I -54

RAPD 마커를 이용한 시라 유전자원의 유전적 다양성 및 집단 구조 분석

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Analysis of genetic diversity and population structure in dill (*Anethumgraveolens*) germplasm using RAPD markers

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Objectives

To analysis of genetic diversity and population structure in dill (*Anethum graveolens*) germplasm using RAPD markers.

Materials and Methods

○ Materials
- One hundred and thirty five accessions of *A. graveolens* germplasm were obtained from the National Agrobiodiversity Center, Rural Development Administration, Republic of Korea

○ Methods
- Data for effective number of alleles (Ne), Nei's genetic diversity (H) and Shannon's information index (I), across all the 135 accessions were also analyzed. Total genetic diversity (Ht) (Nei, 1978) was calculated using POPGENE 32 software.

Results

A total 142 scored bands 89 bands were found polymorphic (77.74) revealing a high degree of polymorphism (Table 1). Percentage of polymorphism was the highest (92.85%) for the primer OPB15 and the lowest (41.17) for the primer OPB20. Observed number of alleles (Na) ranged from 1.91 to 2.00, the average value 1.99, effective number of alleles (Ne) ranged from 1.631 to 1.860, mean value 1.732, Nei's genetic diversity (H) values ranged from 0.346 to 0.444, mean value of 0.401, Shannon's information index (I) ranged from 0.518 to 0.635, the average mean value was observed 0.581 and total gene diversity (Ht) values ranged from 0.346 to 0.444 mean value of 0.401. All the 135 accessions were analysed using 10 RAPD markers.The Nei's genetic distance ranged from 0.034 to 0.995 and genetic identity ranged from 0.353 to 0.966. The dendrogram was developed for 135 accessions of *A. graveolens* using RAPD markers. The genetic relationship among accessions using 10 RAPD markers, were grouped into two major clusters denoted as cluster-I and cluster-II. These contained 87 and 48 accessions, respectively. Cluster-I could be

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subdivided into two sub-clusters denoted as A and B. The sub-cluster A contained 38 accessions and sub-cluster B contained 49 accessions. Although a number of groups can be identified, the dendrogram show little to no geographic structuring of accessions for RAPD markers, those accessions didn't grouped together neither country nor continental of origin

Table 1. RAPD primers used for population genetic diversity and Genetic variability across all the accessions of *A. graveolens* using RAPD marker

Primer	T_B[a]	P_B[b]	H	I	Ht
OPA07	17	10	0.429	0.613	0.429
OPA11	10	7	0.377	0.553	0.377
OPB07	7	5	0.346	0.518	0.346
OPB12	10	9	0.376	0.545	0.376
OPB13	8	7	0.392	0.571	0.392
OPB15	14	13	0.421	0.604	0.421
OPB18	10	9	0.444	0.635	0.444
OPB20	17	7	0.411	0.587	0.411
OPC01	12	10	0.434	0.62	0.433
OPC20	13	12	0.382	0.56	0.382
Total	142	89	–	–	–
Average	11.8		0.4012	0.581	0.401

[a] : Total No. of bands, [b] : No. of polymorphic bands

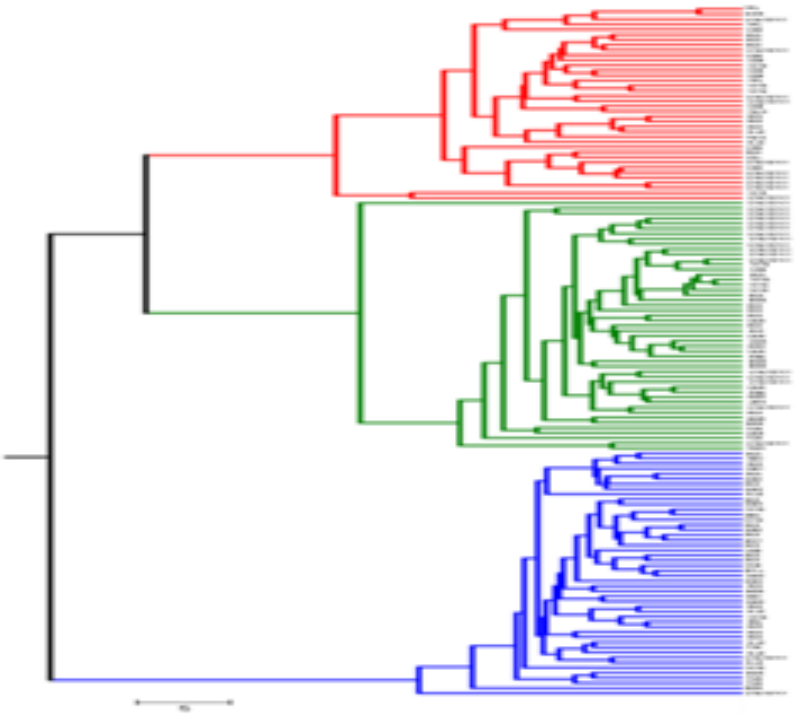

Fig. 1. Dendrogram generated using UPGMA cluster analysis RAPD based on genetic diversity of 135 dill accessions.