Assessment of Genetic Diversity and Association Analysis of Yield Contributory Traits for Selection Criteria in Lentil

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Received March 17, 2019 Accepted May 29, 2019 Published Online June 28, 2019 Abstract: The present investigation was carried out at Gram Breeding Research Station, Kallurkot-Bhakkar, Pakistan, to determine a fruitful selection criteria for genetic improvement in lentil. Twelve elite lentil genotypes were grown under tri-replicate randomized complete block design (RCBD). Data were recorded for primary branches per plant, secondary branches per plant, pods per plant, plant height, days to 90 % maturity and grain yield. The recorded data were subjected to principal component analysis (PCA), path and correlation coefficient analysis. Analysis of variance revealed considerable variation among genotypes for all the recorded traits. PCA distinguished the traits into six PCs. First two components extracted more than 1 Eigen values and collectively contributed 79.86% in genetic variation. Higher positive loadings were extracted by secondary branches ¹ and pods plant ¹ in both components. Path analysis revealed that secondary branches plant ¹ (exhibited the highest direct positive effect (0.846) on grain yield followed by pods plant (0.513). Correlation coefficient analysis also confirmed highest significant contributions of secondary branches plant (92.0%) followed by pods plant (76.0%) and primary branches plant (65.0%). Study suggests that the secondary branches and pods plant may be focused while determining fruitful selection criteria for genetic improvement in lentil.

Keywords: Yield traits, correlation, path analysis, PCA, lentil.

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1. Introduction

Lentil is an important rabi pulse crop grown for its grain. It belongs to family Leguminoceae with diploid chromosome number 2n = 14. It is cultivated in tropical, subtropical and temperate regions across the world (Roy et al., 2013; Nath et al., 2014; Pandey et al., 2015; Noor et al., 2017 and Sakthivel et al., 2019). Legumes are good source of nutrients including protein, carbohydrates and minerals (Dar et al., 2016; Muehlbauer et al., 1985 and Adsuleet al., 1989). Lentil is among the oldest domesticated grain legume crops (Bahl et al., 1993). In addition to nutrient source, lentil also provides various environmental and ecological benefits through biological N2 fixation (Adams et al., 2018; Khazaei et al., 2016; Chowdhury et al., 2019). Pakistan's average lentil production (567 kg ha⁻¹) is far below from the world's average of 936 kg ha⁻¹ (FAO, 2017). Major reason for decline in lentil production is scarcity of high yielding

genotypes and narrow genetic base of cultivated genotypes (Roy et al., 2013; Khazaei et al., 2016 and Rizwan et al., 2017). Varieties in India and Pakistan are vulnerable to a wide range of environmental stresses due to their narrow genetic base (Erskine, 2009; Singh et al., 2014 and Noor et al., 2017).

Researchers seldom take interest in any single character, they also examine other characters and study their mutual relationships (Aghili et al., 2012; Benbrahim et al., 2017; Tejashwini et al., 2018). Various attributes are linked with each other for production of final phenotype (Admas et al., 2018; Mahmood et al., 2018; Mahpara et al., 2017). Higher yield being associated with various other attributes becomes complex in nature (Bakhsh et al., 1971; Saleem et al., 2002 and Yucel et al., 2006). Selection for higher grain yield may be easy when contribution of various attributes to yield is quantified through path coefficient analysis (Dewey and Lu, 1959).

Association analysis may be little more than an intelligent guess for determination of desired criteria for selection (Ahmad et al., 2017; Hawatin, 1978). Correlation coefficient and path analysis may be utilized for the selection of genotypes for future lentil breeding programme (Sakthivel et al., 2019). Correlation and path coefficient analysis have widely been employed by many researchers to examine the direct and indirect effects of different agronomic traits for genetic improvement in lentil (Karadavut, 2009; Aghili et al., 2012; Amin et al., 2015; Pandey et al., 2015 and Tejashwini et al., 2018).

Limited information on genetic variability and correlation among different yield contributory traits are available, so, it is very important to generate the information on the genetic diversity in lentil germplasms and also important to investigate the association among yield components. The present investigation was planned to generate information on genetic variability and association of different yield contributory traits to demonstrate a fruitful selection criteria for genetic improvement in lentil.

2. Materials and Methods

The experiment was carried out at Gram Breeding Research Sub-Station, Kallurkot (71.153°E and 32.923°N), Punjab, Pakistan, during rabi 2017-18. The experimental material consisting of 12 lentil (Lens culinaris) genotypes (LPP 16501, LPP 16502, LPP 16503, LPP16503, LPP 16504, LPP 16505, LPP 16506, LPP 16506, LPP 16507, LPP 16508, LPP 16509, LPP 16510, Markaz-09 and Pb-Masoor-09) was laid down into tri-replicate Randomized Complete Block Design (RCBD). All entries were sown in 4 rows of 4 meter length. Row to row spacing was maintained at 20cm. All the agronomic practices were performed as per requirement of the

Data were recorded for primary branches plant⁻¹, secondary branches plant⁻¹, pods plant⁻¹, plant height (cm), days to 90% maturity and yield kg ha⁻¹. Data were subjected to STAR (Statistical Tool for Agricultural Research version 2.0.1) for principal component analysis. Path analysis was done by the method presented by Dewey and Lu (1959) and correlation analysis was performed following Singh and Chaudhry (1979).

3. Results and Discussion

Results regarding mean performance of various yield contributory traits have been shown in Table (1). Maximum number of primary branches (2.83) were observed in Markaz-09 while minimum (1.60) were recorded in LPP 16502, maxim secondary branches (7) were recorded in LPP 16508 while minimum (3.67) were found in LPP 16509, Maximum number of pods plant-1 (45) were counted in LPP 16508 while minimum (20.67) were recorded in LPP 16509, maximum plant height (34.54) was measured in LPP 16501 while minimum (24.17) was measured in Pb-Masoor-09, most number of days to maturity (138) were recorded in LPP 16501 while less days (124.67) were recorded in LPP 16503, highest yield potential (434.67) was recorded in LPP 16508 while minimum yield (242.90) was found in LPP 16509. Basic analysis of variance revealed that all the genotypes were significantly different ($p \ge 0.01$) for all the traits under study (Table 2).

Table 1. Mean performance of various traits of lentil genotypes

Genotypes	PBPP	SBPP	NPP	PH	DM	YLD
LPP 16501	2.00	6.33	41.00	34.54	138.00	349.31
LPP 16502	1.60	5.00	31.00	27.93	136.67	325.72
LPP 16503	2.50	6.67	46.00	27.87	124.67	393.87
LPP 16504	2.00	5.00	30.67	28.13	130.33	353.94
LPP 16505	2.00	5.00	35.33	25.73	134.00	322.02
LPP 16506	2.00	5.33	32.67	27.80	126.33	314.61
LPP 16507	2.00	4.33	25.33	29.63	137.00	259.09
LPP 16508	2.67	7.00	45.00	31.50	133.33	434.91
LPP 16509	1.67	3.67	20.67	26.10	127.33	242.90
LPP 16510	1.83	5.67	24.33	25.80	135.67	367.82
Markaz-09	2.83	6.33	42.33	26.43	133.00	363.19
Pb-Masoor-09	2.00	5.33	34.67	24.17	135.67	333.12
C.V	15.36	20.60	12.77	5.56	1.12	6.45

Means followed by different letters are significant at 0.05 % level of probability. (PBPP= Primary branches plant⁻¹, SBPP= Secondary branches plant⁻¹, NPP= No of pods plant⁻¹, PH=Plant height at maturity, DM= Days to maturity, Yld= Grain yield kg ha⁻¹).

Table 2. Mean Square values of different traits of Lentil genotypes

Source	DF	PBPP	SBPP	NPP	PH	DM	YLD
Reps	2	0.228	4.694	56.250	95.864	0.583	292.995
Genotypes	11	0.43*	2.876**	205.583**	24.111**	60.424**	8344.752**
Error	22	0.103	1.270	18.947	2.420	2.189	475.55

Table 3. Principal component analysis of agronomic traits among lentil genotypes

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Principal	Eigen	Percentage	Cumulative					
Components	values	of	percentage					
		variance	of variance					
PC 1	3.54	59.00	59.00					
PC 2	1.25	20.86	79.86					
PC 3	0.67	11.12	90.98					
PC 4	0.35	5.77	96.75					
PC 5	0.15	2.58	99.33					
PC 6	0.04	0.67	100					

Principal component analysis employed for estimation of genetic variability distributed the traits into six PCs. A scree plot was also constructed for better illustration of results (Fig. 1). Eigen values expressed by PC1, PC2, PC3, PC4, PC5 and PC6 were 3.54, 1.25, 0.67, 0.35, 0.1547 and 0.0403 respectively. First and second components showed more than 1 Eigen values and exhibited 59.0% and 20.86% contribution in genetic variability with a cumulative share of 79.86% in total genetic diversity (Table 3). Similar results have also been reported by Shahid et al., 2002; Yucel et al., 2006; Benbrahim et al., 2017 and Idrissi et al., 2018 who reported more than 80% of genetic variation through first two components.

Performance of different traits in principle component analysis (Table 4) is evident that higher positive values of secondary branches plant⁻¹ (0.517), number of pods plant⁻¹ (0.499) were revealed in first component. PC2 also presented higher positive loadings for secondary branches plant⁻¹ (0.6123) and number of pods plant⁻¹ (0.4109) indicating that these traits share a considerable amount of genetic variation. These results are in line with earlier reports of (Khazaei et al., 2016; Laskar et al., 2017; Rizwan et al., 2017 and Sakthivel et al., 2019) who also reported

secondary branches and number of pods share a notable amount of genetic variation.

Path coefficient studies were performed to quantify the direct effects of different traits to grain yield as shown in Table 5. Study revealed that highest significant direct effect on yield was presented by secondary branches plant-1 (0.846) followed by number of pods plant⁻¹ (0.513) and plant height (0.275)while negative direct effect of days to maturity and primary branches plant-1 were observed. Positive direct effects of secondary branches and number of pods have also been reported by Yucel et al., 2006; Karadayut, 2009 and Amin et al., 2015. Path coefficient analysis suggested that secondary branches plant⁻¹ and number of pods plant⁻¹ may be considered as most effective agronomic traits contributing maximum towards final grain yield. Results agree with previous findings of Bakhsh et al., 1971 and Tejashwini et al., 2018.

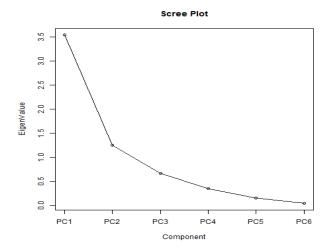


Fig. 1. Scree Plot showing Eigen values

Table 4. Performance of different attributes in Principal Component Analysis

Variables	PC1	PC2	PC3	PC4	PC5	PC6
PBPP	0.4505	0.4109	-0.0638	-0.7082	0.4795	0.0775
SBPP	0.5165	0.6123	-0.105	0.2328	-0.0008	-0.816
NPP	0.4991	0. 5864	0.0386	-0.1889	-0.8042	0.2555
PH	0.2298	-0.2028	0.7523	0.0101	0.1734	0.0846
DM	-0.0292	0.2244	-0.5893	-0.2321	-0.02	0.0349
YLD	0.4769	-0.0201	-0.265	0.5955	-0.3047	0.5044

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Table 5.Direct Effect of different attributes of lentil genotypes

Traits	PBPP	SBPP	NPP	PH	DM	YLD
PBPP	-0.136	-0.237	0.037	0.819	-0.407	0.075
SBPP	-0.063	0.846	0.139	-0.276	0.091	0.349
NPP	0.018	-0.257	0.513	-0.314	-0.143	0.975
PH	-0.133	-0.167	0.103	0.275	-0.326	0.324
DM	0.777	-0.065	0.055	-0.384	-0.326	-0.106

Lentil genotypes

	80	200				
Traits	PBPP	SBPP	NPP	PH	DM	YLD
PBPP	1	0.755**	0.794**	0.172	-0.194	0.656*
SBPP		1	0.884**	0.399	0.013	0.921**
NPP			1	0.374	-0.088	0.765**
PH				1	0.246	0.252
\mathbf{DM}					1	-0.013
YLD						1

Correlation coefficient analysis was performed to observe the association of different traits to grain yield as shown in (Table 6). Correlation analysis revealed that secondary branches plant-1 (0.921) presented highest positive contribution to grain yield followed by number of pods plant⁻¹ (0.765), primary branches plant⁻¹ (0.656) and plant height (0.252) to grain yield. It was also observed that days to maturity were negatively correlated to grain yield. Significant positive contributions to grain yield were exhibited by secondary branches plant⁻¹ (92%) followed by number of pods plant-1 (76%) indicating that these traits are most influential for determination of grain yield. Similar results were reported earlier that secondary branches, number of pods and primary branches are major yield contributory attributes (Saleem et al., 2002; Yucel et al., 2006 and Aghili et al., 2012). Karadavut, 2009 and Amin et al., 2015 also concluded that number of pods and secondary branches plant⁻¹ have higher significant and positive association with the final yield. Results are also in line with Chowdhury et al., (2019), who concluded that the number of primary branches plant-1 and number of pod plant-1 had positive and significant correlation as well as exhibit direct positive effect on seed yield plant⁻¹.

4. Conclusion

Principal component analysis extracted higher positive loadings for secondary branches plant-1 and pods plant-1 in both first and second component indicating that these traits have significant contributions towards genetic diversity. Path and correlation analysis revealed strong parallel association of secondary branches plant-1 and pods plant⁻¹ in determination of grain yield. Therefore, the

Table 6. Correlation Coefficients for Various Traits in genotypes possessing higher numbers of secondary branches and pods plant-1 may be preferred while attempting lentil genetic improvement program.

> List of Abbreviations: RCBD, randomized complete block design; PCA, principle component analysis; N₂, nitrogen; 2n, diploid chromosome number; FAO, food and agriculture organization; Fig, Figure; PBPP, Primary branches plant⁻¹; SBPP,secondary branches plant⁻¹; NPP, number of pods plant⁻¹; PH, plant height; DM, days to maturity; Yld, yield.

> **Competing Interest Statement:** The authors declare that they have no competing interests regarding the publication of this paper.

Author's Contribution:

M.T.M., M.A. M.S. and I.A., involved in the conception, design of the study. M.T.M., A.H., A.U.H., M.S., M.N.M performed experiment; all authors were involved in data collection, analysis, interpretation and manuscript writing.

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