# CROSSOVER AND NON-CROSSOVER INTERACTIONS AND REGRESSION ANALYSIS FOR SEED YIELD AND OTHER TRAITS IN *MACROSPERMA* × *MICROSPERMA* DERIVED GENE POOL OF LENTIL

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### ABSTRACT

Twenty nine advanced bold seeded *macrosperma*  $\times$  *microsperma* derived lines of lentil alongwith check were evaluated in ten environments for six quantitative traits and data were subjected to regression analysis and also the analysis to detect the presence of crossover and non-crossover interactions. Four genotypes HPLC 8855, 8883, 8894 and 8895 were identified to be promising using regression analysis, whereas five genotypes HPLC 8829, 8887, 8888, 8892 and 8895 against standard check Vipasha were identified as potential ones by using crossover and non-crossover interactions concept. Of these genotypes, HPLC 8895 has been identified as high yielding genotype having specific adaptability and responsiveness to higher introgen regimes both by regression analysis and crossover and non-crossover interactions concept.

Key Words : Macrosperma × microsperma derived gene pool, lentil, genotype × environment interaction, crossover and non-crossover interaction, regression analysis.

To enhance the production of lentil it is advocated that breeders should look for environment specific genotypes which are to be responsive to input-intensive agriculture, capable of giving high yield. This becomes more important in case of grain legumes, which are generally not responsive to the better management practices, to breed for their responsiveness to specific environment and better inputs. Keeping in view the above, the present investigation was carried out in a wide range of heterogeneous environmental conditions across the hills of Western Himalayas to identify location-specific and nitrogen- responsive genotypes in lentil using regression analysis [1, 2] and cross and non-crossover interactions concept [3]. Earlier information on this aspect in such type of generated material in lentil is not available.

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# MATERIAL AND METHODS

Twenty nine advanced ( $F_{4}$ ) breeding lines of four macrosperma × microsperma crosses namely, Precoz  $\times$  PL 406, Precoz  $\times$  PL 639, HPL 3  $\times$  L 830 and HPL 4  $\times$  L 830, selected on the basis of high seed yield ( $\geq 2 \text{ gm/plant}$ ) in the background of bold seed size (100-seed weight  $\geq$  4.5 gm) alongwith local check Vipasha were raised in a randomized block design with two replications at five locations namely, Palampur, Sundernagar, Kangra, Dhaulakuan and Berthin, which represent different environmental conditions across the hills of Western Himalayas. At each location two micro-environments were created by applying two doses of nitrogen (N) i.e. 20 kg N/ha and 40 kg N/ha at the time of sowing thus, ten environments (Env.) i.e. Env. I. (20 kg N/ha) and II (40 kg N/ha) at Palampur, Env. III (20 kg N/ha) and Env. IV (40 kg N/ha) at Sundernagar, Env. V (20 kg N/ha) and Env VI (40 kg N/ha) at Kangra, Env. VII (20 kg N/ha) and Env. VIII (40 kg N/ha) at Dhaulakuan and Env. IX (20 kg N/ha) and Env. X (40 kg N/ha) at Berthin were created. The initial soil fertility status of two micro-environments at each location with respect to available N, P and K was worked out and found to be similar. Values for N availability for Palampur, Sundernagar, Kangra, Dhaulakuan and Berthin were found to be 112, 91, 103, 97, and 145 kg/ha., respectively. In each environment plots consisted of single row of 1 m length with row to row and plant to plant distances of 25 and 5 cm., respectively. Recommended doses of P<sub>2</sub>O<sub>5</sub>, i.e., 40 kg P<sub>2</sub>O<sub>5</sub>/ha was also applied at the time of sowing. The data were recorded on five randomly taken plants from each plot in each environment on seed yield/plant (g), biological yield/plant (g), harvest index (direct values were used for statistical analysis), seeds/pod, 100-seed weight (g) and crushing hardness (kg per cm<sup>2</sup>) and data were analysed separately for each environment. Adjusted progeny means were used for the combined analysis and for the traits exhibiting the presence of  $g \times e$  interaction, regression analysis and analysis to detect the presence of crossover and non-crossover interactions were carried out as per Eberhart and Russell [1] and Perkins and Jinks [2], and Gail and Simon [3].

## **RESULTS AND DISCUSSION**

Analysis of variance revealed significant differences among genotypes for the six traits in all ten environments. The combined analysis revealed the presence of g  $\times$  e interaction for seed yield/plant, biological yield/plant, harvest index, seeds/pod, 100-seed weight and crushing hardness. Regression analysis enables breeders to select desirable genotypes with respect to the responsiveness and stability in different environments. In the studied material the genotypes HPLC 8855, 8883, 8894 and

8895 had above average performance and responsiveness with respect to seed yield/plant (Table 1). Among these high yielding genotypes HPLC 8855, 8883 and 8894 can be designated as stable ones with average responsiveness. Though the genotype HPLC 8895 is an above average yielder and also has shown above average responsiveness coupled with instability. It was highest yielder in Env. VIII (Dhaulakuan, 40 kg N/ha) followed by HPLC 8894, 8855 and 8883 and were significantly superior

Table 1. Heterogeneity (H) test of response for the comparison of mean seed yield/plant (g) against the standard variety Vipasha along with  $Q^+$  and  $Q^-$  values for crossover interaction and adaptability parameters for the genotypes

Genotypes	Adaptability parameters			Against Vipasha		
_	u+d <sub>i</sub>	$\beta_i \pm SE$	$\sigma^2 d_i$	Н	Q+	Q-
HPLC 8806	1.23	$0.32^{*} \pm 0.35$	0.39*	84.31#	53.69	32.47 <sup>\$</sup>
HPLC 8815	1.10	$-0.21^{*} \pm 0.18$	0.06*	36.75*	21.62	16.84 <sup>\$</sup>
HPLC 8825	1.01	$0.01^{*} \pm 0.15$	0.03	27.93 <sup>#</sup>	12.00 <sup>\$</sup>	16.08
HPLC 8827	1.02	$0.02^{*} \pm 0.26$	0.20*	53.74 <sup>#</sup>	29.04	24.93 <sup>\$</sup>
HPLC 8829	1.08	$0.01^{*} \pm 0.18$	0.08*	31.12 <sup>#</sup>	17.07	15.03 <sup>\$</sup>
HPLC 8855	$1.58^{*}$	$0.26^{*} \pm 0.15$	0.03	29.61#	24.59	8.34
HPLC 8856	0.99	$-0.61^{*} \pm 0.25$	0.17*	54.64#	20.81 <sup>\$</sup>	34.18
HPLC 8875	1.09	$-0.29^{*} \pm 0.11$	0.00	29.42 <sup>#</sup>	193.78	12.03 <sup>\$</sup>
HPLC 8877	1.16	$-0.37^{*} \pm 0.41$	0.54*	77.27*	79.56	15.24 <sup>\$</sup>
HPLC 8883	1.57*	$-0.01^{*} \pm 0.13$	0.01	21.40#	44.73	0.00
HPLC 8888	1.34	$0.54^{+} \pm 0.37$	0.44*	86.57#	70.73	26.03 <sup>\$</sup>
HPLC 8892	1.26	$-0.04^{*} \pm 0.25$	0.18*	<b>44.58</b> <sup>#</sup>	38.92	13.03 <sup>\$</sup>
HPLC 8894	1.58*	$0.20^{*} \pm 0.14$	0.03	23.44#	44.40	0.01
HPLC 8895	1.71*	$1.02^{*} \pm 0.29$	0.25*	151.54#	183.63	22.39 <sup>\$</sup>
Grand mean (u)	$1.27 \pm 0.18$					
Vipasha	$1.01 \pm 0.13$					

\* Significant at P < 0.05; # H was significant against  $x^2$  0.05 at s-1 df, where s is the number of environments. \$ minimum of either Q<sup>+</sup> or Q<sup>-</sup> was significant against "C" value given by Gail and Simon [3].

to the best check. The genotype HPLC 8895 showed above average performance alongwith instability for biological yield/plant, 100-seed weight and crushing hardness being the best performance of this genotype for these traits again in Env. VIII. The HPLC 8883 showed average performance alongwith stability for harvest index.

The regression technique describes the response pattern of individual genotype without differentiating the kind of  $g \times e$  interaction involving change in magnitude of response or direction among the genotypes [4, 5]. Baker [4] described a test, which was initially proposed by Gail and Simon [3], and illustrated its application to test the kind of interaction in crop plants. The concept of crossover and non-crossover interaction is important in decision making relating to crop improvement strategies [4], since the presence of crossover interaction is a substantial evidence in favour of breeding for specific adaptation to certain situations. Baker [4] further suggested that in the absence of crossover interaction, there is little substance for argument in the favour of breeding for adaptation to specific environment. The genotypes exhibiting crossover interaction against a standard variety can be said to have specific adaptability and can replace that standard variety in the specific environments.

The existence of prior scientific basis to explain crossover interaction is crucial [6]. Thus, it is advantageous to define the varietal combinations among which one has to look for qualitative interaction in advance. There will be enormous multiplicity of all possible varietal pairs for detection of crossover interaction if there is no prior basis for comparison. Such a practice will greatly increase the experiment-wise error rate. In the present case the new genotypes were therefore, compared with the standard check Vipasha for detection of crossover interaction since the aim was to find a suitable alternative to Vipasha.

The H (heterogeneity of response) and Q<sup>+</sup> and Q<sup>-</sup> (for the presence of crossover interaction) against the standard variety Vipasha were estimated for all the 29 genotypes for the traits exhibiting the presence of  $g \times e$  interaction, i.e., seed yield/plant, biological yield/plant, harvest index, seeds/pod, 100-seed weight and crushing hardness and their significance was tested [4]. The genotype exhibiting either significant H or Q<sup>+</sup> and Q<sup>-</sup> are given in Table 2. For seed yield/plant H was significant for the 26 genotypes against Vipasha. The presence of crossover interaction was observed for eleven genotypes, HPLC 8806, 8815, 8825, 8827, 8829, 8856, 8875, 8877, 8888, 8892 and 8895 for seed yield/plant against Vipasha. Four genotypes, HPLC 8871, 8883, 8892 and 36-11 exhibited the presence of crossover interaction for biological yield/plant and twenty one genotypes namely, HPLC 8806, 8810, 8815, 8816, 8824, 8826, 8827, 8829, 36-11, 8855, 8856, 8858, 8864, 8865, 8871, 8877, 8883, 8891, 8892, 8894 and 8895 exhibited the presence of crossover g × e interaction for harvest index and three genotypes namely HPLC 8871, 8894 and 36-11 showed the

presence of crossover  $g \times e$  interaction for seeds/pod and one genotype HPLC 8888 showed the presence of crossover  $g \times e$  interaction for 100-seed weight and three genotypes HPLC 8826, 8827 and 8891 exhibited the presence of crossover  $g \times e$ interaction for crushing hardness. All the genotypes failed to exhibit crossover interaction for all traits against Vipasha thus, presence or absence of crossover interaction was genotype specific and trait specific [7]. The genotype HPLC 8806 in Env.X (Berthin, 40 kg/ha); HPLC 8829, 8877, 8892 and 8895 in Env. VI (Kangra, 40 kg N/ha) had significantly higher seed yield/plant than check Vipasha.

Table 2.	Genotypes exhibiting significant *, #H (heterogeneity of response), and
	Q⁺ and Q⁻ against standard variety Vipasha

Characters	Н	Q <sup>+</sup> and Q <sup>-</sup>
Seed yield/plant (g)	All genotypes except HPLC 8826,8882 and 8891	HPLC 8806, 8815, 8825, 8827, 8829, 8856, 8875, 8877, 8888, 8892, 8895 (11 genotypes)
Biological yield/ plant (g)	All genotypes except HPLC 8824 and 8825	HPLC 8871, 8883, 8892 and 36-11 (4 genotypes)
Harvest index	All 29 genotypes	HPLC 8806, 8810, 8815, 8816, 8824, 8826, 8827, 8829, 36-11, 8855, 8856, 8858, 8864, 8865, 8871, 8877, 8883, 8891, 8892, 8894, 8895 (21 genotypes)
Seeds/pod	All 29 genotypes	HPLC 8871, 8894, 36-11 (3 genotypes)
100-seed weight (g)	All genotypes except HPLC 36-11	HPLC 8888 (1 genotype)
Crushing hardness	All 29 genotypes	HPLC 8826, 8827, 8891 (3 genotypes)

\*H was significant against  $x^2$  0.05 at s-1 df, where s is the number of environments. # minimum of either Q<sup>+</sup> or Q<sup>-</sup> was significant against "C" value given by [3]

The conclusion drawn from regression analysis and crossover and non-crossover interactions concept about identifying genotypes having specific adaptibility differ considerably. The genotypes HPLC 8855, 8883, 8894 and 8895 identified as potential yielder having specific adaptability for Env. VIII, on the basis of regression analysis failed to exhibit significant min ( $Q^+$  or  $Q^-$ ) against standard variety Vipasha except HPLC 8895 which had significant min ( $Q^+$ ,  $Q^-$ ) against Vipasha. On the other hand the five genotypes HPLC 8829, 8877, 8888, 8892 and 8895 identified as potential yielders having specific adaptibility to higher fertility level at Berthin, on the basis

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of crossover and non-crossover interaction concept, failed to exhibit stable above average performance and responsiveness for seed yield/plant except HPLC 8895.

A mention may be made of the genotype, HPLC 8895 which has been identified as a high yielding genotype having specific adaptability both by using regression analysis and crossover and non-crossover interaction concept. HPLC 8895 gave significantly more mean seed yield/plant than the standard variety Vipasha. However, in Env. I, II, III, IV and V it had lower seed yield than Vipasha and in Env. V, VI, VII, VIII, IX and X it had more seed yield than Vipasha. Thus, genotype HPLC 8895 had specific adaptation to high yielding environment, i.e., high nitrogen regimes (40 kg N/ha) rather than possessing general adaptation [8].

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