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Short Communication

Generation mean analysis for yield and its component traits in barley (*Hordeum vulgare* L.)

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The inheritance of genetic parameters were studied from six generations of three crosses of barley (*Hordeum vulgare* L.) namely, RD 2503 × BL 2, Raj Kiran × IBVT 12 and RD 2508 × RD 2052 by using generation mean analysis. Six generations of these crosses *viz.* P_1, P_2, F_1, F_2, BC_1 and BC_2 were grown separately in randomized block design with three replications during *rabi* 2003. Observations were recorded for eleven characters namely, days to heading, days to maturity, flag leaf area, plant height, spike length, number of effective tillers per plant, number of grains per spike, test weight, biological yield per plant, harvest index and grain yield per plant, on randomly selected 5 plants in P_1, P_2, and F_1, 10 plants in back crosses (BC_1 and BC_2) and 20 plants in F_2 generation. The scaling tests 'A', ' B', 'C' and 'D [1, 2] was used to test the adequacy of the additive - dominance model. Six parameter model for estimation of various genetic component in presence of digenic interaction [3, 4] was used. Three-parameter model was also used when scales were significant.

Results of the scaling tests revealed that out of four scaling tests one or two scales were found significant in all the three crosses for most of the characters. This indicated the presence of epistatic interaction. However the additive-dominance (3-parameter) model was fitted in cross RD 2503 × BL 2 for flag leaf area, harvest index and grain yield per plant; in cross RD 2508 × RD 2052 for flag leaf area, spike length, number of grains per spike and test weight and in cross Rajkiran × IBVT 12 for number of grains per spike and test weight. Plant height and effective tillers inheritance were controlled by additive effect than that of dominance. Plant height, spike length, and effective tillers inheritances were governed by "additive-dominance" model was also reported [5].

Both additive (d) and dominance (h) gene effects were significant for days to maturity, plant height and grain yield in cross RD 2508 × RD 2052 and in cross Rajkiran × IBVT 12 for days to heading, days to maturity, biological yield and harvest index. The dominance component (h) was significant and greater in magnitude than additive gene effect (d) for most of the traits in most of the crosses. This indicated predominant role of dominance gene action in the inheritance of the traits in barley. Vimal and Vishwakarma [6] also reported that both additive and dominance gene effects played an important role in the expression of the traits and magnitude of dominance effect (h) had a greater value than additive (d) effect in barley.

Among the digenic interaction effect additive × additive (I) and dominance × dominance (I) interaction were found significant for days to heading and days to maturity in cross RD 2503 × BL 2; days to heading, plant height, number of effective tillers per plant, harvest index and grain yield per plant in cross RD 2508 × RD 2052 and days to heading, days to maturity, number of effective tillers per plant and grain yield per plant in cross Rajkiran × IBVT 12. All the three interactions were found significant for days to heading, days to maturity in cross Rajkiran × IBVT 12 and for plant height and grain yield in cross RD 2508 × RD 2052. The magnitude of additive × additive (i) and dominance × dominance (l) interactions were more than the magnitude of additive × dominance (j) for most of the characters.

The results of dominance (h) effect and dominance × dominance (l) type of interaction revealed that duplicate type of interaction was prevalent in cross RD 2503 × BL 2 for days to heading and days to maturity; in cross RD 2508 × RD 2052 for plant height, number of effective tillers per plant, harvest index and grain yield per plant; and in cross Rajkiran × IBVT 12 for days to heading, days to maturity, number of effective tillers per plant and grain yield per plant. The duplicate type of epistasis played an important role in the expression of majority of the cases in the present study.

Table 1. Estimation of different types of gene action in the three crosses of barley

Characters	Cross	m	d	h	i	j	l	Type of interaction
Days to heading	C1	77.5	–0.3	9.5**	9.7**	–0.5	–11.9**	D
	C2	77.9	–1.1**	–1.4	0.5	–0.9*	–2.6	-
	C3	81.9	4.6**	15.9**	13.4**	1.3**	–11.4**	D
Days to maturity	C1	112.7	–0.1	20.3**	19.5**	–0.1	–22.8**	D
	C2	116.9	–1.6**	–75**	–2.9*	–0.2	–4.0*	-
	C3	121.6	2.3**	5.5**	3.7*	–1.0*	–7.5**	D
Flag leaf area (cm^2)	C1	36.2	7.0**	–19.6	-	-	-	-
	C2	17.7	–0.2	11.3	-	-	-	-
	C3	16.7	2.8	0.9	1.5	0.4	–12.1	D
Plant height (cm)	C1	92.4	3.4	33.4**	25.4**	5.8**	13.7	D
	C2	95.1	6.1**	–49.5**	–56.1**	4.7*	106.3**	D
	C3	87.3	–0.3	–1.3	–7.0	–0.3	–5.3	-
Spike length (cm)	C1	8.9	1.0**	0.4	88.0	0.3	–2.2	D
	C2	10.1	0.2	–3.6	-	-	-	-
	C3	8.2	0.4	0.2	–0.7	0.9**	0.5	-
No. of effective tillers/plant	C1	6.3	0.4	0.8	1.9	2.0**	–4.9*	D
	C2	7.2	0.2	–7.9**	–8.1**	0.7	12.0**	D
	C3	7.8	0.4	–7.6**	–7.3**	0.5	10.4**	D
No. of grains/spike	C1	55.7	25.7**	7.3	16.4	26.9**	2.4	-
	C2	39.8	4.6**	41.3	-	-	-	-
	C3	101.5	1.8	–105.3**	-	-	-	-
Test weight (g)	C1	43.7	–8.9**	–0.8	–3.7	–6.3**	–12.0	-
	C2	38.3	–0.7	–0.3	-	-	-	-
	C3	31.7	–3.7**	4.2	-	-	-	-
Biological yield/plant (g)	C1	28.7	5.3*	8.1	15.9*	8.2**	–10.9	D
	C2	27.1	3.7	–8.4	–10.4	8.0**	13.8	D
	C3	36.4	3.7*	–17.6**	–22.4**	2.5	17.4	D
Harvest index (%)	C1	65.8	0.9	–53.7	-	-	-	-
	C2	52.6	3.7	–45.5**	–43.1**	–1.1	47.9*	D
	C3	33.4	5.6*	–31.3**	22.1*	0.1	19.4	D
Grain yield/plant (g)	C1	14.8	–0.9*	–7.1	-	-	-	-
	C2	12.8	2.3**	–12.6**	–13.2**	3.0**	16.7**	D
	C3	11.4	–0.7	–14.4**	–12.9**	0.4	10.9	D

C1-RD 2503 × BL 12, C2 = RD 2508 × RD 2052, C3 = Rajkiran × IBVT 12, D-duplicate;
*,**, 5% and 1% significant level, respectively

The results of absolute total of non -fixable gene effects were higher than the fixable gene for most of the crosses indicating greater role of non-additive gene effects. Earlier Briga [7] reported the role of non-additive gene effect. Some forms of recurrent selection namely, diallel selective mating [8] or bi-parental mating in early segregating generation might prove to be useful approach for tangible advancement of barley.

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