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Analysis of Genetic Parameters and Trait Relationship for Seed Yield and its Attributing Components in Lentil (*Lens culinaris* Medik.)

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ABSTRACT

Background: Lentil (*Lens culinaris* Medik. ssp. *culinaris*) is the oldest domesticated grain legume. It is cultivated for its nutritious lens-shaped seed in marginal and rainfed areas of temperate countries and most tropical highlands. The present study was carried out to get better insights into genetic variability, trait association and to assess direct and indirect effects of various attributing components on seed yield.

Methods: The experimental material consisted of 43 lentil genotypes, grown in randomized block design with three replications during *Rabi* 2019-20 and 2020-21. The data on 11 quantitative traits was pooled across two seasons and statistical analyses were done using R studio and INDOSTAT software.

Result: High PCV and GCV coupled with high heritability and genetic advance were observed for 100-seed weight, seed yield and biological yield suggesting that expression of these traits is controlled by additive gene action. Most of the quantitative traits were positively correlated with seed yield. Biological yield, harvest index, number of primary branches and number of pods per plant had highest positive direct effect on seed yield. Therefore, genotypes LL 931, L 4717, IPL 316, LH 18-04, LH 17-19 and DPL 15 should be used in crossing programmes to obtain high yielding transgressive segregants.

Key words: Direct effect, Genetic parameters, Heritability, Lentil, Path coefficients, Seed yield, Trait relationship.

INTRODUCTION

Lentil (*Lens culinaris* Medik. ssp. *culinaris*) 2n=2x=14 is the oldest domesticated grain legume that belongs to the family Fabaceae. It is grown extensively for its nutritious lens-shaped seed in marginal and rainfed areas of temperate countries and most tropical highlands. Roots of lentil go as back as 8000-9000 BC (Harlan, 1992) when it was originated from *L. culinaris* Medik. ssp. *orientalis* in Fertile Cresent of Eastern Asia (Cubero, 1981). After soybean and hemp, lentil is having the third-highest seed protein content among plant-based food; making it a vital source of inexpensive protein (Bhatty, 1988). India ranks second in lentil production in the world after Canada with a total production of 1.10 million tons yielding out of 1.30 million hectares (INDIASTAT, 2020). The average productivity of lentil is 847 kg/ha in India which is quite low as compared to average productivity of the world of 1195 kg/ha (FAOSTAT, 2019). Therefore, to address the issue of low productivity, there is a need to tailor large number of superior cultivars using different breeding strategies. Genetic variability is essential in any crop improvement programme. Plant breeders need to know about the variability in primary gene pool and relationship between characteristics and yield to improve complicated traits like seed yield. Seed yield is an economically important trait in virtually all crops. It is complex in nature and under polygenic control and it exhibits multiplicative interactions with its attributing traits and environments (Sharma *et al.*, 2020). Therefore, to yield gains in productivity, information on genetic variability and traits association of seed yield with other attributing traits is highly valuable as it helps in an appropriate selection approach. The pace and magnitude of genetic improvement through selection or hybridization can be determined by the magnitude of genetic variability. Furthermore, selection for seed yield could be made more effective and productive when contribution of each causal effect to yield is quantified through path analysis (Dewey and Lu, 1959). Thus, the current study was carried out to get better insights into genetic variability, trait association between seed yield and its attributing components and to assess the direct and indirect effects of various attributing components on seed yield.

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MATERIALS AND METHODS

Forty-three diverse genotypes of lentil (*Lens culinaris* Medik.) were evaluated in field trials for eleven quantitative traits (Table 1). The accessions were grown in a randomized block design with three replications, with a plot size of 7.2 m^2 (0.30 cm × 4 m × 6 rows) on research farms of Pulses Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar, during 2019-20 and 2020-21 *Rabi* cropping seasons. The experimental site is subtropical region, located on latitude of 29°10′ North and longitude of 75°46′ East and 215.2 m above mean sea level. The crop was raised by adopting all recommended package of practices. The data was observed on 11 quantitative traits *viz*., days to 50% flowering, days to maturity, plant height (cm), number of pods per plant, number of primary branches, number of fruiting branches, seeds per pod, 100-seed weight (g), biological

Table 1: Description of test genotypes of lentil used in present study.

Genotypes	Pedigree	Type of material	Source/Origin
DPL 15	PL 406 × L 4076	Cultivar	IIPR, Kanpur
DPL 58	PL 639 × Precoz	Breeding line	IIPR, Kanpur
DPL 62	JLS 1 × LG 171	Cultivar	IIPR, Kanpur
HUL 57	Mutant of HUL 11	Cultivar	BHU, Varanasi
IPL 220	(DPL 44 × DPL 62) × DPL 58	Cultivar	IIPR, Kanpur
IPL 315	PL 4 × DPL 62	Cultivar	IIPR, Kanpur
IPL 316	Sehore 74-3 × DPL 58	Cultivar	IIPR, Kanpur
IPL 406	DPL 35 × EC 157634/382	Cultivar	IIPR, Kanpur
IPL 81	K 75 × PL 639	Cultivar	IIPR, Kanpur
JL 3	Land race selection from Sagar, MP	Cultivar	JNKVV, Jabalpur
Kota Masoor-1	KLB 339 × SL 94-09	Cultivar	AUK, Rajasthan
Kota Masoor-2	LL 1049 × RKL 11	Cultivar	AUK, Rajasthan
L 4076	PL 234 × PL 639	Cultivar	IARI, New Delhi
L 4147	(L 3875 × P4) × PKVL 1	Cultivar	IARI, New Delhi
L 4717	ILL 7617 × 91516	Cultivar	IARI, New Delhi
L 4727	Sehore 74-3 × Precoz	Cultivar	IARI, New Delhi
LH 16-01	Selection from RKL 605-3	Breeding line	CCS HAU, Hisar
LH 17-16	LH 07-26 × PL 01	Breeding line	CCS HAU, Hisar
LH 17-17	LH 07-26 × PL 01	Breeding line	CCS HAU, Hisar
LH 17-18	LH 07-26 × PL 01	Breeding line	CCS HAU, Hisar
LH 17-19	LH 07-26 × PL 01	Breeding line	CCS HAU, Hisar
LH 18-04	LH 07-26 × PL 01	Breeding line	CCS HAU, Hisar
LH 18-05	LH 07-26 × PL 01	Breeding line	CCS HAU, Hisar
LH 82-6 (Garima)	Pusa 2 × No.- 4	Cultivar	CCS HAU, Hisar
LH 84-8 (Sapna)	L9-12 × JLS-2	Cultivar	CCS HAU, Hisar
LH 89-48 (HM-1)	K 75 × L 4076	Cultivar	CCS HAU, Hisar
LL 1373	IPL 406 × FLIP 2004-7L	Cultivar	PAU, Ludhiana
LL 699	PL 639 × PL 77-2	Cultivar	PAU, Ludhiana
LL 931	LH 90-103 × LL 608	Cultivar	PAU, Ludhiana
Narender Masoor 1	Precoz × PL 406	Cultivar	NDUAT, Faizabad
Narender Masoor 2	Variety identified	Cultivar	NDUAT, Faizabad
Pant L 7	L-4076 × DPL 15	Cultivar	GBPUAT, Pantnagar
Pant L 8	DPL 59 × IPL 105	Cultivar	GBPUAT, Pantnagar
Pant Lentil 01	PL 04 × DPL 55	Breeding line	GBPUAT, Pantnagar
PL 02	PL 04 × DPL 55	Cultivar	GBPUAT, Pantnagar
PL 04	UPL 175 × (PL 184 × P 288)	Cultivar	GBPUAT, Pantnagar
Precoz	Argentina cultivar	Exotic cultivar	ICARDA, Syria
RLG 5	Selection from local germplasm	Cultivar	RARI, Durgapura
RVL 11-6	JL 3 × DPL 62	Cultivar	RVSKVV, Sehore
RVL 13-5	JL 3 × DPL 62	Cultivar	RVSKVV, Sehore
RVL 13-7	JL 1 × Black Masra	Cultivar	RVSKVV, Sehore
RVL 31	Local selection from Shajapur, MP	Cultivar	RVSKVV, Sehore
WBL 77	ILL 7723 × BL × 84176	Cultivar	Berhampore, WB

yield per plot (kg), harvest index (%) and seed yield per plot (kg). Data were pooled across two seasons to carry out statistical analyses. The analysis of variance was carried out as suggested by Fisher (1925). The genetic parameters *viz*., genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as per standard procedure given by Burton and De vane (1953). The heritability in the broad sense and genetic advance were determined by using methodology of Johnson *et al*. (1955). The path coefficients were obtained by following the method of Dewey and Lu (1959). Statistical analyses were done using R studio and INDOSTAT software.

RESULTS AND DISCUSSION

Variation among the pooled mean over two years of 43 diverse genotypes for 11 quantitative traits was highly significant (p<0.01) for all the eleven traits which validated further statistical and genetic analysis (Table 2). The scrupulous analysis of variance, mean, standard errors of mean and critical difference (CD) revealed highly significant differences among the genotypes for all 11 quantitative traits studied. This connoted the presence of ample amount of genetic variability among the genotypes under study. Significant genetic variability in lentil has been reported by several researchers for different traits (Kumar *et al*., 2015; Kumar *et al*., 2020; Sharma *et al*., 2020).

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is a potent tool for estimation of variation in breeding material and determining to what extent environment alterations have their role in output of a trait. The values of variance, coefficient of variation, heritability and genetic advance for different traits are presented in Table 3. Phenotypic variance denoting total variance was maximum for number of pods per plant (172.92) followed by plant height (36.15) and harvest index (14.02). The PCV for all the traits was higher than GCV though the differences were less. The narrow gap between PCV and GCV revealed low influence of environment in the expression of these characters. Al-Aysh (2014), Hussan *et al*. (2018) and Kumar *et al*. (2020) also found PCV values to be slightly higher than that of GCV for all the characters. The GCV and PCV varied from 2.57% to 17.56% and 2.62% to 17.78%, respectively. According to Deshmukh *et al*. (1986), GCV and PCV values less than 10% are regarded as low, whereas values greater than 20% are considered as high and values between 10 and 20% to be medium. Based on this classification, moderate GCV and PCV values were observed for 100-seed weight (17.56% and 17.78%, respectively), seed yield per plot (16.14% and 16.62%, respectively), biological yield per plot (14.93% and 15.61%, respectively), plant height (13.45% and 13.67%, respectively), number of fruiting branches (12.27% and 12.94%, respectively), number of pods per plant (11.24% and 11.61%, respectively), seeds per pod (10.36% and 10.92%, respectively) and harvest index (9.97% and 10.83%, respectively), suggesting that selection for these traits would be amenable for genetic improvement. However, low GCV and PCV values were observed for days to maturity (2.57% and 2.62%, respectively), days to 50% flowering (4.02% and 4.08%, respectively) and number of primary branches (8.49% and 9.18%, respectively).

The estimates of genetic coefficient of variations along with heritability and genetic advance would be beneficial in predicting gain under selection (Assefa *et al*., 1999; Sahu *et al*., 2015). The heritable portion of phenotypic variance considered by value of $\sigma^2 g$ relative to $\sigma^2 p$ expressed as h^2_{BS} was very high (89.9% to 97.5%) for all 11 traits except harvest index (84.7%) and number of primary branches (85.4%) that showed most of the traits had moderate heritability (Table 3). Thus, all the traits except harvest index and number of primary branches were affected by environmental fluctuation to minimal extent. Furthermore, high heritability estimates (h^2_{BS}) with corresponding high genetic advance as percent of mean (GAM) is more efficient and pragmatic approach for selection than that with low GAM. The estimates of heritability in broad sense (h^2_{BS}) and corresponding GAM, both were high for 100-seed weight, seed yield per plot,

Table 2: Mean performance and analysis of variance (ANOVA) for 11 quantitative characters of lentil.

Traits	Mean performance						Source of variation and mean squares		
	Range	Mean	S.E.	CD (5%)	CD (1%)	CV	Replication (DF=2)	Genotypes (DF=42)	Error (DF= 84)
Days to 50% flowering	72.5-86.0	79.0	0.55	1.54	2.05	1.203	3.703	31.23**	0.904
Days to maturity	112.0-130.0	124.3	0.64	1.81	2.40	0.895	11.479	31.82**	1.239
Plant height (cm)	24.9-54.3	44.0	1.07	3.01	3.98	4.210	1.892	108.43**	3.429
Number of pods per plant	82.3-145.8	113.3	3.29	9.25	12.26	5.029	19.649	518.76**	32.464
Number of primary branches	2.3-3.7	2.93	0.10	0.29	0.38	6.072	0.036	0.22**	0.032
Number of fruiting branches	10.5-22.5	15.9	0.65	1.84	2.43	7.098	1.526	12.76**	1.28
Seeds per pod	1.15-2.00	1.64	0.06	0.16	0.21	6.016	0.017	0.10**	0.01
100-seed weight (g)	1.57-3.59	2.46	0.07	0.19	0.26	4.839	0.022	0.58**	0.014
Biological yield per plot (kg)	1.727-4.637	3.224	0.15	0.41	0.55	7.885	0.496	0.76**	0.065
Harvest index (%)	23.7-50.4	34.6	1.46	4.12	5.46	7.339	16.138	42.06**	6.435
Seed yield per plot (kg)	0.564-1.476	1.072	0.04	0.12	0.16	6.892	0.033	0.10**	0.005

DF= Degrees of freedom. **Significant at 1% level of probability.

biological yield per plot, plant height, number of fruiting branches and number of pods per plant. Therefore, expression of these traits was controlled by additive gene action and direct selection would be highly fruitful for their genetic improvement over short span of time. Similar findings were observed for 100-seed weight, seed yield, pods per plant and plant height by Tyagi and Khan (2010), Abdipur *et al.* (2011), Hussan *et al.* (2018) and Kumar *et al.* (2020).

Variability and heritability data provide opportunities for genetic improvement in different traits, but they do not suggest any kind of association between them. As a result, understanding the relationships between the traits is helpful in the indirect selection and improvement of economically important traits for a successful breeding program for any crop (Shabanimofrad *et al.*, 2013). In the present study, seed yield per plot was positively correlated with biological yield per plot, number of pods per plant, plant height, days to maturity, number of primary branches, harvest index, days to 50% flowering and number of fruiting branches (Table 4). Thus, selection for these positively associated yield attributing traits could bring about sufficient gain in seed yield. However, seed yield per plot was found negatively correlated with 100-seed weight (Table 4).

As the number of factors in correlation studies increases, Pearson's correlation coefficient may not provide exact representation of association between yield and its contributing traits. In such perplexing situations, path coefficient analysis allows a more in-depth study of specific direct and indirect efforts of trait and thorough investigation of the precise forces acting and quantifies the relative importance of each causal effect (Khan *et al.*, 2016). In the present study, path coefficient analysis has been conducted taking seed yield per plot as dependent variable. The direct and indirect effects of various traits on seed yield are provided in Table 4. The highest positive direct effect on seed yield was exerted by biological yield (0.854) followed

Table 3: Estimates of genetic parameter for yield and yield contributing characters of lentil.

Traits	σ^2p	σ^2g	σ^2e	GCV	PCV	h^2_{BS} (%)	GA	GAM (%)
Days to 50% flowering	10.41	10.11	0.30	4.02	4.08	97.10	6.45	8.17
Days to maturity	10.61	10.19	0.41	2.57	2.62	96.10	6.45	5.19
Plant height (cm)	36.15	35.00	1.14	13.45	13.67	96.80	11.99	27.27
Number of pods per plant	172.92	162.10	10.82	11.24	11.61	93.70	25.39	22.41
Number of primary branches	0.07	0.06	0.01	8.49	9.18	85.40	0.47	16.15
Number of fruiting branches	4.25	3.83	0.43	12.27	12.94	90.00	3.82	23.98
Seeds per pod	0.032	0.029	0.003	10.36	10.92	89.90	0.33	20.23
100-seed weight (g)	0.192	0.187	0.005	17.56	17.78	97.50	0.88	35.73
Biological yield per plot (kg)	0.25	0.23	0.02	14.93	15.61	91.50	0.95	29.42
Harvest index (%)	14.02	11.88	2.15	9.97	10.83	84.70	6.53	18.90
Seed yield per plot (kg)	0.032	0.030	0.002	16.14	16.62	94.30	0.35	32.28

σ^2p: Phenotypic variance; σ^2g: Genotypic variance; σ^2e: Environmental variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; h^2_{BS}: Heritability (Broad sense); GA: Genetic advance; GAM: Genetic advance as % of mean.

Table 4: Path coefficient analysis showing direct and indirect effects of different characters on seed yield in 43 lentil genotypes.

	DF	DM	PH	NPP	NPB	NFB	SP	HSW	BY	HI
DF	0.018	0.009	0.008	0.007	0.006	0.007	0.005	-0.001	0.008	0.000
DM	0.038	0.078	0.052	0.036	0.019	0.033	0.007	0.018	0.053	-0.015
PH	-0.020	-0.031	-0.046	-0.025	-0.021	-0.018	-0.003	-0.007	-0.028	-0.002
NPP	0.012	0.014	0.016	0.030	0.014	0.014	0.006	0.000	0.014	0.008
NPB	0.023	0.017	0.032	0.031	0.069	0.016	0.015	-0.012	0.020	0.027
NFB	-0.017	-0.019	-0.018	-0.021	-0.011	-0.045	-0.011	-0.006	-0.024	0.008
SP	-0.012	-0.005	-0.003	-0.010	-0.011	-0.012	-0.049	0.022	-0.013	-0.002
HSW	0.002	-0.014	-0.010	0.000	0.011	-0.008	0.027	-0.062	-0.007	0.024
BY	0.357	0.578	0.519	0.389	0.247	0.462	0.236	0.102	0.854	-0.161
HI	0.014	-0.110	0.024	0.162	0.226	-0.106	0.022	-0.228	-0.109	0.579
Pearson's correlation with seed yield	0.414**	0.517**	0.573**	0.600**	0.548**	0.342*	0.256	-0.174	0.766**	0.468**

Residual effect= 0.124. *Significant at 5% level of probability; **Significant at 1% level of probability; DF= Days to 50% flowering, DM = Days to maturity, PH= Plant height (cm), NPP= Number of pods per plant, NPB = Number of primary branches, NFB= Number of fruiting branches, SP= Seeds per pod, HSW= 100-seed weight (g), BY= Biological yield per plot (kg), HI= Harvest index (%), SY= Seed yield per plot (kg).

Table 5: List of ten best lentil genotypes selected from 43 genotypes for each quantitative character.

DF		DM		PH (cm)		NPP		NPB		NFB	
WBL 77	73.00	L 4717	112.33	RLG 5	53.60	LH 17-19	140.10	LH 17-19	3.53	LL 1373	20.60
L 4717	74.33	L 4727	117.17	LH 18-05	52.37	IPL 316	139.87	DPL 58	3.53	DPL 62	20.17
Kota Masoor-2	74.67	RVL 11-6	119.33	LH 82-6	52.07	Pant L -8	131.73	LH 18-04	3.47	HUL 57	19.30
JL 3	75.00	RVL 31	119.50	IPL 81	52.03	Pant L -7	131.10	RVL 11-6	3.37	LH 84-8	18.27
IPL 220	75.00	WBL 77	119.83	LH 17-19	51.07	LH 17-17	129.47	LL 699	3.3	IPL 81	18.23
RVL 31	75.33	RVL 13-7	120.17	LH 17-17	50.83	LH 17-18	127.57	Kota Masoor-2	3.27	L 4147	18.17
RVL 13-7	75.67	JL 3	120.67	LH 18-04	50.30	IPL 81	127.20	L 4147	3.17	IPL 316	18.03
Kota Masoor-1	75.83	Pant L -7	121.00	LH 84-8	49.97	LH 18-04	127.13	LH 17-17	3.13	LH 16-01	17.90
L 4727	75.83	PL 04	121.50	RVL 13-5	49.67	LH 18-05	125.67	IPL 220	3.1	Pant L -8	17.80
Pant L -7	75.83	Precoz	122.67	IPL 406	49.07	RVL 31	123.20	IPL 316	3.07	LH 18-05	17.47
SP		HSW (g)		BY (kg)		HI (%)		SY (kg)			
HUL 57	1.93	LL 1373	3.50	LL 931	4.096	L 4717	44.23	IPL 316	1.373		
Narender Masoor 2	1.92	Precoz	3.39	DPL 15	3.996	LH 18-04	43.53	LH 18-04	1.346		
IPL 81	1.88	IPL 406	3.30	IPL 316	3.972	LH 17-19	40.40	LH 17-19	1.301		
LH 17-16	1.88	DPL 62	3.13	DPL 62	3.935	Kota Masoor-2	40.03	LL 699	1.293		
Pant L -8	1.85	RVL 13-5	3.05	IPL 81	3.905	LH 17-18	39.80	LH 84-8	1.29		
LH 17-19	1.85	Pant L -7	2.80	L 4147	3.855	WBL 77	38.73	LH 82-6	1.28		
WBL 77	1.85	DPL 58	2.74	LH 82-6	3.79	LH 17-17	38.10	Kota Masoor-2	1.244		
L 4147	1.83	DPL 15	2.72	RLG 5	3.638	Pant L -7	37.63	Pant L -8	1.242		
LL 931	1.83	LL 931	2.68	L 4076	3.599	LH 84-8	37.57	IPL 81	1.216		
RVL 11-6	1.80	LH 82-6	2.67	IPL 315	3.592	Kota Masoor-1	37.57	IPL 220	1.209		

DF= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPP= Number of pods per plant, NPB= Number of primary branches, NFB= Number of fruiting branches, SP= Seeds per pod, HSW= 100-seed weight (g), BY= Biological yield per plot (kg), HI= Harvest Index (%), SY= Seed yield per plot (kg).

by harvest index (0.579), days to maturity (0.078), number of primary branches (0.069), number of pods per plant (0.030) and days to 50% flowering (0.018). Hence, these traits should be given high weightage and positive selection should be done to improve seed yield. However, 100-seed weight (-0.062), seeds per pod (-0.049), plant height (-0.046), number of fruiting branches (-0.045) had negative direct effect on seed yield per plot. These results are in accordance with the findings of previous studies of Younis *et al*. (2008), Aghili *et al*. (2012), Dalbeer *et al*. (2015). Furthermore, Latif *et al*. (2010) found negative direct effect of 100-seed weight on seed yield whereas Kumar *et al*. (2020) found negative direct effect of seeds per pod on seed yield. However, days to flowering, number of pods per plant, plant height, number of fruiting branches and seeds per pod had positive indirect effect on seed yield *via* biological yield. These indirect effects had not only validated the low magnitude direct effect but also explained highly significant positive association of these traits with seed yield. The apparent inconsistency between Pearson's correlation and path analysis was most likely due to the fact that the former only evaluates mutual association without taking into account the cause, whereas the latter defines the causes and assesses their relative importance (Bhatt, 1973). The presence of a low residual effect (0.124) showed that the independent characters made a significant contribution to the dependent trait *i.e.* seed yield and the characters selected for path analysis were acceptable and appropriate.

Crop yield is mostly determined by biological yield and partitioning accumulated biomass to reproductive structures (Andrade *et al*., 1999). The fraction of total biomass devoted to reproductive tissues is known as reproductive partitioning (Hay, 1995; Sinclair, 1998). Any crop plant's productivity is determined not only by its photosynthetic efficiency, but also by the successful translocation of assimilates to the seeds, as evaluated by the harvest index. Thus, selection for biological yield, harvest index and seed yield per se could bring about significant genetic gain as these traits have relatively high coefficient of variation along with high heritability and genetic advance as percent of mean. These traits were further reinforced by positive direct effect on seed yield. Therefore, biological yield, harvest index and seed yield may be used as better selection indices for lentil crop improvement. The genotype LL 931 (4.096 kg) is highest biomass yielder followed by DPL 15 (3.996 kg) and IPL 316 (3.972 kg) and for harvest index L 4717 (44.23%) followed by LH 18-04 (43.53%) and LH 17-19 (40.40%). High seed yield potential per se is undoubtedly an important consideration when it comes to selection of genotypes. Amongst the genotypes, IPL 316 (1.373 kg) followed by LH 18-04 (1.346 kg) and LH 17-19 (1.301 kg) were highest seed yielders (Table 5).

CONCLUSION

Genetic improvement and tailoring of high yielding cultivars require knowledge of amount and nature of genetic variability that is present in the primary gene pool. Therefore, we examined genetic variation for 11 quantitative traits of 43 diverse lentil genotypes in order to have better insight into genetic variability, character association and direct and indirect effects of various yield components in lentil. High PCV and GCV coupled with high heritability and genetic advance were observed for 100-seed weight, seed yield per plot and biological yield suggesting that expression of these traits is controlled by additive gene action and selection would be highly fruitful. Most of the quantitative traits were positively correlated with seed yield except 100-seed weight. It is evident from path coefficient analysis that biological yield, harvest index, days to maturity, number of primary branches, number of pods per plant and days to 50% flowering were the highest direct contributor to seed yield. Therefore, to obtain high yielding transgressive segregants, the genotypes LL 931, L 4717, IPL 316, LH 18-04, LH 17-19 and DPL 15 should be used in hybridization programmes to exploit genetic variability present in lentil stocks.

Conflict of interest: None.

REFERENCES

Abdipur, M., Vaezi, B., Bavei, V., Heidarpur, N.A. (2011). Evaluation of morpho-physiological selection indices to improve drought tolerant lentil genotypes (*Lens culinaris* Medik) under rainfed condition. American-Eurasian Journal of Agricultural and Environmental Sciences. 11(2): 275-281.

Aghili, P., Imani, A.A., Shahbazi, H., Yousef, A. (2012). Study of correlation and relationships between seed yield and yield components in lentil (*Lens culinaris* Medikus). Annals of Biological Research. 3(11): 5042-5045.

Al-Aysh, F.M. (2014). Genetic variability, correlation and path coefficient analysis of yield and some yield components in landraces of lentil (*Lens culinaris* Medik). Jordan Journal of Agricultural Sciences. 173(3834): 1-14.

Andrade, F.H., Vega, C.R.C., Uhart, S.A., Cirilo, A.G., Cantarero, M., Valentinuz, O. (1999). Kernel number determination in maize. Crop Science. 39: 453-459. DOI: 10.2135/cropsci1999.0011183X0039000200026x.

Assefa, K., Ketama, S., Tefera, H., Nguyen, H.T., Blum, A., Ayele, M., Bai, G., Simane, B., Kefyalew, T. (1999). Diversity among germplasm lines of the Ethiopian cereal tef [*Eragrostis tef* (Zucc.) Trotter]. Euphytica. 106: 87-97. DOI: 10.1023/A:1003582431039.

Bhatt, G.M. (1973). Significance of path coefficient analysis determining the nature of character association. Euphytica. 22: 338-343. DOI: 10.1007/BF00022643.

Bhatty, R.S. (1988). Composition and quality of lentil (*Lens culinaris* Medik): A review. Canadian Institute of Food Science and Technology Journal. 21: 144-160. DOI: 10.1016/S0315-5463(88)70770-1.

Burton, G.W. and DeVane, E.H. (1953). Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 45: 478-481. DOI: 10.2134/agronj1953.00021962004500100005x.

Cubero, J.I. (1981). Origin, Domestication and Evolution. Commonwealth Agricultural Bureau, In: Lentils. [Webb, C. and Hawtin, G.C., (Eds).], Slough, UK. pp. 15-38.

Dalbeer, S., Verma, O.P., Kavita, K.K. (2015). Correlation and path coefficient analysis for yield attributes in lentil (*Lens culinaris* Medikus). International Journal of Science and Research. 4: 158-161.

Deshmukh, S.N., Basu, M.S., Reddy, P.S. (1986). Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of groundnut. Indian Journal of Agricultural Sciences. 56: 816-821.

Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal. 51: 515-518. DOI: 10.2134/agronj1959.00021962005100090002x.

FAOSTAT, (2019). Available online: https://www.fao.org/faostat/en/#home (accessed on Jan 1, 2022).

Fisher, R.A. (1925). Statistical Methods for Research Workers. Oliver and Boyd, Edinburgh.

Harlan, J. (1992). Crops and Man. American Society of Agronomy, Madison, Wisconsin.

Hay, R.K.M. (1995). Harvest index: A review of its use in plant breeding and crop physiology. Annals of Applied Biology. 126: 197-216. DOI: 10.1111/j.1744-7348.1995.tb05015.x.

Hussan, S., Khuroo, N.S., Lone, A.A., Dar, Z.A., Dar, S.A., Dar, M.S. (2018). Study of variability and association analysis for various agro-morphological traits in lentil (*Lens culinaris* Medikus). Journal of Pharmacognosy and Phytochemistry. 7: 2172-2175.

INDIASTAT, (2020). Available online: https://www.indiastat.com/data/agriculture/agricultural-production (accessed on Jan 1, 2022).

Johnson, H.W., Robinson, H.F., Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 47(7): 314-318. DOI: 10.2134/agronj1955.00021962004700070009x.

Khan, A.M.R., Eyasmin, R., Rashid, M., Ishtiaque, S., Chaki, A.K. (2016). Variability, heritability, character association, path analysis and morphological diversity in snake gourd. Agriculture and Natural Resources. 50(6): 483-489. DOI: 10.1016/j.anres.2016.07.005.

Kumar, A., Gill, R.K., Singh, M. (2020). Genetic variability and association analysis for various agro morphological traits in lentil (*Lens culinaris* M.). Legume Research. 43(6): 776-779. DOI: 10.18805/LR-4326.

Kumar, J. and Srivatava, E. (2015). Impact of reproductive duration on yield and its component traits in lentil. Legume Research. 38(2): 139-148. DOI: 10.5958/0976-0571.2015.00077.6.

Latif, M.A., Hassan, M.M., Sultana, N. (2010). Variability and character association and path coefficient analysis in lentil (*Lens culinaris* Medik.). Bangladesh Journal Environmental Sciences. 18: 49-51.

Sahu, V., Dodiya, N.S., Joshi, A., Rajoriya, S.K., Jain, P., Jain, D. (2015). Genetic diversity among *Withania somenifera* (L.) dunal genotypes using morphological and molecular markers. Journal of Cell and Tissue Research. 15: 4867-4875.

Shabanimofrad, M., Rafii, M.Y., Megat Wahab, P.E., Biabani, A.R., Latif, M.A. (2013). Phenotypic, genotypic and genetic divergence found in 48 newly collected Malaysian accessions of *Jatropha curcas* L. Industrial Crops and Products. 42: 543-551. DOI: 10.1016/j.indcrop.2012.06.023.

Sharma, S.R., Singh, S., Gill, R.K., Kumar, R., Parihar, A.K. (2020). Selection of promising genotypes of lentil (*Lens culinaris* Medik.) by deciphering genetic diversity and trait association. Legume Research. 43: 764-769. DOI: 10.18805/LR-4056.

Sinclair, T.R. (1998). Historical changes in harvest index and crop nitrogen accumulation. Crop Science. 38: 638-643. DOI: 10.2135/cropsci1998.0011183X003800030002x.

Tyagi, S.D. and Khan, M.H. (2010). Studies on genetic variability and interrelationship among the different traits in Microsperma lentil (*Lens culinaris* Medik.). Journal of Agricultural Biotechnology and Sustainable Development. 2(1): 15-20.

Younis, N., Hanif, M., Sadiq, S., Abbas, G., Asghar, M.J., Haq, M.A. (2008). Estimates of genetic parameters and path analysis in lentil (*Lens culinaris* Medikus). Pakistan Journal of Agriculture Science. 45(3): 44-48.