Development and Characterization of Polymorphic Genomic-SSR Markers in Asian Long-Horned Beetle (Anoplophora glabripennis)

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Abstract : The Asian long-horned beetle, Anoplophora glabripennis (Motschulsky) (Coleoptera: Cerambycidae: Lamiinae), is a wood-borer and polyphagous xylophages native to Asia and killing healthy trees. As it causes serious danger to trees, the beetle has been paid close attention in the world. However, the genetic markers limited, especially microsatellite. In this study, 24 novel simple sequence repeat (SSR) molecular markers, a powerful tool for genetic diversity studies and linkage map construction, were developed and characterized from whole genome shotgun sequences. We developed SSR loci of 2 to 6 repeated and perfect units including 9895 points, the density of SSRs was found one SSR per 56.57 kb and the abundance of SSR was 0.02/kb, besides 140 types of repeats motifs were found. Half of the 48 pairs SSR primers (containing 4 di-, 7 tri-, 2 tetra- and 11 hexamers SSRs) we selected randomly from 1222 pairs of primers were polymorphism. The number of alleles for these markers in 48 individuals varied from 3 to 21 with an average of 7.71, the number of effective alleles ranged from 1.22 to 9.97 with an average of 3.54. Besides this, the polymorphic information content (PIC) ranged from 0.18 to 0.89 with a mean of 0.65, And Shannon's Information index (I) ranged from 0.46 to 2.62 with an average of 1.44. The results suggest that the method for screening of SSR in the whole genome is feasible and efficient. SSR markers developed in this study can be used for population genetic studies of A. glabripennis. Moreover, they may also be helpful for the development of microsatellites for other Coleoptera.

Keywords : SSR markers, Anoplophora glabripennis, genetic diversity, whole genome
Conference Title : ICMBE 2015 : International Conference on Molecular Biology and Evolution
Conference Location : Paris, France
Conference Dates : September 21-22, 2015