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Combining Ability, Genetic Diversity and Their Association with Heterosis for Seed Yield in Lentil (*Lens culinaris* Medikus)

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ABSTRACT

Background: In lentil, the information on relationship between combining ability, parental genetic diversity and heterosis is very scanty and need to be explored further.

Methods: The present investigation was carried out in randomized block design with three replications during *rabi* 2020-21 at GBPUAT, Pantnagar with 55 genotypes (10 parents and 4p5 F_1's hybrids). The Griffing's, Method II, Model I was used to estimate combining ability. The D^2 statistics was used to measure genetic diversity (GD). The Pearson's correlation was used to measure correlation between heterosis and different parameters *viz.,* parental mean (PM), specific combining ability (SCA), mean of general combining ability (MGCA) and genetic diversity (GD).

Result: The hybrids *viz.,* PL 8 × PL 4 (2.1 g), PL 8 × L 4147 (2.11 g), PL 8 × L 4076 (2.13 g), PL 8 × PL 406 (2.27 g), PL 8 × PL 5 (2.32 g) and PL 8 × PL 7 (2.52 g) were identified as most promising hybrids for seed yield while the parents PL 8 (2.14 g) and PL 7 (2.07 g) can be used as donors for high seed yield. The SCA were found to be the most reliable parameters to predict heterosis.

Key words: Combining ability, Genetic diversity, Heterosis, Lentil.

INTRODUCTION

Lentil (*Lens culinaris* Medikus sub sp. *culinaris*) is an autogamous annual pulse crop known for its protein rich grains. In India during 2018-19, it was cultivated on 1.5 million hectare area with an annual production of 1.5 million tons and with an average productivity of around 1000 kg/ha (Anonymous, 2018). During last three decades, area under lentil has increased by 85%, production by 151% and productivity by 39%. Despite these tremendous achieve ments, there is still a lot of scope to increase its productivity. Heterosis breeding resulted in quantum jump in productivity of several crops but in case of pulses, it has not yet been properly exploited. The information regarding the genetic mechanism of heterosis is still not adequate in lentil. Diallel analysis is useful in imparting the knowledge about GCA and SCA variances. The amount of heterosis in any cross also relies heavily on the relative performance of inbred parents and amount of genetic divergence between parents. The presence of genetic diversity between parents used in hybridization is considered as an important parameter for obtaining significant heterosis (Tecklewold and Becker, 2006). Keeping all these aspects in mind, the present investigation was carried out with an aim to assess GCA, SCA variances and effects and correlation between combining ability, *per se* performance of parents, genetic diversity and heterosis.

MATERIALS AND METHODS

Plant materials and field experiments

The 10 elite lentil varieties *viz.,* PL 8 (DPL 59 × IPL 105), PL 4 [UPL 175 × (PL 184 × P-288)], PL 406 (Selection from P 495), PL 639 (L9-12 × T 8), PL 5 (L 4126 × LG-171), PL 7 (L 4076 × DPL 15), LH 84-8 (L9-12 × JLS 2), L 4147 [(L 3875 × P4) × PKVL 1], L 4076 (PL 234 × PL 639) and LL 864 (LL 498 × LH 84-8) were crossed in half diallel fashion during the *rabi* 2019-20 to produce 45 F_1's. These 45 F_1's and 10 parents were grown during *rabi* 2020-21 at N.E.B.C.R.C. of GBPUAT, Pantnagar in randomized block design with three replications. The observations were recorded on seven morphological characters *viz.,* days to 50% flowering, days to maturity, number of primary branches/plant, number of pods/plant, number of seeds/pod, 100-seed weight (g) and seed yield/plant (g). The observations on primary branches/plant, pods/plant, seeds/pod, 100-seed weight (g) and seed yield/plant (g) were recorded on five randomly selected plants from each replication and mean values were used for statistical analysis. The observations on days to 50% flowering and days to maturity were recorded on whole plot basis.

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Statistical analysis

The combining ability was evaluated by using Griffing's (1956), Method II, Model I (Fixed effects). If GCA and SCA effects were significant in desirable direction than these effects were considered as good (G) and those significant towards undesirable direction were considered as poor (P) while non-significant effects were designated as average (A). Similarly, in case of *per se* (PM) performance if mean of line is found above overall parental mean than such lines were considered as good (G) but if mean of a parental line was below the overall parental mean than these lines were classified as poor (P). The heterosis over mid parent (MPH) and better parent (BPH) were estimated for seed yield. The GCA effects obtained from both parental lines of a hybrid were averaged to determine the mean GCA (MGCA) effect of the parents (Kumar *et al.,* 2015). The genetic diversity was estimated for various yield and related traits by using Mahalanobis D^2 statistics (Mahalanobis, 1928) and for preparation of clusters, Tocher's method as proposed by Rao (1952) was used. By using the method of Arunachalam (1984), the parents were classified into three genetic diversity classes *i.e.* low, medium and high. The Pearson's correlation coefficients were used to estimate the relation between PM, SCA, MGCA, GD, MPH and BPH.

RESULTS AND DISCUSSION

Estimation of combining ability and genetic diversity

The mean comparison among parents and their hybrids was presented in Fig 1 and Fig 2. In case of maturity, the hybrid mean (87 days) was found to be early as compared to parent mean (90 days). The hybrid PL 5 × LH 84-8 (82 days) was found as earliest maturing hybrid. The primary branches in hybrids ranged from 4.3 (PL 4 × LL 864) to 8 (PL 8 × PL 7) with a mean value of 6.2, which is higher than the parental mean (4.2). The mean for number of pods in hybrids was 36.4 while in parents it was 28.9, the hybrid PL 8 × PL 7 exhibited highest number of pods (51.3). In case of number of seeds per pods and 100-seed weight the hybrid mean was 1.6 and 2.36 respectively while parents mean was 1.6 and 2.18, respectively. The seed yield in hybrids ranged from 1.43 g (PL 639 × LL 864) to 2.52 g (PL 8 × PL 7) with a mean of 1.79 g while in parents it ranged from 1.39 g (L 4147) to 2.14 g (PL 8) and the mean parents yield was 1.66 g. The hybrids *viz.,* PL 8 × PL 4 (2.1 g), PL 8 × L 4147 (2.11 g), PL 8 × L 4076 (2.13 g), PL 8 × PL 406 (2.27 g), PL 8 × PL 5 (2.32 g) and PL 8 × PL 7 (2.52 g) were identified as most promising hybrids for seed yield while the parents PL 8 (2.14 g) and PL 7 (2.07 g) can be used as donor for high seed yield. A close perusal of Table 1 indicated that genotypic differences were significant for all characters which indicated the preponderance of sufficient genetic variability among

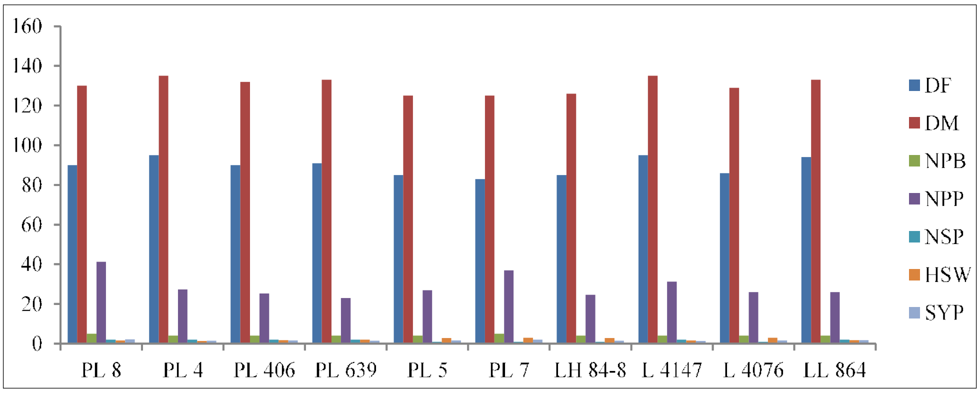

Fig 1: Mean performance of parents for different biometrical traits.

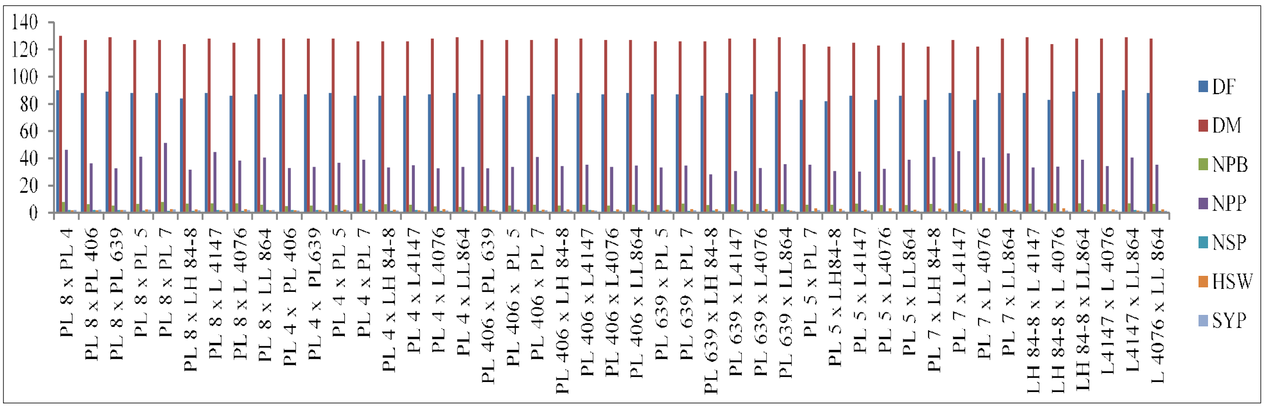

Fig 2: Mean performance of hybrids for different biometrical traits.

the experimental material. The adequacy of genetic variability for these studied traits were also reported earlier by Sellami *et al.,* 2021, Suri *et al.,* 2022 and Tan *et al.,* 2022 in lentil. The diallel ANOVA indicated that MSS due to GCA and SCA effects were highly significant (p<0.01) for all the characters (Table 1). The significance of GCA and SCA effects were also reported earlier by Naik *et al.,* (2020). The estimates of SCA variance were found to be higher than the corresponding GCA variance for all characters except number of seed/pod, hundred seed weight and seed yield/plant. Average degree of dominance was found to be more than unity for the characters *viz.,* days to flowering, days to maturity and number of pods/plant which indicated the presence of over dominance. The parent PL 7 was ranked as the best parent, as it had a good GCA effects for maximum six characters including seed yield (Table 2). The hybrids *i.e.* PL 8 × PL 406, PL 8 × PL 5, PL 8 × PL 7, PL 4 × PL 5 and L 4147 × L 4076 exhibited good SCA effects for seed yield (Table 3). The perusals of Table 4 indicated that for seed yield, out of 45 experimental hybrids seven hybrids *viz.,* PL

Table 1: Diallel analysis of variance for different biometrical characters.

Source of variation	*df*	MSS						
		DF	DM	NPB	NPP	NSP	HSW	SYP
Replication	2	3.660	46.406	0.725*	155.824*	0.005	0.013	0.013
Genotypes	54	20.017**	81.786*	3.489**	99.6603**	0.425**	0.731**	0.185**
Error	108	1.426	48.807	0.109	23.108	0.006	0.005	0.014
Parents	9	49.040**	48.996	0.533**	104.818**	0.801**	1.263**	0.195
Hybrids	44	11.734**	85.826**	1.887**	69.801**	0.358**	0.619**	0.179
Parents *vs* hybrid	1	123.240**	199.111*	100.596**	1367.079**	0.002	0.848**	0.382
GCA	9	24.221**	52.620**	1.576**	107.116**	0.789**	1.357**	0.295**
SCA	45	3.162**	22.190	1.080**	18.440**	0.012**	0.020**	0.015**
					Variances			
σ^2GCA		1.978	3.029	0.128	8.284	0.065	0.113	0.024
σ^2SCA		2.687	5.921	1.044	10.738	0.010	0.018	0.020
$\sqrt{\sigma^2SCA/2\sigma^2GCA}$		1.630	2.994	0.258	6.669	0.018	0.031	0.010

Where, DF, DM, NPB, NPP, NSP, HSW and SYP refers to days to 50 % flowering, days to maturity, number of primary branches/plant, number of pods/plant, number of seed/pod 100- seed weight and seed yield/plant.

Table 2: General combining ability effects of parents for different biometrical traits.

Parents	DF	DM	NPB	NPP	NSP	HSW	SYP
PL 8	0.783* (P)	2.300* (P)	0.534* (G)	5.078* (G)	0.196* (G)	-0.226* (P)	0.354* (G)
PL 4	0.950* (P)	3.606* (P)	-0.368* (P)	-0.589 (A)	0.171* (G)	-0.314* (P)	-0.062* (P)
PL 406	0.533* (P)	0.272 (A)	-0.507* (P)	-1.644* (P)	0.232* (G)	-0.241* (P)	-0.039* (P)
PL 639	0.811* (P)	0.689 (A)	-0.257* (P)	-3.700* (P)	0.201* (G)	-0.100* (P)	-0.136* (P)
PL 5	-1.717* (G)	-2.478* (G)	-0.229* (P)	-1.533* (P)	-0.232* (P)	0.267* (G)	-0.022 (A)
PL 7	-1.856* (G)	-2.450* (G)	0.571* (G)	5.078* (G)	-0.313* (P)	0.428* (G)	0.217* (G)
LH 84-8	-1.661* (G)	-2.367* (G)	0.076 (A)	-2.506* (P)	-0.304* (P)	0.322* (G)	-0.067* (P)
L 4147	1.533* (P)	0.883 (A)	0.229* (G)	0.606 (A)	0.193* (G)	-0.284* (P)	-0.087* (P)
L 4076	-1.106* (G)	-1.228 (A)	-0.016 (A)	-1.561* (P)	-0.335* (P)	0.493* (G)	-0.070* (P)
LL 864	1.728* (P)	0.772 (A)	-0.032 (A)	0.772 (A)	0.193* (G)	-0.345* (p)	-0.089* (P)

*Significant at 5% level, ** Significant at 1% level, G = Good, P= Poor and A= Average.

Table 3: Specific combining ability effects of hybrids for different biometrical traits.

Hybrids	DF	DM	NPB	NPP	NSP	HSW	SYP
1	1.333* (P)	26.058* (P)	1.978* (G)	6.838* (G)	0.032 (A)	0.135* (G)	0.040 (A)
2	-0.250 (A)	-3.275* (G)	0.450* (G)	-2.106 (A)	-0.029 (A)	0.034 (A)	0.180* (G)
3	0.472 (A)	-1.359* (G)	-0.800* (P)	-3.717(A)	0.002 (A)	0.011 (A)	0.075 (A)
4	2.000* (P)	-0.859(A)	0.339(A)	2.783(A)	0.002 (A)	0.057 (A)	0.220* (G)
5	2.472* (P)	-0.886(A)	1.039* (G)	6.172* (G)	-0.018 (A)	0.103* (G)	0.181* (G)
6	-2.389* (G)	-3.970* (G)	0.200(A)	-5.912* (P)	0.007 (A)	-0.005 (A)	-0.131* (P)
7	-1.917* (G)	-3.220* (G)	0.380* (G)	3.977(A)	0.010 (A)	0.055 (A)	0.069 (A)
8	-0.944 (A)	-4.109* (G)	0.625* (G)	-0.189(A)	-0.029 (A)	0.084* (G)	0.072 (A)

Table 3: Continue..

Table 3: Continue..

9	-2.444* (G)	-3.109* (G)	-0.359* (P)	-0.189(A)	0.010 (A)	0.085* (G)	-0.027 (A)
10	-1.083* (G)	-3.914* (G)	0.019 (A)	0.227 (A)	-0.004 (A)	0.067* (G)	0.046 (A)
11	-1.028* (G)	-3.664* (G)	0.103 (A)	2.949 (A)	0.027 (A)	0.183* (G)	0.060 (A)
12	1.833* (P)	-0.831 (A)	0.408* (G)	3.783 (A)	-0.173* (P)	-0.018 (A)	0.156* (G)
13	-0.361 (A)	-3.192* (G)	0.608* (G)	-0.495 (A)	0.007 (A)	-0.082* (P)	-0.013 (A)
14	-0.556 (A)	-2.609* (G)	0.769* (G)	1.422 (A)	-0.101* (P)	0.054 (A)	0.108 (A)
15	-4.417* (G)	-6.192* (G)	0.283 (A)	-0.023 (A)	0.035 (A)	0.093* (G)	0.005 (A)
16	0.556 (A)	-2.081* (G)	-0.806* (P)	-0.189(A)	0.029 (A)	0.093* (G)	0.055 (A)
17	-1.944* (G)	-3.081* (G)	-1.122* (P)	-1.523 (A)	0.035 (A)	0.048 (A)	-0.021 (A)
18	-1.611* (G)	-1.664* (G)	-0.092 (A)	3.005 (A)	-0.035 (A)	0.122* (G)	0.007 (A)
19	0.583 (A)	1.503 (A)	0.214 (A)	1.838 (A)	0.565* (G)	-0.155* (P)	-0.164* (P)
20	0.389 (A)	0.808 (A)	0.080 (A)	2.561 (A)	-0.087* (P)	-0.149* (P)	-0.106 (A)
21	0.861 (A)	1.725 (A)	-0.092 (A)	3.477 (A)	-0.062 (A)	0.127* (G)	-0.022 (A)
22	-1.000 (A)	-1.525* (G)	0.422* (G)	1.366 (A)	-0.026 (A)	0.093* (G)	0.071 (A)
23	0.972 (A)	0.586 (A)	0.011 (A)	1.866 (A)	-0.165* (P)	-0.018 (A)	0.001 (A)
24	-1.528* (G)	-1.081* (G)	0.683* (G)	0.533 (A)	-0.026 (A)	-0.053 (A)	0.093 (A)
25	0.639 (A)	0.086 (A)	0.464* (G)	3.561 (A)	0.029 (A)	-0.222* (P)	-0.019 (A)
26	0.111 (A)	0.391 (A)	0.664* (G)	-1.717 (A)	-0.123* (P)	-0.023 (A)	0.015 (A)
27	-0.083 (A)	-0.359(A)	0.158 (A)	-0.467 (A)	0.068 (A)	0.090* (G)	0.009 (A)
28	-1.278* (G)	-2.275* (G)	0.505* (G)	-1.245 (A)	0.004 (A)	0.279* (G)	-0.064 (A)
29	0.028 (A)	1.836 (A)	0.916* (G)	3.255 (A)	0.032 (A)	-0.015(A)	-0.037 (A)
30	-0.806 (A)	-0.164 (A)	0.766* (G)	3.588 (A)	0.004 (A)	-0.117* (P)	-0.116 (A)
31	-1.361 (A)	1.225 (A)	-0.197 (A)	-3.217 (A)	0.110*(G)	0.250* (G)	0.071 (A)
32	-1.222 (A)	-1.192 (A)	0.297 (A)	-0.301 (A)	-0.065 (A)	0.063 (A)	0.068 (A)
33	-1.083 (A)	-1.442* (G)	0.978* (G)	-3.745 (A)	-0.096* (P)	-0.035 (A)	0.045 (A)
34	-1.778 (A)	-1.331* (G)	0.055 (A)	0.422 (A)	-0.035 (A)	0.225* (G)	-0.142* (P)
35	-1.278 (A)	-0.997 (A)	0.239 (A)	4.755 (A)	-0.062 (A)	0.016 (A)	-0.147* (P)
36	-0.083 (A)	-1.886 (A)	-0.003 (A)	3.422 (A)	0.015 (A)	0.085* (G)	0.093 (A)
37	0.389 (A)	0.864 (A)	0.344* (G)	4.644 (A)	0.018 (A)	0.008* (G)	0.083 (A)
38	-1.306* (G)	-2.359 (A)	0.822* (G)	2.144 (A)	0.046 (A)	0.187* (G)	-0.037 (A)
39	0.861 (A)	1.308 (A)	0.639* (G)	2.811(A)	-0.015(A)	-0.071* (P)	-0.009 (A)
40	0.861 (A)	2.780 (A)	0.505* (G)	0.227(A)	0.143* (G)	-0.083*(P)	0.110 (A)
41	-1.500* (G)	-0.109 (A)	1.083* (G)	3.061(A)	0.038(A)	0.140* (G)	0.023 (A)
42	2.000* (P)	0.891 (A)	1.100* (G)	5.727* (G)	-0.057(A)	-0.095* (P)	0.081 (A)
43	-0.028 (A)	-0.025 (A)	0.264(A)	0.283 (A)	-0.126* (P)	-0.097* (P)	0.187* (G)
44	-0.861 (A)	-0.692 (A)	0.947* (G)	4.283 (A)	0.013 (A)	0.014 (A)	-0.092 (A)
45	-0.556 (A)	0.086 (A)	0.691* (G)	1.116 (A)	0.074 (A)	-0.030 (A)	-0.055 (A)

Where 1 to 45 refers to hybrids PL 8 × PL 4 to L 4076 × LL 864, respectively; G, A and P refers to Good, Poor and average respectively.

Table 4: The estimates of PM, MGCA, GD, MPH and BPH for seed yield.

Hybrids	PM	MGCA	GD	MPH	BPH
1	1.78	0.15	18.69	17.65**	-1.87
2	1.89	0.16	15.71	20.11**	6.07
3	1.83	0.11	15.71	12.26*	-3.74
4	1.91	0.17	46.56	21.47**	8.41*
5	2.10	0.29	46.56	19.71**	17.76**
6	1.80	0.14	46.56	6.93	-9.81*
7	1.76	0.13	15.71	19.55**	-1.40
8	1.87	0.14	46.56	13.90	-0.47
9	1.94	0.13	15.71	3.61	-6.07
10	1.53	-0.05	14.47	12.05*	4.88
11	1.48	-0.10	14.47	10.14*	6.54

Table 4: Continue..

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12	1.55	-0.04	56.67	18.33**	9.52*
13	1.75	0.08	56.67	9.14*	-7.73
14	1.45	-0.06	56.67	20.69**	19.05**
15	1.41	-0.07	14.47	15.60**	13.99**
16	1.51	-0.07	56.76	11.55*	5.62
17	1.58	-0.08	14.47	0.95	-8.05*
18	1.58	-0.09	10.35	0.95	-2.44
19	1.66	-0.03	44.33	-6.63	-7.74
20	1.85	0.09	44.33	-0.81	-11.11**
21	1.55	-0.05	44.33	5.47	0.00
22	1.51	-0.06	10.35	13.53*	4.88
23	1.62	-0.05	44.33	2.47	1.22
24	1.69	-0.06	10.35	2.96	0.00
25	1.60	-0.08	44.33	-0.93	-5.36
26	1.80	0.04	44.33	3.89	-9.66*
27	1.50	-0.10	44.33	5.33	3.27
28	1.46	-0.11	10.35	1.37	-3.27
29	1.56	-0.10	44.33	-2.24	-4.38
30	1.63	-0.11	10.35	-12.54*	-17.82**
31	1.87	0.10	10.11	8.80	-1.45
32	1.57	-0.04	10.11	11.11*	4.17
33	1.53	-0.05	44.33	11.40*	1.79
34	1.64	-0.05	10.11	-6.10	-8.33
35	1.71	-0.06	44.33	-11.70*	-13.22**
36	1.77	0.08	10.11	13.56*	-2.90
37	1.73	0.07	44.33	14.45**	-4.35
38	1.83	0.07	10.11	2.45	-9.18*
39	1.90	0.06	44.33	-0.79	-8.70*
40	1.43	-0.08	44.33	20.98**	17.69**
41	1.53	-0.07	10.11	8.14	3.75
42	1.60	-0.08	44.33	5.92	-2.30
43	1.49	-0.08	44.33	20.40**	12.50**
44	1.56	-0.09	10.35	-4.15	-13.79**
45	1.67	-0.08	44.33	-6.59	-10.34*

Where 1 to 45 refers to hybrids PL 8 x PL 4 to L 4076 x LL 864, respectively and PM, MGCA, GD, MPH and BPH refers to parental mean, mean of general combining ability, genetic diversity, mid parent heterosis and better parent heterosis respectively.

Table 5: Average intra (diagonal) and inter cluster distance (D^2values).

Clusters	I	II	III	IV
I (PL 5, LH 84-8, L 4076, PL 7)	10.11	44.33	56.67	46.56
II (PL 406, PL 639, LL 864, L 4147)		10.35	14.47	15.71
III (PL 4)			0	18.69
IV (PL 8)				

Table 6: The Pearson's correlation between different parameters.

	PM	SCA	MGCA	GD	MPH	BPH
PM	1					
SCA	0.095	1				
MGCA	0.895**	0.303*	1			
GD	0.034	0.097	0.067	1		
MPH	0.037	0.859**	0.414*	0.117	1	
BPH	-0.279	0.760**	0.024	0.169	0.805**	1

8 × PL 5, PL 8 × PL 7, PL 4 × PL 5, PL 4 × LH 84-8, PL 4 × L 4147, LH 84-8 × L 4147 and L 4147 × L 4076 exhibited both significant and positive MPH and BPH for seed yield. The estimation of genetic diversity among parents revealed that four different clusters were present (Table 5). The cluster I (PL 5, LH 84-8, L 4076 and PL 7) and cluster II (PL 406, PL 639, LL 864 and L 4147) contains four parents each while cluster III (PL 4) and IV (PL 8) contains one parent each. The inter cluster distance was greater than the intra cluster distance indicating sufficient genetic diversity among the genotypes. The presence of sufficient genetic diversity in lentil was reported earlier by Gautam *et al.* (2014).

Relationship between PM, SCA, MGCA, MPH and BPH for seed yield

Both MPH and BPH (r=0.805*) were significantly and positively correlated with each other (Table 6). The PM was found to be non-significantly correlated with MPH (r= 0.037) and BPH (r=-0.279) (Table 6). Table 7 and Table 8 indicated that in case of mid parent, highest frequency of heterotic hybrids (65%) was observed when parents having high × low combinations were crossed. In case of BPH, highest frequency of heterotic hybrids (43%) was reported when parents having low x low combination were crossed. These results indicated that parental mean cannot be used as reliable criteria to predict heterosis. The MGCA effects were found to be positively and significantly correlated with MPH (r=0.414*) while positively and non-significantly correlated with BPH (r=0.024), respectively. A close perusal of Table 8 indicated that in case of MPH, 40.00% heterotic frequency was observed by crossing parents having poor × poor GCA effects combination while the good × poor GCA combination showed 35% heterotic frequency. In case of BPH the poor × poor combination showed a heterotic frequency of 57%. The parents having good x good or good × average GCA effects produced a moderate level of heterotic hybrids. The SCA effects were positively and significantly correlated with the MPH (r=0.859**) and BPH (r=0.760**), respectively. In case of MPH, 75% heterotic hybrids showed average SCA effects while 25% showed good SCA effects. In case of BPH, 57% hybrids have shown average SCA while 43 % had good SCA. No heterotic hybrids were obtained having poor SCA. Present finding indicated that high frequency of heterotic hybrids was obtained if crosses possessed average or good SCA. These results indicated SCA as most important factor in heterosis determination. This strong relationship may be due to the reason that both SCA and heterosis are function of non- additive gene action. The presence of genetic diversity between the parents used in hybridization programme is considered as an important parameter for obtaining significant heterosis in hybrids (Tecklewold and Becker, 2006). However, negligible correlation between heterosis and parental diversity was also reported (Devi and Singh, 2011). Heterosis may increase with increase in genetic diversity but greater divergence between parents cannot always results in good heterosis (Cress, 1966). In the present study, GD was found to be positively and non-significantly correlated with MPH (r=0.117) and BPH (r=0.169). In case of MPH the highest frequency of heterotic hybrids were produced when parents having moderate (55%) amount of diversity were crossed while the parents

Table 7: SCA and GCA effects, diversity class and parent mean class.

Hybrids	Cluster	Diversity class	PM class
1	IV × III	M	H × L
2	IV × II	M	H × H
3	IV × II	M	H × L
4	IV × I	H	H × H
5	IV × I	H	H × H
6	IV × I	H	H × L
7	IV × II	M	H × L
8	IV × II	M	H × H
9	IV × II	M	H × H
10	III × II	M	L × H
11	III × II	M	L × L
12	III × I	H	L × H
13	III × I	H	L × H
14	III × I	H	L × L
15	III × II	M	L × L
16	III × I	H	L × H
17	III × II	M	L × H
18	II × II	L	H × L
19	II × I	M	H × H
20	II × I	M	H × H
21	II × I	M	H × L
22	II × II	L	H × L
23	II × I	M	H × H
24	II × II	L	H × H
25	II × I	M	L × H
26	II × I	M	L × H
27	II × I	M	L × L
28	II × II	L	L × L
29	II × I	M	L × H
30	II × II	L	L × H
31	I × I	L	H × H
32	I × I	L	H × L
33	I × II	M	H × L
34	I × I	L	H × H
35	I × II	M	H × H
36	I × I	L	H × L
37	I × II	M	H × L
38	I × I	L	H × H
39	I × II	M	H × H
40	I × II	M	L × L
41	I × I	L	L × H
42	I × II	M	L × H
43	II × I	M	L × H
44	II × II	L	L × H
45	I × II	M	H × H

Where 1 to 45 refers to hybrids PL 8 × PL 4 to L 4076 × LL 864, respectively; H, M, L refers to High, Medium and Low respectively.

Table 8: The heterotic frequency obtained in different class.

Parameters	Classes	Number of heterotic hybrids		Heterotic frequency percent	
		MPH	BPH	MPH	BPH
SCA	P	0	0	0	0
	A	15	4	75	57
	G	5	3	25	43
GCA	G × G	1	1	5	14
	G × A	1	1	5	14
	G × P	7	0	35	0
	P × P	8	4	40	57
	P × A	3	1	15	14
Genetic diversity class	H	6	4	30	57
	M	11	3	55	43
	L	3	0	15	0
Per se performance of parents	H × H	3	2	15	29
	H × L	13	2	65	29
	L × L	4	3	20	43

Where, P, A, G, H, M and L refers to poor, average, good, high, medium and low respectively.

having high level of GD results in 30% heterotic hybrids. In case of better parent heterosis 57% of heterotic hybrids were obtained when parents having high amount of diversity were crossed while parents having moderate amount of diversity resulted in 43% hetrotic hybrids.

CONCLUSION

The hybrids *viz.,* PL 8 × PL 4 (2.1 g), PL 8 × L 4147 (2.11 g), PL 8 × L 4076 (2.13 g), PL 8 × PL 406 (2.27 g), PL 8 × PL 5 (2.32 g) and PL 8 × PL 7 (2.52 g) were identified as most promising hybrids for seed yield while the parents PL 8 (2.14 g) and PL 7 (2.07 g) can be used as donors for high seed yield. The SCA were found to be the most reliable parameters to predict the heterosis.

Conflict of interest: None.

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