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Short Communication

INHERITANCE OF SOME QUANTITATIVE CHARACTERS IN SIX-ROWED BARLEY

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An experiment was undertaken to study the genetic behaviour of yield and certain yield traits using generation mean analysis in six-rowed barley (*Hordeum vulgare*)

The material comprised of parental (P_1, P_2), F_1, F_2, F_3, BC_1 and BC_2 generations of 2 crosses viz., [(RD 137/RS6) × (CN 292/RDB 1)] and [(RD 137/RS 6/CN 292/RDB 1) × (Mexican 19/Russian 20/RS6/Mexican 19)] referred to as cross I and cross II in the present study. The material was grown in RBD with 3 replications. Non segregating generations (P_1, P_2, F_1) were grown in a single row, back cross generations (BC_1 and BC_2) in two rows and F_2 and F_3 in 5 rows of 2 m length. The plant to plant and row to row spacing were maintained 10 cm and 20 cm respectively. Standard agronomic practices were followed to raise a normal crop. Ten competitive plants from each parent and F_1, 20 from BC_1 and BC_2, 40 from F_2 and F_3 per replication were taken at random for recording observations on days to heading, plant height, spike length and grain yield/plant.

Individual scaling tests [1] and joint scaling test [2] were used to estimate the components of gene action. Components of heterosis in the presence of digenic interactions were calculated as suggested by Jinks and Jones [3].

The analysis of variance indicated significant differences among different generations for all the four characters in both the crosses. The scales A, B, C and D were significant for all the characters indicating the presence of epistasis for all the traits.

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The joint scaling test (Table 1) indicated the non-adequacy of 3 and 6 parameter models indicating the role of higher order interactions or presence of linkage. In all the cases, where 6- parameter model was inadequate to explain the total genetic variability for the trait, the estimates of various gene effects were calculated based on digenic interaction model. It was not possible to test the adequacy of the higher order interaction models to such data as only seven generations were available.

The results of digenic interaction model revealed (Table 1) that both additive (d) and dominance (h) gene effects contributed significantly in the inheritance of spike length in the cross II. However, either additive (d) or dominance (h) or both gene effects were also observed to be significant in all the characters studied. This clearly indicate the significant role of the main effects in the inheritance, however, their relative significance, signs and magnitude varied with characters and crosses.

Table 1. Results of joint scaling test for quantitative attributes in barley

Character	Cross	Model	d.f.	χ^2	probability range
Days to heading	Cross I	Additive-dominance	4	185.89	<0.001
		Digenic interactions	1	23.35	<0.001
	Cross II	Additive-dominance	4	1025.80	<0.001
		Digenic interactions	1	43.52	<0.001
Plant height	Cross I	Additive-dominance	4	78.64	<0.001
		Digenic interactions	1	0.47	0.30-0.50
Spike length	Cross I	Additive-dominance	4	76.91	<0.001
		Digenic interactions	1	4.67	0.20-0.50
	Cross II	Additive-dominance	4	11.15	0.20-0.50
Grain yield/plant	Cross I	Additive-dominance	4	110.77	<0.001
		Digenic interactions	1	0.26	0.50-0.70
	Cross II	additive-dominance	4	57.18	<0.001
		Digenic interactions	1	19.74	<0.001

Earliness and short plant height are desirable to achieve high yield but the significant and positive heterosis observed for days to heading and plant height observed in the present study are undesirable. It is noteworthy that significant and positive inbreeding depression was observed for days to heading in both the crosses indicating a possibility for selection of early maturing genotypes in advanced generations.

Table 2. Estimates of the components of heterosis (over better parent) for quantitative traits in barley

Character	Cross	Components of heterosis				Total heterosis (%)	Inbreeding depression (%)
		(d)	(h)	(i)	1/2(j)		
Days to heading	I	6.03	27.51	-2.45	5.87	10.23**	11.03**
						~0.96	~2.75
	II	6.88	-24.74	-1.65	5.58	11.63**	15.37**
						~0.60	~0.76
Plant height	I	13.46	-27.89	14.07	17.99	8.99**	-6.01**
						~1.65	~2.22
Spike length	I	1.63	2.20	-0.40	3.18	-1.67**	0.13
						~0.38	~0.35
	II	0.54	-0.39			-0.88	0.14
						~0.19	~0.15
Grain yield/plant	I	4.22	-7.32	1.09	8.00	-8.89**	-2.44**
						~0.92	~0.58
	II	0.70	17.43	-2.14	-2.24	-2.67*	-3.50**
						~1.11	~0.79

* **Significant at p=0.05 and p=0.01 respectively

Further the results of components of heterosis showed that dominanace effect, additive × dominance (j) interaction more frequently contributed toward significant heterosis. Absence of heterosis for spike length (cross II) could be due to internal cancellation of heterosis components which depend upon the material under study. Pedigree method involving multiple crosses might be used with greater advantage to exploit the additive genetic components for complex traits like grain yield and its component traits.

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