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Early generation selection in microsperma-macrosperma derived gene pool of lentil

N. Kishore and V. P. Gupta

Department of Plant Breeding and Genetics, Himachal Pradesh Krishi Vishvavidyalaya, Palampur 176 062

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Abstract

Evaluation of 475 recombinant lines of 26 crosses in F_3 generation and 409 recombinant lines of 24 crosses in F_4 generation derived from crosses involving *microsperma* and *macrosperma* groups of lentil, raised in augmented design, revealed sufficient genetic variability for seed yield/plant, biological yield/plant, 100-seed weight, harvest index, seeds/pod, days to 50% flowering, and days to maturity. Biological yield/plant and seed yield/plant showed high degree of PCV, GCV and genetic advance. Heritability was high for biological yield/plant and days to maturity whereas moderate for seed yield/plant and most of the traits. Seed yield/plant showed significant positive association with biological yield/plant, harvest index, seeds/pod, 100-seed weight and days to 50% flowering in both F_3 and F_4 generations in almost all the crosses of different groups. Crosses involving Precoz and PL-639 as one of the parents were promising. Crosses L-4145 × PL-639, Precoz × PL-639, Vipasha × PL-639 and Precoz × L-259 were with higher transgressive segregants. About 15% (123) and 10% (92) of the progenies gave higher yield over the better parent and the best check, respectively. Seven per cent (55) bold seeded progenies were identified in the population with nine progenies having both high yield and bold seeds.

Key words : Lentil, *macrosperma - microsperma* derived gene pool, early generation, variability, correlation

Introduction

In self fertilising crops, handling of segregating generations poses a great difficulty to the breeders because of limited available resources. Therefore one is always in search of alternatives to minimize the size of population to be handled in advanced generations but at the same time wants to retain the best recombinant lines for the traits under improvement. Early generation selection is a cogent answer to the problem. Only few reports pertaining to the effectiveness of early generation selection and testing are available and there are conflicting views on the value of selection for yield in early generations [1-5]. Therefore the present investigation was carried out in *microsperma* - *macrosperma* derived populations to study the effectiveness of early generation selection in lentil.

Material and methods

Eight diverse parents of lentil constituting *macrosperma* (Precoz, L-5588 and ILL-2991)and *microsperma* (Vipasha, PL- 406, L-4145, PL-639, and L-259) groups were crossed in different combinations. The experimental material comprising of 900 test lines (progenies) i.e. 475 recombinant lines of 26 crosses in F_3 generation, 409 recombinant lines of 24 crosses in F_4 generation and eight parental lines repeated twice were accommodated in 18 blocks. These test lines along with six checks namely HPLC-8820, HPLC-84-142, HPLC-31S, HPLC-8824, HPLC-8805 and Vipasha were raised in augmented randomized block design. The checks were repeated in each block as per the design. Each plot comprised single row of one metre length with row to row and plant to plant distances of 25 cm and 5 cm, respectively. Data were recorded on row basis (counting total number of plants from each row) for seed yield/plant (g), biological yield/plant (g), harvest index (%), 100-seed weight (g), seeds/pod, days to 50% flowering, days to maturity and reproductive phase. Correlation coefficients were estimated on the basis of observed means in F_3 and F_4 generations separately, both generation wise (F_3 and F_4) across crosses and cross wise in 13 selected crosses in both the generations.

Analysis of variance for the augmented design was done as per Federer [6]. Variability and association studies were estimated following the methods described by Johnson et al. [7-8].

Results and discussion

Microsperma and *macrosperma* hybridization in F_3 and F_4 generations in lentil generated sufficient amount of genetic variability for seed yield/plant, biological yield/plant, harvest index, 100-seed weight, seeds/pod, days to 50% flowering and days to maturity. Rana and

Gupta [9] obtained similar results. Estimates of phenotypic and genotypic coefficients of variation (PCV and GCV), expected genetic advance (GA) and heritability (broadsense) are given in Table 1. High heritability was recorded for biological yield/plant and days to maturity, whereas moderate for seed yield/plant and days to 50% flowering. High estimates of heritability were also obtained by Gupta et al. [10]. This indicates that traits under study are less influenced by the environment or less number of genes are involved.

Table 1. Mean squares, coefficients of variation, heritability, and expected genetic advance for different cross-progenies of F_3 and F_4 generations

Trait	Mean squares	PCV (%)	GCV (%)	h_b^2	GA (%) of mean
Seed yield/plant (g)	0.85*	64.47	51.86	64.71	86.01
Biological yield/plant (g)	9.43*	64.65	57.92	80.28	106.53
Harvest index (%)	77.82*	28.09	17.66	39.55	23.15
100-seed weight (g)	0.26*	22.94	11.24	24.00	11.47
Seeds/pod	0.06*	16.20	7.25	20.00	6.68
Days to 50% flowering	523.26*	17.23	14.62	71.96	25.56
Days to maturity	347.00*	9.72	9.39	93.33	18.62

*Significant at 5% level

For estimating the real effects of selection; high heritability coupled with high genetic advance is an useful index and this was reported for seed yield/plant and biological yield/plant. This result is in line with the finding of Gupta and Kalia[11] and traits showing high heritability with high genetic advance may be controlled by additive gene action.

Improvement of complex character like yield may be accomplished through component breeding in which method there should be strong association of yield with a number of characteristics and simpler inheritance of these yield components than that of yield itself [12]. The estimates of correlation coefficients in F_3 and F_4 generation across crosses are given in Table 2. Seed yield/plant is positively correlated with biological yield/plant and harvest index in both the generations but its positive association with 100-seed weight in F_4 is the most desired one if the breeder wants to evolve high yielding bold seeded varieties. Balayan and Shobir [13] also showed positive association between seed yield and seed size. Negative association of seeds/pod with seed size as obtained by Gupta et al. [14] has also been obtained in F_4 generation. The positive association of seed size (100-seed weight) with biological yield/plant in both the generations indicate that success could be achieved in combining the seed size with that of plant yield by attempting the crosses between bold seeded parent (e.g. Precoz in this study) and high yielding cultivars with higher biomass.

Table 2. Phenotypic correlation coefficients in F_3 (lower half) and F_4 (upper half) generations between different character-pairs

Character	Seed yield/plant	Biological yield/plant	100-seed weight	Harvest index	Seeds/pod	Days to 50% flowering	Days to maturity	Reproductive phase
	1	2	3	4	5	6	7	8
1	-	0.88*	0.13*	0.14*	0.06	0.10*	0.08	−0.06
2	0.83*	-	0.21*	−0.24*	0.05	0.21*	0.17*	−0.15*
3	0.04	0.11*	-	−0.15*	−0.16*	0.16*	0.04	−0.20*
4	0.27*	−0.23*	−0.14*	-	0.06	−0.22*	−0.17*	0.17*
5	0.09*	0.12*	−0.04	−0.05	-	−0.04	0.04	0.11*
6	0.04	0.18*	−0.13*	−0.13*	0.09*	-	0.80*	−0.76*
7	−0.05	0.03	−0.20*	−0.03	0.10*	0.89*	-	−0.26*
8	0.01	−0.09*	−0.08	0.21*	0.00	−0.46*	−0.10*	-

*Significant at 5% level

A list of crosses showing significant phenotypic correlation coefficient for different character pairs is furnished in Table 3. Seed yield/plant was positively associated with biological yield/plant for all the 13 crosses studied in both the generations. Seed yield/plant exhibited positive association with seed size for the crosses ILL-2991 × PL-406 and Precoz × L-5588 in the F_3 and F_4 generations, respectively, whereas it was negative for ILL-2991 × L-259 in F_3 generation. Negative association of seed size with seeds/pod was obtained in F_4 generation for the cross Precoz × Vipasha and positive for the cross ILL-2991 × PL 406 in F_3 generation and is similar to the finding of Gupta et al. [14]. If one association is positive for a particular cross in one generation, then the same association may be negative for the same or other cross in the same or other generation. Biological yield/plant had positive correlation with harvest index in F_3 generation for the cross Vipasha × PL-406 but for the same cross negative association was observed in the F_4 generation. The possible reason for the difference in associations from cross to cross generation to generation may be

Table 3. List of crosses showing significant correlation coefficients in F3 and F4 generations

Character-pair	Cross	
	F3	F4
Seed yield/plant with biological yield/plant	Precoz × PL 406 (0.76) Precoz × L 5588 (0.72) Precoz × PL 639 (0.87) Precoz × L 4145 (0.92) Precoz × Vipasha (0.93) Vipasha × ILL 2991(0.64) Vipasha × PL 406 (0.91) ILL 2991 × L 5588 (0.83) ILL 2991 × L 259 (0.90) ILL 2991 × PL 406 (0.50) L 4145 × PL 639 (0.88) PL 406 × L 4145 (0.91) PL 406 × L 259 (0.69)	Precoz × PL 406 (0.95), Precoz × L 5588 (0.91), Precoz × PL 639 (0.87), Precoz × L 4145 (0.80), Precoz × Vipasha (0.86), Vipasha × ILL 2991 (0.87), Vipasha × PL 406 (0.91), ILL 2991 × L 5588 (0.54), ILL 2991 × L 259 (0.73), ILL 2991 × PL 406 (0.90), L 4145 × PL 639 (0.87), PL 406 × L 4145 (0.76), PL 406 × L 259 (0.87)
Seed yield/plant with 100-seed weight	ILL 2991 × L 259 (–0.55) ILL 2991 × PL 406 (0.63)	Precoz × L 5588 (0.36
Seed yield/ plant with seeds/pod	Precoz × PL 639 (0.52) ILL 2991 × PL 406 (0.63)	Precoz × L 4145 (0.54),
Seed yield/ plant with seeds/pod	Precoz × PL 639 (0.52), ILL 2991 × PL 406 (0.41)	Precoz × L 4145 (0.54), PL 406 × L 4145 (0.57)
Biological yield/plant with harvest index	Vipasha × PL 406 (0.47)	Precoz × L 5588 (–0.67), Vipasha × PL 406 (–0.72)
Biological yield/plant with 100-seed weight	Precoz × PL 406 (0.64), ILL 2991 × L 259 (–0.50)	Precoz × L 4145 (0.49)
Biological yield/plant with seeds/pod	Precoz × PL 639 (0.41), ILL 2991 × PL 406 (–0.36)	Precoz × L 4145 (0.60)
100-seed weight with seeds/pod	ILL 2991 × PL 406 (0.80)	Precoz × Vipasha (–0.65)
100-seed weight with harvest index	ILL 2991 × L 259 (–0.41), L 4145 × PL 639 (–0.59)	Precoz × L 5588 (–0.62)

Note : Figures in parenthesis are significant at 5% level

because of the high degree of segregation and genetic heterogeneity in the F_3 generation leading to the breakdown and formation of new linkage groups and reduction in dominance from F_3 to F_4.

Besides above information, from practical point of view a plant breeder is also interested to select potential crosses for identifying transgressive segregants and high yielding recombinant lines along with desirable traits. The observed frequency (%) of progenies superior

Table 4. Observed frequency (%) and mean values of highest yielding progenies superior to better parent and to the best check in F3 and F4 generation along with the performance of other traits

Cross	Generation	Frequency (%) of progenies superior in seed yield over		Mean seed yield of the best progeny along with the performance of other traits			
		Better parent	Best check	Seed yield/plant (g)	Biological yield/plant (g)	100-seed weight (g)	Harvest index (%)
Precoz × PL 406	F3	0.21	0.21	2.44	6.04	2.84	40.34
	F4	0.98	0.49	5.14	19.62	1.96	26.20
× L 4145	F3	0.42	0.21	3.22	8.22	3.00	39.16
	F4	1.47	0.98	4.50	17.49	2.12	25.72
× L 259	F4	3.18	2.20	7.62	24.01	1.72	31.76
× L 5588	F3	0.63	0.63	3.11	8.81	2.36	35.26
	F4,	1.22	1.22	4.00	11.38	2.64	35.11
× ILL 2991	F3	0.84	0.42	5.53	20.05	2.68	27.59
	F4	0.73	0.73	2.71	5.75	3.40	47.17
× Vipasha	F3	0.63	0.63	4.57	14.47	2.24	31.57
× PL 639	F3	1.05	1.05	4.04	12.50	2.88	32.35
	F4	2.44	2.44	4.58	12.78	2.76	35.87
Vipasha × L 5588	F4	0.49	0.49	4.62	17.90	1.72	25.81
× ILL 2991	F3	0.21	0.21	3.50	9.64	1.76	36.21
	F4	1.22	1.22	4.61	14.99	2.44	30.76
× PL 406	F3	0.63	0.63	3.85	11.08	2.28	34.69
	F4	0.24	0.24	2.93	9.79	2.00	29.92
× PL 639	F4	2.44	2.44	3.58	9.20	2.08	38.96
× L 4145	F3	0.42	0.42	2.74	7.35	2.92	35.23
ILL 2991 × L 4145	F3	0.42	0.21	3.48	9.15	2.00	38.06
× L 259	F3	0.42	0.42	2.64	6.40	1.76	41.18
	F4	1.96	1.71	7.36	16.26	1.56	45.24
× PL 406	F3	0.21	0.21	2.46	5.90	1.80	41.69
	F4	1.71	1.22	4.41	9.56	2.16	46.15
× PL 639	F3	0.21	0.21	2.30	7.44	2.16	30.85
	F4	0.73	0.73	4.12	18.79	1.96	21.91
L 5588 × L 259	F3	0.63	0.73	3.43	6.04	2.28	56.20
L4145 × PL 639	F3	0.21	0.21	2.59	5.86	1.96	44.18
	F4	3.67	3.18	4.75	11.62	2.48	46.85
PL 406 × PL 639	F3	0.42	0.42	2.30	4.75	1.80	48.44

Mean of best check, Vipasha = 1.31, CD (5%) = 1.21

to the better parent and to the best check, Vipasha a released variety for Himachal Pradesh for seed yield/plant along with the performance of other traits in different crosses in F_3 and F_4 generations have been summarized in Table 4. For seed yield/plant the number of progenies superior to the better parent (transgressive segregants) were 55 in F_3 and 88 in F_4 generation and number of progenies superior to the best check were 26 in F_3 and 66 in F_4 generation. It indicated that number of superior progenies were more in F_4 generation than F_3 generation. Highest frequency of progenies having seed yield higher than the best check was observed for the cross L-4145 × PL-639 followed by Precoz × PL-639, Vipasha × PL-639 and Precoz × L-259 and hold promise for exploitation in further generations. About 15 and 10% progenies gave higher seed yield over the better parent and the best check, respectively in both the generations. About 7% (55) bold seeded progenies were identified in the population, out of which, interestingly, nine of the lines also showed superiority in yield over the best check. All the nine progenies had 100-seed weight of more than 3.0 grams over the best check Vipasha and the crossed progenies were of *macrosperma* × *microsperma* nature with Precoz (*macrosperma*) being one of the parent in all the crosses. Therefore, the crosses involving Precoz as one of the parents may be carried forward and exploited with a view to isolate high yielding and bold seeded segregates.

As these views have far reaching consequences it would be desirable to look at this aspect on the basis of present information with respect to economic traits such as seed yield/plant, biological yield/plant, 100-seed weight and promising crosses could be identified on the basis of combination of these characters. Looking at the continuous nature of variation generated in the present lentil population for seed yield and related traits, classification of lentil into sub species i.e. *microsperma* and *macrosperma* appears to be unjustified as reported earlier.

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