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GENETIC DIVERGENCE AND CORRELATION AMONG DIFFERENT YIELD ATTRIBUTING CHARACTERS IN LENTIL (*LENS CULINARIS* MEDIK)

NANCY LEGO[1]*, RAJIB NATH[2] AND D. K. DE[1]
[1]Department of Genetics and Plant Breeding, BCKV, Mohanpur - 741 252, West Bengal, INDIA
[2]Department of Agronomy, BCKV, Mohanpur - 741 252, West Bengal, INDIA
e-mail: legonancy183@gmail.com

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***Corresponding author**

ABSTRACT

Experiments carried out to assess correlation, path coefficient and genetic diversity in 24 genotypes of lentil (*Lens culinaris* Medik) grown in three rowed plots following RBD replicated thrice revealed significant difference among them for all the parameters studied. Plant height, Pods per plant, days to 50% flowering, days to maturity and harvest index showed high heritability coupled with high genetic advance indicating the influence of additive gene action. Seed yield per plant showed highly significant and positive correlation with weight of pods per plant (0.992), number of pods per plant (0.915), primary branches per plant (0.573) and harvest index (0.557). The former two characters had also desirable path value of (0.8466) and (0.0843) respectively and therefore, appeared to be advantageous components for direct selection. D^2 analysis grouped the genotypes into five clusters comprising 16, 5, 1, 1 and 1 accession respectively. The highest genetic diversity was observed between cluster I and V (1396.68) followed by II and V (1219.62). The genotype KLB-134 belonging to cluster V had the highest mean for yield. Hence, accessions belonging to cluster I and V, II and V have been suggested to be used as parents for hybridization programme for the development of high yielding lentil genotypes.

INTRODUCTION

Lentil, (*Lens culinaris* Medik) is cultivated worldwide, with the total area of around 4.6 mha producing 4.2 mt of seeds with an average production of 1095 kg/ha (FAO, 2010). In India, pulses are very important source of protein in the diets as majority of population is vegetarian and it is grown as rainfed crop during rabi season. India ranks second after Canada in the world in respect of production as well as acreage followed by Australia. It is mostly grown in Madhya Pradesh, Uttar Pradesh, Bihar and West Bengal covering about 1.46 mha with total production of 1.08 mt of grain. Thus the present productivity of lentil in India is much less than the potential productivity. By 2030, the world lentil consumption is estimated to be 5.5 mt, indicating an increment in demand of about 2 mt from the present production (Clancey, 2009).

Therefore, much concerted efforts are necessary to improve its yield. For such purpose, collection and evaluation of potentialities of the existing cultivars, genotypes from different geographical origin is essential because it depicts the genetic diversity of the base materials on which the promise for further improvement depends. The success of a breeding programme for the improvement of quantitative attributes depends to a great extent on the magnitude of genetic variability existing in the germplasm. High yield can be achieved by selection of those characters that have high heritability values coupled with high genetic advance. Panse (1957) concluded that a character with high heritability in association with high genetic advance (in % grand mean) is an indication of expression of additive gene action. Yield is a quantitative character dependant on different other characters. Therefore, adequate knowledge about the magnitude and degree of association of yield with its attributing characters is of great significance to the plant breeder particularly when simultaneous improvement of more than one character is considered. Sharma *et al.* (2014) reported significantly positive correlation of yield per plant with number of pods per plant, harvest index, number of branches per plant. Therefore, the present experiment was carried out to have a clear picture about the inheritance pattern of different characters, their inter-relationship, belongingness to different groups to facilitate effective breeding programme.

MATERIALS AND METHODS

Twenty four genotypes of lentil obtained from ICARDA and AICRP on MuLLARP, BCKV, Kalyani, India were evaluated in a Randomised Block Design with three replications during *rabi* season of two consecutive years 2012-13 and 2013-14 at seed farm, AB-block, Kalyani (23.5^0 N, 89.0^{0}E) BCKV. The soil type of the experimental plot was alluvial, sandy loam in texture with good water holding capacity and medium fertility level; pH 6.9. Each genotype was sown in three rows of three metre length with spacing of 25 cm between rows and 10 cm between plants. N:P:K @ 20:40:40 kg per ha was applied. All recommended cultural practices and plant protection measures were followed to raise a healthy crop. Data for ten agronomic characters, viz., plant height (cm), primary branches per plant, number of pods per plant, weight of pods per plant (g), weight of shoots per plant (g), days to 50% flowering, 100 seed weight (g), days to maturity, harvest index and seed yield per plant (g) from five randomly selected competitive plants were collected from middle row of each genotype in both the years and were pooled analysed following Windostat 9.1 software. Phenotypic and genotypic coefficient of variations; heritability (bs) and genetic advance were estimated according to Burton (1952) and Burton and Devane (1953) respectively. The estimates of indirect and direct contribution of various characters to seed yield were calculated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). The quantitative diversity of genotypes was grouped into different clusters following Toucher's method (Rao, 1952).

RESULTS AND DISCUSSION

Analysis of variance revealing significant values among the genotypes for all the characters under study indicated scope for selection. The variability and values for other genetic parameters (Table 1) shows the magnitude of PCV to be higher than the corresponding GCV values for all the characters indicating importance of environment. However, the values were in close proximity with each other as reported earlier by Rathi *et al.* (2002), which indicate genetic control in their expression except in case of primary branches per plant. Very high heritability as has earlier been reported by Bicer and Sakar (2008), Younis *et al.* (2008), Ghulam *et al.* (2010) and Singh *et al.* (2012) was observed for all the characters studied.

Genetic advance as percentage of mean was highest for number of pods per plant followed by seed yield per plant.

Table 1: Variability and genetic parameters for different character of lentil

Sl. no	Characters	Mean	Range	Variance		GCV	PCV	h^2 (broad sense)	GA (genetic advance)	GA as % of mean
				GV	PV					
1	Plant height (cm)	58.684	27.79-76.2967	133.01	134.35	19.653	19.752	0.990	23.639	40.28
2	Primary branches per plant	5.754	3.150-10.5708	1.521	1.813	21.435	23.398	0.839	2.328	40.45
3	Number of Pods per plant	94.604	22.27-504.22	10173.0	10394.56	106.614	107.769	0.979	205.548	217.272
4	Weight of pods per plant (g)	4.517	0.8783-15.858	13.488	13.542	81.311	81.474	0.996	7.550	167.166
5	Weight of shoots per plant (g)	9.120	1.4277-20.379	22.491	22.627	52.000	52.158	0.994	9.740	106.796
6	Days to 50% flowering	76.139	47.833-98.333	256.810	260.235	21.047	21.187	0.987	32.794	43.072
7	100 seed weight(g)	4.077	3.0805-7.107	1.172	1.233	26.556	27.234	0.951	2.175	53.341
8	Days to maturity	146.43	101.83-169.00	460.723	463.197	14.658	14.698	0.995	44.099	30.116
9	Harvest index (%)	28.933	5.9200-54.22	327.848	332.983	62.581	63.070	0.985	37.011	127.92
10	Seed yield per plant (g)	3.813	0.6675-15.213	11.932	11.990	90.598	90.817	0.995	7.099	186.185

Table 2: Mean performance for 10 different morphological characters in 24 genotypes of lentil germplasm

Genotype	Plant Height (cm)	Primary Branches per plant	Number of Pods per Plant	Weight of Pods per plant (g)	Weight of Shoot per plant (g)	Days to 50% Flowering	100 Seed Weight(g)	Days to Maturity	Harvest Index (%)	Seed yield per Plant(g)
ILL 10893	76.2967	5.8167	63.6833	5.1915	7.3720	68.5000	7.1070	133.3333	30.3883	3.8168
ILL 10971	50.4467	5.9667	86.0000	3.8193	2.7537	68.6667	3.0805	135.3333	41.7417	2.7398
ILL 10803	52.8850	4.4167	65.0167	2.4845	5.6217	79.1667	3.7667	147.5000	25.4633	2.0638
ILL 10257	67.4867	5.5833	23.3167	1.0430	11.1855	98.3333	4.5175	169.0000	6.2917	0.7657
ILL 10220	59.1833	5.3833	23.7500	1.4758	12.4408	75.3333	3.6997	147.6667	8.6483	1.2042
ILL 237	58.5683	5.1667	119.1100	6.2590	9.4918	94.8333	3.5455	162.3333	34.7350	5.4697
ILL 10921	27.7900	3.1500	34.6000	1.8512	0.4277	53.1667	3.2217	118.0000	61.2233	1.3965
ILL 10231	57.7067	4.9500	128.0000	4.0785	20.3792	83.8333	3.2717	156.1667	11.8617	2.9028
ILL 10103	53.6450	5.4167	86.6667	4.4598	13.1925	86.1667	4.6367	158.5000	21.6750	3.8250
ILL 10047	70.6800	5.0000	25.3333	1.2542	13.1117	75.6667	3.4070	146.8333	5.9200	0.8513
ILL 10236	59.0667	6.6167	75.7317	4.3670	13.8397	78.5000	3.5958	156.6667	21.4700	3.9068
ILL 10258	62.7333	5.8500	27.1833	0.8783	8.2320	98.1667	3.5430	168.5000	7.3150	0.6675
ILL 6821	68.5917	5.7667	22.2750	1.1102	9.4727	87.6667	3.7900	159.5000	8.2950	0.8783
ILL 10897	47.7500	6.4917	35.0267	3.3193	1.2542	59.8333	6.2042	126.8333	60.6317	2.7605
ILL 10273	66.1900	6.2167	30.9000	1.3958	13.9007	92.1667	3.7562	167.8333	6.5483	1.0018
ILL 8108	68.8700	5.7667	109.1167	7.4965	9.4902	95.1667	6.4223	167.6667	37.0850	6.3008
X2009S170	68.9183	5.9167	72.2500	4.3198	8.1845	74.0000	4.1127	146.5000	29.5767	3.6957
X2009S96	68.0783	5.6167	42.0417	2.4578	8.1207	82.0000	3.6655	166.5000	16.9967	1.7915
X2009S218	64.8883	5.2500	226.9833	12.5167	11.4288	85.6667	3.5578	166.0000	45.8367	10.9692
X2009S219	68.2717	6.1000	138.2367	3.3890	7.4460	85.8333	3.2283	167.3333	23.9117	2.5908
LL 204	34.2467	5.2645	66.0217	4.3457	5.5232	48.8333	3.7223	102.3333	35.5600	3.5093
KLB-134	53.3467	10.5708	504.2267	15.8583	15.9733	47.8333	3.3428	101.8333	47.7983	15.2135
SKUA L-9	51.0492	5.5750	116.4017	6.5265	5.2488	55.8333	5.1860	120.5000	53.8250	6.3273
ASHA(check)	51.7183	6.2487	148.6215	8.5048	4.7888	52.1667	3.4633	121.6667	51.5883	6.8575
Mean	58.6837	5.7542	94.6039	4.5168	9.1200	76.1389	4.0768	146.4305	28.9328	3.8128
C.D	1.3249	0.6174	17.0230	0.2661	0.4230	2.1164	0.2817	1.7989	2.5916	0.2743

Table 3: Genotypic and phenotypic correlations among yield traits in Lentil

Sl. no	Characters		Plant height (cm)	Primary branches per plant	Number of Pods per plant	Weight of pods per plant (g)	Weight of shoots per plant (g)	Days to 50% flowering	100 seed weight (g)	Days to maturity	Harvest index (%)	Seed yield per plant(g)
1	Plant height(cm)	$r_g r_p$	1.0001.000	0.18520.1672*	-0.0793-0.0793	-0.0712-0.0713	0.44870.4448**	0.65200.6431**	0.24310.2405**	0.68080.6753**	-0.5984-0.5931**	-0.0836-0.0833
2	Primary branches per plant	$r_g r_p$		1.0001.000	0.73680.6696**	0.59940.5468**	0.31630.2898**	-0.2290-0.2052*	0.03750.0259	-0.2557-0.2348**	0.10830.0926	0.63280.5732**
3	Number of Pods per plant	$r_g r_p$			1.0001.000	0.91090.9010**	0.31240.3100**	-0.3371-0.3313**	-0.1660-0.1631	-0.3596-0.3550**	0.40360.3982**	0.92630.9153**
4	Weight of pods per plant(g)	$r_g r_p$				1.0001.000	0.17860.1775*	-0.3560-0.3535**	0.04840.0483	-0.3596-0.3585**	0.56970.5639**	0.99530.9916**
5	Weight of shoots per plant (g)	$r_g r_p$					1.0001.000	0.4126 0.4109**	-0.2076-0.2021*	0.38520.3839**	-0.5998-0.5952**	0.19250.1916*
6	Days to 50% flowering	$r_g r_p$						1.0001.000	-0.0039-0.0034	0.96710.9598**	-0.6901-0.6797**	-0.3606-0.3570**
7	100 seed weight(g)	$r_g r_p$							1.0001.000	-0.0473-0.0485	0.21700.2058*	0.03440.0334
8	Days to maturity	$r_g r_p$								1.0001.000	-0.6593-0.6529**	-0.3707-0.3685**
9	Harvest index (%)	$r_g r_p$									1.0001.000	0.55720.5572**
10	Seed yield per plant (g)	$r_g r_p$										1.0001.000

**significant at 1% ; *significant at 5%.

Similar findings have earlier been reported by Tyagi and Khan (2011). Generally, high heritability coupled with low genetic advance indicates non-additive gene action. Such characters can be improved through indirect selection metrics. Whereas, high heritability coupled with high genetic advance in case of plant height, pods per plant, days to 50% flowering, days to maturity and harvest index indicate the characters to be controlled by additive genes and accordingly direct selection in the desired direction can be practiced. These findings were in agreement with Singh *et al.* (2009); Ghulam *et al.* (2010) and Tyagi and Khan (2011) for number of pods per plant and 50% flowering; Kakde *et al.* (2008), Younis *et al.* (2008) and Hussain *et al.* (2014) for days to maturity.

Mean performance

Ten morphological characters considered for comparing the performance of the genotypes revealed significant inter genotypic difference for all the characters under study (Table 2). Three genotypes namely KLB-134, ILL-10897 and ILL-10236 showed higher significant mean for number of primary branches as revealed by the C.D value. Considering the character number of pods per plant, it was noticed that among the seven genotypes that had significantly higher mean KLB-134 produced the highest mean (504.22). In the present experiment only six genotypes viz., ILL 237, ILL 8108, KLB-134, SKUA L-9, X2009S218 and Asha produced significantly higher mean for seed yield.

Harvest index, the ratio of economic yield with the remaining part of the plant, reveals the potentiality of any crop to translocate the photosynthate from the source to the sink. In the present experiment, ten genotypes produced significantly higher harvest index as revealed by the CD value. Considering the number of characters for which a genotype produced significantly superior mean it was noticed that KLB-134, ILL 8108 and X2009S218 could do so for eight, seven, and eight characters including yield.

Correlation and path coefficient analysis

Genotypic correlation values (Table 3) were more than that of respective phenotypic correlation values indicating strong inherent relation between the character pairs. Significantly positive correlation of seed yield could be observed with primary branches per plant (0.573), number of pods per plant (0.915), weight of pods per plant (0.992), weight of shoot per plant (0.192) and harvest index (0.557). These results corroborate the findings of Naresh *et al.* (2009), Kayan *et al.* (2012) and Sharma *et al.* (2014). Two characters may show correlation just because they are correlated with a common third one. In such cases, it becomes necessary to study the causal relationship between the variables in addition to the degree of such relationship. Path coefficient analysis measures the direct influence of one variable upon the other and permits separation of correlation coefficients into components of direct and indirect effects. Residual effect (0.1140) of path coefficient analysis (Table 4) indicated that the numbers of characters chosen for the study were appropriate for yield determination. Path coefficient (phenotypic) analysis revealed that primary branches per plant (0.0311), number of pods per plant (0.0843), weight of pods per plant (0.8466), weight of shoots per plant (0.0463) and harvest index (0.0824) besides positive direct effect on seed yield per plant as earlier observed by

Table 4: Path co-efficient analysis (phenotypic) showing direct and indirect effects of component traits on lentil

Sl.No	Character	Plant Height (cm)	Primary Branches per plant	Number of Pods per Plant	Weight of Pods per plant(g)	Weight of Shoot per plant(g)	Days to 50% Flowering	100 Seed Weight	Days to Maturity	harvest Index(%)	Seed yield per plant (g)
1	Plant Height (cm)	0.0065	0.0011	-0.0005	-0.0005	0.0029	0.0041	0.0016	0.0044	-0.0038	-0.0833
2	Primary Branches per plant	0.0052	0.0311	0.0208	0.0170	0.0090	-0.0064	0.0008	-0.0073	0.0029	0.5732**
3	Number of Pods per Plant	-0.0067	0.0565	0.0843	0.0760	0.0261	-0.0279	-0.0138	-0.0299	0.0336	0.9153**
4	Weight of Pods per plant (g)	-0.0604	0.4629	0.7628	0.8466	0.1503	-0.2993	0.0409	-0.3035	0.4774	0.9916**
5	Weight of Shoot per plant (g)	0.0206	0.0134	0.0144	0.0082	0.0463	0.0190	-0.0094	0.0178	-0.0276	0.1916*
6	Days to 50% Flowering	0.0491	-0.0157	-0.0253	-0.0270	0.0314	0.0764	-0.0003	0.0733	-0.0519	-0.3570**
7	100 Seed Weight	-0.0016	-0.0002	0.0011	-0.0003	0.0014	0.0000	-0.0068	0.0003	-0.0014	0.0334
8	Days to Maturity	-0.0471	0.0164	0.0248	0.0250	-0.0268	-0.0670	0.0034	-0.0698	0.0456	-0.3685**
9	harvest Index(%)	-0.0489	0.0076	0.0328	0.0465	-0.0491	-0.0560	0.0170	-0.0538	0.0824	0.5572**

Residual effect = 0.1140; **significant at 1%; *significant at 5%

Table 5: Grouping of genotypes

Sl no.	Clusters	No. Of genotype	Genotypes
1	I	16	X2009S96, X2009S219, ILL 6821, ILL 10258, ILL 10257,ILL 10258, ILL 10273, ILL 10220, ILL 10047, X2009S170, ILL 10803, ILL 10103, ILL 10236, ILL 237, ILL 10893, ILL 10971, ILL 8108
2	II	5	SKUA L-9, ASHA, LL 204, ILL 10897, ILL 10921
3	III	1	ILL 10231
4	IV	1	X2009S218
5	V	1	KLB-134

Table 6: Intra and Inter cluster distances

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	111.26	351.04	214.99	505.48	1396.68
Cluster 2		180.83	531.87	748.24	1219.62
Cluster 3			0.00	525.72	1180.21
Cluster 4				0.00	584.53
Cluster 5					0.00

Table 7: Cluster means

Clusters	Plant height (cm)	primary branches per plant	Pods per plant	Weight of pods per plant(g)	Weight of shoots per plant(g)	Days to 50% flowering	100 seed weight (g)	Days to maturity	Harvest index (%)	Seed Yield per plant (g)
I	63.74	5.66	63.16	3.21	9.62	83.76	4.12	156.31	20.38	2.60
II	42.51	5.35	80.13	4.91	3.45	53.97	4.36	117.87	52.57	4.17
III	57.71	4.65	128.00	4.08	20.38	83.83	3.27	156.17	11.86	2.90
IV	64.89	5.25	226.98	12.52	11.43	85.67	3.56	166.00	45.84	10.97
V	53.35	10.57	504.23	15.86	15.97	47.83	3.34	101.83	47.80	15.21

Younis *et al* (2008) and Ghulam *et al*. (2010), had significantly positive correlation with seed yield and in addition number of pods per plant, weight of pods per plant and weight of shoots per plant revealed to be under additive genetic control therefore direct selection can be practiced from the genotypes which had desirable mean values.

Days to 50% flowering had negative association with yield though it had positive direct effects indicating that indirect effect of some important characters like number of primary branches per plant, number of pods per plant, weight of pods per plant, 100 seed weight and harvest index was high enough to produce negative correlation. Significantly positive correlation between weight of shoot per plant and seed yield might have been the consequence of high and positive direct effect of this character. Interestingly, there was conspicuously high negative direct effect of 100 seed weight on seed yield but the correlation was significantly positive and high. It may be mentioned here that indirect effect of 100 seed weight via number of pod per plant, weight of shoots per plant, days to maturity had been high enough to negate the negative direct effect so much so that a positive correlation was revealed. Such results find support from Khattab (1999), Yadav *et al*. (2003), Tyagi and Khan (2011), Singh *et al*. (2012) and Singh and Srivastava (2013).

Genetic divergence

The importance of genetic diversity for selecting parents in combination breeding of different autogamous crops to recover transgressive segregants has been emphasized by Singh and Ramanujam (1981); Cox and Murphy (1990). In the present experiment the twenty four genotypes were grouped into 5 clusters as shown in table 5. The clusters were formed on the basis of relative magnitude of D^2 values, following Tocher's method (Rao, 1952). Cluster I comprised the highest number of 16 genotypes followed by cluster II with 5 genotypes and remaining clusters were monogenotypic.

Meena and Baha (2003) and Kumar *et al*. (2015) suggested that strains of diverse clusters may be utilized in crop improvement programme to generate a wide range of transgressive segregations for the development of high yielding crop cultivar. The genotypes of the monogenotypic clusters indicated them to possess completely different genetic makeup from rest of the genotypes and from each other.

Intra and Inter cluster distances

Intra cluster distance indicating the diversity of genotype falling in the same cluster (Table 6) varied from 0 (Cluster III, IV and V) to 180.83 (Cluster II). However, the inter cluster distance varied from 214.99 to 1396.68 between cluster I and III and between I and V respectively. From the divergence analysis it may be concluded that superior genotypes belonging to clusters I and III; I and II separated by high estimated statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among segregants (Kulsum *et al*., 2011).

Cluster mean

Cluster mean for different characters presented in Table 7 indicated that they had marked differences in respect of means for all the characters studied. Since cluster means are highly affected by extreme values of characters included in the same cluster, therefore, it has less reliability for selection of individual genotype but it helps in selection of clusters from where parents should be selected for hybridization.

The cluster means clearly indicate that the genotypes viz.,ILL 10231, ILL 8108, X2009S218, ILL 10921, ILL10897, LL 204, SKUA L-9, KLB-134, ASHA could be selected as parents for future hybridization programme or heterosis breeding as well as to obtain a large number of segregants in segregating generations.

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