

**EARLY GENERATION TESTING AND RESPONSE TO SELECTION IN
MACROSPERMA × MICROSPERMA DERIVED GENE POOL OF LENTIL**

OM VIR* AND V. P. GUPTA

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

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ABSTRACT

F₂ derived lines (160) in F₄ from four *macrosperma* × *microsperma* crosses, selected on the basis of high seed yield/plant (g), and high harvest index in the background of bold seed size from 713 F₂ derived lines in F₃ were evaluated in an augmented randomized block design under two nitrogenous regimes i.e., 20 kg N/ha (E-I) and 40 kg N/ha (E-II). Estimates of correlation coefficients of selected F₂ derived lines in F₃ with the corresponding lines in F₄ were highly significant and positive with respect to seed yield/plant (0.91 and 0.92 in E-I and E-II, respectively), biological yield/plant (0.75 and 0.72 in E-I and E-II, respectively) and 100-seed weight (0.91 and 0.92 in E-I and E-II, respectively). At 5% selection intensity, standardized selection differential was observed to be the highest for all studied traits followed by 10% and 22.5% selection intensities. Standardized response to selection at 5% selection intensity was estimated to be the highest for all traits in E-II and it was equally good in E-I also. However, E-II was observed to be superior for all the traits for estimation of response to selection at different selection intensities. The realized heritability of seed yield/plant was estimated to be high at 5%, 10% and 15% selection intensities in E-II. For 100-seed weight the estimated realized heritability was high in all cases. The present results favour the view that most desirable gene combinations can be identified even in the heterozygotes. On the basis of present results yield test in F₃ is advocated.

Key Words : *Macrosperma* × *microsperma* derived gene pool, standardized selection differential, standardized response to selection, early generation testing, realized heritability.

The breeder is always interested to reduce the amount of material to be handled in the segregating generations due to limited available resources and at the same time he does not want to lose the best recombinant lines for the traits under improvement. The early generation testing is the best answer to this problem.

*Present address: Punjab Agricultural University, Regional Res. Station, PO Box 34, Kapurthala 144 601

Therefore, an important consideration is the response to selection for the traits under improvement. Whan *et al.*, [14] suggested that selection for seed yield in early generation need to be done at many sites simultaneously at an early stage however, keeping in view, in the present investigation selection and evaluation of genotypes were carried out in two micro- environments to get the information on early generation testing, response to selection and realized heritability for adopting efficient selection strategies in *macrosperma* × *microsperma* derived gene pool of lentil for the improvement of yield in the background of bold seed size under two micro- environments.

MATERIAL AND METHODS

One hundred sixty (F_4) recombinant lines from four *macrosperma* × *microsperma* crosses namely, Precoz × PL 406, Precoz × PL 639, HPL 3 × L 830 and HPL 4 × L 830, selected on the basis of high seed yield (> 2.0 gm./plant) in the background of bold seed size (100 seed weight > 4.5 gm.) from 713 lines in F_3 generation of aforesaid crosses alongwith eight checks namely Precoz, HPLC 31 (S), HPLC 36-11, HPLC 84-11, HPLC 84-142, L 830, PL 639 and Vipasha were raised in an augmented randomized block design with eight blocks in two micro-environments created by applying two doses of nitrogen i.e., 20 kg N/ha (E-I) and 40 Kg N/ha (E-II) at the time of sowing in the soil. The initial fertility status of two micro-environments with respect to available N, P and K was worked out and found to be similar. Values for N, P and K availability were found to be 104, 35 and 120 kg./ha, respectively. In each of the micro-environments the plots consisted of single row of 1 m length with row to row and plant to plant spacing of 25 and 5 cm., respectively. Standard agronomic practices were adopted. The data were recorded on five randomly taken plants from each plot in each of the micro-environments on seed yield/plant (g), biological yield/plant, (g) harvest index and 100-seed weight (g). The analysis of variance for augmented randomized block design was carried out as per Federer [5]. Simple correlation coefficients were computed for early generation testing and standardization selection differential, response to selection and realized heritability were estimated as per Falconer [3].

RESULTS AND DISCUSSION

The results obtained with respect to correlation of different traits between generations are given in Table 1. The correlation of seed yield/plant, biological yield/plant, harvest index and 100-seed weight of F_2 derived lines in F_3 with seed yield, biological yield, harvest index and 100-seed weight, respectively of F_3 lines derived from them in F_4 generation is significantly positive in both of the micro-environments thereby, indicating that seed yield, biological yield, harvest index

and 100-seed weight of F_2 derived lines in F_4 generation would be predictable on the basis of yield test in F_3 generation and selection of high yielding lines having high harvest index alongwith bold seed size on the basis of seed yield/plant would be fruitful in F_3 generation itself [8, 12]. Little deviation in the estimates of correlation coefficients in two different micro-environments may be due to the presence of genotypes \times micro-environments interactions.

Table 1. Estimates of correlation coefficients between F_3 and F_4 generation with respect to seed yield/plant (g), biological yield/plant (g), harvest index and 100-seed weight in two micro- environments

Traits	Correlation coefficients	
	E-I	E-II
Seed yield/plant (g)	0.91*	0.92*
Biological yield/plant (g)	0.75*	0.82*
Harvest index	0.76*	0.72*
100-seed weight (g)	0.91*	0.92*

*Significant at 5% level of significance

Weiss *et al.*, [13] reported that selection after F_3 generation among lines is fruitful. Hanson and Weber [6] have also indicated that seed weight on F_2 plant basis is essentially equivalent to selection for seed yield in F_3 . Thorne [11] and Luders *et al.*, [7] have reported significant positive correlation coefficient of F_3 derived lines with F_5 derived lines. Boerma and Cooper [1] reported that selection within highly heterogeneous lines isolated by early generation testing of F_2 derived lines in F_3 , F_4 and F_5 generations can result in improved yield. Sneepe [10] and Cooper [2] emphasized the use of early generation testing in F_2 and subsequent generations for yield.

The high order positive and significant correlations between F_3 and F_4 generations of seed yield, biological yield, harvest index and 100-seed weight are indicative of likely response to selection. When selection is carried out in early generations among F_2 derived lines, the important consideration is response to selection in the later generations when lines are approaching homozygosity. As the selected F_2 derived lines in the present study have been evaluated in F_4 generation in two micro-environments and response to selection has been studied under different selection intensities, the consideration of present results would be useful for better prediction of the improvement expected in a breeding programme than from the correlation analysis alone. The results in details on standardized selection differential (S/σ_p),

standardized response to selection (R/σ_p) and realized heritability (R) have been presented in Table 2. At 5% selection intensity, standardized selection differential

Table 2. Estimates of standardized selection differential, standardized response to selection and realised heritability for different traits in 2 micro-environments under different selection intensities

Characters Traits and Selection intensity	Popula tion mean	No. of selec ted lines	Mean of selec ted lines	Standa rdized selec tion differ ential (S/σ_p)	Progeny mean		Standardized selection response (R/σ_p)		Realized heritability (R/S)	
					E-I	E-II	E-I	E-II	E-I	E-II
Seed yield/plant (g)	1.31									
Selection Intensity										
5%		35	2.72	2.93	2.35	2.47	2.16	2.41	0.74	0.82
10%		71	2.21	1.87	1.97	2.04	1.37	1.52	0.73	0.81
15%		106	2.06	1.56	1.72	1.91	0.85	1.27	0.54	0.80
22.5%		160	1.54	0.48	1.46	1.49	0.31	0.38	0.65	0.78
Harvest index (%)	28.18									
Selection Intensity										
5%		35	42.43	1.61	35.94	39.95	0.87	1.32	0.54	0.83
10%		71	37.51	1.05	32.86	32.95	0.53	0.54	0.50	0.51
15%		106	34.43	0.71	30.86	31.17	0.30	0.33	0.43	0.47
22.5%		160	31.69	0.40	29.55	29.98	0.16	0.20	0.39	0.51
100-seed weight (g)	2.94									
Selection intensity										
5%		35	4.26	2.51	4.05	4.11	2.11	2.22	0.84	0.89
10%		71	3.94	1.90	3.74	3.77	1.52	1.58	0.80	0.83
15%		106	3.83	1.69	3.70	3.71	1.45	1.45	0.85	0.86
22.5%		160	3.77	1.58	3.61	3.64	1.27	1.34	0.81	0.84

Phenotypic standard deviations I) Seed yield/plant = 0.48; II) Harvest Index = 8.84; III) 100-seed weight = 0.53

was estimated to the highest for all the studied traits followed by 10%, 15% and 22.5% selection intensities. Standardized response to selection at 5% selection intensity was observed to be the highest for all traits in E-II and it was equally good in E-I also however, estimated values of response to selection at different selection intensities were higher in E-II. The slight differences for estimated response to selection between two micro-environments could be due to the difference in the nature and magnitude in the correspondence between genetic and non-genetic effects. The realized heritability for seed yield/plant was high at 5%, 10% and 15% selection intensities in E-II whereas, it was moderate at all selection intensities in E-I. For harvest index, realized heritability was high at 5% selection intensity and moderate at 10% and 22.5% selection intensities in E-II. At 5% and 10% selection intensities it was moderate in E-I however, realized heritability was low at 15% selection intensity in both the micro-environments than that at 22.5% selection intensity in E-I. For 100-seed weight, realized heritability was observed to be high in all the cases. The difference between two micro-environments for the estimates of realized heritability could be due to the fact that heritability is a property not only of a character but also of the population the environment and the circumstances to which the genotypes are subjected to [3], its ultimate value depends upon the magnitude of all the components of variance. The influence of environments on the estimates of "R" for seed yield as obtained in the present study has also been reported by Whan *et al.*, [14].

In early generation testing S, R and R/S is more at high selection intensity but it gets low at low selection intensity. According to Fasoulas [4] the high intensity of selection maximizes genetic advance as has also been observed in the present study.

Shebeshki [9] advocated that the most desirable gene combinations can be identified even in the heterozygote, the essential point of this view is that the proportion of plants with the most desirable combination of genes decreases rapidly with the advancing generations and if these are not selected in the earliest generations even if heterozygote, they will be lost. The present results are in favour of the theory given by Shebeshki [9] as the number of superior lines are more when selection is predicted in F₂ generation.

As these views have far reaching consequences it would be desirable to look at this aspect on the basis of the present information with respect to seed yield/plant, biological yield/plant, harvest index and 100-seed weight.

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