Estimation of Genetic Divergence in the Seedling Trees of Pecan Nut (*Carya illinoensis* Koch.)

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Genetic variability, heritability, genetic gain, GCV, PCV and correlation studies were carried out in 18 genotypes of pecan (*Carya illinoensis* Koch.). The maximum range was observed in traits kernel percentage (40.20-63.46 %) and minimum range was recorded in traits shell thickness (0.53-1.26 mm). The coefficient of variance for different traits varied from minimum (6.74) in nut width to maximum (34.97) in shell thickness. High heritability was found for traits nut length (98.7), nut weight (97.68), nut width (95.51), nut height (95.00) and kernel percentage (92.41). High GCV (44.49) was exhibited by kernel weight, nut weight (43.84) and moderate for nut length (29.23) and kernel percentage (24.21), PCV was estimated highest for kernel weight (52.74), nut weight (44.36) and moderate for nut length (29.45) and kernel percentage (25.18). The traits shell thickness and nut width exhibited low GCV (0.73) and PCV (12.97) respectively. The nut weight was positively correlated with the nut length, nut width, kernel weight, shell thickness and shell weight, whereas it had negative correlation with the kernel percentage.

Key Words: ***Carya illinoensis*, Genetic variability, Heritability, Seedling trees, Correlation coefficient, Pecan nut**

Introduction

Nature has endowed Kashmir valley with many temperate fruit crops. Much work has been done on leading fruit crops but scanty information is available in minor fruits. Among these minor fruits, Pecan nut (*Carya illinoensis* Koch.) is one which belongs to hickories group and is the cultivated species in Juglandacae family. These are grown successfully in areas receiving moderate to high snowfall in winter with moderate hot summers. Jammu and Kashmir, Himachal Pradesh and hills of Uttaranchal are the states where pecan is under sporadic cultivation. In India, almost all the pecan trees are of seedling origin and exhibit considerable variability for various nut, shell and kennel characters. Pecan is monoecious and wind pollinated, which also lead to extreme variation in trees raised through seeds. As such, each seedling tree represent itself as an individual selection. Determination of nature and magnitude of genetic diversity and variability in nut and kennel character is pre-requisite for any breeding programme for bringing further improvement by means of selection. Therefore, selection from wild population has proved to be a useful tool for fruit breeders to estimate the genetic variability. Therefore, an attempt was made to evaluate the seedling origin pecan tree in the Kashmir valley and gather necessary information on the nature and degree of genetic divergence present in seedling tree, which could help to select elite type for direct use as clones for mass multiplication by standardized vegetative techniques or for further improvement through selection and hybridization.

Materials and Methods

The present investigation on genetic variability in pecan nut (*Carya illinoensis* Koch.) was carried out on 18 seedling selections growing at Shalimar Campus of SKUAST-K, Srinagar, Jammu and Kashmir during the year 2007-08, situated at an altitude of 1588 m above mean sea level lying between latitude 35º5´-34º7´ North and longitude 74º5´-74º9´ East. The area falls under typical temperate zone environment conditions. To know the magnitude of variability, mature nuts were collected in the months of October and November. The collected samples were properly dehulled and dried at room temperature and then stored for 20 days. Dried nuts were used to record various nut, shell and kernel metric traits. The data were recorded on the nut length (mm), nut width (mm), nut height (mm) and shell thickness (mm) by using digital Vernier Caliper. Nut weight (g), kernel weight (g) and shell weight (g) were estimated by using highly sophisticated digital balance and kernel percentage was calculated by the method described by Westwood (1993). The data were recorded thrice and pooled data were analyzed statistically for estimation of variability as suggested by Panes and Sukhatme (1985) and genetic divergence was determined by statistical formula given by Johnson *et al.* (1956). Genotypic and phenotypic coefficient of variance was calculated as per the formula suggested by Burton and Devane (1953).

Results and Discussion

The genotypes under the study showed significant difference for all traits indicating wide variability among them (Table 1). The maximum range was observed in traits kernel percentage (40.20-63.46 %) followed by nut length (28.14-53.34 mm), however minimum range was recorded in traits shell thickness (0.53-1.26 mm). The coefficient of variance for different traits varied from minimum (6.74) in nut width to maximum (34.97) in shell thickness. The analysis of variance for all eight traits showed that mean square was highly significant for all parameters. Analysis of variance revealed significant difference among all the traits studied indicating the existence of genetic variability among them. However, absolute variability in different traits did not permit in deciding as to which trait was showing the highest degree of variability. Similar trend of result was reported by Sundouri and Sharma (2005). The traits which had highest per cent contribution in the variability was kernel percentage (37.03%), followed by nut length (27.22%) and least was also contributed by trait shell thickness (0.57%). The traits contributing maximum variability were important for the purpose of fixing priority of parent for hybridization programme. These findings are in confirmation with the finding of Srivastava and Sharma (2006) in apricot and Chaturvedi *et al.* (1980) in grapes.

The magnitude of GCV, PCV, ECV and heritability involved in the expression of various traits are presented in Table 2, which can precisely be used for making comparison between traits of different metric parameters. Maximum magnitude of GCV, PCV and ECV were recorded for trait shell weight. High GCV (44.49) was exhibited by kernel weight, nut weight (43.84) and moderate for nut length (29.23) and kernel percentage (24.21), PCV was estimated highest for kernel weight (52.74), nut weight (44.36) and moderate for nut length (29.45) and kernel percentage (25.18). The traits shell thickness and nut width exhibited low GCV (0.73) and PCV (12.97), respectively. ECV was observed high in kernel weight (28.09) and moderate in kernel percentage (6.94) and nut weight (6.60) whereas low in other traits. From the present study, it is quite apparent that all the traits except kernel weight and shell weight had less pronounced difference between GCV, PCV and ECV and the parameters employing that variability was due to genetic constitution. In general, the magnitude of PCV was greater than GCV denoting that environmental factors influenced their expression. Further the wide difference between GCV and PCV for kernel weight and shell weight depicted that they were prone to environmental fluctuations, whereas, narrow difference between GCV and PCV for rest of the traits revealed that they were relatively stable to environmental variations. GCV, PCV and ECV estimates for various traits and characters in various fruits have also been estimated by authors Panday and Bisht (1998) and Attri *et al.* (1999) in pomegranate and mango, respectively.

High heritability was found for traits nut length (98.7), nut weight (97.68), nut width (95.51), nut height (95.00) and kernel percentage (92.41). High heritability for different traits indicate that large proportion of phenotypic variance has been attributed to genotypic variance and therefore, reliable selection could be made from these traits on the basics of their phenotypic expression rather than genetically constitution. High heritability alone with genetic advance and genetic gain was observed for nut length, nut weight and kernel percentage indicating that the traits were controlled by additive gene effect (Panes, 1957) and it would respond very well to continuous selection, so that considerable improvement of these traits might be possible. Moderate to low heritability, genetic advance and genetic gain for the rest of the traits suggested that these were controlled by non-additive gene effect having low genetically gene action. Panes (1957) suggested that high genetic advance, genetic gain and heritability provides good scope for improvement as

Table 1. Range, mean, coefficient of variance and per cent contribution of different traits in seedling trees of pecan nut

Traits	Range	Mean	S.D.	Coefficient of variance	Per cent contribution
Nut length (mm)	28.14-53.34	37.23	0.73	13.40	27.22
Nut width (mm)	16.43-21.76	18.56	0.29	16.74	13.60
Nut height (mm)	15.51-21.98	18.36	0.38	19.58	13.41
Nut weight (g)	3.09-8.74	5.54	0.21	26.58	4.07
Shell weight (g)	1.64-4.97	2.76	0.14	19.15	2.03
Shell thickness (mm)	0.53-1.26	0.78	0.67	34.97	0.57
Kernel weight (g)	1.33-4.73	2.78	0.14	28.87	2.04
Kernel percentage (%)	40.26-63.46	50.37	2.01	16.93	37.03

Table 2. Estimation of various genetic constrains for different nut traits in pecan

Traits	Nut length	Nut width	Nut height	Nut weight	Kernel weight	Shell thickness	Shell weight	Kernel percentage
GCV	29.23	12.68	15.83	43.84	44.49	0.73	51.69	24.21
PCV	29.45	12.97	16.24	44.36	52.74	21.39	59.21	25.18
ECV	3.41	2.69	3.58	6.60	28.09	22.12	28.89	6.94
Heritability	98.70	95.51	95.00	97.68	71.16	30.03	76.21	92.41
G. Advance	22.27	4.73	5.84	24.98	2.15	0.08	2.58	24.15
G. Gain	59.86	25.48	31.78	89.26	77.31	1.88	92.95	47.94

Table 3. Genotypic and phenotypic correlation coefficient in pecan

Traits		Nut width (mm)	Nut height (mm)	Nut weight (g)	Kernel weight (g)	Shell thickness (mm)	Shell weight (g)	Kernel percentage (%)
Nut length (mm)	G	0.330	0.328	0.845	0.744	0.384	0.380	- 0.059
	P	0.223	0.222	0.769	0.696	0.340	0.365	-0.065
Nut width (mm)	G		0.691	0.545	0.229	0.616	0.682	-0.447
	P		0.611	0.480	0.181	0.579	0.656	-0.509
Nut height (mm)	G			0.608	0.313	0.605	0.711	-0.412
	P			0.529	0.288	0.577	0.661	-0.472
Nut weight (g)	G				0.842	0.457	0.881	-0.81
	P				0.810	0.433	0.839	-0.90
Kernel weight (g)	G					0.147	0.487	0.456
	P					0.123	0.429	0.431
Shell thickness (mm)	G						0.611	-0.497
	P						0.561	-0.508
Shell weight (g)	G							0.528
	P							0.496

such characters are grown by additive gene action. Low genetic gain indicates that the involvement of non-additive gene action and improvement through selection for these characters could be rather ineffective.

Correlation studies are essential in evaluating and brining the improvement for many characters and also to access the impact of selection for one trait on other related one. The extent of variation in the studied traits of pecan was mostly by the inherent genetically constitution which appeared in the phenological form while studying the traits. The genotypic and phenotypic correlation coefficients among all the characters are presented in Table 3. The magnitude of correlation coefficient revealed that the genotypic correlation was higher than those of the corresponding phenotypic correlation coefficient indicating the inherent association among the various traits. The nut weight was positively correlated with the nut length, nut width, kernel weight, shell thickness and shell weight, whereas it had negative correlation with the kernel percentage. Shelling percentage had positive correlation only with kernel weight and shell weight. Kernel weight also had positive correlation with nut length, nut weight but negative correlation with shelling percentage. The weight of nut showed a direct correlation with nut length, nut width and kernel weight, which is the important selection criterion for nut crops. The correlation coefficient exerted by kernel percentage with nut weight has low magnitude. Nut length and nut width showed very high correlation and also with other parameters studied and are in accordance with those obtained by Sharma and Sharma (2001) in walnut and Kaushal and Sharma (2003) in pecan.

From the above study on mean performance and other genetic parameters of different nut traits, it is revealed that nut character, *viz*., nut weight, kernel weight, nut length and nut width were most important traits for selection of genotypes from the wild seedling population of the pecan nut fruit. The other traits such as shell thickness and shell weight are considered as second most important characters for selection in pecan nut. Considerable importance has been attached to correlation study in the crop improvement because it plays key role in the simultaneous selection process of a group of characters for breeders, who are always concerned with the selection of superior genotypes.

The phenotypic characters do not lead to excepted genetic advance mainly due to genotypic × environmental (G×E) interaction as well as due to undesirable association between the component characters at genotypic level. The knowledge of nut weight and its attributing characters are of considerable use towards the selection of superior genotypes.

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