

Genetic Architecture of Yield and Three Important Yield Traits in Six Rowed Barley

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Abstract: Inheritance of yield and its components in six rowed barley (*Hordeum vulgare* L.) through generation mean analysis in two crosses revealed the presence of epistasis. The additive and non-additive genetic components were important for the expression of tillers per plant, grains per spike, 100 grain weight and grain yield per plant. Duplicate type of epistasis was observed for most of the traits. Significant heterosis, accompanied by inbreeding depression, was frequently observed for the traits.

Key words: Barley, scaling tests, generation mean, yield.

The success in breeding programme depends on the amount of variability present for different characters in a population and its efficient utilization. Progress in varietal improvement in crops has been slow due to lack of imagination, vision and efficiency in utilizing the components of genetic variation for various important quantitative traits which provide genetic basis for choosing parents for the breeding programme (Krull and Borlaug, 1970). Present investigation was, therefore, undertaken to study the nature and magnitude of gene action, controlling inheritance of yield and its components in barley through generation mean analysis in two crosses.

Materials and Methods

The present study consisted of two crosses, [(RD 137/RS6) x (CN 292/RDB 1)] and [(RD137/RS6/CN 292/RDB 1) x (Mexican 19/Russian 20/RS6/Mexican 19)] referred to as cross I and cross II, respectively. Seven generations namely P₁, P₂, F₁, F₂, F₃, BC₁ and BC₂ were developed from each of the crosses. These generations were evaluated in irrigated conditions in RBD with 3 replications. The P₁, P₂, F₁ consisted of single row plots, BC₁ and BC₂ consisted of two row plots, while F₂ and F₃ consisted of 5 row plots. The rows were 2 m long, with 20 cm spacing. With in row a plant to plant distance of 10 cm was maintained. Ten competitive plants, each from non-segregating generations, 20 from each back-cross generations and 40 cm from F₂ and F₃ generations were selected randomly in both the crosses for recording data on characters (Table 1).

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Table 1. Scaling test estimates of genetic parameters and their relative magnitude (%) for yield and yield traits in barley (I and II indicate cross I and II, respectively)

Parameter	Tillers/plant		Grains/spike		100 grain wt. (g)		Grain yield/plant (g)	
	I	II	I	II	I	II	I	II
Scales								
A	16.6**	1.5	9.8	14.8**	1.7**	0.1	11.3	0.1
	± 6.0	± 1.3	± 10.4	± 3.7	± 0.2	± 0.2	± 7.4	± 0.2
B	7.2**	2.5**	-24.0	4.9	0.4	1.1**	-8.1**	1.1**
	± 1.3	± 0.7	± 13.4	± 3.2	± 0.4	± 0.1	± 1.0	± 0.1
C	-7.5**	-3.4*	-58.3**	1.4	3.2*	0.8**	0.4	0.8**
	± 0.7	± 1.6	± 20.7	± 6.2	± 0.2	± 0.2	± 2.0	± 0.2
D	-15.7**	-3.7**	-21.9**	-9.7**	0.5*	-0.5	-1.6	-0.2
	± 3.1	± 1.0	± 4.2	± 3.4	± 0.2	± 0.1	± 3.8	± 0.1
Genetic parameters								
(m)	67.2	5.3	47.1	38.8	53.2	5.3	18.3	13.8
	± 0.3	± 0.3	± 3.2	± 1.5	± 0.2	± 0.0	± 1.6	± 1.9
(d)	-0.1	-0.2	-12.1**	-3.7*	-0.1**	0.2**	-4.2**	-0.7
	± 0.1	± 0.2	± 2.0	± 1.4	± 0.0	± 0.0	± 0.4	± 0.6
(h)	-7.5**	4.2*	-27.9	14.1*	0.3	0.3	-7.3	17.4**
	± 1.6	± 2.0	± 18.0	± 6.7	± 0.7	± 0.3	± 5.8	± 6.3
(i)	-7.4	1.3**	3.7	1.8	-0.9**	-0.2**	-1.9	2.1
	± 0.3	± 0.4	± 3.6	± 1.8	± 0.2	± 0.0	± 1.7	± 2.2
(j)	-19.4**	2.8*	77.1**	8.9	1.1	-0.1**	16.0**	-4.4
	± 2.6	± 1.3	± 4.6	± 4.9	± 0.4	± 0.2	± 3.0	± 3.8
(l)	8.5**	-2.8	19.8	-16.1**	-1.3**	-0.7	1.6	-17.7**
	± 1.3	± 1.7	± 24.7	± 5.2	± 0.5	± 0.3	± 4.3	± 4.6
Relative magnitude of genetic parameters (%)								
(m)	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
(d)	-0.1	-0.5	-27.3	-9.8	-0.3	3.9	-22.8	-5.2
(h)	-11.5	79.6	-59.6	36.9	0.7	5.7	-39.1	130.7
(i)	-11.2	24.3	7.8	4.9	-1.9	-4.7	-5.8	16.0
(j)	-28.7	-53.8	163.0	23.5	2.2	-20.5	86.3	-33.1
(l)	<u>12.7</u>	<u>-54.5</u>	42.1	<u>-42.8</u>	<u>-2.5</u>	<u>-14.2</u>	8.6	-132.3

*,** Significant at $p = 0.05$ and 0.01 , respectively. The underlined parameters are significant.

The generation mean and their standard errors were first subjected to individual scaling tests (Hayman and Mather, 1955) to determine the presence or absence of non allelic interactions. The parameters of components of variations were estimated

by using mean and weighted variance of seven generations. The 3-parameter model, based on expected mean from the observed generations, was tested by weighted X^2 method (Cavelli, 1952). Relative magnitude of various gene effects in per cent were

Table 2. Results of joint scaling test for yield and yield attributes in barley

Character	Cross	Model	d.f.	χ^2	Probability
Tillers/plant	I	Additive-dominance	4	163.16	<0.001
		Digenic interactions	1	26.62	<0.001
	II	Additive-dominance	4	68.01	<0.001
		Digenic interactions	1	10.44	0.001-0.01
Grains/spike	I	Additive-dominance	4	513.59	<0.001
		Digenic interactions	1	26.52	<0.001
	II	Additive-dominance	4	18.27	0.001-0.01
		Digenic interactions	1	6.28	0.01-0.02
100 grain weight (g)	I	Additive-dominance	4	187.62	<0.001
		Digenic interactions	1	0.146	0.70-0.80
	II	Additive-dominance	4	102.61	<0.001
		Digenic interactions	1	6.28	0.01-0.02
Grain yield/plant (g)	I	Additive-dominance	4	110.77	<0.001
		Digenic interactions	1	0.26	0.50-0.70
	II	Additive-dominance	4	57.18	<0.001
		Digenic interactions	1	19.74	<0.001

calculated by dividing the estimated value of each parameter by mean and then multiplying by 100.

Results and Discussion

Perusal of Table 1 revealed significant differences among the generations of each cross for all the traits. The F_1 mean values were generally within parental limits, excepting for tillers per plant, indicative of overdominance. Similarly, the F_2 mean values were also within the parental limits, excepting for grains/spike (cross II), hundred grain weight and grain yield/plant, indicative of transgressive segregation. F_3 mean were higher than F_2 mean values for all the traits, which may be because of breakage of linkages or due to the accumulation of favorable genes in segregating generations, which is further supported by the superiority of mean of backcross generations (either of the BCs or both) over

recurrent parents. Among the scaling tests (A,B,C and D), either any one or all were found significant, indicating the significant role of nonallelic interaction in the control of yield and its related traits.

Results on joint scaling test (Table 2) indicated highly significant χ^2 values for 3-parameter model, indicating the presence of epistasis in almost all the characters. Therefore, 6-parameter model was applied. The χ^2 values for tillers per plant and grains per spike in both the crosses indicated adequacy of 6-parameter model (Table 2). However, for 100 grain weight and grain yield per plant, even this model was found to be inadequate, indicating the role of still higher order interactions or presence of linkages in the genetic control. Where the 6 and 3 parameter models were adequate, the estimates of various gene effects were calculated.