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Genetic Diversity of Maize Accessions (*Zea mays* L.) by Using SSR Markers

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[Introduction]

Maize represents an actual source of consumption and income for millions of people in several countries over the world. High-yielding hybrid variety development program is very important to increase farmer's income. Therefore, plant breeders needs to develop many homozygous inbred lines to obtain high genetic sources. Potential inbred lines are very significant phenotypic variability and genetic diversity and constitute an essential component of food security, as they provide the raw material used by breeders to improve the quality and productivity of maize. To know genetic diversity, the use of molecular markers provided an opportunity to analyze large-scale of maize populations like previously used to study the structure of plants genetic variation.
In this study, we developed EST-SSR marker and analyzed the genetic diversity of maize by using SSR markers.

[Materials and Methods]

For genetic diversity study, we used 148 potential inbred lines developed by using composite line selection and pedigree methods. Total RNA was isolated from young leaf tissue for design of the cDNA library. A total of 50 cDNAs were cloned in *E. coli* by employing the pGEM-T Easy vector. To confirm the ligation of the plasmid and the cDNA, the extracted plasmid from *E.coli* was cut with a restriction enzyme (*Eco*RI) and analyzed by 1.0% agarose gel electrophoresis. The plasmid DNA sequence was analyzed by SolGent Co.. After analysis of the DNA sequence, The EST-SSR markers were designed using the microsatellites analysis program WebSat and Primer3 web version 4.0.0.

[Results and Discussion]

By doing this experiment, we can develop 15 EST-SSR markers. we can study genetic diversity of maize germplasms (148 inbred lines) by using these EST-SSR markers and other microsatellites markers. Moreover, besides acting as a molecular tag for particular traits, EST-SSR markers can be identify information about polymorphic information content (PIC). Thus, by developing EST-SSR markers, the molecular analysis of maize could be done more efficiently. By doing this experiment, we can develop high-quality maize cultivars (drought resistant and high yield etc.) while overcoming the challenges from climate change and other unfavorable conditions.

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