



RESEARCH ARTICLE

ANALYSIS OF GENETIC VARIABILITY AND DIVERGENCE FOR QUANTITATIVE TRAITS
IN LENTIL (*LENS CULINARIS* MEDIK.)

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ABSTRACT

The present experiment was conducted using one hundred and eighty five genotypes of lentil collected from different locations to determine the genetic variation, association and divergence among them. Data on various characteristics were recorded. Wide range of variations found in mean values suggested variations for all agronomic traits under study. ANOVA showed statistically significant differences among the genotypes for all the traits. Genetic parameters like genotypic and phenotypic variances and correlation coefficient, heritability and genetic advance were estimated. Estimates of phenotypic and genotypic coefficients of variations were high for grain yield (55.10, 51.15), number of pods per plant (49.31, 47.56) and harvest index (53.17, 40.89) while it was very low for days to flowering (3.77, 3.63) and days to maturity (2.46, 2.23). Estimates of genotypic coefficient of variability constituted major component of variability suggested variation in the genetic constitution irrespective of environmental influences. All the characters showed high heritability. The traits grain yield per plant, number of pods per plant, harvest index, number of branches and seed weight showed high genetic advances, suggested selection of genotypes considering these traits will lead to high yielding varieties. Phenotypic and genotypic correlation revealed that all the traits possess positive correlation with grain yield, except days to flowering and days to maturity. Genotypic and phenotypic path coefficient revealed that traits like number of pods per plant, biological yield and harvest index have direct positive effect on grain yield. Genetic divergence analysis grouped 185 genotypes into eight clusters. Cluster VII had highest mean value of grain yield, number of pods per plant and harvest index while lowest was that of II. Hybridization between the genotypes of these clusters may give rise to more valuable transgressive segregates.

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INTRODUCTION

Lentil (*Lens culinaris* Medik) is among the first crop domesticated and has become an important food legume crop in the farming and food systems of many countries. It is a diploid (2n = 14 chromosomes), self-pollinated, high valued annual cool season grain legume crop with a relatively large genome of 4,063 Mpb (Arumuganathan and Earle, 1991).

Globally, lentil ranks sixth in terms of production among the major pulses and constituted 6% of total dry pulse production. The important lentil-growing countries of the world are India, Canada, Turkey, Bangladesh, Iran, China, Nepal and Syria (Ahlawat, 2012). The total cultivated area in the world is around 4.148 million hectares producing 4.43 million tons of seeds with an average production of 1068 kg/ha (FAO, 2010). Lentil ranks first among pulse crops in Nepal. Its area and production is 2,05,939 ha and 2,26,830 metric ton, respectively with productivity of 1,101 kg per hectare (MOAD,2014) It contributes to human diet and plays an

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important role in enhancing the fertility status of soil by fixing atmospheric nitrogen in symbiotic association with bacteria. It can be successfully integrated into the existing rice-maize based cropping pattern. Now the importance of lentil in Nepal is also increasing due to export market to Bangladesh and other foreign countries (Yadav, 2004). There is an urgent need to increase the overall production and productivity through crop improvement. It is important to know genetic base, variability and genetic diversity present in the elite and exotic germplasms. The grain yield is very complex trait and it is multiplicative end product of several basic components of yield (Grafius, 1959) and Whitehouse *et al.* (1958) have doubted the individuality of this character and suggested that there may not be genes for the yield per se but for the various components. The multiplicative inter action of which results in to total effect of yield.

Therefore to clearly understand the genetic architecture of yield, it will be rather important to study it into its various components (Yadav, 1997). Greater the variability, higher the chances of getting the desired types. Further, partitioning it into heritable and non- heritable traits help in effective selection. High heritable and high genetic advance indicates additive gene action (Panse, 1956) whereas high heritability with low genetic advance suggests for non-additive gene action of dominance and epistasis nature. Information of genetic variation along with character association of yield and its contributing character helps breeder for selection. Morphological characters have been frequently used in order to know the diversity in germplasm collections (Erskine and Chaudhary, 1986; Erskine *et al.*, 1989; Sarker *et al.*, 1999). The aim of this study was to study the morphological characteristics to analyze the yield components and find the relationship among the 185 genotypes and grouped it in to different cluster having similarity in one group collected from different sources.

MATERIALS AND METHODS

The present investigation was carried out during winter season (Nov-Apr) in 2011/12 at the crop field of Agronomy Division, Khumaltar, Kathmandu located at latitude 27° 3' 86" north and longitude 85° 35' 52" east and an elevation of 144 meter above sea level with 1340 mm annual rainfall. The experimental materials comprised of 185 genotypes including 5 checks were collected from International Centre for Agricultural Research in the Dry Areas (ICARDA), National Grain Legumes Research Program, Rampur (NGLRP) and National Genetic Resource Center (NGRC), Khumaltar, Kathmandu. Considering each germplasm line as one treatment these genotypes were planted in augmented design with 4 blocks. Plot size was of 2 rows of 1.5 meters length. Crop was planted at spacing of 25 cm row to row and 5 cm plant to plant spacing. Five checks (ILL7715, ILL7164, Bari masuro-4, Sindur and Simal) were planted in each block randomly with 45 test entries. Six plants were randomly selected and tagged to study the inter and intra variations. Eleven quantitative traits *i.e.* leaflet length (LL), days to 50% flowering (DF), days to 90% maturity (DM), plant height (PH), number of primary branches (PB), number of pods per plant (PP), number of seeds per pod (SP), 100 seed weight (SW), biological yield per plant

(BY), grain yield per plant (GY) were recorded following IBPGR descriptors 1985 and harvest index (HI) were estimated. All recommended agronomic practices were followed as per the NGLRP recommendation during the experiment. ANOVA of augmented design was calculated by using method described by Federrer (1961). The genetic parameter, correlation coefficient and path coefficient at genotypic and phenotypic levels were computed following methods given by Panse and Sukhatma (1969) and Singh and Chaudhary (1985). Statistical analysis was performed on the data obtained from 6 plants in each plot while divergence analysis and dendrogram was prepared using Pear sons dissimilarity index.

RESULTS AND DISCUSSION

Analysis of variances (ANOVA) for augmented design revealed significant differences among lentil entries (including checks) and tested genotypes for all 11 characters (Table-1). Genetic variability in the initial breeding materials ensures better chances of producing desired recombinants for crop improvement.

Genetic parameters

The range, mean value, genotypic covariance (GCV) phenotypic covariance (PCV), heritability and genetic advance as percent of mean at 5% levels for all 11 agro-morphological traits analyzed is presented in Table 2

Agronomic traits

Higher the range of variation for all the traits *i.e.* leaflet length (1.77-3.08), days to 50% flowering (88.50-110.67), days to 90% maturity (122.50-148.83), plant height (16.67-35.00), number of primary branches (3.5-12.67), number of pods per plant (6.33-80.17), number of seeds per pod (0.93-2.00), 100 seed weight (0.91-3.31), biological yield per plant (1.24-6.68), grain yield per plant (0.90-3.02) and harvest index (5.50-65.41) were recorded and it indicates selection could be done for any characters (Table-2). Genotypes ILL3236 (13.58), RL-11 (12.98), X94 S-43 (11.98), F2003-49L (10.81), ILL8191 (10.24), X49s-48 (10.08), ILL8132 (9.98), ILL9932 (9.91), Khajura-1 (9.81) produced significantly higher number of branches per plant than best check Simal (8.16), where as genotypes RL-11 (81.46), Aarial (75.55), ILL3236 (74.66), RL-6 (74.66), F2003-49L (74.46), NRX-99s-95-1-1 (71.49), ILL9932 (70.16), khajura-1 (69.12) and RL-39 (68.05) produced significantly higher number of pods per plant than best check Simal (39.7). Significantly high number of seeds per pod were obtained from NRX-99s-95-1-1 (2.00), X49s-48 (2.00), ILL10071 (1.98), ILL7979 (1.96), ILL3236 (1.94), RL-95 (1.93), Arun (1.91), ILL1920 (1.91), ILL6811 (1.90), ILL2712 (1.88), LN-0111 (1.87). Genotypes ILL3236 (3.02g), RL-39 (3.01g), Aarial (2.96g) RL-11 (2.86g) ILL9932 (2.42g), Khajura-1 (2.34g), RL-6 (2.30g) produced significantly higher grain yield per plant than best check Simal (1.0g). Significantly higher biological yield per plant was produced from ILL3236 (7.43g), F2003-49L (6.62g), LN-0137 (6.22g), RL-11 (6.05g), Aarial (5.92g), Khajura-1 (5.87g), RL-6 (5.66g), ILL1704 (5.49g), ILL9932 (5.43g), ILL4139 (5.37g) ILL993

(5.30g), RL-81 (5.21g)) than best check Simal(4.09g). High 100 seed weight were recorded from RL-81 (3.56g), FLIP05-44L (3.31g) RL-83 (3.09g), RL-25 (2.95g) NRX9901-1 (2.75g), RL-47 (2.75g), RL-85 (2.73g). High harvest index % were recorded from RL-39 (65.77), Aarial (60.39), ILL6024 (54.9), Jutpani (54.86), LL2373 (54.77), NRX-99s-95-1-1(54.23), RL-85 (53.88), RL-95 (53.35), ILL9932 (52.89), 39-S-66L (52.5), ILL4139 (52.15), Arun (50.7), ILL7538 (50.5), ILL3236 (50.2), RL-11(50.11) than best check Bari masuro-4(33).

Phenotypic and genotypic coefficient of variation

Genetic variability in the source population is an important pre-requisite for any genetic improvement; however, it is not only the criterion for deciding as to which traits is showing the highest degree of variability. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) can help in this regards. PCV and GCV values of approximately more than 20% are regarded as high, whereas values less than 10 % are regarded as low and between these two values are regarded as medium (Deshmukh and Reddy, 1986). Based on this high GCV and PCV were recorded for grain yield (51.13,55.10), number of pods per plant (47.56,49.31), harvest index (40.88,53.17), biological yield(37.93,48.120, 100 seed weight (26.91,26.93), number of branches per plant, (32.14,35.26) and number of seeds per pod (26.13,28.61) respectively. Medium GCV and PCV were recorded for leaflet length and plant height while low for days to flowering and days to maturity. High genotypic and phenotypic coefficient in lentil were recorded by Tyagi and Khan, 2011

Heritability and genetic advances

The broad sense of heritability (h^2) estimates of the traits ranged from 59.10 to 99.86 per cent. According to Agrawal *et al.*,1976, heritability estimates in cultivable plants can be placed in the following categories, 5-10 low,10-30 medium and value 30 and above as high heritability. Based on this, all the traits showed high heritability. Number of pods per plant showed highest heritability and genetic advance (93.03,94.51), grain yield followed by grain yield per plant (86.18,97.82), High heritability with high genetic advance were also reported by Yainis, *et al.*, 2008 in lentil while by Patel *et al.*, 2012 in green gram. On the basis of these traits early generation selection is possible. Hence, genotypes having higher number of pods and grain yield per plant are RL-11, Aarial, ILL3236, RL-6, F2003-49L NRX-99s-95-1-1, ILL9932, khajura-1 and RL-39 and are selected for future breeding program.

Correlation

Table-3 showed the genetic and phenotypic correlation coefficients of 11 traits recorded on 185 genotypes of lentil. The genotypic correlation coefficients were higher as compared to phenotypic in all the characters indicating high consistence of results. Similar results were also reported by Tyagi and Khan, 2011. Grain yield per plant had positive and significant correlation with all the characters except days to flowering and days to maturity. Number of pods per plant was found positively correlated with plant height, number of branches, leaflet length, number of seeds per pod, biological yield per plant, harvest index, and grain yield per plant.

Table 1. Analysis of variance (ANOVA) for different morphological and economical traits F value (.05)1.93, (.01)2.5

		LL	PH	NB	DF	DM	PP	SP	GY/p	BY/p	SW	HI
Source	DF	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS	MSS
Blocks (b)	3	0.072	104.222	5.923	299.473	71.572	712.313	0.241	2.162	11.269	2.190	713.618
Entries (e)	184	0.067**	7.355**	3.227**	8.237**	8.774**	221.461**	0.069**	0.341**	1.386**	0.208**	159.281**
Checks (c)	4	0.037	6.335	4.956	9.243	11.317	101.516**	0.011	0.140**	2.156**	0.079*	88.261**
Varieties (v)	179	0.068**	7.407**	3.206**	8.250**	8.688**	262.592**	0.071**	0.347**	1.376**	0.206**	161.737**
Check vs. Var	1	0.040	2.118	0.050	1.819	14.090**	183.291**	0.030	0.038	0.065	0.033	46.696**
Error	12	0.012	1.751	0.640	4.800	3.800	33.500	1.430	1.208	2.892	1.743	29.693
GM		2.398	23.475	6.424	95.559	133.973	31.553	12.028	16.116	8.789	10.389	23.014
CV%		4.657	5.636	12.456	2.293	1.455	18.343	12.028	16.116	8.789	10.389	23.014

Note- LL=leaflet length(cm), PH= plant height, NB = number of primary branches per plant, DF = days to 50% flowering, DM = days to 90 maturity,PH = number of pods per plant=, seeds per pods, BY/p= biologic yield per plant(g),GY/p= grain yield per plant(g), SW= 100 seed weight(g), and HI= harvest index **, = significant at 1%,* = significant at 5% probability levels..

Table 2. Genetic Parameter for different morphological traits in Lentil

	Range	Mean	GCV%	PCV%	HA	GA as% mean
LL	1.77-3.08	2.40	16.28	19.62	68.83	27.82
PH	16.67-35.00	23.48	12.81	15.07	72.22	22.42
NB/P	3.5-12.67	6.42	32.11	35.26	82.93	60.25
DF	88.50-110.67	95.56	3.63	3.77	92.75	7.20
DM	122.50-148.83	133.97	2.23	2.46	81.98	4.16
P/P	6.33-80.17	31.55	47.56	49.31	93.03	94.51
S/P	0.93-2.00	1.43	26.13	28.61	83.39	49.15
BY/P	1.24-6.68	2.89	37.93	48.12	62.13	61.59
SW	0.91-3.31	1.74	26.91	26.93	99.86	55.39
HI	5.50-65.41	29.69	40.88	53.17	59.10	64.73
GY/P	0.09-3.02	1.21	51.15	55.10	86.18	97.82

Note- LL=leaflet length (cm), DF = days to 50% flowering, DM = days to 90 maturity,, PH= Plant height,, P/P = number of pods per plant, NB/p = Number of primary branches per plant, seeds per pods, BY/p= biologic yield per plant (g), GY/p= Grain yield per plant (g), SW= 100 seed weight (g) and HI= harvest index

Table 3. Estimates of Phenotypic and Genotypic correlation coefficients among the eleven traits

Traits		PH	BP	DF	DM	P/P	S/P	SW	BY/Pt	HI	GY/pt
Leaflet length	Pheno	0.072	0.059	0.024	0.008	0.112	0.034	0.017	0.074	0.054	0.081
	Geno	0.324**	0.333**	0.083	0.069	0.347**	0.226**	0.055	0.445**	0.192**	0.320**
Plant height	Pheno		0.209**	-0.338**	-0.193**	0.310**	0.144**	0.333**	0.501**	0.095	0.390**
	Geno		0.315**	-0.456**	-0.256**	0.381**	0.306**	0.446**	0.692**	0.273**	0.507**
Number of branches/pt	Pheno			-0.119	-0.042	0.474**	0.122	-0.023	0.564**	0.057	0.395**
	Geno			-0.189**	-0.071	0.675**	0.358**	-0.036	0.757**	0.317**	0.587**
Days to flowering	Pheno				0.632**	0.024	-0.036	-0.353**	-0.188**	0.002	-0.118
	Geno				0.715**	0.027	-0.075	-0.367**	-0.325**	0.005	-0.151
Days to maturity	Pheno					0.114	0.039	-0.253**	-0.049	0.043	-0.036
	Geno					0.130	0.094	-0.279**	-0.072	0.055	-0.047
Pods per plant	Pheno						0.372**	0.015	0.580**	0.608**	0.797**
	Geno						0.695**	0.016	0.781**	0.777**	0.888**
Seeds per pod	Pheno							0.099	0.331**	0.616**	0.623**
	Geno							0.209**	0.523**	0.838**	0.756**
100 seed wt	Pheno								0.214**	0.271**	0.317**
	Geno								0.350**	0.353**	0.393**
Biological yield per plant	Pheno									0.099	0.677**
	Geno									0.490**	0.801**
Harvest index	Pheno										0.732**
	Geno										0.882**

Note: r value at 5% = 0.138, r at 1% = 0.181 * significant at 5%, ** significant at 1%

Table-4a. Phenotypic path coefficient analysis

	Direct	LL	PH	B/P	DF	DM	P/P	S/P	SW	BY/P	HI	SUM PATH
LL	-0.008	-0.008	0.001	0.000	0.001	-0.001	0.019	0.002	0.001	0.036	0.028	0.081
PH	0.016	-0.001	0.016	0.000	-0.012	0.012	0.052	0.010	0.017	0.245	0.050	0.390
NB/P	0.001	0.000	0.003	0.001	-0.004	0.003	0.079	0.009	-0.001	0.276	0.030	0.395
DF	0.035	0.000	-0.005	0.000	0.035	-0.039	0.004	-0.003	-0.018	-0.092	0.001	-0.118
DM	-0.062	0.000	-0.003	0.000	0.022	-0.062	0.019	0.003	-0.013	-0.024	0.023	-0.036
P/P	0.368	-0.001	0.005	0.000	-0.100	-0.101	0.368	0.027	0.001	0.284	0.319	0.797
S/P	0.072	0.000	0.002	0.000	-0.001	-0.002	0.062	0.072	0.005	0.162	0.323	0.623
SW	0.052	0.000	0.005	0.000	-0.012	0.016	0.002	0.007	0.052	0.105	0.142	0.317
BY/P	0.489	-0.001	0.008	0.000	-0.007	0.003	0.097	0.024	0.011	0.489	0.052	0.677
HI	0.525	0.000	0.002	0.000	0.000	-0.003	0.102	0.044	0.014	0.048	0.525	0.732

Note: Residual 0.2929

Table-4b Genotypic path coefficient analysis

	Direct	LL	PH	B/P	DF	DM	P/P	S/P	SW	BY/P	HI	SUM PATH
LL	-0.050	-0.050	-0.007	-0.008	0.009	-0.008	-0.090	-0.037	-0.008	0.342	0.177	0.320
PH	-0.020	-0.016	-0.020	-0.008	-0.049	0.029	-0.099	-0.050	-0.065	0.532	0.252	0.507
NB/P	-0.024	-0.017	-0.006	-0.024	-0.020	0.008	-0.175	-0.059	0.005	0.582	0.293	0.587
DF	0.107	-0.004	0.009	0.005	0.107	-0.081	-0.007	0.012	0.053	-0.250	0.005	-0.151
DM	-0.114	-0.004	0.005	0.002	0.077	-0.114	-0.034	-0.015	0.041	-0.055	0.050	-0.047
P/P	0.429	-0.202	-0.018	-0.016	0.007	-0.015	0.429	-0.114	-0.003	0.400	0.417	0.888
S/P	-0.164	-0.011	-0.006	-0.009	-0.008	-0.011	-0.180	-0.164	-0.030	0.402	0.774	0.756
SW	-0.145	-0.003	-0.009	0.001	-0.039	0.032	-0.004	-0.034	-0.145	0.269	0.326	0.393
BY/P	0.769	-0.022	-0.014	-0.018	-0.035	0.008	-0.203	-0.086	-0.051	0.769	0.453	0.801
HI	0.923	-0.010	-0.005	-0.008	0.001	-0.006	-0.201	-0.137	-0.051	0.377	0.923	0.882
Residual	0.182											

Plant height has significant positive correlation with number of branches, number of pods per plant, number of seeds per pod, seed weight, biological yield, harvest index and grain yield while significant negative correlation with days to flowering and days to maturity. Number of branches had positive correlation with number of pods per plant, number of seeds per pod, biological yield and harvest index. Hundred seed weight had positive and significant correlation with harvest index. This positive association was earlier reported by Chauhan and Singh (2001). Moreover, positive association of pods per plant, biological yield/plant, plant height and 100-seed weight was Genotypes having high number of Pods per plant are RL-11, Aarial, F2003-49L, Khajura1, Simal, ILL6811, RL-39,

ILL2373, while genotypes having higher harvest index are RL-39, Aarial, ILL6024, ILL2373, 39s-66L, RL-1, ILL3236, Khajura-1, ILL9932, ILL8132, RL-95, NRX-99s-1, x49s-8, RL-11, ILL3236. These genotypes were selected for further study.

Path coefficient

The direct and indirect effects of the casual variables on seed yield per plant were shown in Table-4. The grain yield per plant is influenced by several characteristics (causes) and these characteristics show various degrees of relationship among themselves.

Table 5. Clustering pattern of 185 lentil genotypes based on Pearson similarity analysis for 11 characters

S.N	No. of genotypes	Entries name
1	145	Arun,Baitadi 6A,Bari masuro -4,Cumara,DIGGER,DPL-62,FLIP 2009-54L,FLIP 95-1L, FLIP05-52(ILL10073), Flip2006-55L, FLIP-2006-99L, FLIP2009-59L, FLIP2009-60L, HUL-57, IL-1,ILL10068, ILL10134, ILL1672, ILL1704, ILL1920, ILL1970, ILL2501, ILL2526, ILL2527, ILL2573, ILL2701-1, ILL2712, ILL2716, ILL3111, ILL3280, ILL3338, ILL3490, ILL3491, ILL3496, ILL3768, ILL590, ILL6021, ILL6025, ILL6260, ILL6408, ILL6447, ILL6458, ILL6465, ILL6468, , ILL6818, ILL6821, ILL6829, ILL7157, ILL7162, ILL7163, ILL7164, ILL7220, ILL7537R, ILL7616, ILL7664, ILL7715, ILL7723, ILL7978, ILL7980, ILL7986, ILL7990, ILL8186, ILL8187, ILL8188, ILL8191, ILL8605,ILL9881,ILL9885, ILL9924,ILL9926,ILL9927, ILL9949,ILL9976,, LL9992, ILL9993, ILL9996, ILL1970, khajura-2, LG-12, LN-0111,LN-0135, LN-0136, LN-3885, Mangal Bazar, M-Bharatai, NRX2001-71-3, NRX2001-71-4, NRx2001-, 2-3, NRX9801-1, NRX9901-1, NRx-99S-95-1-12, PL-4, PL-406, PL-4402,PL-639, RL-12, RL-13,RL-15, RL-21, RL-22, RL-23, RL-25, RL-26, RL-28, RL-35, RL-38, RL-4, RL-41, RL-42, RL-43, RL-45, RL-47, RL-49, RL-51, RL-55, RL-56, RL-58, RL-60, RL-62, RL-67, RL-69, RL-71, RL-73, RL-74, RL-76, RL-77, RL-78, RL-79, RL-8,RL-80, RL-81,RL-83, RL-84, RL-85, RL-9,RL-94,RL-95, Shikhar, Shisir, Simal, Simrik, Sindur, WBL-77, X39S-66L, X49s-48
2	1	RL-68
3	26	39-S-66L, F2003-49L, FLIP05-44L(ILL100), ILL10045, ILL10071, ILL2373, ILL4139, ILL6024, ILL6256, ILL6467, ILL6811, ILL7538, ILL7979, ILL8132, ILL9932, ILL9943, ILL9990, Jutpani, Khajura-1, LN-0137, NRX-99s-95-1-1, RL-39, RL-44, RL-6, X94s-48, X95S-83
4	7	FLIP04-60L(ILL10013), FLIP2008-7L, ILL10065, ILL6256, ILL6458, RL-70, RL-75
5	2	Sagun, X94 S-43
6	1	RL-20
7	1	Aarial
8	2	ILL3236, RL-11

Table 6. Genotypic means of each cluster for 11 characters

Cluster	NO.CLUSTER	LL	PH	B/P	DF	DM	P/P	S/P	GY/P	BY/P	SW	HI
I	145	2.37	23.18	6.04	95.20	133.83	26.58	1.38	0.66	2.64	1.71	26.38
II	1	2.10	23.08	4.17	95.83	122.50	8.83	1.40	0.23	1.24	1.93	20.76
III	26	2.51	25.10	7.95	95.47	134.16	55.70	1.67	1.72	4.09	1.89	45.84
IV	7	2.42	19.67	5.90	104.38	140.62	31.21	1.45	0.72	2.33	1.55	32.98
V	2	2.72	23.29	11.25	92.25	130.08	35.67	1.28	0.78	3.66	1.48	21.42
VI	1	2.90	35.00	6.33	92.83	131.67	17.83	1.23	0.64	2.89	2.81	21.20
VII	1	2.13	30.83	6.67	102.50	131.00	73.33	1.77	2.95	6.00	2.21	60.03
VIII	2	2.50	27.71	12.42	93.00	131.08	72.33	1.90	2.77	6.11	2.02	49.95

Table 7. Intra and inter cluster distance between clusters

Cluster	I	II	III	IV	V	VI	VII	VIII
I	0	4.54	4.03	4.30	4.03	5.47	7.81	7.85
II		0	7.30	7.60	6.55	6.92	9.80	10.42
III			0	5.94	4.43	6.27	4.83	4.20
IV				0	6.79	8.22	8.85	9.62
V					0	6.08	8.44	6.36
VI						0	8.68	8.67
VII							0	4.90
VIII								0

The correlation coefficients of the causal characteristics with grain yield per plant were partitioned into direct and indirect effects through path coefficient analysis at phenotypic and genotypic levels. Present study revealed that higher positive direct effect on grain yield was recorded by harvest index (0.525) followed by biological yield (0.489), and pods per plant (0.368) at phenotypic level (Table-4a) while it was 0.923,0.769 and 0.429- respectively at genotypic level (Table-4b). The results are consistent with those of Ghafoor *et al.* (1990), and Yaqoob *et al.* (1997). Seed weight showed negative direct effect while it had positive indirect effect via biological yield and harvest index on grain yield. Selection of genotypes having high harvest index and biological yield /plan are RL-39, Aarial, ILL6024,ILL2373 ,39s-66L, RL-11, ILL 3236,Khajura-1,ILL9932,ILL8132, F2003-49L,LN-0137,RL-6', and selection for future breeding program considering those traits will certainly lead to fruitful results.

Genetic divergence

The genetic divergence is an outcome of several factors such as changing of breeding material, genetic drift, natural variation and artificial selection rather than ecological and geographical diversification (Sirohi and Dar, 2009). Through multivariate analysis, the 185 genotypes were grouped into eight clusters based on Pearson' dissimilarity index. The composition of different clusters varied from 1 to 145 genotypes, their number and names are recorded in Table -5. The cluster I has 145 genotypes while clusters II, VI and VII have 1 each. Cluster mean for 11 characteristics are presented in Table-6. Cluster VII has highest number of pods per plant, (73.33), highest grain yield (2.95); and highest harvest index (60.03) followed by cluster VIII. Seed per pod (1.90) and biological yield per plant (6.11) was highest for Cluster VIII followed by Cluster VII whereas the highest seed weight (2.81)

was that of Cluster VI. The distribution of genotypes from different eco-geographical regions into these clusters was apparently random. Genotypes of similar origin were grouped into different cluster and vice versa, thereby indicating non-relationship between geographical and genetic diversity. Similar results were obtained by Jeena and Singh, 2002 and Tyagi and Khan, 2010. This tendency of genotypes to occur in cluster cutting across geographical isolations is not the only factor causing genetic diversity (Singh *et al.*, 2004). This also suggests that genotypes falling in a cluster may have some degree of ancestral relationship and distributed during the process of human civilization and migration. Similar finding were reported by Sirohi *et al.*, 2007, Solanki, 2007 and Jeena and Singh, 2002. Breeding program may initiated involving the genotypes of superior clusters having high mean value for almost all required traits are selected for further testing. Inter cluster distances between cluster is presented in Table-6 .Highest cluster distance 10.41 was observed between cluster II and VIII followed by between II and VIII (9.8) and between IV and VIII (9.62). Hybridization between the genotypes of these clusters may give rise to more valuable transgressive segregates.

Conclusion

Analysis of variance revealed significant differences among the treatments (including checks) and varieties (tested line) for all the traits. Significant genotypic differences supported by wide range of variation for mean values suggested variability present in the experimental materials. Genotypes viz (RL-39, RL-11, ILL 3236, Khajura-1, ILL6024, ILL9932, ILL8132, ILL 2373 produced significantly higher grain per plant than best check (Simal). These genotypes also possessed significantly higher number of pods per plant than best check. High heritability along with high genetic advance as percentage of mean were observed for number of pods per plant, grain yield per plant, biological yield per plant and harvest index suggested early generation selection for these traits would be very effective. At phenotypic and genotypic level grain yield has significant positive correlation with , number of pods per plant, number of seeds per pod, biological yield per plant and harvest index ,these traits should be consider in selecting the variety in lentil. Non-significant correlation with days to flowering and days to maturity suggesting that high yielding short duration variety could be selected simultaneously. Genetic divergence analysis indicated highest mean value for number of pods (77.33) and grain yield per plant (2.95g) obtained by cluster V and lowest for cluster II (8.83,0.23g), selection of high mean value and crosses between these groups resulted in raising the average productivity of lentil in the country.

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