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Assessment and exploitation of genetic divergence in pecan nut

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ABSTRACT

Sixty genotypes of pecan nut having unknown seedling origin were selected after thorough survey to assess the nature and magnitude of genetic divergence. Genetic divergence was analyzed in these 60 bearing trees of pecan nut growing at various geographical locations in Jammu Division of UT of Jammu and Kashmir. The data were subjected to non- hierarchical Euclidean cluster analysis based on seven nut and kernel characters viz nut length, lateral nut width, ventral nut width, shell thickness, kernel weight, kernel length and nut weight High heritability coupled with higher genetic advance was observed for kernel length (94.80% and 46.61 %).Further kernel weight showed positive and significant correlation with nut length and nut weight. Clustering of selected genotypes was done by using D^2 statistics and dendrogram was made as per Ward's method. All the 60 seedling pecan nut genotypes were grouped into 8 clusters. The maximum inter cluster distance was recorded between selections of cluster VII and V. Cluster VII was the most diverse as more clusters showed maximum inert cluster distance with it. Considering high magnitude of genetic advance and heritability (broad sense) in various traits of horticultural interest, the existing biodiversity was gainfully exploited by direct selection and three genetically diverse genotypes were selected and compared with three commercial cultivars and out of these five genotypes one was selected for commercial cultivation based on yield and nut characters. The selected genotype has been released as variety for cultivation in North West Himalayan region and the same has been notified by central Variety Release committee and released under name SKJPP 25 /Jammu pecannut.

Key words: *Carya illinoensis* (Wang) K. Koch., correlations, genetic divergence, heritability.

INTRODUCTION

The pecan nut [*Carya illinoensis* (Wangenheim) C. Koch], native to North America (Andersen and Crocker, 1) is one of the better known hickories, belonging to "Juglandaceae" family. In India, pecans were introduced from USA by Punjab government in 1937. Eight cultivars were planted at Government Fruit Farm, Palampur, Himachal Pradesh, which became major source of planting material in Himalayan region. At present pecan nut is one of the most important temperate nuts grown in India, and mainly cultivated in Jammu and Kashmir and Himachal Pradesh. The total area under pecan nut production is increasing due its high economic returns and adaptation to intermediate zone of Jammu (Ravindran *et al.*, 10). The area under pecan nut in Jammu region is around 0.524 thousand ha with production of about 0.077 thousand MT in 2020-21 (Anon, 2). Pecan nut has the recognition of being called "queen of nuts" because of its excellent kernel characteristics. Pecan is superior to walnut in quality and flavor(65-70% fats, 8-10% proteins, high in phosphorous, potassium and vitamins A, C, E and B complex), and thrives best in areas (warm and humid), which are unfit for walnut cultivation (Rani *et al.*, 9).

Though introduced in Palmpur, Himachal Pradesh, way back in 1930 (Singh *et al.*, 14), this nut crop could not assume commercial status among orchardists due to non-availability of suitable cultivars. Pecan nut is having great commercial scope in the Union Territory of Jammu and Kashmir, being hardy to climatic vagaries with huge export potential. The existing vast gene pool of seedling origin in Poonch, Rajouri, Kathua, Udhampur and Doda districts, has shown tremendous variability in respect of growth, yield and quality attributes, providing an opportunity to exploit for commercial use. Meager efforts have been made in India for selection of superior seedling pecan genotypes with desirable traits especially economically important nut and kernel traits (Rani *et al.*, 8). To commercialize pecan, there is need to select/ develop ideal variety(ies) having desirable horticultural traits in order to establish the productive pecan orchard. There is an urgent need to identify suitable trees from native seedling populations or to introduce cultivars from other countries; however, it takes a long time to commercialize introduced cultivars after assessing their location specific performance. Keeping in view the available genetic

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wealth around Rajouri and Poonch districts, the present study was conducted to select/develop improved progenies and hybrids in the future. The measurement of correlation between characters is a matter of considerable influence in selection practice. The better understanding of the association is provided by the path analysis co-efficient in relation to direct and indirect effects of various component traits on nut weight, hence this study was conducted on genetic variability, heritability, correlation and cluster analysis of different naturally occurring pecan nut genotypes.

MATERIALS AND METHODS

The present investigation was carried out in the Division of Fruit Science, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Chatha, J&K during 2018-19 to study the extent of variability and selection of superior pecan trees from a population of seedling origin in Jammu Division. Various locations of Rajouri (33.77°N 74.1°E) and Poonch (33°23′N 74°18′E) districts of Jammu Division, ranging from 915 and 981 m elevation were surveyed for selecting pecan nut trees of seedling origin. Out of total population, 60 pecan nut trees were selected based on superior nut and kernel characteristics. All the trees selected were bearing and were between the age group of 12 to 15 years old. The data recorded during the investigation were statistically analyzed with the help of INDOSTAT statistical package (version 7.00. Hyderabad, India). Analysis of variance, cluster analysis based on Ward's method using squared Euclidean distance was performed using the statistical software Indostat and statistical package for agricultural research (SPAR) version 7.0 programme. The D^2 statistic was used for assessing the genetic divergence among the population (Mahalanobis, 5).

RESULTS AND DISCUSSION

The analysis of variance exhibited significant differences for all the traits indicating the substantial amount of genetic variation present in the gene pool. The estimates of range in variation, average mean performance, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percentage of mean are presented in Table 1. The range in variation was observed from 20.03 to 52.40 for nut length (mm), 15.50 to 28.50 for lateral nut width (mm), 15.50 to 33.40 for ventral nut width (mm), 0.30 to 1.89 for shell thickness (mm), 2.06 to 6.59 for kernel weight (g), 11.21 to 39.27 for kernel length (mm) and 3.56 to 8.63 for nut weight (g). However, the overall mean values were as low as 0.30 mm for shell thickness and as high as 52.40 mm for nut length.

Singh *et al*. (13) also reported variation in lateral nut width and ventral nut width . Singh *et al.* (14) reported wide range of variation in thickness of shell in pecannut. Similar variability for kernel weight and kernel length have also been reported by Shah *et al*. (11) and for nut weight by Kaushal and Sharma (4)

Phenotypic coefficient of variability were higher in magnitude than the genotypic coefficient of variability for all the characters under study. The highest phenotypic (28.67%) and genotypic (24.69 %) coefficients of variability were found for kernel weight and whereas these were lowest in nut length (14.00 % and 12.90 %, respectively). Heritability (broad sense) varied from 43.10% in shell thickness to 94.80% in kernel length. Highest heritability was observed for kernel length (94.80%) followed by ventral nut width (89.10%), nut length (84.90%), lateral nut width (77.60%) and kernel weight (74.10%). It was moderate for the remaining traits *i.e.* nut weight (59.80%) and shell thickness (43.10 %). Highest genetic advance as percentage of mean was found

Table 1. Estimates of variability parameters for various nut and kernel traits in pecan nut selections.

Characters	Mean ± SE	Range	Coefficient of variation (%)		Heritability (% Broad sense)	Genetic advance	Genetic advance as % age of mean
			PCV	GCV			
Nut length (mm)	37.00 ± 1.16	20.03 – 52.40	14.00	12.90	84.9	9.06	24.49
Lateral Nut width (mm)	20.57 ± 0.81	15.50 – 28.40	14.46	12.74	77.6	4.76	23.12
Ventral nut width (mm)	23.18 ± 0.88	15.50 – 33.40	20.03	18.91	89.1	8.52	36.78
Thickness of shell (mm)	1.55 ± 0.13	0.30 – 1.89	19.01	12.47	43.1	0.26	16.85
Kernel weight (g)	4.00 ± 0.34	2.06 – 6.59	28.67	24.69	74.1	1.75	43.79
Kernel length (mm)	24.28 ± 0.76	11.21- 39.27	23.86	23.23	94.8	11.32	46.61
Nut weight (g)	5.77 ± 0.47	3.56 – 8.63	22.43	17.34	59.8	1.59	27.62

for kernel length (46.61 %) followed by kernel weight (43.79). It was lowest for shell thickness (16.85 %). The ratio of genetic variance to the total variance called heritability is a useful measure in predicting the progress to be achieved through selection. selection can be done more quickly for the characters having high heritability. High heritability estimates were accompanied with high genetic gain in case of kernel weight and kernel length indicating additive gene action control for the inheritance of these traits and these traits are likely to respond more to selection. The analysis of variance for various nut characters showed the significant difference among selections. These differences indicated the presence of substantial amount of variability and considerable scope for improvement for various characters namely nut length, lateral nut width, ventral nut width, thickness of shell, kernel weight, kernel length and nut weight in the material under study.

Phenotypic and genotypic correlation coefficients among seven characters in 60 pecan nut selections were computed, and presented in the Table 2. Nut length was positively and significantly associated with nut weight, kernel length, lateral nut width, kernel weight, ventral nut width, while nut length showed the inverse relationship with shell thickness. Nut width(lateral and ventral) showed significant and positive correlation with nut weight, kernel weight and kernel length showed positive correlation with shell thickness. Thickness of shell was positively correlated with nut weight and kernel weight whereas negatively correlated with kernel length. Kernel weight and length showed positive and significant correlation with nut weight, Present study revealed that genotypic correlation coefficients were higher in magnitude than the phenotypic ones for most of traits except thickness of shell establishing predominant role of heritable factors. These results are in conformity to the findings of Shah *et al.* (11) who also observed that magnitude of genotypic correlation coefficients were higher than the phenotypic ones in almond selections.

It is evident from correlation studies that nut length was positively and significantly correlated with nut weight both at phenotypic and genotypic levels and these results are in line with earlier work of Rana *et al*. (7) who also observed positive and significant correlation between nut length and nut weight in walnut. The characters which had non-significant correlations suggest that they are independent of each other. The present correlation findings are similar to those obtained by Singh *et al*. (13) in seedling pecan nut trees growing in Himachal Pradesh.

The direct and indirect effects of various characters were worked out as presented in Table 3. Maximum positive direct effect on nut weight was shown by nut width in lateral view followed by kernel weight, nut width in ventral view, shell thickness, kernel length and nut length. Kernel weight has highest positive indirect effect on nut weight which was followed by kernel length and nut width in ventral view via nut width in lateral view. Maximum negative indirect effect on nut weight was via kernel length for shell thickness, followed by nut length for shell thickness and shell thickness for nut length. Present studies revealed that nut width in lateral view had maximum positive direct effect on nut weight at genotypic level followed by

Table 2. Phenotypic (P) and Genotypic (G) correlation coefficients among various nut and kernel traits in pecan nut selections.

Character		Nut length (mm)	Lateral Nut width (mm)	Ventral nut width (mm)	Thickness of shell (mm)	Kernel weight (g)	Kernel length (mm)	Nut weight (g)
Nut length (mm)	(G)	-	0.637**	0.507**	-0.047	0.574**	0.898**	0.708**
	(P)	-	0.513**	0.462**	-0.036	0.470**	0.804**	0.495**
Lateral Nut width (mm)	(G)		-	0.711**	0.001	0.781**	0.711**	0.992**
	(P)		-	0.584**	-0.030	0.608**	0.610**	0.676**
Ventral nut width (mm)	(G)			-	0.031	0.718**	0.476**	0.853**
	(P)			-	0.034	0.597**	0.430**	0.621**
Thickness of shell (mm)	(G)				-	0.046	-0.125	0.100
	(P)				-	-0.020	-0.062	0.070
Kernel weight (g)	(G)					-	0.586**	0.956**
	(P)					-	0.488**	0.582**
Kernel length (mm)	(G)						-	0.742**
	(P)						-	0.559**

**Significant at 1% level of significance

Table 3. Path analysis at genotypic level showing direct (diagonal) and indirect (off diagonal) effects of various nut and kernel traits on nut weight in pecan nut selections.

Character	Nut length (mm)	Nut width in lateral view (mm)	Nut width in ventral view (mm)	Shell thickness (mm)	Kernel weight (g)	Kernel length (mm)	Genetic correlation coefficient of nut weight
Nut length (mm)	0.029	0.018	0.015	-0.001	0.017	0.026	0.708**
Nut width in lateral view (mm)	0.329	0.517	0.367	0.005	0.404	0.367	0.992**
Nut width in ventral view (mm)	0.087	0.122	0.172	0.005	0.123	0.082	0.853**
Shell thickness (mm)	-0.004	0.001	0.002	0.081	0.004	-0.010	0.100**
Kernel weight (g)	0.216	0.293	0.269	0.017	0.375	0.220	0.956**
Kernel length (mm)	0.051	0.040	0.027	-0.007	0.335	0.057	0.742**

**Significant at 1% level of significance

kernel weight and nut width in ventral view. Maximum negative indirect effect on nut weight was via kernel length for shell thickness which was followed by nut length for shell thickness and shell thickness for nut length. The results are in agreement with the earlier findings of Singh *et al*. (13) where it was reported that kernel weight followed by nut width had maximum direct effect on nut weight in pecan nut.

On the basis of Euclidean cluster analysis sixty selections of pecan nut were grouped into eight clusters. Sixty diverse selections included in the present study varied significantly for all the characters under investigation. The perusal of data presented in Table 4 and Fig. 1 depicted that cluster I had maximum number of selections (13) namely SKJPR1, SKJPP16, SKJPP28, SKJPR27, SKJPP19, SKJPR30, SKJPP56, SKJPP34, SKJPP49, SKJPP33, SKJPR3, SKJPP29, SKJPR4, SKJPP22, SKJPP12, SKJPP18, SKJPP17, SKJPP9 followed by cluster VI (SKJPR6, SKJPP40, SKJPP42, SKJPP58, SKJPP51, SKJPP53, SKJPP41, SKJPP52, SKJPP57, SKJPP36, SKJPP38, SKJPP46, SKJPP43), cluster IV (SKJPR7, SKJPP48, SKJPP32, SKJPP10, SKJPP20, SKJPP14, SKJPP15, SKJPP60), cluster III (SKJPR 2, SKJPP50, SKJPP31, SKJPP24, SKJPP55, SKJPP26, SKJPP54), cluster VIII (SKJPP13, SKJPM21, SKJPP23, SKJPP35, SKJPP37, SKJPP39, SKJPP44), cluster IV (SKJPP11, SKJPP59, SKJPP47, SKJPP59) and cluster VII (SKJPP8, SKJPP25). Cluster V consisted only one selection (SKJPR5). Singh *et al.* (13) reported five clusters with 36 selections of pecan nut. Thakur *et al.* (15) reported eight clusters in 63 diverse selections of almond growing in Kinnaur district of Himachal Pradesh.

Data given in Table 5 reveals maximum inter-cluster distance (266.26) between cluster VII and V followed by cluster VII and IV (186.20). Cluster VII was the most diverse as more clusters showed maximum intercluster distance with it *i.e.* cluster

Table 4. Distribution of different pecan nut selections into clusters based on D^2 statistics.

Cluster	Number of selections in the cluster	Accession number of the selection
I	18	SKJPR1, SKJPP16, SKJPP28, SKJPR27, SKJPP19, SKJPR30, SKJPP56, SKJPP34, SKJPP49, SKJPP33, SKJPR3, SKJPP29, SKJPR4, SKJPP22, SKJPP12, SKJPP18, SKJPP17, SKJPP9
II	4	SKJPP11, SKJPP45, SKJPP47, SKJPP59
III	7	SKJPR 2, SKJPP50, SKJPP31, SKJPP24, SKJPP55, SKJPP26, SKJPP54
IV	8	SKJPR7, SKJPP48, SKJPP32, SKJPP10, SKJPP20, SKJPP14, SKJPP15, SKJPP60
V	1	SKJPR5
VI	13	SKJPR6, SKJPP40, SKJPP42, SKJPP58, SKJPP51, SKJPP53, SKJPP41, SKJPP52, SKJPP57, SKJPP36, SKJPP38, SKJPP46, SKJPP43
VII	2	SKJPP8, SKJPP25
VIII	7	SKJPP13, SKJPM21, SKJPP23, SKJPP35, SKJPP37, SKJPP39, SKJPP44

Table 5. Mean intra and inter cluster (D^2 Values) distance values.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	(9.38)	19.15	20.42	33.31	85.44	35.38	121.08	62.10
II		(5.03)	33.08	31.43	78.21	58.63	161.74	75.97
III			(10.04)	49.75	102.41	34.31	71.65	28.88
IV				(18.86)	64.08	99.90	186.20	80.87
V					(0.00)	151.11	266.26	133.28
VI						(20.36)	88.92	77.61
VII							(18.64)	45.22
VIII								(9.47)

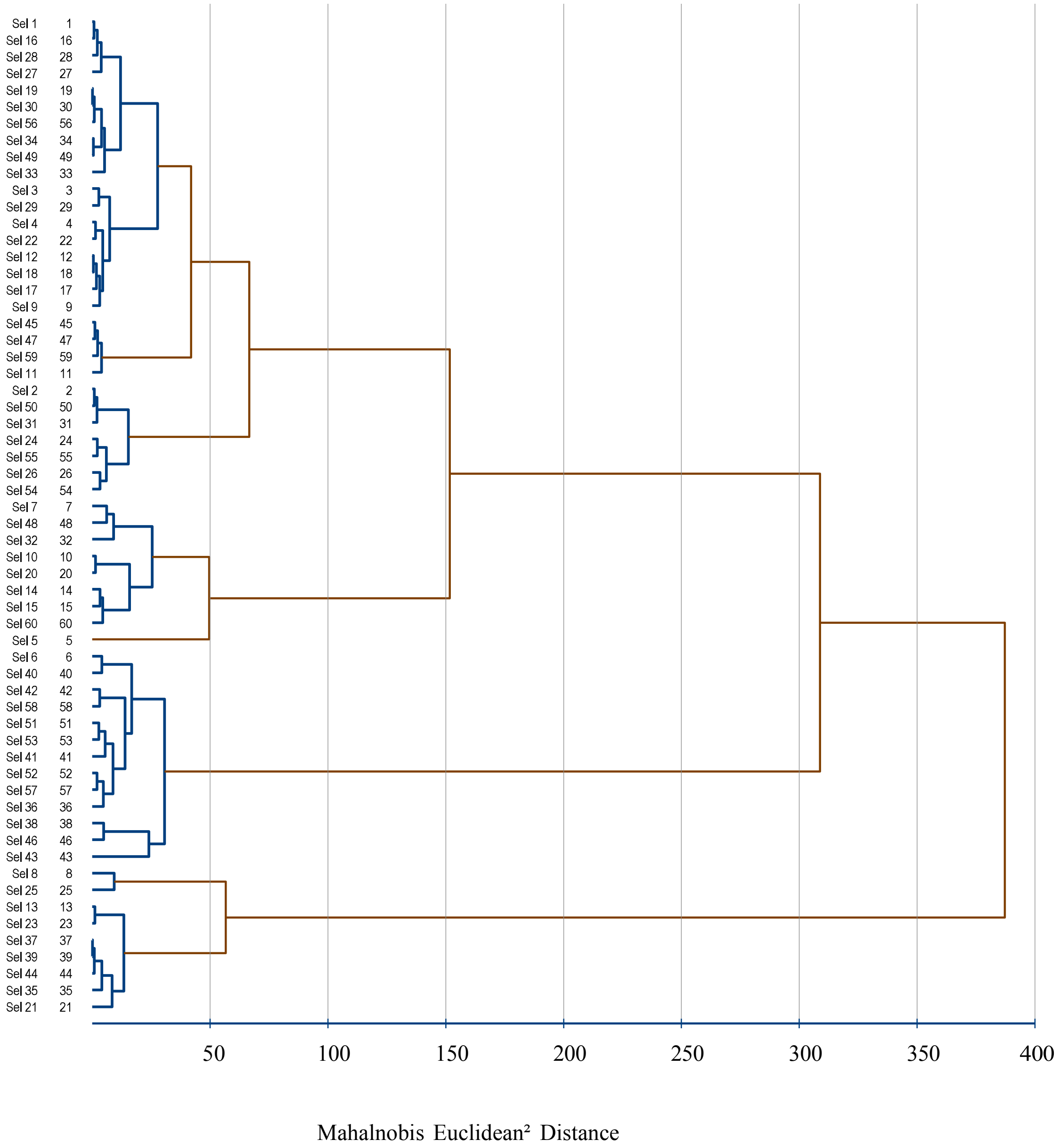

Fig. 1. Dendrogram showing clustering of pecan nut selections by Ward's method.

A. Mother I tree selected of SKJPP-25

B. Nut and Kernel of SKJPP-25

Plate 1. (A and B). Tree, nuts and kernel of pecan nut SKJPP-25.

V, IV and II. Intracluster distance for 60 selections was recorded maximum for cluster VI (20.36) while it was recorded zero in cluster V which contain only one selection. Cluster VII was the most diverse as more clusters showed maximum intercluster distance with it *i.e.* cluster V, IV and II. Selections belonging to clusters separated by genetic distance may be used in hybridization programme to obtain a wide spectrum of variation among the seggregants. Parents with good nut and kernel characters can be selected from clusters VII and V for isolation of useful recombinants in segregation generation. These genotypes can be used for transfer of their useful traits in commercial pecan nut cultivars. Similar segregation into different clusters have also been reported earlier by hierarchial Euclidean cluster analysis in seedling pecan by Singh *et al*. (15). Genotypically distant parents are able to exert high heterosis was also reported by Ramanujam *et al*. (6) and Falconer (3).

On the basis of cluster mean obtained, seventeen best pecan nut selections were analysed biochemically and based on biochemical analysis three selections namely SKJPP8, SKJPM21 and SKJPP25 were regarded as best. Based on dissimilarity coefficient selections SKJPP8 & SKJPM21 and SKJPM21 & SKJPP25 are most distantly related. Out of these three selections based on biochemical characters, yield and nut characters SKJPP 25 was selected for direct release and the has been notified by central Variety Release committee with name Jammu Pecannut (Plate 1 (A and B) for cultivation in mid hill areas of North West Himalayas. The accession has been conserved at NBPGR centre at Central Institute of Temperate Horticulture(IC no 642157).

AUTHORS' CONTRIBUTION

Conceptualization of research (SR, AS, KK), designing of experiment (AR, KK), execution of field/lab experiment and data collection (AR, KK), Analysis of data and interpretation (AR and MS).

DECLARATION

The authors declare no conflict of interest.

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