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COMPARISON OF HYBRIDIZATION AND INDUCED MUTATION AS SOURCES OF CREATING GENETIC VARIABILITY FOR VARIOUS TRAITS IN LENTIL (*Lens culinaris* Medik.)

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SUMMARY

Three distinct sets comprising of 8 variable populations developed through different sources of creating genetic variability, viz; hybridization, induced mutation and mutation of hybrids were evaluated in nested design. The results showed the phenotypic superiority of individual plants over parents and standard varieties for studied traits. Sufficient amount of variability was present for days to mature, plant height, pods per plant and 100-seed weight in F_3M_2 (AB_{HM}) and can be used for the genetic improvement of these traits. However, greatest variability within F_3 (AB_H) population in Set-3 may be due to both environmental and genetic factors. Mutated populations in all sets had more variability among plants as compared to recombinant and recombinant mutant generations. However, F_3M_2 (AB_{HM}) population had maximum economic worth in Set-3. The estimates of genotypic variance and heritability for the traits under study in all segregating populations of all sets were found to be significant which indicated the presence of heritable genetic variability for all these traits. The recombinant populations, viz; F_3 (AB_H) and F_3M_2 (AB_{HM}) included large number of genetic variants. The selection of such genetic variants exhibiting desirable features may be helpful for breeders to identify best performing true breeding lines in succeeding generations.

Key words: Hybridization, induced mutations, genetic variability, nested (hierarchical)

Key findings: Recombination or hybridization itself or in combination with mutation has proved to be the best source of creating genetic variation. Moreover, the parents in Set-1, viz; NLH 03381 and NLH 96475B possessed a diverse genetic nature which contributed in creating maximum genetic variability.

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INTRODUCTION

The narrow genetic base and use of unproductive exotic genetic material are the major causes of low genetic improvement in lentil (Ali *et al.*, 2010). The pre-requisite for the genetic improvement of a crop is the extent of genetic variability which is more important than the total variability (Khan *et al.*, 2005). Evaluation of genetic variability through different genetic parameters is thus compulsory for the identification of desired traits that can contribute towards the improvement of seed yield (Sarwar *et al.*, 2010).

Among various sources of creating genetic variability in lentil, hybridization is the most common conventional method but it needs tedious efforts and commitment. Since the

emasculation and pollination of little floral buds of lentil is difficult and time consuming thus the manipulation of genetic variability through hybridization seams less feasible as compared to other technologies. (Shah *et al.*, 2008) reported that mutagens may cause genetic changes in an organism, break the linkages and produce many new promising traits for the improvement of crop plants. Creation of genetic variability through mutagenesis proved best for strengthening crop improvement programs and represents a more efficient source of genetic variability than the gene pool conserved by nature (Satpute and Fultambkar, 2012). But it is also a well-known fact that out of one million mutations, only one may be desirable. Mutated F_3 generation may have more genetic variability, so the evaluation of different sources of creating genetic variability and identify the best one (s) which may aid the breeders to develop high yielding and disease resistant varieties. The objectives of present research work include (1) To measure the extent of exploitable genetic variability in F_3 (hybridized), M_3 (mutated) and F_3M_2 (mutated hybrid) generations along with parents (P_1 and P_2) and standard varieties (SV_1 and SV_2) and (2) To evaluate and compare the genetic variability already created at NIAB through different sources, viz; hybridization, induced mutation (atomic radiations) and mutation of hybrids and (3) To study the nature of inheritance patterns of various morphological traits.

MATERIALS AND METHODS

The research work was conducted in the experimental fields of Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad and the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. Different segregating generations, their parents and standard varieties already constituted at NIAB through hybridization and induced mutations were used as experimental material in this study. Three distinct sets were constituted from the available breeding material. Each set comprised of 8 populations, viz; 4 segregating generations (recombinant, mutant and recombinant mutant), their 2 parents and 2 standard varieties. Various populations, their abbreviations and symbols along with details of genetic nature of parents, segregating generations and standard varieties are placed in Table 1.

The experiment was laid out in nested (hierarchical) design and the layout of all sets was same. In each population of true breeding genotypes (parents and standard varieties), 2 rows were taken as progenies and 20 plants of each progeny were sown in field. These plants were further divided into 2 rows to obtain 2 observations (replicates) of a trait in 10 plants of a progeny. Similarly, in each population of segregating generations (recombinant, mutant and recombinant mutant), 2 progenies of phenotypically selected single plants were taken as such and 20 plants of each progeny were sown in field. These plants were equally divided into 2 rows to obtain 2 observations (replicates) of a trait in 10 plants of a progeny. Two observations (replicates) of a trait may also be considered as 2 measurements of a single plant in case of true breeding populations or measurements of 2 different single plants of a progeny in case of segregating populations. Each experimental unit was of 1 m length keeping plant-to-plant and row-to-row distances of 10 and 30 cm, respectively. The data on days to mature (DM), plant height (PH) in centimeters, and pods per plant (NPP), 100-seed weight (SDWT) in grams and seed yield in gram per plant (SY) were recorded on all plants of each progeny in each population of a set.

Analysis of variance was carried out for each plant trait in each population following (Montgomery, 2008) and (Anonymous, 2005) on computer software, MSTATC. The mean squares from the analysis of variance of nested design were equated to their expected values to obtain the estimates of different genetic parameters as outlined by (Robinson *et al.*, 1951). The format of analysis of variance has been presented in Table 2. Genetic parameters including components of variance, coefficients of variability, estimates of broad-sense heritability, expected genetic advance and relative expected genetic advance were determined from the expected mean squares to compare genetic variability among the populations using Microsoft Excel (v.2010).

Table 1. Various populations, their abbreviations and symbols along with details of genetic nature of parents, segregating generations and standard varieties in each set used in present study.

Set #	Name of population	Abbreviations	Symbols	Genetic nature
1	Parent-1	P_1	A	[§]NL 03381
	Parent-2	P_2	B	NL 96475B
	Recombinant segregating generation	F_3	AB_H	NL 03381 × NL 96475B
	Mutant segregating generation-1	$M_3(P_1)$	A_M	NL 03381/100 Gy*
	Mutant segregating generation-2	$M_3(P_2)$	B_M	NL 96475B/100 Gy
	Recombinant mutant segregating generation	F_3M_2	AB_{HM}	NL 03381 × NL 96475B/100 Gy
	Standard variety-1	SV_1	C	Punjab Masoor 2009
	Standard variety-2	SV_2	D	Markaz 2009
2	Parent-1	P_1	A	NL 03381
	Parent-2	P_2	B	NL 66184
	Recombinant segregating generation	F_3	AB_H	NL 03381 × NL 66184
	Mutant segregating generation-1	$M_3(P_1)$	A_M	NL 03381/100 Gy
	Mutant segregating generation-2	$M_3(P_2)$	B_M	NL 66184/100 Gy
	Recombinant mutant segregating generation	F_3M_2	AB_{HM}	NL 03381 × NL 66184/100 Gy
	Standard variety-1	SV_1	C	Punjab Masoor 2009
	Standard variety-2	SV_2	D	Markaz 2009
3	Parent-1	P_1	A	NL 96475B
	Parent-2	P_2	B	NL 66184
	Recombinant segregating generation	F_3	AB_H	NL 96475B × NL 66184
	Mutant segregating generation-1	$M_3(P_1)$	A_M	NL 96475B /100 Gy
	Mutant segregating generation-2	$M_3(P_2)$	B_M	NL 66184/100 Gy
	Recombinant mutant segregating generation	F_3M_2	AB_{HM}	NL 96475B × NL 66184/100 Gy
	Standard variety-1	SV_1	C	Punjab Masoor 2009
	Standard variety-2	SV_2	D	Markaz 2009

*Irradiation unit, [§] = NIAB Lentil

RESULTS

The mean phenotypic values of different populations for various traits in 3 sets are presented in Table 3. In Set-1, the parental means were greater for plant height and pods per plant and lesser for days to mature than their corresponding variety means. However, the standard varieties had more seed size and seed yield as compared to parents. In Set-2, parental means were better than standard varieties for almost all the traits except seed yield. Likewise, in Set-3, mean phenotypic values of parents were better than standard varieties for plant height, pods per plant and seed yield per plant. These results implied that parents selected for present study had more genetic potential for the mentioned traits as compared to standard varieties. The parental means of remaining traits were lower than standard varieties.

In all sets, the generation means of all segregating populations, viz; F_3 (AB_H), M_3 (A_M), M_3 (B_M) and F_3M_2 (AB_{HM}) for maturity were smaller than parents and standard varieties which indicated the presence of early maturing plants within these populations. The presence of non-significant variation within true breeding populations, viz; parents and standard varieties as evident from their mean squares revealed that the variability within these populations was not genetic rather various environmental factors, e.g. temperature, moisture etc. might be involved (Table 4). Considering these facts further genetic analyses of these populations was not performed since it may be misleading. Therefore, different genetic parameters were computed only for segregating populations for the assessment and comparison of genetic variability among plants within these populations.

In Set-1, days to mature, pods per plant and seed yield showed maximum genotypic and phenotypic variation in F_3 (AB_H) population. In Set-2 highest genotypic and phenotypic variability was observed for days to mature in F_3 (AB_H) and M_3 (B_M), plant height in F_3M_2 (AB_{HM}), number of pods per plant and 100-seed weight in M_3 (A_M), and seed yield in F_3 (AB_H) populations (Table 6). In Set-3, higher values of genotypic and phenotypic variation were exhibited by days to mature, plant height and pods per plant, however, 100-seed weight and seed yield per plant revealed similar findings in M_3 (A_M) population (Table 7).

Table 2. Format of analysis of variance with 'n' replication, 'p' progeny, 'k' number of plants per population and 'e' environment.

Sources of variation	Degrees of freedom	Mean squares	Expected mean squares
Between progenies	p-1 = 1	MS_3	$\hat{\sigma}^2_e + n\hat{\sigma}^2_k + nk\hat{\sigma}^2_p$
Among plants within progeny	p(k-1) = 18	MS_2	$\hat{\sigma}^2_e + n\hat{\sigma}^2_k$
Within plants (Error)	pk(n-1) = 20	MS_1	$\hat{\sigma}^2_e$
Total	pkn-1 = 39		

$\hat{\sigma}^2_p$ = Variance between progenies, = Variance among plants within progenies, = Variance within plantsMS2, MS1 = Estimates of among plants within progeny mean square and error mean square, respectively, MS3 = Estimate of progeny mean square.

Table 3. Mean phenotypic values of different populations for various traits in 3 sets along with parental, generation and cultivar means.

Set #	Population	DM	PH	NPP	SDWT	SY
1	NL 03381 (A*)	140.43	38.23	280.03	2.28	14.43
	NL 96475B (B)	141.58	37.05	265.48	2.44	14.30
	Parental Mean	141.01	37.64	272.76	2.36	14.37
	F_3 (AB_H)	139.18	37.33	275.05	2.60	14.63
	M_3 (A_M)	138.78	37.50	265.98	2.56	14.98
	M_3 (B_M)	138.35	36.98	270.90	2.69	14.78
	F_3M_2 (AB_M)	137.68	37.43	268.55	2.55	14.20
	Generation Mean	138.50	37.31	270.12	2.60	14.65
	SV-1 (C)	142.35	37.90	252.83	2.55	14.85
	SV-2 (D)	141.05	37.10	270.00	2.67	15.18
	Cultivar Mean	141.70	37.50	261.42	2.61	15.02
2	NL 03381 (A)	140.35	34.55	265.48	2.77	15.33
	NL 66184 (B)	141.18	28.38	265.98	2.68	16.80
	Parental Mean	140.77	31.47	265.73	2.73	16.07
	F_3 (AB_H)	139.50	37.28	268.78	2.61	15.18
	M_3 (A_M)	136.73	36.80	270.48	2.65	15.73
	M_3 (B_M)	138.78	35.85	270.15	2.63	15.35
	F_3M_2 (AB_M)	140.35	35.68	268.18	2.65	15.40
	Generation Mean	138.84	36.40	269.40	2.64	15.42
	SV-1 (C)	142.95	31.53	257.75	2.53	16.58
	SV-2 (D)	142.65	24.43	250.58	2.62	16.20
	Cultivar Mean	142.80	27.98	254.17	2.58	16.39
3	NL 96475B (A)	142.40	30.75	252.15	2.51	16.53
	NL 66184 (B)	142.10	29.33	257.58	2.53	16.50
	Parental Mean	142.25	30.04	254.87	2.52	16.52
	F_3 (AB_H)	140.60	37.73	267.65	2.64	16.15
	M_3 (A_M)	138.75	37.15	284.65	2.61	15.13
	M_3 (B_M)	136.68	36.15	275.45	2.65	14.55
	F_3M_2 (AB_M)	138.58	23.58	267.83	2.64	15.05
	Generation Mean	138.65	33.65	273.90	2.64	15.22
	SV-1 (C)	142.90	26.35	252.10	2.63	16.08
	SV-2 (D)	141.23	25.40	256.33	2.58	16.05
	Cultivar Mean	142.07	25.88	254.22	2.61	16.07

Table 4. Mean squares from the analyses of variance of different traits in all populations of Set-1, Set-2 and Set-3.

Source of Variation	df	Set-1					Set-2					Set-3				
		DM	PH	NPP	SDWT	SY	DM	PH	NPP	SDWT	SY	DM	PH	NPP	SDWT	SY
Between Progenies																
P1 (A)	1	9.03	119.03**	390.63*	0.48*	7.23	0.90	25.60	27.23	0.01	2.02	6.40	6.40	518.40	0.04	38.02**
P2 (B)	1	55.22	0.40	1380.63*	0.04	2.50	50.63	18.22	50.63	0.04	10.00*	40.00*	18.22	27.23	0.02	0.40
F_3 (AB_H)	1	24.03**	3.03	250.00	0.01	0.23	8.10*	5.63*	93.02	0.02	0.02	48.40**	2.03	144.40	0.07	0.10
M_3 (A_M)	1	65.03**	1.60	697.23**	0.02	11.02**	30.63**	0.10	18.23	0.00	15.63**	0.90	4.90	0.90	0.00	9.02*
M_3 (B_M)	1	2.50	7.22	1.60	0.01	0.23	13.22	4.90	230.40*	0.02	0.40	265.22**	72.90**	313.60	0.08	14.40*
F_3M_2 (AB_M)	1	5.63*	1.22	62.50	0.06	3.60*	19.60*	1.22	0.23	0.06*	4.90*	24.03**	416.03**	2449.23	0.03	4.90
SV-1 (C)	1	28.90	40.00	354.02	0.34	1.60	0.90	4.22	504.10	0.13	0.02	10.00	16.90	202.50	0.07	2.02
SV-2 (D)	1	3.60	2.50	280.90	0.08	11.02*	12.10	27.23	731.02*	0.00	44.10**	2.03	62.50	275.63	0.08	44.10**
Among Plants																
P1 (A)	18	22.13	14.52	77.60	0.12	3.72	17.01	32.07	363.63	0.10	5.74	11.84	20.51	227.37	0.14	4.80
P2 (B)	18	31.50	24.47	479.33	0.20	5.72	26.54	12.70	415.05	0.12	2.52	16.98	19.34	250.78	0.11	2.64
F_3 (AB_H)	18	43.90**	11.35**	138.05**	0.18**	15.20**	47.11**	11.60**	890.80**	0.30**	13.46**	27.84**	6.69*	508.93**	0.14**	7.56**
M_3 (A_M)	18	37.80**	8.52*	983.40**	0.17**	10.64**	30.66**	8.52**	825.29**	0.33**	12.16**	29.14**	23.96**	1464.51**	0.13**	18.66**
M_3 (B_M)	18	36.87**	147.25**	584.89**	0.32**	7.07**	48.74**	17.73**	513.59**	0.20**	10.43**	32.84*	14.18*	697.57**	0.23**	18.31**
F_3M_2 (AB_M)	18	33.26**	10.17**	586.19**	0.15*	6.82**	46.69**	21.79**	561.67**	0.10**	11.26**	48.63**	34.63**	714.22**	0.20**	13.22**
SV-1 (C)	18	23.79	19.37	269.51	0.14	5.42	16.61	21.18	246.08	0.07	3.13	16.31	20.79	227.95	0.13	1.74
SV-2 (D)	18	20.74	21.84	477.12	0.15	3.29	16.72	34.45	305.68	0.06	4.13	16.75	30.28	271.31	0.14	4.10
Within plants																
P1 (A)	20	11.23	8.93	73.28	0.06	3.08	10.10	22.75	244.48	0.09	4.48	7.00	18.50	221.40	0.07	3.58
P2 (B)	20	15.88	17.95	296.08	0.11	3.55	13.98	6.93	208.38	0.11	2.15	8.70	14.03	210.13	0.06	2.00
F_3 (AB_H)	20	2.08	0.78	77.75	0.01	0.48	1.10	0.98	56.98	0.02	1.98	4.20	2.68	14.90	0.07	0.85
M_3 (A_M)	20	1.68	3.55	24.73	0.02	0.83	3.38	1.45	25.53	0.03	0.98	1.50	5.65	76.65	0.05	1.28
M_3 (B_M)	20	1.55	74.5	23.20	0.05	0.58	3.53	3.45	36.20	0.01	1.75	14.73	5.25	61.70	0.10	1.90
F_3M_2 (AB_M)	20	1.13	1.88	35.80	0.06	0.60	3.85	3.73	9.38	0.01	1.10	2.73	11.73	558.5	0.05	1.85
SV-1 (C)	20	13.60	15.45	211.53	0.11	2.80	14.50	10.43	232.00	0.04	2.98	8.30	21.30	250.70	0.09	1.18
SV-2 (D)	20	11.95	18.60	242.55	0.13	1.68	9.90	18.33	169.93	0.05	3.20	9.18	19.90	137.08	0.09	2.60

The mean genotypic variability and rank scores of different segregating populations for various traits in 3 sets displaying the cumulative genotypic variability are given in Table 8. The comparison of segregating populations indicated that in Set-1 and Set-2, F_3 (AB_H) Population had maximum genetic variability as it secured highest rank scores (19 and 17) followed by M_3 (A_M) and M_3 (B_M) populations, respectively. In Set-3, F_3M_2 (AB_{HM}) population appeared to be the most variable one securing highest rank score (17) followed by M_3 (A_M) and M_3 (B_M) populations.

The mean genetic variability among plants within segregating populations determined from their genetic variances indicated the cumulative worth of all segregating populations in different sets. In Set-1, there was maximum genetic variability in all segregating populations for traits like plant height and pods per plant. Similarly, in Set-2, highest genetic variability was observed in all segregating populations for days to mature and 100-seed weight. However, in Set-3, highest genetic variability in all segregating populations was noted only for seed yield per plant.

Cumulative rank scores of all sets had ranked different sets with Set-1 followed by Set-2 and Set-3 securing cumulative rank scores of 11, 10 and 09, respectively. The results revealed that the recombinant populations, viz; F_3 (AB_H) and F_3M_2 (AB_{HM}) possessed large number of genetic variants within these populations. The selection of such genetic variants exhibiting desirable features may be helpful for a breeder to identify best performing true breeding lines in succeeding generations. Furthermore, recombination or hybridization itself or in combination with mutation has been proved to be the best source of creating genetic variation. In all sets, mutated populations were also found to be a good or normal source of creating genetic variability.

DISCUSSION

In Set-1, the generation means of pods per plant, 100-seed weight and seed yield per plant were higher than those of parents. The results are in accordance with (Idahosa *et al.*, 2010) who found higher mean values for above mentioned characters in cowpea. But lower than standard varieties. Similarly, in Set-2, generation means were greater than parents and standard varieties for plant height, pods per plant and 100-seed weight. The mean phenotypic values of segregating generations for traits like days to mature, plant height, pods per plant and 100-seed weight were also found to be exceeding both parents and standard varieties in Set-3. The remaining traits had lower mean phenotypic values. These results showed the phenotypic superiority of individual plants over parents and standard varieties for some traits in Set-3.

Similarly greater variation was observed for plant height in F_3 (AB_H) followed by F_3M_2 (AB_{HM}) while 100-seed weight in M_3 (B_M) population (Table 5). These results are in line with (Tyagi and Khan, 2010) who also observed maximum genetic variation for all these traits in lentil. Highest heritable variation was observed for all studied traits in F_3 (AB_H) and F_3M_2 (AB_{HM}) populations while moderate to high heritability was noted for all traits in M_3 (A_M) and M_3 (B_M) populations. Chakraborty and Haque (2000) reported high heritability for pods per plant, 100-seed weight and seed yield. Singh *et al.* (2009) also observed similar results for days to mature and plant height. Maximum response to selection was observed for plant height, pods per plant, 100-seed weight and seed yield in $F_3(AB_H)$ and $M_3(B_M)$ populations and for pods per plant, 100-seed weight and seed yield in $M_3(A_M)$ and $F_3M_2(AB_{HM})$ populations (Table 5). Similar findings were presented by Kumar *et al.* (2010).

Chauhan and Singh (1998) also found highest genetic variability for all these characters. All traits revealed greatest heritability in all segregating populations. Similar findings have also been reported in literature (Kausar, 2005; Adeyanju and Ishiyaku, 2007). Lowest response to selection was noted for days to mature in all segregating generations indicating the presence of earliness features in all these populations. Arshad *et al.* (2003) observed low genetic advance for days to mature. Plant height showed highest relative expected genetic advance in F_3 (AB_H), M_3 (B_M) and F_3M_2 (AB_{HM}) populations except in M_3 (A_M) population where it was moderate. Pods per

Table 5. Different genetic parameters of 5 traits for various segregating populations in Set-1.

Populations	DM	PH (g)	NPP	SDWT (g)	SY (g)
$F_3(AB_H)$					
$\sigma^2_k \pm SE(\sigma^2_k)$	$20.91^+ \pm 4.61$	$5.29^+ \pm 1.19$	$530.15^+ \pm 119.61$	$0.08^+ \pm 0.02$	$7.36^+ \pm 1.59$
σ^2_e	1.04	0.39	38.88	0.01	0.24
σ^2_r	21.95	5.67	569.02	0.09	7.60
$h^2 \pm SE (h^2)$	$0.95^+ \pm 0.21$	$0.93^+ \pm 0.21$	$0.93^+ \pm 0.21$	$0.93^+ \pm 0.21$	$0.97^+ \pm 0.21$
ΔG	7.83	3.89	39.00	0.50	4.69
REGA (%)	5.63	10.43	14.18	19.13	32.03
$M_3(A_M)$					
$\sigma^2_k \pm SE(\sigma^2_k)$	$18.06^+ \pm 3.97$	$2.49^+ \pm 0.96$	$479.34^+ \pm 103.17$	$0.08^+ \pm 0.02$	$4.91^+ \pm 1.12$
σ^2_e	0.84	1.78	12.36	0.01	0.41
σ^2_r	18.90	4.26	491.70	0.09	5.32
$h^2 \pm SE (h^2)$	$0.96^+ \pm 0.21$	$0.58^+ \pm 0.23$	$0.97^+ \pm 0.21$	$0.91^+ \pm 0.21$	$0.92^+ \pm 0.21$
ΔG	7.29	2.11	37.94	0.45	3.73
REGA (%)	5.25	5.63	14.26	17.64	24.91
$M_3(B_M)$					
$\sigma^2_k \pm SE(\sigma^2_k)$	$17.66^+ \pm 3.87$	$2.23^+ \pm 17.15$	$280.84^+ \pm 61.39$	$0.13^+ \pm 0.03$	$3.25^+ \pm 0.74$
σ^2_e	0.78	1.86	11.60	0.03	0.29
σ^2_r	18.43	4.09	292.44	0.16	3.53
$h^2 \pm SE (h^2)$	$0.96^+ \pm 0.21$	$0.54^+ \pm 0.23$	$0.96^+ \pm 0.21$	$0.84^+ \pm 0.21$	$0.92^+ \pm 0.21$
ΔG	7.22	7.44	28.82	0.59	3.03
REGA (%)	5.22	20.12	10.64	22.02	20.49
$F_3M_2(AB_{HM})$					
$\sigma^2_k \pm SE(\sigma^2_k)$	$16.07^+ \pm 3.49$	$4.15^+ \pm 1.08$	$275.19^+ \pm 61.58$	$0.05^+ \pm 0.02$	$3.11^+ \pm 0.72$
σ^2_e	0.56	0.94	17.90	0.03	0.30
σ^2_r	16.63	5.08	293.09	0.08	3.41
$h^2 \pm SE (h^2)$	$0.97^+ \pm 0.21$	$0.82^+ \pm 0.23$	$0.94^+ \pm 0.21$	$0.61^+ \pm 0.22$	$0.91^+ \pm 0.21$
ΔG	6.91	3.23	28.21	0.29	2.96
REGA (%)	5.02	8.62	10.50	11.31	20.81

plant revealed similar results except in M_3 (B_M) population where it was moderate. Highest response to selection was observed for 100-seed weight and seed yield per plant in all segregating populations (Table 6). These results are in accordance with Kausar (2005).

Moderate to high heritability was noted for days to mature and 100-seed weight, respectively. Haddad *et al.* (1982) and Ranganatha *et al.* (2013) also reported similar findings. Plant height, pods per plant and seed yield per plant showed higher values of heritable variation in all segregation populations. The results are in line with Bicer and Sakar (2010) and Sarwar *et al.* (2013) who also found highest heritability for above mentioned traits. Again lowest response to selection was observed for days to mature in all segregating populations which revealed the presence of early maturing character in them (Arshad *et al.*, 2003). Highest response to selection was found for plant height, 100-seed weight and seed yield per plant in F_3M_2 (AB_{HM}) population while for pods per plant in M_3 (A_M) population (Table 7). Dhananjay *et al.* (2009) and Sarwar *et al.* (2013) noted maximum genetic advance in lentil for the characters studied.

CONCLUSIONS

Our results suggested that the parents in Set-1, viz; NLH 03381 and NLH 96475B possessed diverse genetic nature which contributed in creating maximum genetic variability. Moreover, the existence of maximum genetic variability in Set-1 may be exploited in the selection of superior single plants with desirable features for further evaluation in breeding programs.

Table 6. Different genetic parameters of 5 traits for various segregating populations in Set-2.

Populations	DM	PH (g)	NPP	SDWT (g)	SY (g)
$F_3(AB_H)$					
$\sigma^2_k \pm SE(\sigma^2_k)$	$23.00^+ \pm 4.94$	$5.31^+ \pm 1.22$	$416.91^+ \pm 93.60$	$0.14^+ \pm 0.03$	$5.74^+ \pm 1.43$
σ^2_e	0.55	0.49	28.49	0.01	0.99
σ^2_r	23.55	5.80	445.40	0.15	6.73
$h^2 \pm SE (h^2)$	$0.98^+ \pm 0.21$	$0.92^+ \pm 0.21$	$0.94^+ \pm 0.21$	$0.93^+ \pm 0.21$	$0.85^+ \pm 0.21$
ΔG	8.32	3.87	34.67	0.63	3.88
REGA (%)	5.96	10.38	12.90	24.31	25.58
$M_3(A_M)$					
$\sigma^2_k \pm SE(\sigma^2_k)$	$13.64^+ \pm 3.23$	$3.53^+ \pm 0.91$	$399.88^+ \pm 86.59$	$0.15^+ \pm 0.03$	$5.59^+ \pm 1.28$
σ^2_e	1.69	0.73	12.76	0.02	0.49
σ^2_r	15.33	4.26	412.65	0.17	6.08
$h^2 \pm SE (h^2)$	$0.89^+ \pm 0.21$	$0.83^+ \pm 0.21$	$0.97^+ \pm 0.21$	$0.89^+ \pm 0.21$	$0.92^+ \pm 0.21$
ΔG	6.11	3.01	34.55	0.65	3.98
REGA (%)	4.47	8.17	12.77	24.46	25.29
$M_3(B_M)$					
$\sigma^2_k \pm SE(\sigma^2_k)$	$22.61^+ \pm 5.12$	$7.14^+ \pm 1.89$	$238.70^+ \pm 53.99$	$0.09^+ \pm 0.02$	$4.34^+ \pm 1.11$
σ^2_e	1.76	1.73	18.10	0.01	0.88
σ^2_r	24.37	8.87	256.80	0.10	5.21
$h^2 \pm SE (h^2)$	$0.93^+ \pm 0.21$	$0.81^+ \pm 0.21$	$0.93^+ \pm 0.21$	$0.94^+ \pm 0.21$	$0.83^+ \pm 0.21$
ΔG	8.04	4.21	26.14	0.53	3.34
REGA (%)	5.79	11.74	9.68	20.05	21.73
$F_3M_2(AB_{HM})$					
$\sigma^2_k \pm SE(\sigma^2_k)$	$21.42^+ \pm 4.91$	$9.03^+ \pm 2.32$	$276.15^+ \pm 58.92$	$0.05^+ \pm 0.01$	$5.08^+ \pm 1.19$
σ^2_e	1.93	1.86	4.69	0.00	0.55
σ^2_r	23.35	10.90	280.83	0.05	5.63
$h^2 \pm SE (h^2)$	$0.92^+ \pm 0.21$	$0.83^+ \pm 0.21$	$0.98^+ \pm 0.21$	$0.92^+ \pm 0.21$	$0.90^+ \pm 0.21$
ΔG	7.78	4.80	28.92	0.35	3.75
REGA (%)	5.54	13.46	10.78	13.33	24.37

Table 7. Different genetic parameters of 5 traits for various segregating populations in Set-3.

Populations	DM	PH (g)	NPP	SDWT (g)	SY (g)
$F_3(AB_H)$					
$\sigma^2_k \pm SE(\sigma^2_k)$	$11.82^+ \pm 2.95$	$2.01^+ \pm 0.75$	$247.01^+ \pm 53.40$	$0.04^+ \pm 0.02$	$3.35^+ \pm 0.80$
σ^2_e	2.10	1.34	7.45	0.03	0.43
σ^2_r	13.92	3.35	254.46	0.07	3.78
$h^2 \pm SE (h^2)$	$0.85^+ \pm 0.21$	$0.60^+ \pm 0.22$	$0.97^+ \pm 0.21$	$0.53^+ \pm 0.23$	$0.89^+ \pm 0.21$
ΔG	5.56	1.92	27.18	0.23	3.03
REGA (%)	3.95	5.10	10.15	8.79	18.75
$M_3(A_M)$					
$\sigma^2_k \pm SE(\sigma^2_k)$	$13.82^+ \pm 3.06$	$9.15^+ \pm 2.58$	$693.93^+ \pm 153.79$	$0.04^+ \pm 0.01$	$8.69^+ \pm 1.96$
σ^2_e	0.75	2.83	38.33	0.02	0.64
σ^2_r	14.57	11.98	732.26	0.06	9.33
$h^2 \pm SE (h^2)$	$0.95^+ \pm 0.21$	$0.76^+ \pm 0.21$	$0.95^+ \pm 0.21$	$0.60^+ \pm 0.22$	$0.93^+ \pm 0.21$
ΔG	6.35	4.64	45.01	0.28	4.99
REGA (%)	4.58	12.50	15.81	10.55	3.00
$M_3(B_M)$					
$\sigma^2_k \pm SE(\sigma^2_k)$	$9.06^+ \pm 3.75$	$4.46^+ \pm 1.58$	$317.94^+ \pm 73.42$	$0.06^+ \pm 0.03$	$8.20^+ \pm 1.93$
σ^2_e	7.36	2.63	30.85	0.05	0.95
σ^2_r	16.42	7.09	348.79	0.11	9.15
$h^2 \pm SE (h^2)$	$0.55^+ \pm 0.23$	$0.63^+ \pm 0.22$	$0.91^+ \pm 0.21$	$0.57^+ \pm 0.23$	$0.90^+ \pm 0.21$
ΔG	3.92	2.92	29.88	0.34	4.76
REGA (%)	2.87	8.14	10.85	12.69	32.71
$F_3M_2(AB_{HM})$					
$\sigma^2_k \pm SE(\sigma^2_k)$	$22.95^+ \pm 5.11$	$11.45^+ \pm 3.82$	$343.15^+ \pm 93.44$	$0.08^+ \pm 0.02$	$5.69^+ \pm 1.40$
σ^2_e	1.36	5.86	13.96	0.02	0.93
σ^2_r	24.31	17.31	357.11	0.10	6.61
$h^2 \pm SE (h^2)$	$0.94^+ \pm 0.21$	$0.66^+ \pm 0.22$	$0.96^+ \pm 0.26$	$0.77^+ \pm 0.22$	$0.86^+ \pm 0.21$
ΔG	8.17	4.83	7.23	0.42	3.88
REGA (%)	5.89	20.48	2.70	15.77	25.79

SE= Standard error, ΔG= Genetic advance and REGA= Relative expected genetic advance, h^2= heritability,
σ^2_r, σ^2k, σ^2_e = Components of variance, ± = Standard error value, + = The estimate of genetic variation/broad-sense heritability differs significantly from zero as its absolute magnitude exceeded twice its respective standard error.

Table 8. Mean genetic variability within different segregating populations for various traits in 3 sets and cumulative rank scores.

Population	DM	PH	NPP	SDWT	SY	Total
Set-1						
$F_3(AB_H)$	20.91[¥]	5.29	530.15	0.08	7.36	
	(4)	(4)	(4)	(3)	(4)	(19)
$M_3(A_M)$	18.06	2.49	479.34	0.08	4.91	
	(3)	(2)	(3)	(3)	(3)	(14)
$M_3(B_M)$	17.66	2.23	280.84	0.13	3.25	
	(2)	(1)	(2)	(4)	(2)	(11)
$F_3M_2(AB_{HM})$	16.07	4.15	275.19	0.05	3.11	
	(1)	(3)	(1)	(2)	(1)	(08)
Mean (Set-1)	18.17	12.07	391.38	0.09	4.66	
	(2)[§]	(3)	(3)	(2)	(1)	(52/11)
Set-2						
$F_3(AB_H)$	23.00	5.31	416.91	0.14	5.74	
	(4)	(2)	(4)	(3)	(4)	(17)
$M_3(A_M)$	13.64	3.53	399.88	0.15	5.59	
	(1)	(1)	(3)	(4)	(3)	(12)
$M_3(B_M)$	22.61	7.14	238.70	0.09	4.34	
	(3)	(3)	(1)	(2)	(1)	(10)
$F_3M_2(AB_{HM})$	21.42	9.03	276.15	0.05	5.08	
	(2)	(4)	(2)	(1)	(2)	(11)
Mean (Set-2)	20.17	6.25	332.91	0.11	5.19	
	(3)	(1)	(1)	(3)	(2)	(50/10)
Set-3						
$F_3(AB_H)$	11.82	2.01	247.01	0.04	3.35	
	(2)	(1)	(1)	(2)	(1)	(07)
$M_3(A_M)$	13.82	9.15	693.93	0.04	8.69	
	(3)	(3)	(4)	(2)	(4)	(16)
$M_3(B_M)$	9.06	4.46	317.94	0.06	8.20	
	(1)	(2)	(2)	(3)	(3)	(11)
$F_3M_2(AB_{HM})$	22.95	11.45	343.15	0.08	5.69	
	(4)	(4)	(3)	(4)	(2)	(17)
Mean (Set-3)	14.41	6.77	334.19	0.05	6.48	
	(1)	(2)	(2)	(1)	(3)	(51/09)

[¥] = Rank scores of 4 segregating populations and 3 sets were determined from their ranking for genetic variance (Exceeds 3 populations = 4, Exceeds 2 populations = 3, Exceeds 1 populations = 2, Exceeds none = 1)
[§] = Rank scores of 3 sets were determined from their ranking for genetic variance (Exceeds 2 sets = 3, Exceeds 1 set = 2, Exceeds none = 1).

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