Scaling Tests Estimates of Gene Effects and Type of Epistasis for Different Yield related Traits in Barley (*Hordeumvulgare L.*) Genotypes for late sown Condition

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Abstract

This research sought to determine the six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of three barley crosses were used for computation of generation mean analysisunder late sown conditions for yield contributing traits. Deviation from zero in simple scaling tests denote the presence of epistasis. Epistatic interaction was found significant in all the traits except a few traits under late sown condition where additive: dominance model was adequate to explain genetic variation. Both additive (d) and dominance (h) gene effects were important for all the traits. It is obvious that non-fixable gene effects (h) (j) and (l) were higher than the fixable (d) (i) in all the crosses for all the characters, indicating greater role of non-additive effects in the inheritance of all the characters studied.
Key words: *Barley, gene action, generation mean analysis*

Introduction

Barley (Hordeumvulgare; 2n = 14, family Poaceae) is an important rabi cereal rank fourth after maize, rice and wheat. Barley has a long history of use as human and animal food, health benefits and malting and brewing in many countries around the world. Since pre-historic times, barley was consumed primarily, as human food in the form of Chapatti and Sattu but due to alternate use of barley in field of brewing and medicine industry, it is considered as highly needed crop of present era. From nutritional point of view, barley grain is considered as superior grain over other cereals due to its higher biological value and rich source of β-glucon, acetylcholine, thiamin, riboflavin, total dietary and water soluble digestiblefiber. Barley is also used in breakfast as soup. It is beneficial in treating hyper cholesteremia[1]. Its bran and bran oil have medicinal value, which considerably reduce the serum cholesterol level in the blood. β-glucon and water soluble digestible fiber fraction present in barley decreases the blood plasma cholesterol[7]. Superior nutritional qualities, water soluble fiber, higher malt extract, low gluten, easy digestibility, cooling and soothering effect of its products are desirable features of barley. Barley based diet reduces the risk of coronary heart diseases by lowering down undesirable level of cholesterol.

A lot of information on nature and relative magnitude of genetic components of variation (additive and dominance) have been generated by generation mean analysis, but literature on barley in respect of fixable and non fixable gene effect is meager. Therefore, the present study was planned to investigate genetics of days to ear emergence, days to maturity, no. of effective tillers/plant, weight of grains/main spike (g), no. of grain/spike and 1000-grain weight (g) by using six-generations of the three crosses under normal and late sown condition conditions.

Materials and Methods

The inheritance of genetic parameters were studies using six generations of three crosses of barley namely DWRB 92 x HUB 113, DWRB 101 x RD 2849, BH 959 x DWRB 123 by applying 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 in two environments, one sown in normal soil and other sown in late sown condition during the same season. Planting were done in row of 3 m long. Row to row distance was kept 25 cm apart. The parent (P_1 and P_2) and F_1s were sown in 2 rows, while back cross generations and F_2 generation were sown in 5 and 6 respectively 6 rows of 3 m length. The experiment was carried out during the 2020-21 at Research Farm of JNKVV, College of Agriculture Tikamgarh (MP) India. Fifteen random plants in parent and F_1 generation, 60 plants in F_2 generation and 45 plants in back cross generations were used for recording observations for six traits in each replication. The analysis of variance for RBD was carried out. The scaling test was performed to test the estimates of six-parameter model using the digenicepistatic model[4]. The scaling tests 'A', 'B' 'C' and D was used to test the adequacy of the additive-dominance model.

Results and Discussion

Results of the simple 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. Therefore, the six-parameter model to detect gene effects was applied in all the characters. The estimates of m, d, h, i, j and l of six parameter model for all the characters are presented in Table 1.

Cross I (DWRB 92 x HUB 113**):**

A careful study same cross under late sown condition, revealed that, additive (d) and dominance (h) gene effects and (i), (j) and (l) type of non-allelic interaction were significant for days to ear emergence, number of effective tiller per plant, weight of grains per main spike and 1000-grain weight (Table 1). Duplicate type of epistasis was for days to ear emergence, number of effective tillers per plant weight of grains per main spike and 1000-grain weight while complementary type of epistasis was recorded for days to maturity.

Cross II (DWRB 101 x RD 2849**):**

It is apparent from Table 2 that under late sown condition significant estimates of additive (d) as well as dominance (h) gene effects and (i) and (j) type of epistatic interaction effects were noted for number of effective tillers per plant and number of grains per spike while dominant (h) gene effects with (i) and (l) type of gene interaction were observed for days to maturity and weight of grains per main spike. Dominance (h) gene effects with (j) type gene interaction were significant for 1000-grain weight while dominance (h) gene effects and (l) type of gene interaction were found for days to ear emergence. Duplicate type of epistasis was predominated in case of days to ear emergence, days to maturity and weight of grains per main spike.

Cross III (BH 959 x DWRB 123**):**

However, the magnitude of dominance (h) gene effect was higher than additive (d) effect, indicating the preponderance of dominance effect over the additive effect. Similar results for these traits, were also reported earlier[2, 6, 3, 9, 10, 11].

Table 1 Simple scaling tests, gene effects and type of epistasis for 09 metric traits in cross- I(DWRB 92 x HUB 113)late sown condition

Characters	Gene effects						Scales				Type of epistasis
	m	d	h	i	j	l	A	B	C	D	
Days to ear emergence	97.000** ±0.570	-3.670** ±0.940	11.170** ±3.070	10.000** ±2.980	2.830* ±1.330	-46.330** ±4.740	21.000** ±1.700	15.330** ±1.700	26.330** ±2.870	-5.000** ±1.490	D
Plant height (cm)	55.000** ±0.720	-0.733 ±1.084	-4.283 ±3.686	0.133 ±3.607	0.316 ±1.137	-5.967 ±5.422	3.233 ±1.684	2.600 ±1.802	5.700 ±3.257	-0.087 ±1.804	-
No. of effective tillers/plant	10.700** ±0.208	-3.467** ±0.353	-10.717** ±1.134	-10.933** ±1.091	-4.383** ±0.358	8.233** ±1.753	-3.033** ±0.567	5.733** ±0.617	13.633** ±1.039	5.467** ±0.545	D
Length of main spike (cm)	7.600** ±0.100	0.000 ±1.094	-0.250 ±0.486	-0.666 ±0.442	0.083 ±0.191	-0.299 ±0.683	0.567 ±0.384	0.400* ±0.159	1.633** ±0.569	0.333 ±0.221	-
Days to maturity	146.000** ±1.000	-3.000* ±1.290	12.830** ±4.780	10.000* ±4.760	-1.500 ±1.400	23.000** ±6.670	5.000* ±2.490	8.000** ±1.370	3.000 ±4.200	-5.000* ±2.380	C
Weight of grains/main spike (g)	2.033** ±0.0667	0.133* ±0.0667	0.733* ±0.315	0.933** ±0.298	0.199* ±0.084	-1.867** ±0.429	0.667** ±0.141	0.267 ±0.156	0.000 ±0.337	-0.467** ±0.149	D
No. of grains/spike	50.267** ±0.498	8.567** ±0.917	27.150** ±2.746	22.200** ±2.706	10.083** ±0.950	2.367 ±4.276	-2.200 ±1.575	-22.367** ±1.199	-46.767** ±2.197	-11.100** ±1.353	-
1000-grain weight (g)	30.500** ±0.057	5.233** ±0.715	-10.433** ±1.750	-6.601** ±1.450	5.066** ±0.742	44.067** ±3.478	-13.667** ±1.578	-23.800** ±1.947	-30.867** ±1.974	3.300** ±0.725	D
Grain yield/plant (g)	20.500** ±0.513	11.933** ±0.398	13.533** ±2.262	11.200** ±2.202	14.800** ±0.457	12.267** ±2.797	3.067** ±0.899	-26.533** ±0.680	-34.667** ±2.299	-5.600** ±1.101	C

*, ** Significant at 5% and 1% level of probability, respectively; C = complementary epistasis and D = Duplicate epistasis.

Table 2 Simple scaling tests, gene effects and type of epistasis for 09 metric traits in cross II(DWRB 101 x RD 2849) late sown condition

Characters	Gene effects						Scales				Type of
	m	d	h	i	j	l	A	B	C	D	epistasis
Days to ear emergence	76.330** $\pm$0.880	-1.530 $\pm$1.100	7.670* $\pm$4.200	4.670 $\pm$4.160	1.670 $\pm$1.270	-20.000** $\pm$5.830	7.330** $\pm$1.630	7.000** $\pm$2.000	8.670 $\pm$3.800	-3.330 $\pm$2.080	D
Plant height (cm)	75.233** $\pm$0.762	-6.433** $\pm$0.853	22.567** $\pm$3.545	24.999** $\pm$3.493	-12.366** $\pm$0.916	2.667 $\pm$4.731	-25.700** $\pm$1.548	1.033 $\pm$1.205	-43.667** $\pm$3.275	-10.500** $\pm$1.746	-
No. of effective tillers/plant	10.567** $\pm$0.120	-1.467* $\pm$0.667	9.933** $\pm$1.498	7.200** $\pm$1.417	-1.533* $\pm$0.702	-5.599 $\pm$2.879	-2.333** $\pm$1.112	0.733 $\pm$1.054	-8.800** $\pm$1.085	-3.600** $\pm$0.708	-
Length of main spike (cm)	10.067** $\pm$0.088	-2.767** $\pm$0.278	-3.750** $\pm$0.698	-4.733** $\pm$0.659	-4.250** $\pm$0.295	2.833* $\pm$1.256	-3.300** $\pm$0.489	5.200** $\pm$0.442	6.633** $\pm$0.579	2.367** $\pm$0.329	D
Days to maturity	113.330** $\pm$0.330	1.000 $\pm$0.470	15.670** $\pm$2.210	16.000** $\pm$1.630	1.330 $\pm$2.030	-30.000** $\pm$5.290	7.330 $\pm$4.000	6.670** $\pm$2.000	-2.000 $\pm$4.940	-8.000** $\pm$0.820	D
Weight of grains/main spike (g)	1.666** $\pm$0.088	0.099 $\pm$0.094	2.950** $\pm$0.413	3.400** $\pm$0.400	0.117 $\pm$0.108	-5.100** $\pm$0.556	0.967** $\pm$0.125	0.733** $\pm$0.216	-1.700** $\pm$0.408	-1.700** $\pm$0.200	D
No. of grains/spike	98.667** $\pm$1.006	-20.733** $\pm$1.812	45.533** $\pm$5.439	-23.999** $\pm$5.423	26.433** $\pm$1.830	10.933 $\pm$8.336	-19.900** $\pm$1.934	32.967** $\pm$3.139	37.067** $\pm$4.116	12.00** $\pm$2.716	-
1000-grain weight (g)	32.767** $\pm$1.334	-0.899 $\pm$0.704	11.150* $\pm$5.557	7.667 $\pm$5.521	1.826* $\pm$0.828	-8.699 $\pm$6.168	-0.667 $\pm$1.311	-4.300** $\pm$1.206	-12.633* $\pm$5.488	-3.833 $\pm$2.760	-
Grain yield/plant (g)	21.067** $\pm$0.338	-15.067** $\pm$0.638	62.649** $\pm$1.956	43.467** $\pm$1.861	-17.883** $\pm$0.727	-51.567** $\pm$3.133	-13.833** $\pm$1.076	21.933** $\pm$1.203	-35.367** $\pm$1.814	-21.733** $\pm$0.930	D

*, ** Significant at 5% and 1% level of probability, respectively; C = complementary epistasis and D = Duplicate epistasis.

Table 3 Simple scaling tests, gene effects and type of epistasis for 09 metric traits in cross III(BH 959 x DWRB 123) late sown condition

Characters	Gene effects						Scales				Type of epistasis
	m	d	h	i	j	l	A	B	C	D	
Days to ear emergence	77.670** ±0.880	1.000 ±0.940	12.670** ±4.100	12.670** ±4.000	8.000** ±1.300	-13.330** ±5.600	8.330** ±2.310	-7.670** ±1.150	12.000** ±4.140	6.330** ±2.000	D
Plant height (cm)	85.467** ±0.296	-2.467** ±0.667	-10.583** ±1.932	0.799 ±1.785	0.517 ±0.799	-51.367** ±3.272	25.800** ±1.395	24.467** ±1.146	49.767** ±1.895	-0.400 ±0.893	C
No. of effective tillers/plant	11.067** ±0.241	2.799** ±0.339	-5.583** ±1.246	6.933** ±1.178	2.183** ±0.359	5.167** ±1.856	3.067** ±0.702	-1.300* ±0.576	8.700** ±1.264	3.467** ±5.882	D
Length of main spike (cm)	10.133** ±0.176	0.833** ±0.067	1.417 ±0.730	2.333** ±0.718	1.250** ±0.121	7.099** ±0.801	3.633** ±0.116	1.133** ±0.247	2.433** ±0.754	-1.167** ±0.358	-
Days to maturity	125.330** ±0.330	0.330 ±1.250	19.170** ±2.850	16.670 ±2.830	0.830 ±1.270	-30.330** ±5.230	7.670** ±2.450	6.000** ±0.820	-3.000 ±1.560	-8.330* ±1.410	D
Weight of grains/main spike (g)	4.633** ±0.088	0.033 ±0.120	4.667** ±0.447	5.533** ±0.0427	0.667** ±0.131	-6.800** ±0.051	1.300** ±0.188	-0.033 ±0.249	-4.267** ±0.439	-2.767** ±0.213	D
No. of grains/spike	56.667** ±0.669	5.467** ±1.290	15.083** ±4.439	14.667** ±3.718	22.883** ±1.343	8.233 ±7.573	11.433** ±3.305	-34.333** ±2.791	-37.567** ±5.542	-7.333** ±1.858	-
1000-grain weight (g)	32.500** ±0.208	-2.800** ±0.610	4.333** ±1.591	4.933** ±1.478	6.199** ±0.714	-2.000 ±2.855	7.667** ±1.119	4.733** ±1.035	-7.867** ±1.481	-2.467** ±0.738	-
Grain yield/plant (g)	34.067** ±0.134	4.000** ±0.505	-5.600 ±1.295	-20.000** ±1.143	-9.999** ±0.620	14.267** ±2.419	2.767** ±0.938	2.967* ±1.067	25.733** ±1.328	10.00** ±0.571	-

*, ** Significant at 5% and 1% level of probability, respectively; C = complementary epistasis and D = Duplicate epistasis.

It is obvious that non-fixable gene effects (h), (j) and (l) was higher than the fixable (d) (i) for all the three crosses in all the characters, indicating greater role of non-additive effects in the inheritance of the characters studied. Hence normal breeding method would not work and some forms of recurrent selection namely, diallel selective mating or biparental mating in early segregating generation might prove to be effective way of intermating the most desirable sergeants followed by selection might also be useful breeding strategy for the exploitation of both additive as well as non-additive type of gene actions. The duplicate type of gene action was recorded for, majority of the traits under study where (h) and (l) effect had opposite signs. Thus it indicated that non-fixable gene effects are expressing that particular traits i.e., greater role of non-additive gene effects in such cases.

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