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Diversity level of genomic microsatellites in redbay (Perseaborbonia L.) generated by Illumina sequencing

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Abstract

Redbay, Perseaborbonia (L.) Spreng., is a common evergreen tree or shrub native to the swamp forests of the Atlantic and Gulf Coastal Plains in the United States. In the past decade, redbay populations have suffered extensive mortality caused by the vascular disease Laurel wilt (Raffaelealauricola Eichhoff), which has been spread by the exotic redbay ambrosia beetle (Xyleborusglabratus Eichhoff). The disease is threatening the economic, ecologic and aesthetic functions of redbay. Early efforts to preserve genetic diversity of the threatened species, through seed and vegetative propagule collections have occurred without the benefit of guidance from a molecular characterization of existing genetic variation. Molecular markers may prove useful in guiding efficient conservation efforts for this species. Here we surveyed 51 genomic microsatellite (gSSR) markers derived from low-coverage whole genome sequencing of redbay with a panel of 25 unrelated redbay trees from eastern South Carolina. When analyzed in an ABI 3730 Genetic Analyzer, 24 markers demonstrated highly informative scores with a polymorphic information content of at least 0.50 and an estimated null allele frequency ≤0.1. The mean observed and effective number of alleles of these 24 sSSRs were 5.29 and 3.06, respectively. The observed heterozygosity ranged from 0.17 to 1.00 with a mean of 0.65, while the expected heterozygosity ranged from 0.16 to 0.90 with a mean of 0.62. Nei's expected heterozygosity and Shannon's Information index were 0.60 and 1.17, respectively. These results indicate high diversity level in the 24 redbay gSSR markers. This is the first report of genetic variation of redbay DNA markers. The gSSRs exhibiting high levels of polymorphism can be applied in characterization of genetic composition and diversity of seed collection and resistant genotypes in redbay germplasm conservation and breeding programs.

Keywords: Perseaborbonia, gSSR, microsatellite, next-generation sequencing

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