Variability and Association Studies in Land Races of Lentil Collected From South-Eastern Rajasthan

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Abstract: Evaluation of the existing variability in the available germplasm and working out the inter-relationship among yield and its contributing traits is necessary to develop high yielding cultivars of any crop. Keeping this in view, variability and association studies were conducted in a set of 55 diverse lines of lentil (including two checks) collected from South-Eastern parts of Rajasthan, India. Sufficient variability was present in the germplasm for days to flowering, plant height, number of fruiting branches per plant, number of pods per plant, 100- seed weight and seed yield. Days to flowering and plant height had high heritability coupled with high genetic advance while days to maturity had high heritability with moderate genetic advance. Seed yield showed significant positive genotypic correlation with all the traits studied. Pods per plant had maximum direct effect on seed yield followed by 100- seed weight and plant height. Number of fruiting branches per plant had negative direct effect on yield. Pods per plant and 100- seed weight were identified as important yield components; hence selection should be focused on these traits for yield improvement in lentil.

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1. Introduction

Lentil (*Lens culinaris* Medikus) is an important crop for human food, animal feed and cropping systems in West Asia, the Indian subcontinent, Ethiopia, North Africa, and to a lesser extent in Southern Europe. It is considered to be the oldest and widely adapted *rabi* pulse crop. As food, it provides 24-25 % protein along with vitamins and micronutrients *viz*., Fe, Zn, a-Carotene. It is considered to be the most efficient crop in fixing atmospheric nitrogen through rhizobium. In India, it is being cultivated in 1.51 m ha area with production of 0.95 m tones (Singh, 2009). The crop being drought tolerant and moderately cold resistant is remunerative for dry areas. Therefore, it becomes necessary to develop lentil varieties best suited for the dry conditions with conserved moisture. Genetic improvement, in turn, will require information on the extent of genetic variability in the available germplasm. The effectiveness of selection depends on magnitude of variability for yield and component traits. Study of inter-relationship among yield and contributing traits is also necessary. When more variables are correlated with yield, it is important to identify appropriate traits for selection. In such case, path analysis provides an effective means of finding out direct and indirect contribution of different component traits towards seed yield. Keeping all these facts in view, the present investigation was planned to study variability and association between yield and its components in indigenous advance breeding lines of lentil.

2. Materials and methods

The experimental material comprised of 55 indigenous genotypes of lentil including two checks DPL 62 and JL 3, grown in the experimental field of the Agricultural Research Station, Ummedganj, Kota, Rajasthan, India during *rabi* 2008-09 under rainfed condition. These genotypes were collected from different areas of South-Eastern Rajasthan. The trial was laid down in Randomized Block Design with three replications with the spacing of 30 cm and 5 cm between and within the rows, respectively. Each genotype was accommodated in paired rows of 4 m length. The crop was raised following the recommended cultural practices without irrigation. The Observations were recorded on ten randomly selected competitive plants from each plot per replication on 10 metric traits *viz*., plant height (cm), number of fruiting branches per plant, number of pods per plant, number of seeds per pod, 100 – seed weight (g), seed yield per plant (g), incidence of root rot/wilt % at 35 days after sowing and at 110 days after sowing. The observations on days to 50 % flowering and days to maturity were recorded on plot basis. Genotypic and phenotypic coefficient of correlation was computed according to (Jibouri *et al.*, 1958). The correlations were further partitioned into direct and indirect effects as suggested (Dewey and Lu, 1959).

3. Results

The analysis of variance revealed significant differences among the genotypes for all the traits studied indicating the existence of sufficient genetic variability in the experimental material. A few genotypes were found to be significantly superior to the checks *viz.* DPL 62 and JL 3 (Table 1).Out of fifty three genotypes, eight genotypes for days to 50 % flowering and nine genotypes for days to maturity were found significantly superior to the checks. Eight genotypes were also superior to the checks for producing fruiting branches per plant. The genotypes namely RKL 14 (123.20); RKL 308 (119.90); RKL 310 (117.20) and RKL 11 (107.60) were found significantly superior over the checks for pods per plant. While, only two genotypes RKL 37 (2.70) and RKL 300 (2.10) were found superior to the checks for number of seeds per pod. On the other hand, five genotypes for 100-seed weight and eight genotypes for yield per plant were significantly superior to the checks. Appearance of disease was optimum to evaluate disease reaction of the genotypes. Some of the genotypes showed moderate to high susceptibility reaction to root rot/wilt disease after 35 days and 110 days of sowing. Five genotypes were found resistant to root rot/wilt each at 35 and 110 days after sowing.

The general mean, range and estimates of different parameters of genetic variability were presented in Table 2. The phenotypic coefficient of variation (PCV) was maximum for number of pods per plant followed by yield per plant, fruiting branches per plant, 100-seed weight, plant height, and days to flowering, whereas days to maturity and number of seeds per pod had low estimates of PCV. Similar trend was observed for genotypic coefficient of variation (GCV) for almost all the traits, though they were slightly low compared to PCV. The heritability estimate was the highest for days to 50 % flowering (99.19 %), followed by 100-seed weight, days to maturity and plant height. Number of pods per plant and number of seeds per pod had showed moderate heritability, whereas number of fruiting branches per plant and yield per plant showed low estimates of heritability.

The highest genetic advance was observed for number of pods per plant followed by days to 50 % flowering, plant height and days to maturity, whereas number of fruiting branches per plant, number of seeds per pod, 100-seed weight and yield per plant showed low estimates of genetic advance.

Genotypic and phenotypic correlation coefficients among different traits are presented in Table 3. Seed yield had significant positive genotypic correlation with all the yield contributing traits, whereas number of fruiting branches per plant and pods per plant showed significant positive phenotypic correlation with seed yield. Days to 50 % flowering showed significant positive correlation with days to maturity, 100-seed weight, number of fruiting branches per plant and pods per plant. Days to maturity exhibited significant positive correlation with 100- seed weight, plant height, number of fruiting branches per plant and pods per plant. Plant height was positively associated with branches per plant which in turn was positively associated with number of pods per plant. Number of pods per plant was positively correlated with number of seeds per pod.

The results obtained from path analysis on genotypic levels taking seed yield as dependent and other characters as independent variables are presented in Table 4. Pods per plant exhibited the highest positive direct effect (0.90) towards seed yield followed by 100-seed weight, plant height and days to maturity. The direct effect of number of branches per plant was negative. All the characters showed negative indirect effect on seed yield *via* number of branches per plant while the branches per plant showed highest positive indirect effect *via* number of pods per plant. The indirect effect of all the major yield contributing characters (days to 50 % flowering, days to maturity, number of seeds per pod) *via* number of pods per plant were high and positive. Low value of residual effect indicated high contribution of component traits studied towards seed yield.

Table 1. Superior lentil genotypes in comparison to check DPL 62 and JL 3 for different traits

S. No.	Characters	Test genotypes	DPL 62 (check)	JL 3 (check)
1	Days to 50 % flowering	RKL 03 (64.00), RKL 001(63.50), RKL 44, RKL 45 (56.00), RKL 48 (55.00), RKL 46, RKL 303 (56.50); RKL 311 (57.00)	79.00	68.00
2	Days to maturity	RKL 23, RKL 305 (113.50); RKL 34 (112.50); RKL 44, RKL 45, RKL 48, RKL 302, RKL 303, RKL 311 (112.00)	118.00	117.00
3	Plant height(cm)	RKL 308 (58.4);RKL 306 (59.5); RKL 301 (59.80); RKL (58.70)	57.70	65.00
4	No. fruiting branches/plant	RKL 310 (6.30); RKL 306, RKL 11 (6.10); RKL 300, RKL 43, RKL 41(6.00); RKL 23 (6.70); RKL 15 (6.40)	6.80	5.85
5	No. of pods per plant	RKL 308 (119.90); RKL 310 (117.20); RKL 11 (107.60); RKL 14 (123.20)	99.30	69.50
6	No. seeds /pod	RKL 37 (2.70); RKL 300 (2.10)	2.00	2.00
7	100-seed wt(g)	RKL 08 (3.44); RKL 14 (3.45); RKL 300 (3.49); RKL 306, RKL 310(3.34)	3.37	2.55
8	Yield per plant(g)	RKL 11 (7.11); RKL 14 (5.80), RKL 23 (5.96); RKL 47 (6.42); RKL 300 (8.44); RKL 306 (6.08); RKL 308 (6.34); RKL 310 (7.78)	5.01	4.61
9	Root rot/wilt (in % after 35 days of sowing)	RKL 26; RKL 302; RKL 46; RKL 308; RKL 311	resistant	2.50
10	Root rot/wilt (in % after 110 days of sowing)	RKL 27; RKL 26; RKL 42; RKL 302; RKL 307	resistant	5.00

Table 2. Genetic variability for yield and its component traits in indigenous germplasm of lentil.

Characters	Mean	Range	GCV (%)	PCV (%)	h^2 (%)	Genetic Advance as per cent of mean
Days to flowering	70.35	55-85	12.40	12.45	99.19	17.90
Days to maturity	116.38	112-121	2.03	2.18	87.11	4.55
Plant height (cm)	48.74	38.80-65	11.36	12.46	83.13	10.40
Branches/plant	4.96	3-6.70	13.29	21.08	39.77	0.86
No. of pods per plant	88.24	39.20-214.70	31.70	36.27	76.40	50.37
No. seeds /pod	1.89	1.40-2.70	8.00	9.60	69.41	0.26
100-seed wt (g)	2.54	1.90-3.49	18.11	18.44	96.43	0.93
Yield per plant (g)	4.43	2.72-8.44	18.03	33.74	28.55	0.88

Table 3. Phenotypic (P) and genotypic (G) correlation coefficients in germplasm of lentil

Character		Days to maturity	Plant height (cm)	Fruiting branches per plant	No. of pods per plant	No. seeds /pod	100-seed wt (g)	Yield per plant (g)
Days to 50% flowering	G	0.64**	0.20	0.34**	0.27*	0.02	0.36**	0.41**
	P	0.60**	0.19	0.22	0.23	0.02	0.36**	0.22
Days to maturity	G		0.29*	0.30*	0.29*	0.06	0.45**	0.55**
	P		0.24	0.18	0.22	0.10	0.41**	0.25
Plant height (cm)	G			0.32*	0.13	0.12	0.22	0.42**
	P			0.21	0.10	0.07	0.19	0.19
Fruiting branches per plant	G				0.60**	0.16	0.19	0.46**
	P				0.58**	0.12	0.14	0.63**
No. of pods per plant	G					0.32*	0.05	0.84**
	P					0.24	0.05	0.74**
No. seeds /pod	G						-0.15	0.28*
	P						-0.13	0.18
100-seed wt (g)	G							0.42**
	P							0.24

*, ** Significant at 5 and 1 per cent level of significance, respectively

Table 4. Direct (in bold) and indirect effects of different component characters at genotypic level on seed yield.

Character	Days to 50 % flowering	Days to maturity	Plant height (cm)	Fruiting branches/ plant	No. of pods per plant	No. seeds per pod	100-seed wt(g)	Correlation with seed yield
Days to 50 % flowering	**0.00**	0.09	0.06	-0.09	0.24	0.00	0.11	0.41**
Days to maturity	0.00	**0.14**	0.08	-0.08	0.26	0.00	0.14	0.55**
Plant height (cm)	0.00	0.04	**0.28**	-0.09	0.12	0.00	0.07	0.42**
Branches/plant	0.00	0.04	0.09	**-0.28**	0.54	0.00	0.06	0.46**
Pods per plant	0.00	0.04	0.04	-0.16	**0.90**	0.01	0.02	0.84**
No. seeds per pod	0.00	0.01	0.03	-0.04	0.29	**0.03**	-0.04	0.28*
100-seed wt (g)	0.00	0.06	0.06	-0.05	0.05	-0.00	**0.31**	0.42**

Residual = 0.1857, *, ** Significant at 5 and 1 per cent level of significance, respectively

4. Discussion:

The estimates of different genetic variability parameters revealed that sufficient variability was present in the collected germplasm for days to flowering, plant height, number of fruiting branches per plant, pods per plant, 100-seed weight and yield per plant. This variability can be utilized effectively to develop high yielding early maturing cultivars through hybridization followed by selection. Genotype RKL 23 had better yielding ability (5.96 g/plant) along with early maturity (113.5 days) as compared to checks. Besides this, RKL 48, RKL 44 and RKL 45 were also early in flowering (55.00 days) and maturity (122.00 days) as compared to check varieties. RKL 11 (7.11 g); RKL 310 (7.78 g), and RKL 308 (6.34 g) have good yield potential.. These genotypes were also promising in other yield attributing traits such as number of fruiting branches per plant, number of pods per plant etc. (Table 1). Utilization of these promising genotypes in breeding programme can be helpful in development of short duration varieties, The PCV estimates were higher than their corresponding GCV for all the traits, however, the difference between the two was narrow for almost all the traits except seed yield per plant and number of branches per plant indicating that most of the characters were comparatively stable to environmental variation (Table 2). These results were in conformity with the findings of Rao and Yadav (1995) and Singh *et al.,* (2009).

Although GCV is an indicative of the presence of high degree of genetic variation, the amount of heritable portion of variation can be determined with the help of heritability estimates coupled with genetic advance. In the present study, days to flowering, 100-seed weight, days to maturity and plant height showed very high heritability. This suggests that selection for these traits may respond high to breed ideal genotypes in lentil. The high value of broad sense heritability may be due to additive gene effects, reports are also there in lentil to support the similar findings of Vir and Gupta, (1998) and Singh *et al.,* (2009). Though high heritability indicates the effectiveness of selection on the basis of phenotypic performance, it does not show any indication of the amount of genetic progress for selecting the best individuals. Therefore, heritability in conjunction with genetic gain is more useful than heritability alone in predicting the resultant effect for selecting the best genotype for a given trait. In the present study, high heritability estimates coupled with high genetic advance (Table 2) were observed for number of pods per plant, days to flowering and plant height indicating that these traits were under the additive genetic control and simple selection can be used for further improvement of these traits.

The genotypic correlations were generally higher than phenotypic correlation coefficients, which indicated the inherent relationship among the characters and masking effects of environments on the genotypic correlations. Seed yield was associated positively with all the yield attributing traits studied (Table 3). Yadav *et al.*, (2003) and Singh *et al.,* (2009) also reported positive association of seed yield with pods per plant. While making indirect selection for grain yield based on the correlated response, appropriate design and statistical tools should be used to reduce confounding effect of environmental factors and their interaction with genotypes in lentil. The path analysis results indicated that number of pods per plant, 100-seed weight, plant height, days to maturity and number of seeds per pod was important yield contributing characters (Table 4). The positive contribution of days to maturity indicates that our selection criteria should be focused on long reproductive phase to improve yield.

5. Conclusion

On the basis of correlation and path analysis studies, it can be concluded that number of pods per plant and 100- seed weight exerted high direct influence on seed yield per plant resulting in strong positive correlation and this should be taken into consideration while selecting desirable genotypes for higher seed yield in lentil. Since lentil is mostly grown under the receding moisture conditions during *rabi* season, earliness along with high biomass through rapid dry matter accumulation in pods should also be taken into account in selection process.

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