



Development and characterization of novel EST-SSR markers and their application for genetic diversity analysis of Jerusalem artichoke (*Helianthus tuberosus* L.)

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ABSTRACT. Jerusalem artichoke (*Helianthus tuberosus* L.) is a perennial tuberous plant and a traditional inulin-rich crop in Thailand. It has become the most important source of inulin and has great potential for use in chemical and food industries. In this study, expressed

sequence tag (EST)-based simple sequence repeat (SSR) markers were developed from 40,362 Jerusalem artichoke ESTs retrieved from the NCBI database. Among 23,691 non-redundant identified ESTs, 1949 SSR motifs harboring 2 to 6 nucleotides with varied repeat motifs were discovered from 1676 assembled sequences. Seventy-nine primer pairs were generated from EST sequences harboring SSR motifs. Our results show that 43 primers are polymorphic for the six studied populations, while the remaining 36 were either monomorphic or failed to amplify. These 43 SSR loci exhibited a high level of genetic diversity among populations, with allele numbers varying from 2 to 7, with an average of 3.95 alleles per loci. Heterozygosity ranged from 0.096 to 0.774, with an average of 0.536; polymorphic index content ranged from 0.096 to 0.854, with an average of 0.568. Principal component analysis and neighbor-joining analysis revealed that the six populations could be divided into six clusters. Our results indicate that these newly characterized EST-SSR markers may be useful in the exploration of genetic diversity and range expansion of the Jerusalem artichoke, and in cross-species application for the genus *Helianthus*.

Key words: Jerusalem artichoke; EST-SSR markers; Development; Genetic diversity