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Heritability estimates and correlation studies in homogamous walnut (*Juglans regia* L.) accessions from South Kashmir

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ABSTRACT

Thirty two homogamous walnut trees were pre-selected from a total of four hundred and eighty two trees in district Pulwama of South Kashmir and were used to study the genetic variability, heritability, genetic advance and correlation among flowering and yield contributing characters. High genotypic coefficient variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for nut yield (23.43 and 24.75), trunk girth (23.77 and 24.66), TCSA (42.83 and 44.68), yield efficiency (34.12 and 36.80), number of days synchronized (17.98 and 21.15), degree of dichogamy (35.61 and 35.63) and number of catkins per bud (21.25 and 21.62). High heritability coupled with high genetic gain was found for the character TCSA (91.88 % and 84.58 %), yield efficiency (85.97 % and 65.16 %) and degree of dichogamy (99.89 % and 73.31 %), whereas, high heritability coupled with moderate genetic gain was obtained for the characters viz., trunk girth (92.96 % and 47.21 %), nut weight (97.74 % and 24.30 %), kernel weight (97.57 % and 26.54 %) and number of catkins per bud (96.58 % and 43.02 %). Highly significant and positive genotypic correlations of nut yield were found with nut weight (0.894), nut length (0.896), nut width (0.817) and kernel weight (0.362). The study concluded that the parameters viz., TCSA, trunk girth, nut weight, kernel weight and number of days synchronized could serve as selection indices for higher yield with good nut and kernel quality cultivars in walnut.

***Keywords*:** walnut, homogamous, correlation, heritability, accessions

INTRODUCTION

Walnut (*Juglans regia* L.) is one of the most important nut crops of temperate regions of the world belonging to family Juglandaceae and is considered native to Persia and North Western Himalayas which further extends to Jammu and Kashmir, Himachal Pradesh and Uttaranchal. The possible health benefits of walnuts may include boosting the cardiovascular system and bone health, reducing the risk of gallbladder disease, and treating epilepsy. In traditional folk medicine, young, green fruits were used as a health supplement. A decoction of nuts was imbibed to treat high arterial pressure, cardiac diseases, and to rinse the mouth to treat gum disease. Juice from the fruit husk was applied as an ointment to treat mild skin conditions, such as eczema. A tea made from the leaves has been used to treat diabetes (Burmistrov, 1996). The major walnut-producing countries are USA, China, France, Turkey and Italy. In India, it is cultivated at an altitude of 1,200–2,200 m above the sea-level. However, in India there are no systematic orchards of walnut and trees of mainly seedling origin are grown which exhibit wide variation for tree, foliage and floral characters (Sharma *et al.*, 2010). Being heterozygous and cross-pollinated crop, the seedling origin populations of walnut exhibit extreme variations. Importance of walnut in terms of enormous export potential and with a scope of diversification with suitable high value crop in an otherwise apple dominating region, walnut becomes a viable alternative for commercial cultivation in hilly states. Presently the major walnut production comes from seedling tree population grown under natural forests and farmers backyards without any cultural operation. *Juglans regia* is heterodichogamous species *i.e.* having dichogamous and homogamous genotypes. Dichogamous includes protandrous and protogynous genotypes forcing outcrossing (Sutyemez, 2006). In natural populations, protandry is more pronounced than protogyny (Germain *et al*., 1981). On the other hand, homogamy i.e. overlapping pollen shedding period and stigma receptivity periods results in good pollination and consequent higher yield, however homogamy in walnut is quite rare (Sharma and Sharma, 2000, Sutyemez, 2001) as compared to protandry and protogyny. Since genetic variability is the basis of all plant improvement programmes and sufficient genetic variability if present can be exploited for developing superior cultivars. Knowledge of heritability for different traits is essential for any crop improvement programme because the heritable component is the part of total variance which is inherited from one generation to the other. Correlation coefficient is a measure of the degree of association between the two traits worked out at the same time (Hayes *et al*., 1955). Therefore the study was conducted on seedling origin walnut trees to estimate the genetic variability in respect of various parameters and to understand inherent relationship in highlighting the walnut accessions with high degree of homogamy to achieve optimum fruit set and yield with desirable nut and kernel characters.

MATERIALS AND METHODS

In a preliminary survey four hundred and eighty two walnut trees were marked in fourteen villages of district Pulwama of South Kashmir. All the marked trees are of seedling origin ranging an age of between (20 to 60 years). The trees were marked on the basis of health, plant vigour, regular bearing and desirable nut and kernel characters and observations were taken. The weather and geographical features of the studied location are represented in the Fig. 1. Observations on flowering characters were recorded as per IPGRI walnut descriptors (IPGRI, 1994). To determine the nature and extent of dichogamy, observations were recorded at the time of maturation of male catkins and female flower by selecting four branches on each tree. Degree of dichogamy was calculated as per methods of Solar *et al*. (1997) and expressed in per cent.

$$\text{Degree of dichogamy} = 1 - \frac{\text{Number of days when male \& female flowering coincides}}{\text{Number of days of female flowering}} \times 100$$

Latitude	33°N
Longitude	74°E
Altitude	1500-1600 m
Annual rainfall	500-850 mm
Mean temperature (from bud burst to fruit harvest)	
Maximum	15.9 – 31.6°C
Minimum	04.3 – 16.5°C

Fig. 1: Weather and geographical features of the area surveyed

The selected trees showing less than 25 per cent degree of dichogamy (Kumar, 2000; Kumar *et al*., 2005) were categorized as homogamous. The homogamous selections were further evaluated for their nut, kernel and yield characteristics for two consecutive years. Nut yield (kg/tree) was calculated on the basis of total weight of all the nuts harvested after dehulling and drying. Yield efficiency (kg/cm^2) and trunk cross sectional area was calculated as per the method suggested by Westwood (1993). Trunk cross sectional area (TCSA) = ðr^2 where 'r' is the radius of the tree trunk. For recording observations on nut and kernel characters, 20 randomly selected nuts from each selected tree were taken. Nut weight and kernel weight were recorded on digital balance whereas

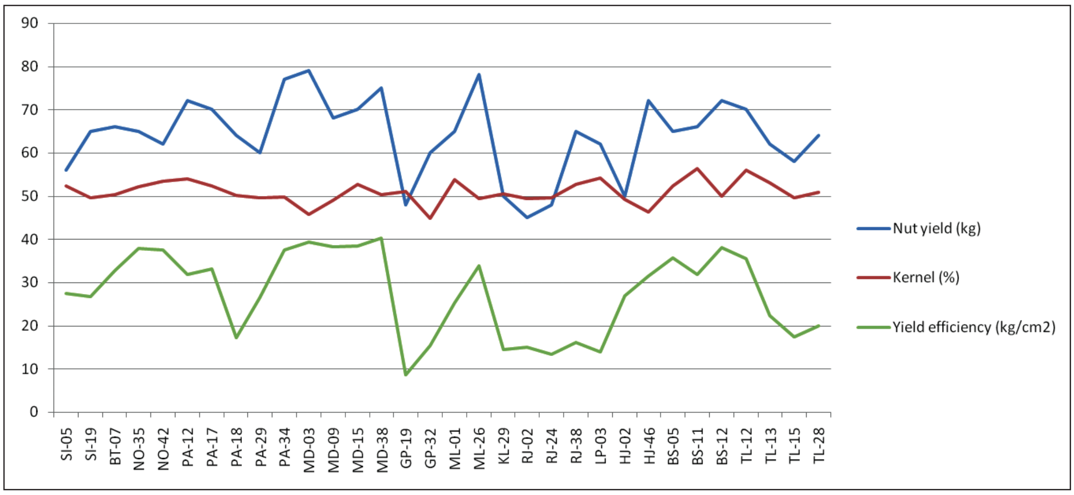

Fig. 2: Nut yield, kernel per cent and yield efficiency of different homogamous walnut accessions from South Kashmir

kernel percentage was determined by dividing kernel weight with nut weight and multiplying with 100. Shell thickness was measured at near centre of half shell with the help of digital vernier calliper. The genotypic and phenotypic coefficients of variation and heritability (in broad sense) were calculated as per Singh and Chaudhary (1979) while genetic advances were estimated as per the procedure of Johnson *et al.* (1955). Data collected on various parameters were statistically analyzed as per the procedure given by Snedecor and Cochran (1994).

RESULTS AND DISCUSSION

Variability studies

The extent of variability was measured in terms of range, mean, co-efficient of variation, PCV, GCV, heritability, genetic advance and genetic gain (Table 1). Wide range of variation was observed in all the studied characters among different homogamous accessions of walnut. Nut yield and nut weight varied from 45.00 (RJ-02) to 79.00 (MD-03) and 10.23 (TL-12) to 17.73 (ML-01) with a mean value of 64.03 and 13.83, respectively. The coefficient of variation for nut yield and nut weight was 6.12 and 1.82, respectively. Maximum and minimum values for trunk girth and TCSA were recorded in accession GP-19 (72.00 cm and 420.38 cm^2) and MD-03 (198.00 cm and 3124.73 cm^2) with a mean value of 147.09 and 1825.29, respectively. Trunk girth and TCSA recorded 6.54 per cent and 12.73 per cent values for coefficient of variations. Accessions TL-12 (29.26 mm) and LP-03 (26.12 mm) recorded minimum nut length and nut width, respectively whereas maximum nut length and nut width was recorded in accessions ML-01 (40.88 mm) and KL-29 (36.84 mm), respectively. Average mean values and coefficient of variation for nut length (34.40 mm and 0.48 %) and nut width (30.69 mm and 0.47 %), respectively. Yield efficiency varied from 8.64 kg/cm^2 (GP-19) to 40.37 kg/cm^2 (MD-38) with a mean value 27.58 kg/cm^2 and coefficient of variation 13.78 per cent (Table 1 and Fig 2). High coefficient of variation obtained in case of yield efficiency may be due to variation in the age of vine and other yield attributes such as trunk girth. Similar types of variations for various vegetative, yield and nut characters have been reported by Mehta *et al.* (2005), Sharma *et al.* (2010), Sharma *et al.* (2014a) and Sharma *et al.* (2014b).

Kernel characters recorded wide variation among all the accessions. Minimum kernel weight (5.20 g) and kernel percentage (44.83 %) was recorded in GP-32 accessions whereas maximum kernel weight was obtained in ML-01 (9.55 g) and maximum kernel percentage in BS-11 (56.35 %). Average mean value and coefficient of variation for kernel weight was 7.03 g and 2.05 per cent and for kernel percentage, mean and coefficient of variation was 50.95 g and 0.35 per cent (Table 1 and Fig 2). Accession SI-05 (0.87 mm) measured minimum shell thickness whereas maximum shell thickness was measured in accession TL-12 (1.34 mm). Average mean value and coefficient of variation for shell thickness was 1.12 mm and 7.12 per cent, respectively. The results pertaining to kernel characters studied presently are in accordance with the findings of Sharma *et al.* (2010) and Sharma *et al.* (2014b).

Minimum duration of male flowering (8.0 days), duration of female flowering (7.0 days) and number of days synchronized (6.0 days) was observed in accession MD-09 whereas maximum duration of male flowering (15.0 days) was observed in accessions SI-05, PA-34, MD-38, KL-29 and TL-12. Maximum duration of female flowering (16.0 days) and number of days synchronized (13.0 days) was recorded in accession KL-29. Average mean value for duration of male flowering, duration of female flowering and number of days synchronized was 12.11 days, 11.44 days and 9.50 days, respectively with coefficient of variation as 10.63 per cent, 10.98 per cent and 11.14 per cent. Earlier Kumar (2000) also reported similar results with respect to duration and synchronization of male and female flowers. In the previous studies, Kumar and Sharma (2013) and Kumar (2016) also reported less than 25 per cent dichogamy in seedling origin walnut plants. Degree of dichogamy varied from 0.00 per cent in HJ-46 to 25.00 in BT-07, NO-42, PA-29, RJ-02, BS-12 and TL-12 with a mean value of 17.50 per cent and coefficient of variation as 1.19 per cent. Accession GP-32 (3.20) obtained minimum number of catkin per bud whereas accession RJ-02 (7.50) observed maximum number of catkin per bud. Average mean value and coefficient of variation for number of catkin per bud was 5.48 and 4.00 per cent. Catkin length ranged between 7.00 cm (MD-03) and 11.75 cm (BS-11) with a mean value 8.83 cm and coefficient of variation was 2.01 per cent. In the previous studies, Kumar *et al.* (2005), Kumar and Sharma (2013) and Kumar (2016) also reported less than 25 per cent dichogamy.

A perusal of the data presented in Table 1 revealed that the magnitude of the phenotypic coefficients of variation (PCV) values were higher than genotypic coefficients of variation (GCV) values for all the characters. The estimates of PCV and GCV were high for nut yield (23.43 and 24.75), trunk girth (23.77 and 24.66), TCSA (42.83 and 44.68), yield efficiency (34.12 and 36.80), number of days synchronized (17.98 and 21.15), degree of dichogamy (35.61 and 35.63) and number of catkins/bud (21.25 and 21.62) indicated the presence of adequate genetic variation among the accessions and suitability of these attributes for further improvement by selection. Lower values of GCV than PCV indicated close association between phenotype and genotype. Present results are in agreement with those reported by Singh *et al.* (2009), Dogra *et al.* (2018) in walnut and Gond *et al.* (2019) in Water chestnut.

Heritability is a parameter of tremendous significance to the breeders as its magnitude indicates the reliability with which a genotype can be recognized through its phenotypic expression (Table 1). Johnson *et al.* (1955) stressed that for estimating the real effect of selection, heritability estimates along with genetic advance are more meaningful. Heritability in broad sense was observed to be high in nut weight (97.7 %), nut length (99.7 %), nut width (99.6 %), kernel weight (97.6 %), kernel percentage (99.5 %), degree of dichogamy (99.9 %), number of catkins/bud (96.6 %) and catkins length (98.4 %). High heritability estimates for nut yield, nut weight, kernel weight were observed by Dogra *et al*. (2018). Heritability estimates alone are not an ideal parameter for predicting the effect of selecting the desired individual. Heritability estimates along with genetic advance are more useful than heritability values alone in predicting the selection of best individuals.In the present study, trunk girth, TCSA, yield efficiency, nut weight, kernel weight, number of days synchronized, degree of dichogamy, number of catkins/bud catkin length exhibited high genetic advance as percentage of mean along with high heritability. These results indicated the influence of additive gene action. In general, the characters which showed high heritability with high genetic advance as per cent of mean are genetically controlled by additive gene (Panse, 1957) and can be improved through mass selection, progeny selection or any other modified selection procedures.

Table 1. Genetic variability components for major characters in homogamous walnut accessions

Characters	Range	Mean	CoV	Coefficient of variance (%)		Heritability (%)	Genetic advance	Genetic gain (%)
				GCV	PCV			
Nut yield (kg/tree)	45.00 – 79.00	64.03	6.12	23.43	24.75	82.8	16.12	25.17
Trunk girth (cm)	72.00 – 198.00	147.09	6.54	23.77	24.66	93.0	69.45	47.21
TCSA (cm^2)	420.38 – 3124.73	1825.29	12.73	42.83	44.68	91.9	1543.77	84.58
Yield efficiency (kg/cm^2)	8.64 – 40.37	27.58	13.78	34.12	36.80	86.0	17.98	65.16
Nut weight (g)	10.23 – 17.73	13.83	1.82	11.93	12.07	97.7	3.36	24.30
Nut length (mm)	29.26 – 40.88	34.40	0.48	8.66	8.67	99.7	6.13	17.80
Nut width (mm)	26.12 – 36.84	30.69	0.47	7.91	7.92	99.6	4.99	16.26
Kernel weight (g)	5.20 – 9.55	7.03	2.05	13.04	13.20	97.6	1.87	26.54
Shell thickness (mm)	0.87 – 1.34	1.12	7.12	11.73	13.72	73.1	0.23	20.65
Kernel (%)	44.83 – 56.35	50.95	0.35	5.16	5.17	99.5	5.40	10.61
Duration of male flowering	8.00 – 15.00	12.11	10.63	13.83	17.44	62.9	2.74	22.59
Duration of female flowering	7.00 – 16.00	11.44	10.98	15.83	19.26	67.5	3.06	26.79
Number of days synchronized	6.00 – 13.00	9.50	11.14	17.98	21.15	72.3	2.99	31.48
Degree of dichogamy	0.00 – 25.00	17.50	1.19	35.61	35.63	99.9	12.83	73.31
Number of catkins/bud	3.20 – 7.50	5.48	4.00	21.25	21.62	96.6	2.36	43.02
Catkin length (cm)	7.00 – 11.75	8.83	2.01	15.77	15.90	98.4	2.85	32.23

Table 2 : Genotypic and phenotypic correlation coefficient of different characters in homogamous walnut accessions

Characters		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	(G)	1.000	0.223*	0.204*	-0.173	0.894**	0.896**	0.817**	0.362**	0.185	0.005	-0.046	-0.226*	-0.101	-0.167	-0.170	-0.108
	(P)	-	0.198	0.187	-0.164	0.805**	0.793**	0.641**	0.330**	0.144	0.007	-0.064	-0.185	-0.090	-0.152	-0.152	-0.085
2	(G)		1.000	0.995**	0.988**	-0.134	-0.053	-0.179	-0.082	0.099	0.067	-0.122	-0.396**	-0.313**	-0.013	-0.168	-0.160
	(P)		-	0.992**	0.969**	-0.127	-0.049	-0.166	-0.081	0.072	0.064	-0.080	-0.320**	-0.255*	-0.016	-0.153	-0.152
3	(G)			1.000	-0.982**	-0.117	-0.044	-0.164	-0.081	0.107	0.039	-0.109	-0.385**	-0.304**	-0.010	-0.164	-0.170
	(P)			-	0.969**	-0.113	-0.039	-0.151	-0.076	0.077	0.037	-0.068	-0.299**	-0.238*	-0.013	-0.149	-0.162
4	(G)				1.000	-0.085	0.019	-0.102	-0.034	0.075	0.091	-0.161	-0.449**	-0.382**	0.047	-0.158	-0.163
	(P)				-	-0.079	0.021	-0.086	-0.032	0.037	0.083	-0.083	-0.336**	-0.297**	0.039	-0.136	-0.156
5	(G)					1.000	-0.938**	0.790**	0.932**	0.203*	-0.015	-0.193	-0.055	-0.173	0.138	0.127	-0.192
	(P)					-	0.924**	0.781**	0.913**	0.179	-0.016	-0.139	-0.059	-0.156	0.136	0.129	-0.190
6	(G)						1.000	0.778**	0.894**	0.200	0.049	-0.232*	-0.184	-0.259*	0.115	0.133	-0.089
	(P)						-	0.774**	0.881**	0.174	0.047	-0.192	-0.143	-0.223	0.115	0.131	-0.086
7	(G)							1.000	0.703**	0.129	-0.076	0.020	0.048	-0.039	0.067	0.155	0.005
	(P)							-	0.692**	0.113	-0.075	0.031	0.038	-0.034	0.067	0.152	0.004
8	(G)								1.000	0.283**	0.353**	-0.205*	-0.168	-0.288**	0.223*	0.216*	0.005
	(P)								-	0.257*	0.350**	-0.162	-0.132	-0.230*	0.222*	0.211*	0.000
9	(G)									1.000	0.186	-0.094	-0.283**	-0.394**	0.478**	0.221*	-0.097
	(P)									-	0.157	-0.133	-0.137	-0.237*	0.414**	0.156	-0.067
10	(G)										1.000	-0.028	-0.285**	-0.297**	0.239*	0.244*	0.481**
	(P)										-	-0.027	-0.232*	-0.242*	0.238*	0.242*	0.477**
11	(G)											1.000	0.688**	0.692**	-0.244*	-0.269**	0.129
	(P)											-	0.290**	0.401**	0.197	-0.212*	0.069
12	(G)												1.000	1.064**	-0.152	-0.439**	-0.088
	(P)												-	0.721**	0.129	-0.378**	-0.061
13	(G)													1.000	-0.517**	-0.362**	0.022
	(P)													-	-0.434**	-0.304**	0.033
14	(G)														1.000	-0.027	-0.252*
	(P)														-	-0.027	-0.250*
15	(G)															1.000	0.213*
	(P)															-	0.206*
16	(G)																1.000
	(P)																-

G: genotypic, P: phenotypic, **Significant at 1%, *Significant at 5%

1 Nut yield (kg/tree) 5 Nut weight (g) 9Shell thickness (mm)13Number of days synchronized
2 Trunk girth (cm) 6 Nut length (mm) 10 Kernel (%) 14Degree of dichogamy
3 TCSA (cm^2) 7 Nut width (mm) 11Duration of male flowering 15Number of catkins/bud
4 Yield efficiency (kg/cm^2) 8 Kernel weight (g) 12Duration of female flowering 16Catkin length (cm)

Correlation studies

Genotypic and phenotypic correlation of sixteen yield and yield attributing characters showed that most of the correlation coefficients at genotypic level were greater than on the corresponding phenotypic level (Table 2). This suggested the predominance of genotypic effects over environmental factors. The variation in correlation coefficient may be due to heterogeneous population having differences in genetic makeup of individual trees. Nut yield was positively and highly significantly correlated with trunk girth (0.223), TCSA (0.204), nut weight (0.894), nut length (0.896), nut width (0.817) and kernel weight (0.362) however negative but significant correlation was observed between nut yield and duration of female flowering (- 0.226). At genotypic level trunk girth showed positive and highly significant correlation with TCSA (0.995) and yield efficiency (0.988) whereas negative and significant correlation was revealed with duration of female flowering (0.396) and number of days synchronized (0.313). Positive and highly significant correlation was observed among TCSA and yield efficiency, however TCSA showed negative but highly significant correlation with duration of female flowering (0.385) and number of days synchronized (0.304). Yield efficiency also had negative but highly significant correlation for duration of female flowering (0.449) and number of days synchronized (0.382). Sharma and Sharma (2001) and Bayazit (2012) also observed positive correlation between nut yield and trunk girth, TCSA and yield efficiency.

Nut weight had positive and highly significant correlation with nut length (0.938), nut width (0.790), kernel weight (0.932) and shell thickness (0.203) at genotypic level. Nut length showed positive and significant correlation with nut width (-0.778), kernel weight (0.894) but negatively correlation with duration of male flowering (-0.232) and number of days synchronized (-0.259). Nut width also showed positive and significant correlation with kernel weight (0.703). Kernel weight showed positive and significant correlation with shell thickness (0.283), kernel percentage (0.353), degree of dichogamy (0.223) and number of catkins per bud (0.216) whereas negative but significantly correlation with duration of male flowering (-0.205) and number of days synchronized (-0.288). Shell thickness had positive and significant correlation with degree of dichogamy (0.478) and number of catkins per bud (0.221) however negative and highly significantly correlation was observed with duration of female duration (-0.283) and number of days synchronized (-0.394). Kernel percentage was positively and significantly correlated with degree of dichogamy (0.239), number of catkins per bud (0.244) and catkin length (0.481) whereas negatively but significantly correlated with duration of female flowering (-0.285) and number of days synchronized (-0.297). Sharma and Sharma (2001), Eskandari *et al.* (2006) and Dogra *et al.* (2018) also observed positive and significant correlation between nut weight and nut length, nut width and kernel weight.

Duration of male flowering had positive and significant correlation with duration of female flowering (0.688) and number of days synchronized (0.692) whereas negative but significant correlations with degree of dichogamy (-0.244) and number of catkins per bud (-0.269). Duration of female flowering was positively and significantly correlated with number of days synchronized (1.064) however negatively and significantly correlated with number of catkins per bud (-0.439). Number of days synchronized was negatively correlated with degree of dichogamy (-0.517) and number of catkins per bud (-0.362) whereas degree of dichogamy was negatively correlated with number of catkins per bud (-0.252). Number of catkins per bud showed positively and significant correlation with catkin length (0.213).

CONCLUSION

The present study indicated sufficient genetic variability among genotypes for all the traits studied.The parameters viz. trunk girth, TCSA, yield efficiency, degree of dichogamy and number of catkins per bud showed high heritability along with high to moderate genetic gain, thereby, indicating the additive gene action for these traits and hence simple selection procedure based on phenotypic expression of these traits would be more reliable. Beside this, these traits had shown significant and positive genotypic correlation with nut yield which revealed the inherent relationship among them.

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