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## A Study on Genetic Advance and Heritability for Yield Components in Barley (Hordeum vulgare L.)

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## Abstract

Genetic advance predicts the quantum gain expected by imposing a particular intensity of selection. High magnitude of both the parameters is expected due to presence of additive gene action. Estimates of heritability and genetic advance for 9 characters including yield and quality have been investigated by studying six generations in barley crosses. Under normal soil heritability in broad sense and narrow sense varied cross to cross. High heritability (>75%) coupled with high genetic advance (>40%) were recorded for weight of grains per main spike (cross I and II), number of grains per spike (cross V), grain yield per plant (cross I, II and III) in normal soil. The traits, number of effective tiller per plant (cross I), weight of grains per spike (cross IV), grain yield per plant (cross II, III and IV) and lysine content (cross III) had high heritability with high genetic advance in saline sodic soil.

Key Words: Barley, Heritability and Genetic advance.

## Introduction

Since pre-history 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 industry and medicine, now it is considered as highly needed crop of present era. From the nutritional point of view, barley grain is considered as superior over wheat due to its higher biological value and rich source of βglucon, thiamin, riboflavin, total dietary and soluble fibre. Barley is also used in breakfast as soup. The major function of heritability estimates is to provide information on transmission of characters from the parents to the progeny. The effectiveness of selection in improving characters by exploiting genetic variability depends largely upon the extent of **Materials and Methods** 

Ten homogygous and genetically divers varieties of barley namely, DL-88, K 560, K 603, Azad, RD 2552, NDB transmissibility of the character. The estimate of heritability provides the index of transmissibility of a character and serves as a useful guide to the breeder for its selection.

Such estimates facilitate evaluation of hereditary and environmental effects in phenotypic variation and thus aid in selection. Heritability estimates can be used to predict genetic advance under selection so that breeder can anticipate improvement from different kinds and intensities of selection. Information on estimates of heritability and genetic advance in early segregating generations on seed yield and its components in barley is very limited, thus present investigation was planned to get precise information.

1020, RD 2618, PL 708, NDB 1173 and Lakhan were selected for building up the experimental materials. The  $F_{1}s$  were

obtained by crossing 10 diverse parents during 2018-19. In the next season, a part of  $F_1$  seed of these crosses and 10 parents were sown in a crossing block to obtain  $F_2$ , BC<sub>1</sub> and BC<sub>2</sub> generations in each cross. A final comparative studies with  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ , BC<sub>1</sub> and BC<sub>2</sub> were made in Randomized Block Design with three replications in two environments, one set was sown in normal soil during 2019-20 at JNKVV, College of Agriculture Tikamgarh. Planting were done in rows of 3 m long. Row to row distance was **Results and Discussion** 

It is evident from Table 2 that estimates of narrow sense heritability was found negative for all the traits in most of crosses except for days to maturity (cross V), number of effective tillers (cross II, IV and V), length of main spike (cross IV and V), grain yield per plant (cross I), in normal soil condition. These results were also supported by findings of several kept 25 cm apart. The parent ( $P_1$  and  $P_2$ ) and  $F_1$ s were sown in 2 rows, while back cross generations and  $F_2$  generations were sown in 5 and 6 rows, respectively, of 3 m length. 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 in each replication. The heritability in narrow sense and broad sense were computed and genetic advance was worked out.

scientists<sup>[2,7,8]</sup> who noticed that inheritance of positive estimates of related components were controlled by additive and dominance effects. Thus, heritability in broad sense and genetic advance in per cent of mean in combination provide clear picture regarding the effectiveness of selection in improving the plant characters.

Characters	Heritability (%)					
	Cross I	Cross II	Cross III	Cross IV	Cross V	
Days to ear emergence	70.40	95.80	90.60	97.90	96.52	
Plant height (cm)	85.20	97.48	99.20	96.56	96.56	
No. of effective tillers/plant	92.03	74.06	90.75	74.79	57.60	
Length of main spike (cm)	44.25	96.73	93.25	95.05	67.55	
Days to maturity	66.10	76.20	95.10	41.70	93.85	
Weight of grains/main spike (g)	93.88	88.30	97.19	81.81	81.06	
No. of grains/spike	99.59	98.52	98.62	100.51	99.55	
1000-grain weight (g)	98.07	98.98	90.87	88.57	93.70	
Grain yield/plant (g)	99.80	99.94	99.67	99.81	60.71	

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Table 1 Heritabilit	v in broad sense (	(h <sup>-</sup> b%) for 9	) metric traits in	cross I-V in barley

On the other hand, the high magnitude of broad sense heritability (more than 75%) was estimated for most of the crosses for plant height, weight of grains per main spike, grain yield per plant, number of grains per spike, husk content, protein content, lysine content and amylose content in both the environments,

except grain yield per plant in cross V. High heritability (h<sup>2</sup>b) coupled with high genetic advance were recorded for weight of grains per main spike in cross I and II, number of grains per spike in cross V, grain yield per plant in cross I, II and III in normal soil<sup>[5]</sup>.

Characters	Heritability (%)					
Characters	Cross I	Cross II	Cross III	Cross IV	Cross V	
Days to ear emergence	-	-	-	-	14.39	
Plant height (cm)	-	-	-	-	-	
No. of effective tillers/plant	-	66.23	-	57.92	64.37	
Length of main spike (cm)	-	-	-	63.85	15.21	
Days to maturity	-	-	-	-	-	
Weight of grains/main spike (g)	-	-	-	-	-	
No. of grains/spike	-	-	-	-	-	
1000-grain weight (g)	-	-	-	-	-	
Grain yield/plant (g)	14.37	-	-	-	-	

Table 2 Heritability in narrow sense  $(h^2n\%)$  for 9 metric traits in cross I-V in barley

## - indicates negative estimates

Low heritability (<50%) coupled with low genetic advance (<20%) denoted that such characters were highly influenced by environmental effects<sup>[2]</sup>. This indicated that much improvement is not possible through selection in this characters due to low value of heritability. Genetic analysis had also shown that these characters are mainly governed by dominance components. High heritability with low genetic advance indicated the presence of non-additive gene action, therefore, selection in early generation for above cited traits may not be effective due to linkage.

Table 3 Genetic advance in per cent of mean (Ga %) for 9 metric traits in cross I-V in
barley

Characters	Cross I	Cross II	Cross III	Cross IV	Cross V
Days to ear emergence	5.20	17.08	8.88	19.05	16.85
Plant height (cm)	11.20	15.49	21.34	22.89	24.3
No. of effective tillers/plant	22.97	12.75	28.07	21.31	20.88
Length of main spike (cm)	6.23	32.54	19.20	31.59	10.43
Days to maturity	4.51	3.50	11.00	3.30	5.05
Weight of grains/main spike (g)	51.40	23.06	56.15	16.47	16.19
No. of grains/spike	25.27	22.68	35.97	28.18	55.90
1000-grain weight (g)	34.79	38.69	16.32	12.92	22.94
Grain yield/plant (g)	46.27	64.21	48.83	34.72	8.46

Under a situation, where dominance gene effect plays major role, one can go for heterosis breeding otherwise use of intermating followed by selection in early generations to exploit both types of gene effects. These were advocated by several scientists<sup>[1,4,8]</sup>. They suggested that value of heritabilities obtained for grain yield were more consistent among broad sense than narrow sense estimates. Genetic advance estimates were low due to lack of additive variance. Nevertheless, the moderate narrow sense heritabilities ranged from 18 to 62% and the considerable proportion of additive variance found under nutrient shortage suggest that on improvement of rooting ability under less favourable nutrition through conventional selection is an important objective in barley breeding<sup>[3,6]</sup>. The overall review of gene effects for metric traits under study revealed that, simple selection procedure may not bring the expectacular gains. This has also been indicated by low genetic advance for exploitation for part of total genetic **References** 

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variation i.e. additive gene effects and additive type of epistatic effects.

However, the degree of improvement attained through selection is not only dependent on heritability but also on the amount of genetic variation present in the breeding population and the extent of selection pressure applied by the breeder.

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