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Genetic variability, correlation and path coefficient analysis for yield and yield components of selected lentil (*Lens culinaris* M.) genotypes

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ABSTRACT

Genetic variability, correlation coefficient and path coefficient were estimated for different morpho-physiological traits of 20 lentil genotypes. A significant genetic variation was observed for all the observed traits. Significantly higher PCV values than those of GCV for all the traits indicated that the traits are more influenced by the environment. The highest estimates of GCV and PCV were observed for seed yield plant^{-1} (23.80% and 24.03%, respectively) followed by number of pods peduncle^{-1} (16.91% and 19.80%, respectively). All the studied traits expressed high heritability ranging from 64.89% to 98.46% and the maximum was recorded for seed plant^{-1} (98.46%) followed by pod plant^{-1} (98.35%) and seed yield plant^{-1} (98.10%). High heritability along with high genetic advance was noticed for number of pods plant^{-1} (98.35% and 50.63, respectively) and number of seeds plant^{-1} (98.46% and 96.01, respectively) and high heritability coupled with high genetic advance as per cent of mean was observed for number of seeds plant^{-1} (98.46%, 39.80%) followed by number of pods plant^{-1} (98.35%, 33.03%) reflected the accumulation of additive gene and phenotypic selection for these characters will be effective for seed yield improvement. The study of associations among the different traits revealed that seed yield plant^{-1} was significantly and positively correlated with number of primary branches plant^{-1}, pods plant^{-1} and seeds plant^{-1} and 100-seed weight. Path analysis also reported that number of pods plant^{-1}, seeds pod^{-1} and 100-seed weight was related to the seed yield mostly through the direct positive effect. So, the traits viz., number of primary branches plant^{-1} and pod plant^{-1} and 100-seed weight should get the major importance during traits selection for lentil yield improvement as those traits had positive and significant correlation as well as direct positive effect with seed yield plant^{-1} and the information of wide genetic diversity for this traits could be used in future systematic lentil breeding programs for the improvement of seed yield.

Keywords: Lentil, genotype, genetic variability, correlation, path analysis

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1 Introduction

Lentil (*Lens esculenta* M.) is one of the most important pulse crops (Nath et al., 2014) and the third most ranked cool-season grain legume crops cultivated in the world after chickpea (*Cicer arietinum* L.) and pea (*Pisum sativum* L.) (FAO, 2015). It is cultivated in different parts the world including tropical, subtropical, and temperate regions (Nath et al., 2014). It one of the first domesticated grain legumes originated from the Near East center of origin (Zohary, 1999) and subsequently spread to central Asia and the Mediterranean Basin (Cubero, 1981; Lev-Yadun, 2000). Now, lentil (*Lens culinaris* Medik. subsp. culinaris) is an important cool season pulse crop of the Indian Subcontinent, the Middle East, North America, North Africa and West Asia including Bangladesh (Erskine et al., 1996). Lentil is grown in a total of 1.8 million hectares of land worldwide 60% cover South Asian region which includes Bangladesh, Burma, India, Nepal and Pakistan (Nazir et al., 1994). In Bangladesh, lentil is the second most legume crops considering cultivating area and production after grasspea but consumer's preference its rank first among pulse crops (Ahamed et al., 2014). In Bangladesh, the total land used for cultivation of lentil is 70983 ha resulting the production of 60537 tons lentil (BBS, 2009). Lentil like other legumes provides various environmental and ecological benefits through biological N_2 fixation (Khazaei et al., 2016). Regarding its cultivation, the most important factors of low production of lentil was the cultivation in marginal land, poor management practice and cultivation of local variety as well as sub-consciousness of farmers (Noor et al., 2017). In this perspective, the lentil genotypes must be characterized for so that breeders of Bangladesh can use the valuable information further for yield improvement (Gupta et al., 2013).

Genetic variation between and within populations of crop species is a major interest of plant breeders and geneticists for its improvement (Hayward and Breese, 1993). Knowledge of genetic variation and genetic relationship between lentil genotypes is important for efficient utilization of germplasm resources (Saini et al., 2004). Lentil is also a short, slender, self-pollinated annual diploid crops ($2n = 2x = 14$) which showed wide range of morphological variations and considerable variations among different quantitative characters have also been reported for use in breeding and selection programs in lentil (Sarker and Erskine, 2001). Therefore, the breeders have a great scope for yield improvement by utilizing the genetic variations exist in lentil germplasms (Roy et al., 2013). In most cases, direct selection for grain yield is misleading because it is greatly influenced by component characters and environment. Moreover, grain yield depends on a number of yield contributing characters (Nath et al., 2014). So, seed yield along with contributing characters should be studied through estimation of correlation among the characters for yield improvement (Das and Sarma, 2015). Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are very useful tool in detecting the amount of variability present in the germplasm (Idris, 2012).

The information on genetic diversity and correlation among different growth parameters for the improvement on lentil is limited in Bangladesh, so, it is very important to generate the information on the genetic variability exist in lentil germplasms and also important to investigate the association among yield components in lentil crops. Therefore, the present study was undertaken to evaluate the genetic variability and association correlation among the different morphological and physiological traits with total yield by determining the trait that contributed maximum to the variation for lentil yield improvement through breeding programs.

2 Materials and Methods

2.1 Plant materials

Twenty lentil genotypes collected from Plant Genetic Resources Centre (PGRC), Bangladesh Agricultural Research Institute (BARI), Gazipur, Bangladesh were used as experimental materials (Table 1).

2.2 Experimental details

The experiment was laid by randomized complete block design (RCBD) with three replications at the field laboratory of the Department of Genetics and Breeding, Bangladesh Agricultural University (BAU), Mymensingh. The seeds of 20 lentil genotypes were sown in the field on 8th November 2016. The land was prepared properly by 5-6 ploughing and cross ploughing. Urea, triple super phosphate and muriate of potash were used as source of nitrogen, phosphorus, potassium at the rate of 49.4, 98.8 and 49.4 kg ha^{-1}, respectively at the time of final land preparation (Akter et al., 2004). Three lines were maintained for each genotype and the length of line was 1.2 m; line to line distance was 30 cm. Application of different intercultural operations like weeding and thinning were done as and when necessary.

Five plants of each genotype were selected from each replication and uprooted to collect data. Days to first flowering was recorded from sowing date to the date when opening of a first flower were seen in the line. Days to fifty percent flowering and days to maturity were recorded from the date to sowing to the date when 50% of the plant had flowered and 90% of the pods turned brown, respectively. Plant height (cm) was taken from the ground level of the stem to tip of a plant was measured by centimeter scale. The

Table 1. List of lentil genotypes used in this experiment with their characters

Sl. No.	Genotypes	Characters
1	BARI Masur-6	Bushy plant, medium leaflet size and violet color flower
2	BARI Masur-7	Bushy plant, large leaflet size and violet color flower
3	BD-3804	Semi-erect plant, medium leaflet size and white color flower
4	BD-3806	Erect plant, medium leaflet size and violet color flower
5	BD-3808	Semi-erect plant, medium leaflet size and white color flower
6	BD-3810	Semi-erect plant, medium leaflet size and white color flower
7	BD-3945	Semi-erect plant, medium leaflet size and white color flower
8	BD-3948	Bushy plant, medium leaflet size and white color flower
9	BD-3975	Bushy plant, medium leaflet size and white color flower
10	BD-3985	Semi-erect plant, large leaflet size and white color flower
11	BD-3986	Bushy plant, large leaflet size and white color flower
12	BD-3995	Bushy plant, large leaflet size and white color flower
13	BD-4028	Semi-erect plant, large leaflet size and violet color flower
14	BD-4088	Bushy plant, medium leaflet size and violet color flower
15	BD-4090	Semi-erect, medium leaflet size and white color flower
16	BD-4095	Bushy plant, large leaflet size and white color flower
17	BD-4134	Bushy plant, medium leaflet size and white color flower
18	BD-5958	Semi-erect, small leaflet size and white color flower
19	BD-5959	Semi-erect, medium leaflet size and white color flower
20	BD-5983	Semi-erect, medium leaflet size and white color flower

total number of primary branches, the total number of pods per peduncle, the total number of pods, the number of seeds and the total number of seeds per pod for individual plant was counted of each genotype and the average was taken. 100-seed weight (g) was measured by taking one hundred clean sun dried seeds and weighed in gram (g) by digital weighing machine. Weight of the total seeds from individual five plants was recorded of each genotype and the average was taken to measure seed yield plant^{-1} (g).

2.3 Statistical analysis

Correlation co-efficient were estimated by using MSTATC and analysis of path coefficient was done with BASICA (Wright, 1921). Genotypic and phenotypic coefficient of variations were estimated according to Burton (1952) and Singh and Choudhury (1985). Heritability in broad sense (h^2b) was estimated according to the formula suggested by Johnson et al. (1955). Estimation of genetic advance was done by the formula of Johnson et al. (1955) and Allard (1960). Genetic advance as per cent of mean also was calculated by the formula of Comstock and Robinson (1952).

3 Results

3.1 Estimation of variability parameters

A wide range of variation was observed for eleven traits among twenty lentil genotypes. The scrutiny of data revealed that variance due to treatment was highly significant for all the traits (Table 2). Coefficient of variation study indicated that PCV was higher than the corresponding GCV for all the traits. Among the traits, seed yield plant^{-1} exhibited high estimates of GCV and PCV (23.80% and 24.03%, respectively) followed by number of pods peduncle^{-1} (16.91% and 19.80%, respectively) and number of seeds plant^{-1} (19.48% and 19.63, respectively). Other characters like days to maturity, days to 50% flowering and days to first flowering exhibited low GCV and PCV. The low difference between GCV and PCV was observed for most of the traits though slightly higher difference between GCV and PCV was observed for number of primary branches plant^{-1} and pods peduncle^{-1}. The traits under study exhibited quite high heritability estimates ranging from 64.89% in number of primary branches plant^{-1} to 98.46% in number of seeds plant^{-1}.

The maximum value of heritability was found for seed plant^{-1} (98.46%) followed by pod plant^{-1} (98.35%) and seed yield plant^{-1} (98.10%). Among all the traits, genetic advance was the highest in number of seeds plant^{-1} (96.01) followed by number of pods plant^{-1} (50.63) and the lowest was observed in number of seeds pod^{-1} (0.23) followed by 100-seed weight (0.28). Genetic advance as per cent of mean was the highest in seed yield plant^{-1} (48.56%) followed by number of seeds plant^{-1} (39.80%) and number of pods plant^{-1} (33.03%) while the lowest value was recorded in days to maturity (5.78%) followed by days to 50% flowering (7.98%) and days to first flowering (9.86%). Heritability in just a po-

Table 2. Quantitative traits of studied lentil genotypes

Traits†	PCV	GCV	PCV (%)	GCV (%)	Heritability (%)	GA	GA (%)
Days to first flowering	9.99	9.56	5.01	4.9	95.64	6.23	9.86
Days to 50% flowering	9.46	8.84	4.15	4.01	93.44	5.92	7.98
Days to maturity	10.64	10.15	2.95	2.88	95.3	6.41	5.78
Plant height (cm)	8.53	7.41	8.27	7.71	86.86	5.23	14.8
Primary branch plant^{-1} (no.)	1.21	0.79	16.29	13.12	64.89	1.47	21.77
Pods peduncle^{-1} (no.)	0.14	0.1	19.8	16.91	72.93	0.56	29.74
Pods plant^{-1} (no.)	624.56	614.25	16.3	16.17	98.35	50.63	33.03
Seeds plant^{-1} (no.)	2240.4	2206.03	19.63	19.48	98.46	96.01	39.8
Seeds pod^{-1} (no.)	0.014	0.013	7.56	7.29	92.86	0.23	14.47
100-seed weight (g)	0.023	0.02	9.69	9.25	91.18	0.28	18.17
Seed yield plant^{-1} (g)	0.79	0.77	24.03	23.8	98.1	1.79	48.56

† PCV = penotypic coefficient of variation, GCV = genotypic coefficient of variation, GA = genetic advance

sition with genetic advance would provide a more trustworthy index of selection value (Johnson et al., 1955). High heritability coupled with high genetic advance as per cent of mean was observed for number of seeds plant^{-1} (98.46%, 39.80%) followed by number of pods plant^{-1} (98.35%, 33.03%) and seed yield plant^{-1} (98.10%, 48.56%).

3.2 Estimation of correlation coefficients

The correlation coefficients among the eleven traits are presented in Table 3. Positive and significant correlation was found in number of primary branches plant^{-1}, number of pods plant^{-1}, number of seeds plant^{-1} and 100-seed weight with seed yield plant^{-1} (0.56*, 0.88**, 0.86**, and 0.73**, respectively) where days to maturity, number of pods peduncle^{-1} and number of seeds pod^{-1} had positive but non-significant correlation with seed yield plant^{-1} (0.03, 0.22 and 0.44, respectively). Other characters showed negative and non-significantly correlated with seed yield. Days to 50% flowering showed highly significant and positive correlation with days to first flowering (0.92**). Days to first flowering and days to 50% flowering represent positive and highly significant correlation with days to maturity (0.85** and 0.89**, respectively). Number of primary branches plant^{-1} and pods plant^{-1} showed positive and highly significant correlation with number of seeds plant^{-1} (0.63** and 0.94**, respectively). Number of primary branches plant^{-1} and number of seeds plant^{-1} showed positive and highly significant correlation with number of seeds pod^{-1} (0.50* and 0.68**, respectively).

3.3 Estimation of path coefficients

The result of direct and indirect effects of ten yield contributing characters is presented in Table 4. Path coefficient analysis shown that, days to maturity, number of primary branches plant^{-1}, pods peduncle^{-1} (0.09), pods plant^{-1} and seeds pod^{-1} and 100-seed weight had direct positive effect on seed yield plant^{-1} (0.15, 0.02, 0.09, 1.34, 0.44 and 0.39, respectively). The highest positive indirect effects on seed yield plant^{-1} were obtained from number of seed plant^{-1} (1.13) via number of pods plant^{-1} followed by number of primary branches plant^{-1} (0.74) via number of pods plant^{-1}, 100-seed weight (0.58) via number of pods plant^{-1} and number of seed pod^{-1} (0.52) via number of pods plant^{-1}. In this study, days to first flowering, days to 50% flowering, plant height, number of seeds plant^{-1} had direct negative effect on seed yield plant^{-1}. The residual effect was 0.202.

4 Discussion

A wide range of variation for seed yield and yield contributing traits among the lentil genotypes indicating the presences of genetic differences among the traits and the use of these traits might be effective in crop improvement program. The difference between PCV and GCV indicates the influences of environmental factors on these traits (Table 2). So, there is adequate scope for the improvement of genotypes through selection based on these traits (Biçer and Şakar, 2008; Haddad et al., 1982; Solanki, 2006).

The higher value of PCV was found for all the traits than GCV indicating that environmental factors affecting the expression of traits to some extent (Pandey et al., 2015). The results of present study showed that seed yield plant^{-1} exhibited high estimates of GCV and PCV followed by seed yield plant^{-1} and number of pods peduncle^{-1} and seeds plant^{-1} reflected greater genetic variability among the accessions and responsiveness of this attributes for making further selection for improvement. Higher values of PCV for seed yield have also been reported by Sadiq et al. (2000) and Idress et al. (2006). Tyagi

Table 3. Coefficient of correlation among quantitative traits of studied lentil genotypes

Traits†	DFF	DPF	DTM	PHT	PBP	PPD	PPP	SPP	SPD	HSW
DPF	0.92**									
DTM	0.85**	0.89**								
PHT	0.14	0.1	0.05							
PBP	−0.1	−0.11	−0.15	−0.1						
PPD	0.05	−0.04	0.03	−0.3	0.25					
PPP	−0.03	0.000009	−0.06	−0.18	0.55*	0.05				
SPP	0.01	0.02	0.01	−0.16	0.63**	0.18	0.94**			
SPD	0.09	0.02	0.11	−0.03	0.50*	0.33	0.39	0.68**		
HSW	−0.05	0.04	0.16	−0.31	0.28	0.11	0.43	0.37	0.08	
SYP	−0.07	−0.02	0.03	−0.32	0.56*	0.22	0.88**	0.86**	0.44	0.73**

* and ** indicate significant at $p \leq 0.05$ and $p \leq 0.01$ probability, respectively

Table 4. Partitioning of phenotypic correlation coefficients into direct and indirect effects of quantitative traits of studied lentil genotypes by path analysis

Traits†	DFF	DPF	DTM	PHT	PBP	PPD	PPP	SPP	SPD	HSW	Cor. SYP
DFF	**−0.09**	−0.07	0.13	−0.01	−0.002	0.01	−0.04	−0.01	0.03	−0.02	−0.07
DPF	−0.08	**−0.08**	0.14	−0.004	−0.002	−0.004	0.00001	−0.01	0.001	0.02	−0.02
DTM	−0.07	−0.07	**0.15**	−0.002	−0.003	0.002	−0.08	−0.01	0.05	0.06	0.03
PHT	−0.01	−0.01	0.01	**−0.04**	−0.002	−0.03	0.24	0.13	−0.01	−0.12	−0.32
PBP	0.01	0.01	−0.02	0.004	**0.02**	0.02	0.74	−0.55	0.22	0.11	0.56*
PPD	−0.004	0.003	0.003	0.01	0.01	**0.09**	0.07	−0.15	0.14	0.04	0.22
PPP	0.002	0	−0.01	0.01	0.01	0.004	**1.34**	−0.82	0.17	0.17	0.88**
SPP	−0.001	−0.001	0.002	0.01	0.01	0.02	1.13	**−0.87**	0.3	0.15	0.86**
SPD	−0.01	−0.002	0.02	0.001	0.01	0.03	0.52	−0.59	**0.44**	0.03	0.44
HSW	0.004	−0.003	0.02	0.01	0.01	0.01	0.58	−0.32	0.03	**0.39**	0.73**

† DFF = days to first flowering, DPF = days to 50% flowering, DTM = days to maturity, PHT = plant height (cm), PBP = primary branches plant^{-1} (no.), PPD = pods peduncle^{-1} (no.), PPP = pods plant^{-1} (no.), SPP = seeds plant^{-1} (no.), SPD = seeds pod^{-1} (no.), HSW= 100-seed weight (g), SYP = seed yield plant^{-1} (g), Cor. SYP = correlation to SYP; Bold figures indicate the direct effect of different yield contributing characters on grain yield plant^{-1}; Residual effect = 0.202 probability, respectively

and Khan (2011) also reported high GCV and PCV in seed yield plant^{-1}. The low difference between GCV and PCV for days to first flowering, days to 50% flowering, days to maturity, plant height, number of pods plant^{-1}, seeds plant^{-1} and seeds pod^{-1}, 100-seed weight and seed yield plant^{-1} indicated very little influence of environment is on these characters of lentil. Gautam et al. (2014) also found low difference between GCV and PCV for days to 50% flowering and days to maturity. The difference between GCV and PCV was slightly higher for number of primary branches plant^{-1} and pods peduncle^{-1} which indicates that influence of environment is a bit more. Crippa et al. (2009) also observed more difference between GCV and PCV for number of primary branches plant^{-1} and pods per plant in lentil.

Heritability is an important parameter for studying quantitative traits. GCV and PCV are not quite enough to determine the heritable portion. Thus, a population expressing a larger proportion of genetic variability for a particular character or group of characters will be more amenable to selection (Furlan et al., 2012). All the traits in the present investigation showed high heritability indicating their importance for getting priority for the improvement of seed yield of lentil through the selection of different traits. Singh and Srivastava (2013), Biçer and Şakar (2008) and Tyagi and Khan (2011) also found high heritability for these traits. The genetic advance is a suitable indicator of the progress that can be expected as result of exercising selection on the pertinent genotypes. Heritability in combination with genetic advance would give a more dependable selection importance (Johnson et al., 1955). Because of environmental contact heritability estimation is not alone sufficient to measure genetic potentiality. In this investigation, high heritability along with high genetic advance was found in number of pods plant^{-1} and number of seeds plant^{-1} indicates the accumulation of more additive genes leading to further improvement of their performance. High heritability joined with high genetic advance also observed by Chakraborty and Haque

(2000) for grain yield, 100- grain weight and number of pods plant^{-1}. High heritability joined with high genetic advance as per cent of mean was observed for the traits number of primary branches plant^{-1}, pods peduncle^{-1}, pods plant^{-1} and seeds plant^{-1}, and seed yield plant^{-1}indicates the role of additive gene expression for these traits and would facilitate better scope for improvement of these traits through direct selection. These results are in agreement with Rasel et al. (2018). Pandey et al. (2015) also found high heritability along with high genetic advance as per cent of mean for number of pods plant^{-1}, seed yield plant^{-1}, seeds plant^{-1}, number of effective pods plant^{-1} and total number of pods plant^{-1}.

Yield is the outcome of combine interaction of several contributing characters and environment (Sharifi et al., 2017). Direct selection for yield trait may not be much effective and therefore, other correlated yield component traits should be taken in to consideration (Kumar et al., 2017). The positive and significant correlation of number of primary branches plant^{-1}, number of pod plant^{-1}, number of seed plant^{-1} and 100-seed weight with seed yield plant^{-1} indicates that additive gene is less affected by the influence of environment and seed yield plant^{-1} can be directly improved by selecting those characters. Similar results also observed by Mekonnen et al. (2014), Tadele et al. (2014) and Abo-Hegazy et al. (2012) who stated positive and significant correlation in number of pods plant^{-1}, number of seeds plant^{-1} and 100-seed weight with seed yield plant^{-1}. Similar finding were also noticed by Singh et al. (2016), Solanki (2006), Chauhan and Singh (2001). Besides, days to maturity, number of pods peduncle^{-1} and number of seed pod^{-1} were correlated positively but non-significantly with seed yield plant^{-1}.

The correlation coefficient alone is enough to interpret the cause and effect relationships among the traits and ultimately with yield. In this case, path coefficient analysis partitions into direct and indirect matrix presenting correlation in a more meaningful way for better interpretation of cause and effect (Wright, 1921; Mohsin et al., 2009). The results of present study reported days to maturity, number of primary branches plant^{-1}, number of pods peduncle^{-1}, number of pods plant^{-1}, number of seeds pod^{-1} and 100-seed weight had positive direct effects on seed yield plant^{-1} suggested that direct selection of those characters for the improvement of seed yield plant^{-1} in lentil would be more effective. Earlier Mekonnen et al. (2014) and Abo-Hegazy et al. (2012) also showed positive direct effects of number of pods plant^{-1} on seed yield plant^{-1}. Days to first flowering, days to 50% flowering, plant height, number of seeds plant^{-1} earn direct negative effect on seed yield plant^{-1}. Tadele et al. (2014) also observed negative direct effect on seed yield with plant height, days to 50% flowering, 90% maturity and 100-seed weight at genotypic level. In this study, the residual effect indicating that the ten characters contributed 80 percent of variability in seed yield plant^{-1} studied in path analysis. This may be due to several reasons such as may be other causal factors (characters) that not involved in the analysis contribute more towards yield and sampling errors. Das and Sarma (2015) also reported residual effects of genotypic and phenotypic paths were 5.24 and 14.94 per cent respectively, indicating major contribution of the characters under study toward the causal relationships, and hence most of the variation in yield.

5 Conclusions

Genetic variability parameters revealed that number of pods peduncle^{-1}, number of pods plant^{-1} and number of seeds plant^{-1} could be the important parameters for the improvement of lentil genotypes for seed yield. On the other hand, number of primary branches plant^{-1}, number of pod plant^{-1} and 100-seed weight had positive and significant correlation as well as direct positive effect with seed yield plant^{-1}, so these traits should get the major priority for the yield improvement in lentil.

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Conflict of Interest

The authors declare that there is no conflict of interests regarding the publication of this paper.

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