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Genetic diversity and character association in different seedling pecan (*Carya illinoensis*) genotypes

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ABSTRACT

The extent of variability, heritability, character association, path analysis and genetic divergence with respect to nut and kernel characters in thirty six seedling pecan genotypes were studied. The analysis of variance showed substantial amount of variability for majority of traits. The estimates of PCV were higher for all the traits investigated. High heritability estimation coupled with high genetic advance was observed for nut length and kernel oil (%) but, higher genetic gain coupled with moderate to high heritability was recorded for kernel protein and shell thickness. Further nut weight had positive and significant association with nut width, shell thickness, kernel weight, kernel width and kernel length. Based on path coefficient analysis, nut length, kernel weight, kernel percentage, kernel width, kernel length and kernel protein showed positive effects towards nut weight and kernel percentage.

Key words: Correlations, Genetic divergence, Heritability, Path analysis, Pecan

Pecan [*Carya illinoensis* (Wang) K. Koch.] is an important edible nut crop which can be grown successfully in areas having an elevation of about 914-1829 m above mean sea level and free from spring frost. Pecan is superior to walnut in quality and thrives best in the areas which are considered somewhat lower and hotter for walnut cultivation (Singh *et al*. 2009 b).

Till date in India, this nut crop could not assume commercial status for the want of suitable cultivars among the orchardists. Nevertheless, there is a huge potential of this nut crop to commercialize being hardy to climatic vagaries and having export value. The existing population comprising the trees of seedling origin exhibit tremendous variability in growth, yield and quality attributes (Singh *et al.* 2010 a), thereby providing a platform for exploitation of vast gene pool. The assessment of variability is the first step of a breeding programme and the progress depends on the extent of genetic variability present in various biometric characters of the gene pool. Since, most of the plant characters of economic importance are polygenic in nature and are highly influenced by environmental fluctuations therefore, it is difficult to judge whether the observed variability is due to environment or genetics of an individual. This suggests the imperative need of partitioning the phenotypic variation into its heritable and non-heritable components. For a successful hybridization programme with efficient utilization of the resources, knowledge of association of different characters is the most useful prerequisite. This will help to screen the progeny at an early stage. The information on nature and degree of genetic divergence present in existing plantations could help to select elite trees for direct use as clone or further improvement through use in hybridization. The present studies were therefore undertaken to estimate the genetic variability in respect of various quantitative and qualitative traits and evaluate relationship among various nut and kernel characters of the seedling trees of pecan so as to bring about improvement in yield and quality through future breeding programmes. Till date, meagre efforts have been made for selection of superior pecan nut genotypes from seedling population having heterozygous and cross-pollinating nature.

MATERIALS AND METHODS

The study material included 36 bearing (22–25 years old) pecan tree selections of seedling origin, presently growing at Research Farm of KVK, Chamba, University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh were evaluated during 2008–09. A random sample of 30 nuts from each tree selection was taken and observations on

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various nut and kernel characters were recorded as per descriptors described by L J Grauke and T E Thompson (http://aggie-horticulture.tamu.edu/carya/manual/descripoorv.html.)

Nut and kernel weight was weighed on digital balance, whereas kernel percentage was calculated as under:

$$\text{Kernel (\%)} = \frac{\text{Kernel weight}}{\text{Nut weight}} \times 100$$

Shell thickness was measured at near centre of half shell with the help of digital vernier calliper (Mitutoyo, Japan – CD – 6” CS). For estimation of kernel protein, nitrogen content was estimated by conventional Kjeldahl method in Kjeltech auto analyser from Foss Tecator, Sweden. Protein content was worked out by multiplying N content with a factor of 5.3 suggested for tree nuts (Khanizadeh *et al.* 1995). Kernel oil was determined by oil extraction apparatus, Sortec (ER 148/3, Milano, Italy). Thus the data recorded on the nut and kernel characters were statistically analyzed using standard randomized block design (RBD).

Further the mean performance of each character for individual selection was subjected to analysis of variance. The variability parameters studied were analysed using standard statistical methods and genetic divergence was computed using non-hierarchical Euclidean cluster analysis as described in Singh *et al.* 2009 a . However, the direct and indirect effects of independent traits on nut weight/tree were estimated as per Singh *et al.* 2010a,b.

RESULTS AND DISCUSSION

Variability studies

The analysis of variance exhibited significant differences for all the traits indicating the substantial amount of genetic variation present in the gene pool (Table 1). The estimates of range in variation, average mean performance, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic gain are presented in Table 2. The range in variation was observed from 3.97 to 10.03 for nut weight (g), 17.94 to 26.62 for nut width (mm), 28.84 to 50.75 for nut length (mm), 0.30 to 1.85 for shell thickness (mm), 2.32 to 5.73 for kernel weight (g), 37.54 to 73.74 for kernel percentage, 14.17 to 23.60 for kernel width (mm), 22.05 to 37.82 for kernel length (mm), 0.78 to 11.33 for kernel protein (%) and 44.28 to 74.40 for kernel oil (%). However, the overall mean values were as low as 0.30 mm for shell thickness to as high as 74.40 (%) for kernel oil. A wide range of variation has been observed for various characters by previous workers in seedling pecan trees growing in different areas Singh *et al.* 2011 a. Further, phenotypic coefficient of variation was higher than that of genotypic coefficient of variation in all the traits studied. Highest phenotypic coefficient of variation and genotypic coefficient of variation were recorded as 30.92 and 28.93 respectively in kernel protein and minimum as 8.57 and 7.72 respectively in case of nut width. Maximum heritability (broad sense) has been recorded as 93.0% in kernel oil followed by 87.6% in kernel

Table 1 Analysis of variance for nut and kernel characters in pecan nut

Source of variance	df	Mean squares									
		X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}
Replication	2	0.93	1.63	2.33	0.01	0.93	192.03	0.58	14.68	2.28	8.45
Treatment	35	5.05**	10.26**	76.11**	0.41**	1.80**	230.29**	10.49**	42.98**	11.90**	184.96**
Error	70	0.85	0.74	3.72	0.04	0.38	92.71	0.88	2.50	0.54	4.49

**Significant at 0.05

Table 2 Estimates of range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (H), genetic advance (GA) and genetic gain (GG) in seedling pecan trees

Character	Range	Mean + SE	PCV (%)	GCV (%)	Heritability (%)	Genetic advance	Genetic gain
Nut weight (g)	3.97–10.03	7.46±0.75	20.09	15.87	62.4	1.93	25.87
Nut width (mm)	17.94–26.62	23.07±0.70	8.57	7.72	81.2	3.31	14.35
Nut length (mm)	28.84–50.75	38.94±1.57	13.55	12.62	86.6	9.42	25.19
Shell thickness	0.30–1.85	1.22±0.17	33.09	28.45	73.9	0.62	50.82
Kernel weight (g)	2.32–5.73	4.14±0.50	22.29	16.65	55.7	1.06	25.60
Kernel percentage	37.54–73.74	55.45±7.86	20.23	10.38	26.3	6.08	10.96
Kernel width (mm)	14.17–23.60	18.74±0.77	10.82	9.58	78.4	3.27	17.45
Kernel length (mm)	22.05–37.82	30.28±1.29	13.21	12.13	84.4	6.95	22.95
Kernel protein (%)	0.78–11.33	6.73±0.60	30.92	28.93	87.6	3.75	55.72
Kernel oil (%)	44.28–74.40	60.87±1.73	13.21	12.74	93.0	15.41	25.31

protein, 86.6% in nut length, 84.4% in kernel length and 81.2% in nut width. The high estimates of heritability coupled with low genetic advance were observed in all the traits except kernel oil revealing the presence of non-additive gene effects. However, high heritability coupled with higher genetic gain (GG) was recorded for the character kernel protein and shell thickness. The high heritability is being exhibited due to favourable influence of environment rather than genotype and selection for traits may not be straight rewarding. These results are in consonance with the earlier studies conducted by various workers in different cultivars and seedling trees in different pecan growing areas (Singh *et al*. 2010 b).

Correlation and path analysis studies

Genotypic and phenotypic correlation coefficients among ten characters are presented in Table 3. Nut weight had significant and positive association with nut width, nut length, kernel weight, kernel width, kernel length and kernel protein. Nut width revealed positive correlation with kernel weight, kernel width and kernel protein. Nut length showed positive and significant association with kernel weight and kernel length. Likewise, kernel weight revealed positive and significant association with kernel length and kernel width. The present findings under present studies are in agreement with those of Singh *et al.* (2011b). The deviation in correlation coefficients may be due to heterogenous population having differences in genetic makeup of individual seedling trees. In path analysis, nine different nut and kernel characters were considered as casual variables and nut weight was taken as dependent variable. The direct and indirect effects of various characters were worked out and presented in Table 4. Nut length, kernel weight, kernel width, kernel length and kernel protein (%) revealed significant and positive effects towards nut weight and these positive correlations are due to higher direct and some indirect effects. The significant and positive correlation between different pairs can be helpful for genetic improvement of different characters in a single step, if the higher or lower value of each is required, while the negatively associated traits where increased or decreased value of both the characters is required cannot be improved in a single step. The characters which had non-significant correlations suggests that they are independent of each other. The present correlation findings are similar to those obtained by several workers (Singh *et al.* 2010a,b; Dashora and Sastry 2011; Kumar *et al*. 2011; Kumar *et al.* 2012) in various crop species.

Genetic divergence

On the basis of Euclidean cluster analysis, 36 pecan

Table 3 Correlation coefficients at genotypic (G) and phenotypic (P) level with respect to nut weight and its component traits in seedling pecan

Character		X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}
X_1	G	1.000									
	P	1.000									
X_2	G	0.616**	1.000								
	P	0.447	1.000								
X_3	G	0.509**	0.131	1.000							
	P	0.332	0.12	1.000							
X_4	G	0.307	0.216	-0.002	1.000						
	P	0.221	0.133	0.002	1.000						
X_5	G	0.906**	0.391*	0.497**	0.165	1.000					
	P	0.526	0.312	0.364	0.047	1.000					
X_6	G	-0.299	-0.328	-0.007	-0.261	0.218	1.000				
	P	-0.387	-0.109	0.051	-0.153	0.446	1.000				
X_7	G	0.447**	0.699**	-0.119	0.135	0.390*	-0.124	1.000			
	P	0.319	0.579	-0.1	0.125	0.247	-0.055	1.000			
X_8	G	0.550**	0.203	0.925**	-0.165	0.617**	-0.007	-0.084	1.000		
	P	0.457	0.205	0.786	-0.115	0.43	-0.043	-0.006	1.000		
X_9	G	0.388*	0.374*	0.201	0.141	0.268	0.258	0.223	0.223	1.000	
	P	0.29	0.338	0.16	0.137	0.386	0.097	0.203	0.191	1.000	
X_{10}	G	-0.007	0.309	-0.19	0.208	-0.159	-0.249	0.278	-0.236	0.236	1.000
	P	-0.004	0.258	-0.181	0.189	-0.105	-0.11	0.227	-0.199	0.22	1.000

*Significant at 5% level of significance, **Significant at 1% level of significance

X_1, Nut weight (g); X_2, nut width (mm); X_3, nut length (mm); X_4, shell thickness (mm); X_5, kernel weight (g); X_6, kernel percentage; X_7, kernel width (mm); X_8, kernel length (mm); X_9, kernel protein (%); X_{10}, kernel oil (%)

Table 4 Direct (in diagonal) and indirect effects (others) of various nut and kernel characters on nut weight in seedling pecan

Character	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	Correlation coefficient
X_1	**0.855**	0.303	-0.199	1.092	0.255	-0.808	–0.716	–0.251	0.085	0.616**
X_2	0.112	**2.318**	0.002	1.389	0.006	0.138	–3.268	–0.135	–0.052	0.509**
X_3	0.184	–0.004	**–0.924**	0.462	0.202	–0.157	0.581	–0.095	0.057	0.307
X_4	0.334	1.152	–0.153	**2.794**	–0.169	–0.450	–2.178	–0.382	–0.043	0.906**
X_5	–0.280	–0.017	0.241	0.608	**–0.777**	0.143	0.026	–0.174	–0.068	–0.299
X_6	0.597	–0.277	–0.125	1.089	0.096	**–0.156**	0.295	–0.150	0.076	0.447**
X_7	0.173	2.145	0.152	1.723	0.006	0.097	**–3.531**	–0.150	–0.064	0.550**
X_8	0.319	0.466	–0.130	1.586	–0.201	–0.257	–0.788	**–0.672**	0.065	0.388*
X_9	0.264	–0.441	–0.192	–0.444	0.194	–0.321	0.832	–0.159	**0.274**	0.007

Residual effect = –0.468

X_1, Nut width (mm); X_2, nut length (mm); X_3, shell thickness (mm); X_4, kernel weight (g); X_5, kernel percentage; X_6, kernel width (mm); X_7, kernel length (mm); X_8, kernel protein (%); X_9, kernel oil (%)

seedling trees were grouped in five different clusters on the basis of their genetic distinctness (Table 5). Maximum number of genotypes, i e nine were accommodated in cluster I and minimum as six in cluster IV.

Data given in Table 6 reveals inter-cluster distance of 4.656 between cluster I and IV followed by 4.493 between cluster III and IV, 4.286 between cluster II and III, 3.446 between cluster I and II, 3.400 between cluster II and, 3.125 between cluster III and V, 3.022 in cluster IV and V, 2.805 in cluster II and V and 2.706 in cluster II, 0.706 in cluster I and III. Maximum intra-cluster distance of 2.240 was observed among the genotypes of cluster, III followed by 2.196 in cluster II, 2.171 in cluster I, 2.016 in cluster IV and 1.987 in cluster V. Relatively lower value of intra-cluster distance indicates lower genetic variation between the members of a cluster. Parents for hybridization can be selected from the clusters I, III and IV for isolation of useful recombinants in the segregating generations. These genotypes can also be utilized for transfer of their useful traits in the commercial pecan cultivars. Similar segregation into different clusters have also been reported earlier by using non-hierarchical Euclidean cluster analysis in the seedling pecan (Singh *et al.* 2010b) and wild raspberry population (Singh *et al.* 2009a) and suggested their use in further breeding.

Table 5 Distribution of different genotypes in different clusters

Cluster no.	Genotypes
I	Tree no. 20, Tree no. 34, Tree no. 22, Tree no. 54, Tree no.62, Tree no. 4, Tree no. 53, Tree no. 59, Tree no. 58
II	Tree no. 48, Tree no. 61, Tree no.2, Tree no. 21, Tree no. 15, SP 2, SP 3
III	Tree no.63, Tree no. 14, Tree no. 49, Tree no. 37, Tree no. 6, Tree no. 44, Tree no. 15
IV	Tree no. 42, Tree no.43, Tree no. 40, Tree no. 39, Tree no. 36, Tree no 41
V	Tree no.9, Tree no. 10, Tree no. 13, Tree no. 3, Tree no. 1, Tree no. 47, SP 1

Table 6 Inter and intra-cluster (bold figures) distances between different clusters in different pecan genotypes

Clusters	1	2	3	4	5
I	**2.171**				
II	3.446	**2.196**			
III	2.706	4.286	**2.240**		
IV	4.656	3.400	4.493	**2.016**	
V	2.420	2.805	3.125	3.022	**1.987**

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