify migrants with both NJ clustering and the Bayesian methods. These markers will be useful for molecular

ecology studies of this highly polyphagous species in order to understand the processes that determine genetic differentiation in the complex agro-ecosystems that it infests and improve local integrated pest management practices.

Key words: Fall armyworm; Genetic structure; Candidate migrant; SSRs; Molecular markers; Insect resistance management