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Research Note

Studies on genetic variability, interrelationships association and path analysis in indigenous germplasm of Lentil in Madhya Pradesh, India

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Abstract
One hundred thirty nine lentil germplasm lines (collected from different parts of Madhya Pradesh) including 3 checks were studied for seed yield and its components for estimating genetic variability and correlation co-efficient. Analysis of variance for seed yield and its component showed significant differences among the genotypes for all ten traits. High heritability estimates were observed for all the traits except number of primary branches per plant. In general phenotypic coefficients of variation were greater than their corresponding genotypic coefficients of variation. High estimates of heritability coupled with high genetic advance and moderate to high GCV were observed for total number of pods per plant, number of effective pods per plant, number of seeds per plant, number of seeds per pod, 100 seed weight and seed yield per plant indicating that selection in such traits might be effective. Seed yield per plant exhibited positive and highly significant correlations with days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, total number of pods per plant, number of effective pods per plant, number of seeds per plant and number of seeds per pod. Path coefficient analysis showed that number of effective pods per plant, number of seeds per plant, and 100 seed weight showed maximum and positive direct effect on seed yield per plant. Hence these traits could be used for the improvement of seed yield resulting in the evolution of high yielding varieties of lentil.

Keywords
Lentil, Germplasm, Heritability, Variability

The lentil or daal or Masoor dal (*Lens culinaris* Medik) is a bushy annual plant of the legume family, grown for its lens-shaped seeds. With 26% protein, lentils have the third highest level of protein from any plant-based food after soybeans and hemp and is an important part of the diet in many parts of the world, especially in Indian subcontinent which have large vegetarian populations. In India, lentil is being grown in 1.56 M ha area with production 1.06 M t and productivity 678 kg/ha. Uttar Pradesh, Madhya Pradesh, Jharkhand, Bihar and West Bengal are the major lentil growing states in India, sharing 85% and 90% of the total area and production, respectively. Madhya Pradesh covers 6.2 Lakh ha area with production 2.3 Lakh tones and productivity 371 kg/ha (FAOSTAT 2012-13).

The Main concern with lentil is low yield potential because of narrow genetic base of the local cultivars. Therefore, the key to increase lentil yield in South Asia including Bangladesh is through widening the available genetic base (Erskine and Saxena, 1993). Indian lentils are exclusively of pilose type and show limited variations. This narrow genetic variability among indigenous germplasm has restricted breeding progress. Lentil is a short, slender, self-pollinated annual diploid (2n= 14) which exhibits a wide range of morphological variations. Considerable variations among the characters for use in breeding and selection programmes have been reported for various morphological characters (Sindhu and Mishra, 1982; Ramgiry *et al.*, 1989; Sarker and Erskine, 2001). The knowledge of genetic variation and relationships between populations is important to understand the available genetic variability and its potential use in breeding programs. Genetic variation between and within populations of crop species is a major interest of plant breeders and geneticists (Hayward & Breese, 1993). Quantitative traits provide an estimate of genetic diversity. Various numerical taxonomic techniques have been successfully used to classify and measure the pattern of phenotypic diversity in the relationship of germplasm collections in a variety of crops by many scientists in lentil (Fratini *et al*., 2007 and Tullu *et al.*, 2008), pea (Amurrio *et al*., 1995) and alfalfa (Smith *et al*., 1995).

The traditional approach of characterization and evaluation involves cultivation of accession sub samples and their morphological and agronomical description; a procedure facilitated by the use of internationally recognized descriptor lists (Erskine and Williams, 1980). Morphological characterization is the first step in the classification and description of any crop germplasm (Smith and Smith, 1989). One of the approaches for gene pool assembly is to collect material from diverse geographical origins with a concentration of accessions from proposed centres of diversity in individual samples (Laghetti *et al.*, 1998). Germplasm collection of crop plants is an excellent source of economically useful plant characters. However, in many crops the number of available accessions greatly surpasses the time a breeder can devote in a screening operation. The breeders must have a means of choosing the accessions that most likely possess the traits of interest. Targeted and more efficient utilization of germplasm by plant breeders can be achieved if the trait characteristics of accessions are known. Therefore, present study was undertaken to access and evaluate the genetic variability in lentil germplasm collected from different district and tribal areas of Madhya Pradesh on the basis of quantitative traits and to identify superior genotypes for future use.

One hundred thirty nine germplasm lines collected from different districts and tribal areas of Madhya Pradesh were used as material and were planted in a randomized block design with three replications at the Seed Breeding Farm, Department of Plant Breeding and Genetics, JNKVV, Jabalpur during *Rabi* 2013-14. Observations were recorded on five plants from each replication for ten economic traits *i.e.* days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, total number of pods per plant, number of effective pods per plant, number of seeds per plant, number of seeds per pod, 100-seed weight and seed yield per plant. Standard statistical procedure were used for the analysis of variance, genotypic and phenotypic coefficients of variation (Burton, 1952), heritability (Hanson *et al*., 1956) and genetic advance (Johnson *et al*., 1955). The genotypic and phenotypic correlation coefficients were computed using genotypic and phenotypic variances and co-variances (Al. Jibouri *et al*., 1958). The path coefficient analysis was done according to the method by Dewey and Lu (1959).

Evaluation of 139 germplasm accessions showed significant differences for the traits studied. The estimates of mean, range, genotypic and phenotypic coefficient of variation (GCV and PCV), heritability and genetic advance for various traits studied are presented in Table 1. The range was maximum (8.80-231.80) for number of seeds per plant, followed by total number of pods per plant (15.30-163.0), number of effective pods per plant (5.97-139.0) and days to maturity (85.67-123.7), whereas minimum range (0.73-3.23) for number of seeds per pod, followed by seed yield per plant (0.2-4.5). The traits showing wide range of variation furnish sample scope for efficient selection.

The phenotypic and genotypic coefficient of variation for seed yield per plant (65.50, 63.55), number of seeds per plant (62.27, 62.17), number of effective pods per plant (51.28, 50.99) and total number of pods per plant (41.59, 41.37) was high which reflected greater genetic variability among the accessions and responsiveness of the attributes for making further selection. This indicated the presence of maximum amount of genetic variability. However, moderate PCV and GCV was observed for number of seeds per pod (23.29, 22.59), number of secondary branches (20.73, 19.63) and 100 seed weight (20.54, 19.91), which accentuate the wide scope of selection for the improvement of these traits from a considerable amount of variability present.

The magnitude of GCV and PCV was low for the remaining traits. The genetic constants for the characters revealed that magnitude of phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits, its denoting environmental factors affecting their expression to some degree or other. Close correspondence between PCV and GCV for all the observed traits implied that it is relatively stable to environmental alteration. However the magnitude of difference between PVC and GVC was less for all the traits while the existent variation for the traits were mainly due to the genetic factor. There is adequate scope for selection based on these traits (Bicer and Sakar, 2004; Haddad, *et al.*, 2004, Solanki, 2006). Younis *et al*. (2008) found greater phenotypic coefficient of variation for pods per plant, seed yield and biomass. Higher values of phenotypic coefficients of variation for seed yield and biological yield have also been reported by Sadiq *et al*. (2000) and only for seed yield by Idrees *et al*. (2006).

The estimates of heritability in broad sense were high for all the observed traits except number of primary branches per plant (68 %), which suggested that the characters are least influenced by the environmental factors and also indicate the dependency of phenotypic expression which reflects the genotypic ability of cultivars to transmit the genes to their off-springs. Similar results were also reported by Rao and Yadav (1988), Chauhan and Singh (1998), Bicer and Sarkar (2008), Younis *et al*. (2008) and Rasheed *et al*. (2008). Jain *et al.* (1995) found high heritability for number of branches per plant, number of pods per plant, pod weight per plant, number of seeds per plant, seed index and harvest index except plant height and biological yield, Bicer and Sakar (2004) for seed weight and number of days to 50 % flowering and Singh and Srivastava (2013) for seed yield per plant, number of primary branches per plant and number of secondary branches per plant.

The genetic advance as percentage of mean was maximum for number of seeds per plant (127.87), seed yield per plant (127.01), number of effective pods per plant (104.42) and total number of pods per plant (84.75), whereas moderate genetic advance were observed for number of seeds per pod (45.12) and 100 seed weight (39.77), which explained that could be uplifted to a large extent. Characters showing high heritability with high genetic advance can be considered as favorable attributes for the improvement through selection and thus, could be improved upon by adapting selection without progeny testing.

High heritability coupled with high genetic advance was observed in total number of pods per plant, number of effective pods per plant and number of seeds per plant. Tyagi and Khan (2011) informed that pods per plant, days to 50% flowering and 100 seed weight showed high variability coupled with high genetic advance (per cent mean). According to Chakrabaorty and Hague (2000) high estimates of heritability in conjuction with high genetic advance was observed for grain yield, 100 grain weight and number of pods per plant. Studies on heritability and genetic advance indicate that simple selection among germplasm accessions can bring about significant improvement in these traits as the heritability and genetic advance were high. The expected genetic advance could have been biased towards higher side as it is based on the estimates of heritability in broad sense.

Estimation of simple correlation coefficient was made among ten important yield components with yield of the 139 lentil accessions. Genotypic and phenotypic correlation coefficients between different pairs of traits are presented in Table 2. In most of the events, genotypic correlation coefficient was higher than phenotypic correlation coefficient. This suggests that there was inherent affiliation among the traits but the environment minimized the phenotypic affiliation (Rathi, *et al.*, 2002).

The correlation coefficient revealed that seed yield per plant had positive association with days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, total number of pods per plant, number of effective pods per plant, number of seeds per plant and number of seeds per pod. Significant positive relationship between yield and vegetative growth represented by plant height could be assigned to photosynthetic factors. Similar finding were noticed by Solanki (2006); Singh *et al.* (2004), Chauhan and Singh, (2001) and Kumar *et al*.(2002).

The genotypic path coefficient for yield and yield contributing traits are presented in Table 3. Number of effective pods per plant showed high positive direct effect (0.468) on seed yield per plant, followed by number of seeds per plant (0.417) and 100 seed weight (0.168). The trait number of effective pods per plant showed substantial indirect positive contribution on seed yield per plant *via* total number of pods per plant (0.454) and number of seeds per plant (0.436). The indirect contribution of number of seeds per plant on seed yield was in high order through total number of pods per plant (0.378), number of effective pods per plant (0.386) and number of seeds per pod (0.227). Similar results were observed by Vir *et al*. (2001), Kumar *et al*.(2004), Singh *et al.* (2009) and Tyagi and Khan (2011). Tadesse *et al.* (2014) found negative direct effect for 100 seed weight.

The above finding illustrated that number of effective pods per plant, number of seeds per plant was the important components in selection for higher seed yield of lentil. This substantiated that the productivity of lentil is directly related with assimilation rate as reported earlier by Dixit and Dubey, (1984); Chakraborty and Haque ,(2000); Bicer and Sakar, (2004) and Kakde *et al*. (2005).

The unexplained variations in phenotype and genotype were 0.5363 and 0.5002, respectively. It further described the existence of some more factors, not considered here, and needed to be included in this study to account fully for the variation in seed yield of lentil. The result of the present experiment revealed that a wide variability existed among the collected lentil accessions. Also there was correlation of different yield elements with the yield of lentil.

It was also concluded from the results that very few germplasm accessions belonged to superior or highly desirable category like early maturity in < 90 days, number of effective pods per plant > 70, very large seed size > 3g/100 seed weight and >3g seed yield per plant and such germplasm lines may prove useful donors (Table 4 Figure 1, 2,3,4) for yield improvement.

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Table 1. Estimation of genetic parameters of different characters

Characters	Mean ±SEM	Range	PCV (%)	GCV (%)	Heritability (%)	Genetic advance (As % Mean)
DM	109.1 ± 0.57	85.7-123.7	8.38	8.33	98.9	17.06
PH (cm)	33.5 ± 0.63	20.3-46	14.48	14.10	94.9	28.31
PB	2.7 ± 0.12	2.2-3.5	13.56	11.18	68.0	18.99
SB	5.2 ± 0.20	3.1-9.5	20.73	19.63	89.6	38.28
TP	50.7 ±1.27	15.3-163	41.59	41.37	98.9	84.75
EP	37.1 ± 1.18	5.97-139	51.28	50.99	98.9	104.42
S/P	59.2 ±1.20	8.8-231.8	62.27	62.17	99.7	127.87
S/Pod	1.6 ±0.005	0.7-3.2	23.29	22.59	94.0	45.12
100 SW (g)	2.3 ±0.07	1.2-3.4	20.54	19.91	94.0	39.77
SY/P (g)	1.2 ±0.11	0.2-4.5	65.50	63.55	94.1	127.01

DM= days to maturity, PH= plant height, PB= number of primary branches per plant, SB= number of secondary branches per plant, TP= total number of pods per plant, EP= number of effective pods per plant, S/P= number of seeds per plant, S/Pod= number of seeds per pod, 100 SW= 100 seed weight, SY/P= seed yield per plant

Table 2. Correlation coefficients for different characters in 139 genotypes of lentil

Characters		Days to maturity	Plant height (cm)	Number of primary branches	Number of secondary branches	Total number of pods / Plant	Number of effective pods / plant	Number of seeds/Plant	Number of seeds /pod	100 Seed weight (g)	Seed yield /plant (g)
Days to maturity	rp	1.000									
	rg	1.000									
Plant height (cm)	rp	0.417**	1.000								
	rg	0.433	1.000								
Number of primary branches	rp	-0.124*	0.253**	1.000							
	rg	-0.163	0.274	1.000							
Number of secondary branches	rp	0.0004	0.066	0.497**	1.000						
	rg	-0.002	0.055	0.537	1.000						
Total number of pods / Plant	rp	0.355**	0.308**	0.211**	0.354**	1.000					
	rg	0.360	0.316	0.245	0.375	1.000					
Number of effective pods / plant	rp	0.322**	0.286**	0.173**	0.336**	0.967**	1.000				
	rg	0.326	0.293	0.199	0.352	0.970	1.000				
Number of seeds/Plant	rp	0.424**	0.325**	0.133**	0.294**	0.903**	0.924**	1.000			
	rg	0.427	0.334	0.156	0.309	0.906	0.926	1.000			
Number of seeds /pod	rp	0.464**	0.234**	-0.077	-0.007	0.234**	0.208**	0.528**	1.000		
	rg	0.481	0.251	-0.084	-0.010	0.250	0.232	0.546	1.000		
100 Seed weight (g)	rp	-0.338**	-0.103*	-0.063	-0.194**	-0.178**	-0.130**	-0.198**	-0.230**	1.000	
	rg	-0.356	-0.106	-0.074	-0.211	-0.184	-0.133	-0.204	-0.249	1.000	
Seed yield /plant (g)	rp	0.353**	0.291**	0.127**	0.282**	0.780**	0.806**	0.822**	0.358**	-0.030	1.000
	rg	0.365	0.307	0.148	0.303	0.798	0.825	0.841	0.383	-0.029	1.000

* and ** significant at 5% and 1% probability rg = genotypic correlation coefficient, rp = phenotypic correlation coefficient

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Table 3. Estimation of genotypic path coefficient for yield and yield contributing traits

Characters		Maturity	PH (cm)	PB	SB	TP/ Plant	EP/ Plant	S/Plant	S/Pod	100 SW (g)	Correlation of yield
DM	P	0.072	0.030	-0.010	0.000	0.026	0.023	0.031	0.034	-0.024	0.353
	G	0.084	0.036	-0.014	-0.0001	0.030	0.027	0.036	0.040	-0.030	0.365
PH (cm)	P	0.007	0.018	0.005	0.001	0.005	0.005	0.006	0.004	-0.002	0.291
	G	0.009	0.020	0.006	0.001	0.006	0.006	0.007	0.005	-0.002	0.307
PB	P	0.001	-0.001	-0.005	-0.003	-0.001	-0.001	-0.001	0.0004	0.0003	0.127
	G	0.001	-0.002	-0.007	-0.004	-0.002	-0.001	-0.001	0.001	0.001	0.148
SB	P	0.000	0.004	0.032	0.065	0.023	0.022	0.019	-0.001	-0.013	0.282
	G	-0.0001	0.004	0.043	0.079	0.030	0.028	0.025	-0.001	-0.017	0.303
TP/ Plant	P	-0.016	-0.014	-0.010	-0.016	-0.045	-0.043	-0.041	-0.011	0.008	0.780
	G	-0.030	-0.027	-0.021	-0.031	-0.084	-0.081	-0.076	-0.021	0.016	0.798
EP/ Plant	P	0.140	0.124	0.075	0.146	0.421	0.435	0.402	0.091	-0.056	0.806
	G	0.152	0.137	0.093	0.165	0.454	0.468	0.436	0.109	-0.062	0.825
S/Plant	P	0.171	0.131	0.054	0.119	0.364	0.372	0.403	0.212	-0.080	0.822
	G	0.178	0.139	0.065	0.129	0.378	0.386	0.417	0.227	-0.085	0.841
S/Pod	P	0.029	0.015	-0.005	-0.001	0.015	0.013	0.033	0.063	-0.014	0.358
	G	0.031	0.016	-0.005	-0.001	0.016	0.015	0.035	0.065	-0.016	0.383
100 SW (g)	P	-0.051	-0.016	-0.010	-0.029	-0.027	-0.020	-0.030	-0.035	0.151	-0.030
	G	-0.060	-0.018	-0.012	-0.035	-0.031	-0.022	-0.034	-0.042	0.168	-0.029

DM= days to maturity, PH= plant height, PB= number of primary branches per plant, SB= number of secondary branches per plant, TP= total number of pods per plant, EP= number of effective pods per plant, S/P= number of seeds per plant, S/Pod= number of seeds per pod, 100 SW= 100 seed weight, SY/P= seed yield per plant

Residual effect: P= 0.5363 G= 0.5002

Table 4. Promising germplasm lines for different traits

Desirable categories	Genotypes
Early (< 90 days)	JLC-134, JLC-135, JLC-136, JLC-137, JLC-138, JLC-139, JLC-140
Number of effective pods per plant (>70)	JLC-54, JLC-67, JLC-81, JLC-82, JLC-106, JLC-109, JLC-131, JLC-132
Very large seed size (>3g/100 seed wt)	JLC-2, JLC-3, JLC-5, JLC-6, JLC-7, JLC-10, JLC-78, JLC-80, JLC-83, JLC-93, JLC-137
Seed yield per plant (>3g)	JLC-35, JLC-67, JLC-106, JLC-117, JLC-132