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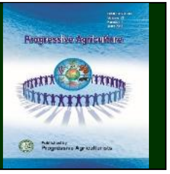

Evaluation of genetic variability and trait association for yield improvement of Lentil

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ABSTRACT

Lentil is a nutritious food and one of the world's oldest domesticated legumes. The present studyevaluatedthe nature and magnitude of variability, heritability, genetic advance and association among the yield and yield contributing traits in 24 lentils (*Lens culinaris* M.) genotypes. From the 13 traits considered, phenotypic coefficients of variation (PCV) were found higher than genotypic coefficient of variation (GCV) which indicates less effect of the environment for the expression of traits studied. Seed weight per plants demonstrated the highest PCV and GCV (60.26 & 59.87) followed by number of seeds per plant (49.14 & 48.97) and number of pods per plant (48.58 & 47.95, respectively). Most of the traits showed high heritability as days to maturity exhibited the highest heritability (99.96%) followed by number of seeds per plant (99.33%). Genetic advance as percent of mean was higher for seed weight per plant (122.58%) and number of seeds per plant (100.56%). Among the traits, number of seeds per plant (0.95& 0.94) and number of pods per plant (0.94 & 0.92) showed positive and significant correlation with seed weight per plant at both phenotypic and genotypic correlation. Consequently, path analysis revealed positive and direct effect of number of pods per plant (0.310&372) and number of seeds per plant (0.770&0.659) on seed weight per plant in both genotypic and phenotypic level, respectively. Based on the genetic analysis of 13 characters, number of pods per plant, number of seeds per plant,1000-seed weight and seed weight per plant were found as the most superior traits can be used in hybridization program for the development of high yielding lentil genotypes.

Introduction

Lentil (*Lens culinaris* M.) is an edible legume and a member of the genus *Lens* of the Viceae tribe in the Leguminosae (Fabaceae) family. It's an essential legume crop in North Africa, West Asia, the Middle East, the Indian Subcontinent and North America (Erskine, 1996). In Bangladesh, it plays a vital role in diet as a cheap source of protein. Total 2.22% of the cultivated land area in Bangladesh is under in pulse cultivation (BBS, 2019). Among pulses, in terms of area (349109 acre) and production (177354 M.ton) lentil is the top most important pulse crop and ranks highest in total consumptions (BBS, 2020). Lentil contains 28% protein for human consumption and its

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straw is a valued animal feed, consisted of 2% minerals and 59% carbohydrates (Frederick et al., 2006).

For crop improvement genetic variability is of prime importance and genetic variation between and within crop species populations is a major interest for plant breeders and geneticists for its improvement (Hayward and Breese, 1993). For efficient utilization of germplasm resources, the knowledge of genetic variation and genetic relationship between lentil genotypes is very important (Saini et al., 2004). If the variability of the population is high, the opportunity of producing desired crop variety will be also high (Allard, 1960). Worldwide, lentil possesses wide range of morphological variations, especially prominent variations among various quantitative characters also have been noted for use in breeding and selection programs in lentil (Sarkar and Erskine, 2001).

On the basis of nature and importance of genotypic and phenotypic correlations, breeding programs may calculate such characters to provide the most wanted genotype (Bicer and Sakar, 2008). So, it is necessary to evaluate genotypic and phenotypic correlation among the yield attributing characters (Tyagi and Khan, 2011). Grain yield of lentil is correlated with primary yield components and also with morphological and physiological characters. The yield contributing characters are also correlated between themselves (Cristobal et al., 2014). Therefore, the relationship between grain yield and yield contributing characters establishes a complex chain of network and it can be analyzed by the way through path coefficient analysis (Rahman and Sarwar, 1982). Therefore, to set up the selection criteria more specific for breeding of lentil, path analysis is important method to address (Rahman and Sarwar, 1982). Moreover, the breeders have a great scope for yield improvement by utilizing the genetic variations exist in lentil germplasms (Sarker and Erskine, 2001). In most cases,a number of yield contributing characters influence grain yield (Nath et al., 2014).In Bangladesh, the information of genetic diversity and correlation among different parameters for the improvement on lentil is limited. So, generating information on the extent of genetic variability exists in lentil germplasm as well and investigating character association among yield components of lentil is very important. Therefore, the aim of this experiment was to study the genetic variability and character association among yield attributing morphological characteristics by analyzing the different genetic components.

Materials and Methods

***Experimental materials*:** A total of 24 lentil genotypes were collected from Bangladesh Agricultural Research Institute (BARI), Bangladesh Institute of Nuclear Agriculture (BINA), Bangladesh Agricultural University (BAU) and International Center for Agricultural Research in the Dry Area, Syria (ICARDA) to conduct the experiment (Table1).

***Experimental details*:** The study was carried out at the Farm Laboratory of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU), Mymensingh during November 2017 to April 2018, following Randomized Complete Block Design (RCBD) experiment with three replications. The individual plot size was 1.5x25 cm, replication to replication distance was 50 cm. The plot was prepared by ploughing with power tiller followed by harrowing and with the help of ladder clods were broken into small pieces. After laddering all the weeds and stubbles were removed from the field. The seeds of 24 lentil genotypes were sowing in the field on 12 November, 2017. Thinning was done 25 days after sowing and weeding was done twice, the first during thinning and the second about two months of sowing. Different genotypes matured at different times. The harvesting was completed by 4 April 2018.Ten plants from each plot were randomly selected to collect data and these were harvested by uprooting. Data were recorded for 13 yield and yield contributing traits, *viz.*, days to 50% flowering, days to maturity, plant height, number of primary branches, number of secondary branches, number of tertiary branches, number of pods per plant.

seed length, seed width, seed length width ratio, number of seeds per plant, weight of 1000 seeds, seed weight per plants from 10 randomly selected plants per genotypes in each replicate.

Table 1. List of lentil genotypes used in this study with their origin.

Sl No.	Genotypes	Source
1	BARI Mashur-1	BARI
2	BARI Mashur-4	BARI
3	BARI Mashur-5	BARI
4	BARI Mashur-6	BARI
5	BARI Mashur-7	BARI
6	BARI Mashur-2	BARI
7	BARI Mashur-3	BARI
8	Binamasur-1	BINA
9	Binamasur-8	BINA
10	Binamasur-9	BINA
11	Binamasur-5	BINA
12	Binamasur-6	BINA
13	BM 507	BAU
14	BM 868	BAU
15	BLX04004-12	ICARDA
16	1LL2508	ICARDA
17	BLX08008-1	ICARDA
18	1LL2530	ICARDA
19	BLX08800-12	ICARDA
20	1LL5127	ICARDA
21	1LL4707	ICARDA
22	BLX088025	ICARDA
23	1LL5099	ICARDA
24	BLX08832	ICARDA

***Statistical analysis*:** Analysis of variance was performed using Minitab 18©.Genotypic and phenotypic variance and heritability in broad sense (h^2_b) were calculated following the formula given by Johnson et al., (1955) and Hanson et al., (1956). Genotypic and phenotypic coefficients of variations were estimated according to Burton (1952) and Singh and Chaudhury (1985). Genetic advance (GA) was calculated according to the formula of Johnson et al., (1955) and Allard (1960). Estimation of genetic advance in percent of mean (GA%) was done with the help of formula given by Comstock and Robinson (1952). The phenotypic and genotypic correlations were estimated by the formula suggested by Miller et al. (1991). Path coefficient was estimated according to the method described by Lynch and Walsh, (1998).

Results and Discussion

***Estimation of genetic variability*:** Estimates of phenotypic and genotypic variances, PCV and GCV, heritability (%), GA and GA% for yield contributing traits were shown in Table 2. For all the traits phenotypic variances were found higher than the genotypic variances (Table 2). Among the traits, number of seeds per plant demonstrated high phenotypic and genotypic variances (1293.86 and 1285.17, respectively) followed by number of pods per plant (690.73 & 673.09, respectively). On the other hand, lowest phenotypic and genotypic variances were found for seed width (0.14 & 0.13, respectively) followed by seed length width ratio (0.18 & 0.16, respectively).

For all the traits, phenotypic coefficients of variances (PCV) were found slightly higher or equal to genotypic coefficients of variance (GCV). Seed weight per plants was found with the highest PCV (60.26) and GCV (59.87) followed by number of seeds per plant (49.14 & 48.97) and number of pods per plant (48.58 & 47.95). On the other hand, the lowest values of PCV and GCV were demonstrated by days to maturity (8.46, 8.46, respectively) and days to 50% flowering (9.76, 9.71, respectively).

For agronomic and economic advantages by improving plant characters, breeding is the ultimate method (Ezzat and Ashmawy, 1999). Here, genotypes showed a wide range of variation, which provides a large scope for selection of superior and desired genotype by the plant breeders for the improvement of lentil.

In the present study, number of seeds per plant showed highest phenotypic and genotypic variances followed by number of pods per plant. These two traits are very important because genotypes with higher number of pods might result higher seed yield. Here, high genotypic and phenotypic variances were observed for this character suggested that the characters have low environmental effects. This finding is similar to Tattimani et al. (2011) and Tyagi and Khan (2011).

Table 2. Estimation of genetic parameters for 13 characters associated with 24 lentil genotypes.

Characters	Mean	Range		Phenotypic variance	Genotypic variance	PCV	GCV	h^2b	GA	GA%
		Maximum	Minimum							
DFF	89.04	107.00	74.00	75.54	74.72	9.76	9.71	98.91	19.90	17.72
DM	115.04	135.00	89.00	94.77	94.73	8.46	8.46	99.96	19.85	17.25
PH	33.35	56.77	20.53	67.60	64.65	24.64	24.10	95.64	16.26	48.72
NPB	2.52	4.80	2.00	0.46	0.38	26.80	24.41	82.07	1.14	45.14
NSB	5.72	11.60	2.80	4.33	4.20	36.34	35.77	96.77	4.15	72.47
NTB	23.85	49.40	8.20	108.22	106.90	43.62	43.35	98.78	21.17	88.75
NPP	54.10	118.27	18.13	690.73	673.09	48.58	47.95	97.45	52.76	97.51
SL	3.74	4.51	1.85	0.312	0.26	14.91	13.61	83.47	0.96	25.62
SW	1.93	2.25	0.48	0.14	0.13	19.31	18.60	91.24	0.72	36.00
SLWR	2.00	3.85	1.65	0.18	0.16	21.19	19.98	85.84	0.76	37.86
NSP	73.19	169.87	23.07	1293.86	1285.17	49.14	48.97	99.33	73.60	100.56
1000SW	20.24	26.50	13.50	13.96	12.31	18.46	17.33	88.18	6.79	33.53
SWP	1.47	3.91	0.44	0.80	0.79	60.26	59.87	98.01	1.81	122.58

Note: DFF=Days to 50% flowering, DM= Days to maturity, PH=Plant height, NPB= Number of primary branches, NSB= Number of secondary branches, NTB= Number of tertiary branches, NPP=Number of pods per plant. SL= Seed length, SW= Seed width, SLWR= Seed length width ratio, NSP= Number of seeds per plant, 1000 SW= Weight of 1000 seeds, SWP= Seed weight per plants.

The low environment effects on trait expression have been also confirmed by the narrow gap between the PCV and GCV for all the characters as it suggested Gautam et al. (2014). On the other hand, higher environmental influence was found on days to 50% flowering and days to maturity as these traits were characterized with lower values of GCV and PCV. The low values of GCV and PCV for days to maturity and days to 50% flowering were also reported in lentil by Gautam et al. (2014).

Analysis of heritability is used to calculate the comparative performance of inequality in genetic and non-genetic factors in a population's total phenotypic variance. In selective breeding it is an important concept. Here, high heritability (>80%) was found for all the traits considered.

Among all the traits, number of seeds per plant was showed highest genetic advance (73.60) followed by number of pods per plant (52.76) and the lowest was found for seed width (0.72) followed by seed length width ratio (0.76) and seed length (0.96).

Genetic advance as percent of mean (GAM) recorded highest for seed weight per plants (122.58%) followed by number of seeds per plant (100.56%). By contrast, days to maturity (17.25%) was provided with lowest GAM value followed by days to 50% flowering (17.72%). High heritability combined with high genetic advance as percent mean was found for days to maturity (99.96%, 17.25%) followed by number of seeds per plant (99.33%, 100.56%) and days to 50% flowering (98.91%, 17.72%).

An assessment of heritability and non-heritable components in the total variability observed is indispensable in adopting suitable breeding procedure (Gautam et al., 2014). In this experiment, all the traits showed high heritability which indicates their importance for getting priority for the improvement of yield of lentil through the selection of different traits. Tyagi and Khan (2011) also enlisted high heritability for the traits considered in the present study of lentil.

The estimation of high heritability accompanied by high GA observed indicates that heritability is mainly due to additive gene effect and selection may be effective to improve that trait. In the present investigation, highest GA was obtained by number of seeds per plant followed by number of pods per plant, but lowest GA was found in seed width followed by seed length width ratio and seed length. These traits were found also found similar GA by previous studies by Gautam et al. (2014) in lentil.

High genetic advance along with high heritability usually considered as the best reliable selection criteria for breeding (Johnson et al., 1955). High heritability combined with high GA% was found for days to maturity followed by number of seeds per plant and days to 50% flowering. Pandey et al., (2015) also found the similar result in lentil.

***Estimation of correlation coefficients*:** Estimation of correlation coefficient at genotypic and phenotypic level for individual traits was presented in Table 3 & 4.

Table 3. Genotypic correlation coefficient between yield and yield contributing characters in lentil.

Characters	DM	PH	NPB	NSB	NTB	NPP	SL	SW	SLWR	NSP	1000SW	SWP
DFF	0.59**	0.38	0.03	0.09	0.46*	-0.21	-0.24	-0.29	0.22	-0.21	-0.32	-0.28
DM		0.64**	0.19	0.29	0.52**	-0.23	-0.23	-0.24	0.19	-0.24	-0.31	-0.29
PH			0.33	0.23	0.46*	-0.17	-0.43*	-0.34	0.17	-0.27	-0.49*	-0.34
NPB				0.38	0.45*	0.31	0.14	0.07	-0.06	0.24	-0.25	0.33
NSB					0.37	0.15	-0.18	-0.18	0.12	0.17	-0.37	0.12
NTB						0.29	-0.19	-0.23	0.04	0.16	-0.54**	0.11
NPP							-0.14	-0.14	0.02	0.90**	-0.25	0.94**
SL								0.96**	-0.78**	-0.22	0.40	0.01
SW									-0.87**	-0.21	0.40	-0.02
SLWR										0.08	-0.15	-0.04
NSP											-0.30	0.95**
1000SW												-0.15

Note: * and ** indicate significant at 5% and 1% level of probability, respectively.

A highly significant and positive correlation at both genotypic and phenotypic level was found for days to 50% flowering with days to maturity (0.59) and number of tertiary branch (0.46), number of pods per plants with seed weight per plant (0.94 and 0.92) and number of pods per plant (0.90 and 0.89). Besides, at genotypic and phenotypic level days to maturity demonstrated a highly significant correlation with plant height (0.64 and 0.63) and number of tertiary branch (0.52 and 0.53). Moreover, significant correlation between number of primary branch and number of tertiary branch (0.45) was only found at genotypic level. Plant height exhibited a positive correlation with number of tertiary branch (0.46) at genotypic level but negative significant correlation was found with seed length (-0.43 and -0.42) and 1000 seed weight (-0.49 and -0.44) at both genotypic and phenotypic level, respectively. Moreover, seed length showed highly significant and positive correlation with seed width (0.96 and 0.84) and negative correlation with seed length width ratio (-0.78 and -0.56) at genotypic and phenotypic level, respectively. Number of tertiary branches showed highly significant and negative correlation with 1000 seed weight (-0.54) at genotypic level but positive correlation (0.51) at phenotypic level.

Table 4. Phenotypic correlation coefficient between yield and yield contributing characters in lentil.

Characters	**DM**	**PH**	**NPB**	**NSB**	**NTB**	**NPP**	**SL**	**SW**	**SLWR**	**NSP**	**1000SW**	**SWP**
DFF	0.59**	0.39	0.03	0.09	0.46*	-0.21	-0.22	-0.28	0.21	-0.20	-0.28	-0.28
DM		0.63**	0.21	0.30	0.53**	-0.23	-0.21	-0.23	0.18	-0.24	-0.28	-0.29
PH			0.28	0.24	0.46*	-0.16	-0.42*	-0.32	0.14	-0.27	-0.44*	-0.33
NPB				0.34	0.39	0.31	0.14	0.07	-0.04	0.22	-0.18	0.29
NSB					0.36	0.14	-0.18	-0.17	0.10	0.17	-0.04	0.11
NTB						0.28	-0.18	-0.22	0.04	0.16	0.51**	0.12
NPP							-0.12	-0.13	0.02	0.89**	-0.23	0.92**
SL								0.84**	-0.56**	-0.19	0.37	0.01
SW									-0.87**	-0.21	0.35	-0.03
SLWR										0.07	-0.13	-0.03
NSP											-0.27	0.94**
1000SW												-0.15

Note: * and ** indicate significant at 5% and 1% level of probability, respectively; DFF=Days to 50% flowering, DM= Days to maturity, PH=Plant height, NPB= Number of primary branches, NSB= Number of secondary branches, NTB= Number of tertiary branches, NPP=Number of pods per plant. SL= Seed length, SW= Seed width, SLWR= Seed length width ratio, NSP= Number of seeds per plant, 1000 SW= Weight of 1000 seeds, SWP= Seed weight per plants.

The relationship between grain yield and different yield contributing characters of lentil were studied through analysis of correlation coefficient at genotypic and phenotypic level.

The positive correlations of number of pods per plants and number of seeds per plants with seed yield is expected, as increased number of pods and seeds ensures increased yield (Singh et al. 2012; Malek et al. 2014). Therefore, number of pods and seeds per plants should be considered as selection criteria for developing high yield lentil varieties. For obtaining higher seed yield per plant, number of pods per plants should be increased as well, and a positive correlation between number of pods per plant and number of seed per plant in the present study should be utilized for developing high yielding lentil varieties through selection or hybridization (Gupta et al. 2012). Besides, negative correlation in plant height with seed length and 1000 seed weight in the present study indicate that bushy plant type provides better seed size and weight which are also desirable for lentil breeding as selection criteria (Malek et al. 2014).

***Estimation of path coefficients*:** The genotypic and phenotypic path analyses for grain yield performed with 12 independent traits were presented in Table 5 and Table 6, respectively.

T**able 5.** Direct and indirect effects of different yield contributing characters on grain yield in lentil at genotypic level.

Characters	**DFF**	**DM**	**PH**	**NPB**	**NSB**	**NTB**	**NPP**	**SL**	**SW**	**SLWR**	**NSP**	**1000SW**	**SWP**
DFF	**-0.127**	0.039	0.022	.0009	-0.0013	0.028	-0.066	-0.238	-0.157	0.069	-0.162	0.049	-0.284
DM	-0.075	**0.067**	0.036	0.006	-0.004	0.032	-0.072	0.023	-0.130	0.060	-0.185	-0.048	-0.294
PH	-0.048	0.043	**0.057**	0.011	-0.003	0.028	-0.053	0.041	-0.184	0.054	-0.208	-0.076	-0.336
NPB	-0.004	0.013	0.019	**0.031**	-0.563	0.027	0.097	-0.014	0.037	-0.018	0.185	-0.038	0.331
NSB	-0.011	0.019	0.013	0.012	**-0.0148**	0.023	0.047	0.018	-0.097	0.037	0.131	-0.057	0.116
NTB	-0.058	0.035	0.026	0.014	-0.548	**0.061**	0.091	0.018	-.0125	0.012	0.123	-0.083	0.110
NPP	0.026	-0.015	-0.009	0.009	-0.002	0.017	**0.314**	0.0138	-0.075	0.006	0.694	-0.038	0.941**
SL	0.03	-0.015	-0.023	0.004	0.002	-0.012	-0.043	**-0.099**	0.520	-0.246	-0.169	0.062	0.004
SW	0.036	-0.016	-0.019	0.002	0.002	-0.014	-0.043	-0.095	**0.541**	-0.275	-0.162	0.062	-0.231
SLWR	-0.028	0.012	0.009	-0.002	-0.007	0.003	0.006	0.077	-0.472	**0.316**	0.061	-0.023	-0.035
NSP	0.026	-0.016	-0.015	0.007	-0.0025	0.009	0.283	0.021	-0.114	0.025	**0.770**	-0.046	0.95**
1000SW	-0.040	-0.020	-0.028	-0.008	0.005	-0.032	-0.078	-0.039	0.217	-0.047	-0.231	**0.155**	-0.154
Residual value: 0.115													

Note: * and ****** indicates significant at 5% and 1% level of probability, respectively.

The results demonstrated that at both genotypic and phenotypic level, days to maturity (0.067, 0.038), number of primary branches (0.031, 0.041), number of pods per plant (0.314, 0.372), seed width (0.541, 0.139), seed length width ratio (0.316, 0.093), number

of seeds per plant (0.770, 0.659) and 1000 seed weight (0.155, 0.028) showed a direct positive effect on grain yield. At genotypic level plant height and number of tertiary branches (0.057, 0.061) exhibited direct positive effect but in phenotypic level it showed direct negative effect (-0.013, -0.045). Conversely, seed length (-0.099) showed direct negative effect at genotypic level but had direct positive effect (0.083) with yield at phenotypic level.

Furthermore, the highest indirect positive effect was found in number of pods per plant (0.694, 0.587) via number of seeds per plant at both levels. In this study, days to 50% flowering (-0.127, -0.019) and number of secondary branches (-0.0148, -0.028) had direct negative effect on grain yield at genotypic and phenotypic level, respectively. Residual value was 0.115 and 0.214 at genotypic and phenotypic path coefficient, respectively.

Furthermore, in path coefficient analysis positive direct effect of one trait with yield ensures importance of the former trait for selecting and developing higher yielding variety (Dalbeer et al. (2013). Based on the present study, days to maturity, plant height, number of primary branches, number of tertiary branches, number of pods per plants, seed width, seed length, seed length width ratio, number of seeds per plants, 1000 seed weight should be considered for direct selection of high yield lentil genotype. In lentil, present findings were in agreement with the findings of Tyagi and Khan (2011). Days to 50% flowering, numbers of secondary branches, seed length have negative direct effect on seed yield. However, these negative effects directly or indirectly affect the yields and these results are similar to the report of Bicer and Sakar (2008).

Table 6. Direct and indirect effects of different yield contributing characters on grain yield in lentil at phenotypic level.

Characters	DFF	DM	PH	NPB	NSB	NTB	NPP	SL	SW	SLWR	NSP	1000SW	SWP
DFF	**-0.019**	0.022	-0.005	0.001	-0.002	-0.021	-0.078	-0.018	-0.038	0.019	-0.132	-0.008	-0.283
DM	-0.011	**0.038**	-0.008	0.008	-0.0084	-0.023	-0.085	-0.017	-0.032	0.016	-0.158	-0.008	-0.294
PH	-0.0075	0.024	**-0.013**	0.012	-0.006	-0.021	-0.059	-0.035	-0.044	0.013	-0.178	-0.012	-0.326
NPB	-0.0005	0.008	-0.003	**0.041**	-0.009	-0.018	0.115	0.012	0.009	-0.004	0.145	-0.005	0.295
NSB	-0.0017	0.011	-0.003	0.014	-**0.028**	-0.016	0.052	-0.015	-0.023	0.009	0.112	-0.001	0.112
NTB	-0.008	0.020	-0.006	0.016	-0.010	**-0.045**	0.104	-0.015	-0.031	0.004	0.105	-0.014	0.114
NPP	0.040	-0.008	0.002	0.0128	-0.004	-0.012	**0.372**	-0.010	-0.018	0.0018	0.587	-0.006	0.92**
SL	0.004	-0.008	0.005	0.006	0.005	0.008	-0.044	**0.083**	0.116	-0.052	-0.125	.0106	0.004
SW	0.054	-0.008	0.004	0.003	0.0047	0.009	-0.048	0.071	**0.139**	-0.081	-0.138	0.010	-0.032
SLWR	-0.041	0.006	-0.0019	-0.002	-0.0045	-0.0018	0.007	-0.047	-0.121	**0.093**	0.046	-0.003	-0.024
NSP	0.0038	-0.009	0.0037	0.009	-0.005	-0.007	0.330	-0.015	-0.029	0.006	**0.659**	-0.007	0.94**
1000SW	0.055	-0.0107	0.006	-0.007	0.001	0.022	-0.085	0.031	0.048	-0.012	-0.178	**0.028**	-0.151
Residual value 0.2137													

Note: * and ** indicates significant at 5% and 1% level of probability, respectively; DFF=Days to 50% flowering, DM= Days to maturity, PH=Plant height, NPB= Number of primary branches, NSB= Number of secondary branches, NTB= Number of tertiary branches, NPP=Number of pods per plant. SL= Seed length, SW= Seed width, SLWR= Seed length width ratio, NSP= Number of seeds per plant, 1000 SW= Weight of 1000 seeds, SWP= Seed weight per plants.

Conclusion

In conclusion, it has revealed that all the traits showed higher level of heritability which indicates that, all the traits are good estimator for the improvement of lentil yield. The importance of days to maturity, plant height, number of primary branches, number of tertiary branches, number of pods per plants, seed width, seed length, seed length width ratio, number of seeds per plants, 1000 seed weight has been confirmed by correlation and path coefficient. These traits can be therefore, used as selection criteria for choosing high yielding lentil genotypes were also confirmed by correlation and path coefficient analysis.

References

Allard RW (1960). Principles of Plant Breeding.John Wiley and Sons. Inc., New York. pp. 1-7

BBS (2019). Yearbook of agricultural statistics, Bangladesh Bureau of Statistics.Statistics and Informatics Division (SID), Ministry of Planning, Government of the People's Republic of Bangladesh.

BBS (2020). Yearbook of agricultural statistics, Bangladesh Bureau of Statistics.Statistics and Informatics Division (SID), Ministry of Planning, Government of the People's Republic of Bangladesh.

Biçer B, Sakar D (2008). Heritability and path analysis of some economical characteristics in lentil. Journal of Central European Agriculture, 9:175-180.

Burton GW (1952). Quantitative inheritance in Grasses. Proc. 6th International Grassland Congress, 1: 277-283.

Comstock RE, Robinson HF (1952). Genetic parameters, their estimate and significance. Proc. 6th Intl. Grassland Congress, 1: 284-291.

Cristobal MD, Pando V, Herrero B (2014). Morphological characterization of lentil (*Lens culinariesMedik*) landraces from Castilla Leon, Spain, 46(4): 1373-1380.

Dalbeer, Nath S, Verman OP, Kavita, Kumar K (2013). Correlation and path coefficient analysis for yield attributes in lentil (*Lens culinaris* L.). International Journal of Science and Research, 4(8): 557-585.

Erskine W (1996). Lessons for breeding from land races of lentil. Euphytica. pp. 107-112, https://doi.org/10.1023/A:1002939704321

Ezzat ZM, Ashmawy F (1999). Performance of some exotic Lentil genotypes and path coefficient analysis lentil.Assiut. Agric. Sci., 18(3): 103-118.

Frederick M, Cho S, Sarker A, McPhee K, Coyne C, Rajesh P, Ford P (2006). Application of biotechnology in breeding lentil for resistance to biotic and abiotic stress. Euphytica, 147:149-165. https://doi.org/10.1007/s10681-006-7108-0

Gautam NK, Singh N, Iquebal MA, Singh M, Akhtar J, Khan Z, Ram B (2014). Genetic diversity analysis for quantitative traits in lentil (*Lens culinaris*Medik.) germplasm.Legume Research, 37(2):139-144. https://doi.org/10.5958/j.0976-0571.37.2.021

Gupta R, Begum SN, Islam MM, Alam MS (2012). Characterization of lentil (Lens culinaris M.) germplasm through phenotypic marker. Journal of the Bangladesh Agricultural University, 10:197–204. http s://doi.org/10.3329/jbau.v10i2.14682

Hanson G, Robinson HF, Comstock RE (1956). Biometrical studies on yield in segregating population of Korean Lespedeza. Agronomy Journal, 48: 268-274. https://doi.org/10.2134/agronj1956.00021962004800060008x

Hayward M, Breese E (1993). Population structure and variability. In: Hayward MD, Bosemark NO, Romayosa I (Eds), Plant Breeding: Principles and Prospects. Chapman and Hall, London, UK. https://doi.org/10.1007/978-94-011-1524-7

Johnson HW, Robinson HW, Comstock RE (1955). Estimation of genetic and environmental variability in Soybean, 47: 314-318. https://doi.org/10.2134/agronj1955.00021962004700070009x

Lynch M, Walsh B (1998). Genetics and Analysis of Quantitative Traits.Sinauer Associates, Sunderland, MA. pp. 47-49

Malek MA, Rafii MY, Afroz SS, Nath UK, Mondal MMA (2014). Morphological characterization and assessment of genetic variability, character association and divergence in Soybean Mutants.The Scientific World Journal, pp. 12. https://doi.org/10.1155/2014/968796

Miller BC, Hill JE, Roberts SR (1991). Plant population effects on growth and in water seeded rice. Agronomical Journal, 83: 291-297. https://doi.org/10.2134/agronj1991.00021962008300020006x

Nath UK, Rani S, Paul MR, Alam MN, Horneburg B (2014). Selection of superior lentil (Lens esculenta M.) genotypes by assessing character association and genetic diversity. The Scientific World Journal, 1-6. https://doi.org/10.1155/2014/372405

Pandey S, Bhatore A, Babbar A (2015). Studies on genetic variability, interrelationships association and path analysis in indigenous germplasm of Lentil in Madhya Pradesh, India. Electronic Journal of Plant Breeding, 6: 592–599.

Rahman AR, Sarwar MD (1982). Path coefficient analysis in lentil. Bangladesh Journal of Agricultural Science, 7(4): 121-127.

Saini N, Jain N, Jain S, Jain RK (2004). Assessment of genetic diversity within and among Basmati and non-Basmati rice varieties using AFLP, ISSR and SSR markers. Euphytica, 140: 133–146. https://doi.org/10.1007/s10681-004-2510-y

Sarker A, Erskine W (2001). Utilization of genetic resources in lentil improvement. In: Proceedings of the Genetic Resources of Field Crops. Genetic Resources Symposium, EUCARPIA, Poznam, Poland.

Singh RK, Chaudhury BD, (1985). Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Dillhi. pp. 225-252.

Singh RS, Sood BC, Kumar N (2012). The nature and magnitude of variability and disease genotypes across cropping system, 32(1): 66-70.

Tattimani M, Shilpa B, Biradar, Hakkalappanavar S, Danaraddi CS, Satyareddi SA (2011). Evaluation of different agronomic practices on nodule and yield attributes of lentil (*Lens culinaris*Medic). Advance Research Journal of Crop Improvement, 2(2): 168-173.

Tyagi SD, Khan MH (2011). Correlation, pathcoefficient and genetic diversity in lentil (*Lens culinaris*Medik) under rainfed conditions. International Research Journal of Plant Science, 2: 191- 200.