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Development Of Cross-Species Transferable Microsatellite Markers For Evaluating Biotypic Diversity In The Aphid Pest Greenbug (Hemiptera: Aphidinae)

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The greenbug, *Schizaphis graminum* (Rondani) is an important aphid pest of wheat and sorghum in the Southern Great Plains of the U.S. Biotypic variation in the greenbug has been well characterized at the phenotypic level based on the abilities of different greenbug clones to damage a set of selected plant genotypes. In the present study, we investigated the genetic diversity of different greenbug biotypes with microsatellite or simple sequence repeat (SSR) markers. The abundance and distribution of SSRs were explored in the EST and genomic sequences of the pea aphid, *Acyrtosiphon pisum* (Harris), and the green peach aphid, *Myzus persicae* (Sulzer). A total of 108 newly developed, together with 40 published SSR markers were investigated for their cross-species transferability among 6 aphid species. Genetic diversity among 44 greenbug biotypes was further examined with 30 SSR markers. It was found that the pea aphid genome is abundant in SSRs with unique frequency and distribution of SSR motifs. Cross-species transferability of EST-derived SSRs is dependent upon phylogenetic closeness between SSR donor and target species, but is higher than that of genomic SSRs. Neighbor joining analysis of SSR data revealed host-adapted genetic divergence as well as regional differentiation of greenbug biotypes. This is the first report of large scale development of SSR markers in aphids, which should have wide use in aphid genetic, ecological, and evolutionary studies.