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Analysis of molecular variance and population structure of sesame (*Sesamum indicum* L.) genotypes using SSR markers

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[Introduction]

Sesame (2*n*=2*x*=26, 357 Mb) belongs to the *Sesamum* genus of the Pedaliaceae family, very rich in compounds like lignan, sesamin and sesamolin. All these properties show the nutritional significance and medicinal importance making it highly valued crop. Since genetic base of cultivated sesame is narrow, genetic characterization plays a key role in sesame breeding programs.

[Materials and Methods]

A set of 129 genotypes (*n*=129) of cultivars and landraces from Korea and different parts of the world obtained from the Gene Bank of Rural Development Administration. DNA extraction was done according to the manual for DNA isolation from plant tissue using DNeasyPlant Maxi Kit (QIAGEN, Germany). The study downloaded 109528 SSR markers with known physical position (http://www.sesame-bioinfo.org/PMDBase). A set of 70 primer pairs were selected at least 4 to 5 primer pairs for each sesame linkage group (SLG). Phylogenetic analysis was conducted using Jaccard's similarity coefficient through NTSYS-pc software ver. 2.11. Genetic diversity parameters were calculated using the software programmes PowerMarker ver. 3.25 and POPGENE ver. 1.32. Population structure was investigated using a Bayesian clustering method implemented in the software STRUCTURE 2.3.4. The optimum *K* 10 run (*K*=1 to *K*=10) was determined from replicate runs for each of *K* with the length of burn-in set to 500K and the Markov chain Monte Carlo repeats to 500K run length. The Analysis of Molecular Variance (AMOVA) was performed to examine molecular variance within and between the populations (clusters) and correlation of alleles of pairwise estimates between populations, *Fst*, was calculated using software Arlequin ver. 3.5.2.

[Results and Discussions]

Twenty three SSRs found to be polymorphic in our study. PIC and He (expected heterozygosity) values ranged from a low of 0.33 and 0.38 to a high of 0.86 and 0.88 with average values of 0.65 and 0.72, respectively. The phylogenetic analysis using NTSYSpc software grouped 129 sesame genotypes into eight clusters. Cluster I and II contained maximum number of genotypes 64 and 39 whereas, clusters III, IV, V, VI, VII and VIII and consisted of 5, 7, 4, 3, 2, and 5 genotypes, respectively. The majority of the germplasm from Korea fell into cluster I and II. The model-based STRUCTURE analysis grouped sesame genotypes into three populations; Pop1, Pop2, and Pop3 and 35 accessions as admixture group. Pair-wise estimates of *Fst* (AMOVA) indicated a high degree of differentiation varying from 0.15 between Pop2 and Pop1 to 0.21 between Pop3 and Pop1, whereas low *Fst* (0.08) were between Pop2 and Pop3. The results given in this study demonstrated that SSR markers were useful for genetic diversity assessment in sesame. The phylogenetic cluster and STRUCTURE results indicated relatively high genetic dissimilarity among studied genotypes and may assist in selecting distant genotypes as parents for future hybridization to improve the degree of genetic variation in sesame.

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