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Genetic divergence among *Corylus colurna* genotypes based on morphological characters of hazelnut

Kanchan Kumar Srivastava[1], Khurseed Ahmad Zargar[2] & Shyam Raj Singh[1]

[1]Central Institute of Temperate Horticulture, ICAR, Old Airfield, Rangreth, Srinagar, Jammu &Kashmir, 190 007, India, e-mail: kanchanpom@gmail.com
[2]Division of Pomology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar, J&K, 191 121, India

Abstract: Genetic divergence was studied in 41 genotypes of *Corylus colurna* on the basis of 15 morphological characters of nuts. The divergence among genotypes was estimated by the Mahalanobis' method and the studied genotypes were grouped into clusters by Tocher's method. The obtained data were analysed using the PCA and CA. As a result, 9 genotype clusters were distinguished and a wide diversity among genotypes originating from the same locality was found. It has been proposed that for obtaining the most desirable transgressive segregates in *Corylus colurna*, genotypes from the genetically most distant clusters should be crossed.

Keywords: hazelnut, genetic divergence, variability, genotype, Mahalanobis distance

1. Introduction

Hazelnut is one of the world's major nut crop, popularly known as Virin in Kashmir. World production of hazelnut is 778 thousand tons (Faostat data 2007). Turkey is a leading producer and exporter of hazelnut, accounting for about 70% of the total production in the world. In USA, hazelnut is so popular that it has been declared as Oregon State Nut. Hazels are deciduous trees and shrubs scattered over the temperate region of northern hemisphere. *Corlyus colurna* (Turkish hazel) is native of south-eastern Europe and south-western Siberia and south to western Himalayas – from Kashmir to Kumaon. It is a very important and costly nut used in confectionary and chocolate. The tree is very useful in binding soil, which helps to prevent soil erosion, and provides also valuable timber. Leaves are used to feed the cattle and nuts are eaten by wild animals. Turkish hazel that grows in the Kashmir valley exhibits a wide genetic variability. Trees are large, multi-branched, multi- to single stemmed, leaves are leathery, big glabrous; the species spreads by suckers from the roots of a parent plant. However, no systematic orcharding is practiced in the Kashmir valley, though it is a very important nut for diversification of orchard ecosystems and a good crop for higher altitudes, where other fruit crops are not possible. Furthermore, there are available good genetic resources for enhancing the species cultivation and development of new, promising cultivars. Hence, the survey and documentation of hazelnut genotypes were carried out from 2006 to 2008, to identify a superior genotype in the Kashmir valley area for the further hybridisation purpose. Selection of genetically diverse genotype is important for the exploitation of heterosis and development of desirable recombinants, in addition, an assessment of the nature and magnitude of diversity between genotypes will help to choose proper parents for hybridisation.

2. Material and methods

The present investigation was carried out during 2006-2008. For the study, 41 genotypes were detected in the Dachigam Wild Life Sanctuary and at the Sher-e-Kashmir University of Agricultural Sciences of Kashmir, Shalimar, Srinagar, 15 km away from the sanctuary. The Kashmir is located at the longitude of 34°45' N and latitude of 74°50' E, at the altitude of 1640 m a.s.l.

At maturity, 15 nuts per a genotype were randomly collected in three replications for two consecutive years. The number of nuts per genotype cluster, nut length, nut width, nut thickness, kernel length, kernel thickness and shell thickness were recorded by digital vernier calliper; nut and kernel weight were measured with an electronic balance and nut roundness index was calculated by the formula: nut roundness index = X+Y/2Z, where X and Y are two cross diameters (width and thickness) and Z is the height or length of a nut from an apex to scutellum. Nut size was calculated by the method suggested by Botu *et al*. (1999). Fat content was estimated by the method following Sadasivam and Manickam (1992a). The protein content of a kernel was estimated according to the Micro-Kjeldahl method and was multiplied by the conversion factor (N x 6.25) for the crude protein content (it included also the non-protein nitrogen) (Sadasivam & Manickam 1992b).The genetic divergence among the genotypes was estimated by Mahalanobis D^2 statistics and all genotypes were grouped into clusters according to Tocher's method, as describe by Rao (1952). Canonical analysis was carried out by calculating canonical roots according to Singh and Choudhary 1979; for the factor analysis (Principal Components Analysis) of various parameters, the SPSS software version 10.0 was used (Norusis 1994).

3. Results

On the basis of the relative magnitude of D^2 values, 41 genotypes were grouped, using Tocher's method,

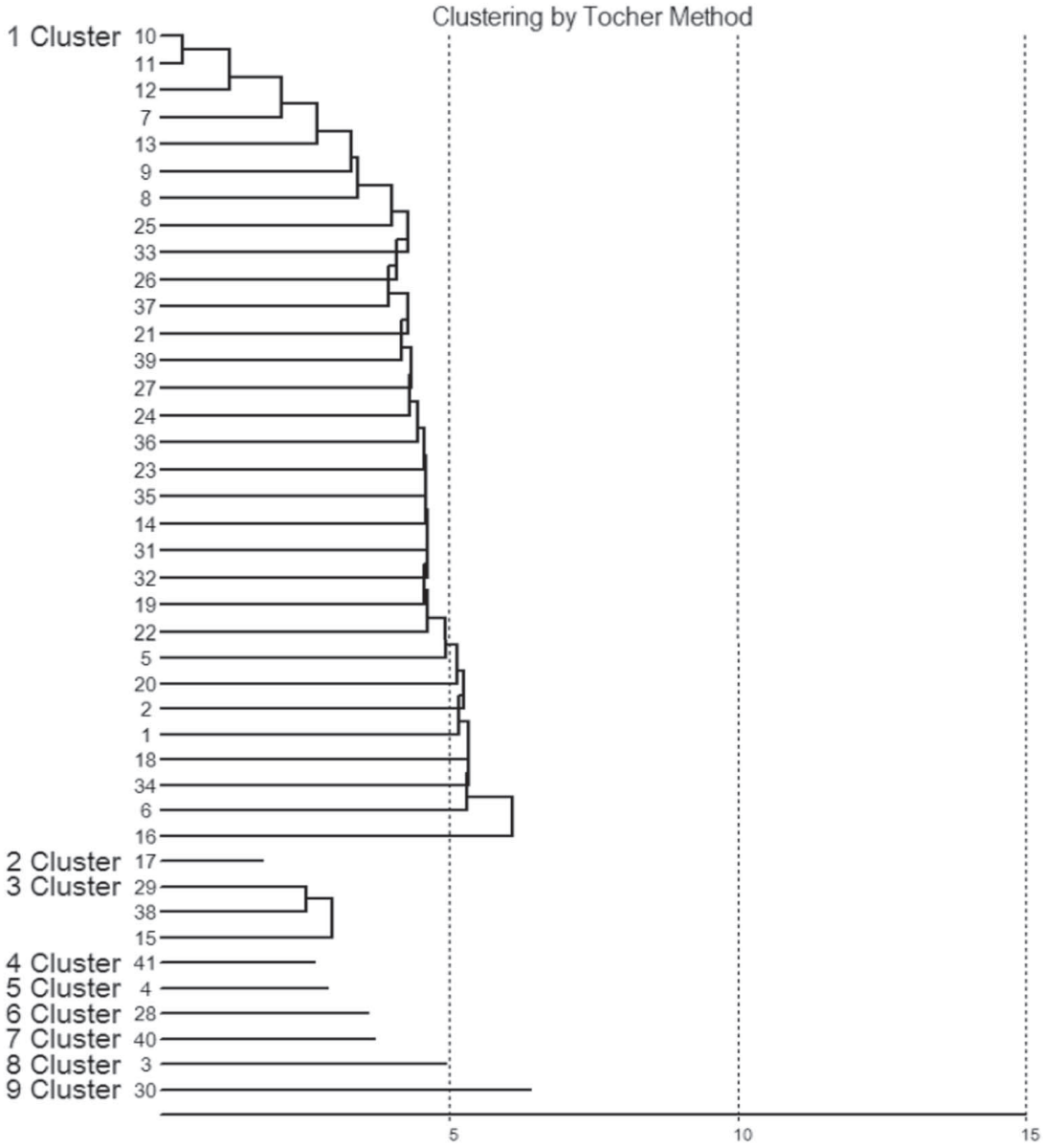

Fig. 1. Dendrogram showing different clusters of genotypes, grouped by Tocher's method, in *Corylus colurna* germplasm

Table 1. Clustering pattern of 41 genotypes of *Corylus colurna*

Cluster	Number of genotypes	Genotypes
I	31	SKAU-H 0016, SKAU-H 0006, SKAU-H 0034, SKAU-H 0018, SKAU-H 0001, SKAU-H 0002, SKAU-H 0020, SKAU-H 0005,SKAU-H 0022, SKAU-H 0019, SKAU-H 0032, SKAU-H 0031, SKAU-H 0014, SKAU-H 0035, SKAU-H 0023, SKAU-H 0036,SKAU-H 0024, SKAU-H 0027, SKAU-H 0039, SKAU-H 0021, SKAU-H 0037, SKAU-H 0020, SKAU-H 0033, SKAU-H 0025, SKAU-H 0008, SKAU-H 0009, SKAU-H 0013, SKAU-H 0007, SKAU-H 0012, SKAU-H 0011, SKAU-H 0010
II	1	SKAU-H 0017
III	3	SKAU-H 0029, SKAU-H 0038, SKAU-H 0015
IV	1	SKAU-H 0041
V	1	SKAU-H 0004
VI	1	SKAU-H 0028
VII	1	SKAU-H 0040
VIII	1	SKAU-H 0003
IX	1	SKAU-H 0030

into 9 clusters. Cluster I was the largest one, with 31 genotypes, cluster III had 3 genotypes, while clusters II, IV, V,VI,VII,VIII and IX were mono-genotypic (Fig. 1 and Table 1). However, the genotypes SKAU-H-0041 and SKAU-H-0040, located in cluster IV and cluster VII, have different distances. The highest intra-cluster distance was registered in cluster I (2.25), while the rest of clusters had intra-cluster distance equal to 0.00. The highest inter-cluster D^2 value was observed between clusters VII and IX (3.90), followed by cluster IX and cluster VI (3.76). This indicates a wide genetic distance between these groups (Table 2). Since these clusters showed the highest inter-cluster distances, selection of parents from such clusters for hybridisation programme

Table 2. Mean intra and inter cluster values for the studied nut characters (see Table 3) in nine genotype clusters of *Corylus colurna*

Cluster Number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
I	2.25	2.59	2.61	2.54	2.70	2.83	2.72	2.82	3.09
II		0.00	2.91	2.75	2.69	3.23	2.59	2.02	3.27
III			0.00	2.92	3.14	2.84	3.20	3.08	3.10
IV				0.00	2.95	2.31	3.02	2.90	3.12
V					0.00	3.77	2.62	2.55	3.44
VI						0.00	3.29	3.42	3.76
VII							0.00	2.93	3.90
VIII								0.00	3.59
IX									0.00

Table 3. Cluster means for the studied nut characters in 41 genotypes of *Corylus colurna*

Traits	Cluster Means								
	I	II	III	IV	V	VI	VII	VIII	IX
Nut/ cluster	3.45	3.48	3.42	3.11	3.51	2.83	3.49	3.53	3.49
Nut length (mm)	16.41	16.86	16.28	17.28	16.46	18.13	16.59	16.44	16.31
Nut breadth (mm)	17.37	17.88	17.29	17.06	17.68	16.36	17.34	17.42	16.78
Nut thickness (mm)	12.34	12.37	12.29	12.54	12.42	12.08	11.67	11.90	12.41
Nut roundness Index	0.90	0.90	0.90	0.86	0.91	0.79	0.87	0.83	0.89
Nut size (mm)	15.34	15.70	15.28	15.62	15.52	15.52	15.20	15.26	14.61
Nut weight (g)	1.59	1.50	1.29	1.75	1.63	1.55	1.65	1.52	1.42
Kernel length (mm)	12.03	12.16	11.89	14.27	12.35	14.34	11.99	12.01	11.70
Kernel breadth (mm)	12.00	11.15	12.10	10.92	12.61	11.05	12.12	12.09	11.70
Kernel thickness (mm)	7.41	7.52	7.24	8.21	7.93	7.91	7.70	7.53	7.39
Kernel weight (g)	0.49	0.51	0.53	0.53	0.55	0.48	0.45	0.50	0.47
Kernel percent	31.18	33.93	41.17	29.85	33.81	31.13	28.70	33.09	33.15
Shell thickness (mm)	1.91	1.66	1.72	1.57	1.72	1.47	2.03	1.68	1.70
Fat (%)	49.81	46.55	49.00	45.23	56.15	43.01	48.75	48.38	49.53
Protein (%)	14.49	17.35	16.68	13.74	20.99	12.99	17.70	17.07	16.30

Table 4. Principal component values of the studied nut characters in *Corylus colurna*

Traits	V1	V2	V3	V4	V5	V6	V7
No of nuts/ cluster	0.139	0.076	0.372	0.300	0.008	0.037	0.437
Nut length (mm)	0.165	-0.049	0.130	0.040	0.171	-0.027	0.152
Nut breadth (mm)	-0.228	0.347	-0.101	-0.189	0.346	-0.134	0.279
Nut thickness (mm)	-0.044	-0.372	0.038	0.296	-0.295	0.091	0.058
Nut roundness Index	-0.028	0.152	0.017	0.035	0.071	-0.309	0.090
Nut size (mm)	0.007	0.251	-0.223	-0.259	0.230	0.089	0.209
Nut weight (g)	-0.240	0.235	-0.147	0.405	-0.171	-0.023	-0.415
Kernel length (mm)	0.070	-0.202	0.363	0.155	0.599	-0.394	-0.433
Kernel breadth (mm)	-0.042	-0.040	0.038	-0.212	0.251	0.715	-0.361
Kernel thickness (mm)	0.644	0.379	-0.282	0.195	-0.131	-0.068	0.170
Kernel weight (g)	0.195	-0.128	0.243	0.014	-0.088	0.121	0.184
Kernel per cent	-0.236	-0.188	0.134	-0.422	-0.341	-0.270	-0.032
Shell thickness (mm)	-0.419	0.435	0.217	0.078	-0.200	-0.082	-0.154
Fat (%)	-0.077	0.346	0.522	0.159	-0.009	0.298	0.083
Protein (%)	0.376	0.204	0.387	-0.483	-0.265	-0.103	-0.255
Eigen value	27.83	19.11	12.12	10.88	9.80	9.25	6.60
Percent variance	22.62	15.80	9.84	8.84	7.95	7.51	5.37
Cumulative percent of variance	22.62	38.39	48.24	57.08	65.04	72.56	77.92

would help to develop novel hybrids. In turn, cluster II and cluster VIII had the lowest inter-cluster distance (2.02), which indicates close relationship and similarity of most traits of the genotypes. Hence selection of parents from these clusters should to be avoided. The cluster mean values for the quantitative traits are presented in Table 3. Cluster V has the highest mean values for such traits as nut roundness index (0.91), kernel width (12.61mm), kernel weight (0.55g), fat content (56.15%) and protein content (20.99%), while cluster IV shows the highest values for nut weight (1.75g), kernel length (14.27mm) and kernel thickness (8.21mm). The highest percentage of kernels (41.17%) was recorded in cluster III. Clusters IV and V are expected to give promising and desirable recombinations in segregating generations, because they comprise desirable features as evident from their cluster means. The principal component analysis data are presented in Table 4. The first vector shows the highest eigen value (27.83) and accounts for 22.62% of the total variation. The first vector is the combination of kernel thickness, protein content, kernel weigh, nut length and the number of nuts per cluster. The second vector has an eigen value of 19.41 and explains 15.80% of the total variation. This factor is mainly the combination of shell thickness and kernel thickness. The third vector has an eigen value of 12.12 and the total variation of 9.84%; it is the combination of fat content and protein content. The fourth vector has an eigen value of 10.88 and the total variation of 8.84%, with the maximum contribution of nut weight. The fifth vector has an eigen value of 9.80 and the total variation of 7.95%; it is mainly the combination of kernel length and nut width. Vector sixth has an eigen value of 9.25 and the total variation of 7.51%, with the highest contribution of kernel width. Vector seven has an eigen value of 6.60, with the total variation of 5.37% and, the highest contribution of kernel weight and nut size. In this case, canonical root value accounts for 77.92% of the cumulative variance.

The genetic diversity among genotypes could be due to various factors, like heterogeneity, genetic architecture of populations and developmental traits, as described by (Murty & Arunanchalam 1966). In the case of *Corylus colurna*, genotypes originating from the same locality were grouped in separate clusters, which indicates a wide diversity among genotypes originating from the same place. Rao *et al*. (2003) reported that geographical distribution and genetic diversity are correlated and concluded that eco-geographically different cultivars also differ genetically from each other. A clustering pattern similar to our pattern was reported in walnut by Pandey and Tripathi (2007). Grouping of genotypes from the same locality in different clusters may result from different genes controlling the most important characters and different genetic constituents. Sardana *et al*. (1997) observed that cluster means reveal the inner diversity in the material under study. De *et al*. (1988) proposed that traits contributing maximum towards the D^2 values should be given priority in choosing a cluster for the further selection and choice of parents for hybridisation.

4. Final remarks

Based on the present findings of genetic divergence and its component analysis it can be concluded that inter-crossing between genotypes of genetically diverse clusters that show a superior mean outcome may be helpful for obtaining desirable segregates. In the case of *Corylus colurna*, the highest genetic diversity was registered between cluster VII and IX. Comparison of

the cluster means for 15 clusters indicated that the studied characters considerably differed between the clusters. Therefore, it is suggested to cross genotypes selected from the most distant clusters, with the high mean outcome, to get desirable transgressive segregates.

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