

Genetic variability in biparental progenies of feed barley (*Hordeum vulgare* L.) under drought environment

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ABSTRACT

The present investigation was carried out to study genetic variability parameters in bi-parental progenies of Barley (*Hordeum vulgare* L.) under drought condition. To achieve the objectives of present investigation F₂ population of RD 2715 x RD 3002 were raised and backcross to both the parents according to North Carolina Design III (Biparental mating Design). Three random F₂ plants as males and backcrossing them to both the original parents. Six progenies generated in this way make up one set and likewise, three sets were generated using random samples of plants in F₂ population. BIPs of cross RD 2715 x RD 3002 under drought condition showed twelve high heritable characters with maximum was for days to maturity (88%). Additive variance due to male was greater than the females and average additive variance was greater than dominance variance indicating the predominant role of additive gene action in the inheritance of these characters.

Keywords: North carolina design III, drought, additive variance, heritability

INTRODUCTION

Barley (*Hordeum vulgare* L.) is an ancient, annual, self-pollinating, monocotyledonous, diploid (2n=14) species that belongs to the family Gramineae (Poaceae) and tribe Hordea. Barley, which is natively known as Jau, was domesticated around 11,000 years ago in the Near East (Harwood, 2019). The genus *Hordeum* comprises of 32 species, for a total of 45 taxa in the genus, all with the basic chromosome no. x=7 (Bothmer *et al.*, 1991). Farmers widely cultivate this poor man's crop due to its better adaptability to abiotic and biotic stresses (Wang *et al.*, 2018). It is enriched with biologically active constituents such as tocotrienols, tocopherols, phenolic compounds, hordenine, and soluble dietary fibre beta-glucan (De Paula *et al.*, 2017). To address the growing

demand for agricultural production in future climate scenarios, an efficient and cost-effective strategy involves breeding crop varieties to enhance drought tolerance. The increase in barley yield has primarily been achieved by modifying genes related to drought and disease resistance, making the barley plant more responsive to agricultural practices. The situation can be improved by inter-mating during the F₂ and F₃ generations, which increases the likelihood of recombination between favourable and unfavourable genes, leading to the emergence of superior but rare recombinants. To effectively harness genetic variability, it is crucial to comprehend the nature and extent of gene effects associated with the inheritance of key agronomic traits. Genetic analysis techniques like diallel analysis, line x tester are both reliable and informative, they do impose limitations on recom-

bination rates and maintain tight linkage. North Carolina-III design initially developed by Comstock and Robinson (1948, 1952) can address the above problems.

MATERIAL AND METHODS

The experimental material was received from All India Co-ordinated Research Project on Wheat and Barley, RARI, Durgapura. Material was consisted of F_2 population of *viz.*, RD 2715 x RD 3002 cross.

During the *rabi* season of 2022-23, F_2 generations from cross RD 2715 x RD 3002 was raised in non-replicated rows to generate bi-parental progenies using NCD III (Comstock and Robinson, 1948, 1952). The bi-parental progenies was developed by designating three random F_2 plants as males and backcrossing them to both the original parents. Six progenies generated in this way make up one set and likewise, three sets were generated using random samples of plants in each F_2 population. During *rabi* season of 202-234 generated BIPs were evaluated in replicated trial in accordance with randomized block design. Narrow sense heritability was calculated using the formula suggested by Allard (1960). Genetic advance as percent of mean (GAM) was computed and categorized according to Johnson *et al.* (1955).

RESULTS

In BIPs generated from the base population of cross 'RD 2715 x RD 3002', additive variance due to males was greater in magnitude than additive variance due to females. Magnitude of average additive component of variance was higher than dominant component of variance in all the characters. Variances less than zero was considered as zero.

Results of the BIPs generated from RD 2715 x RD 3002 demonstrated that the variance components of the current investigation were negative in some cases. Robinson *et al.* (1955) and Miller *et al.* (1958) pointed out that the true values of negative estimates were either zero or small positive value, and that the negative result from sampling error. Consequently the negative estimates of variance components obtained either for σ^2_A or for σ^2_D appeared to have resulted due to sampling error. Such variances were considered as zero (Table 1).

High narrow sense heritability (h^2_{NS}) estimates in BIPs from cross 'RD 2715 x RD 3002' was observed for most of the traits in restricted irrigated environments in which maximum was for days to maturity (88%) followed by days to heading (87%), days to reproductive phase (85%), 100-grain weight (72%), biological yield per plant

Table 1. Genetic parameters of different characters in drought environment of BIPs of Cross I: RD 2715 x RD 3002

S.No.	Character	AV M	AV F	AV	DV	DV/AV	h^2 (%)	GA	GAM
1	Days to heading	8.33	0.00	8.33	0.00	0.00	87	5.55	9.03
2	Days to maturity	12.26	0.00	12.26	0.00	0.00	88	6.76	6.34
3	Days to reproductive phase	12.25	0.00	12.25	0.00	0.00	85	6.66	14.79
4	Plant height	27.35	0.00	27.35	0.00	0.00	66	8.74	12.04
5	Spike length	0.85	0.00	0.85	0.00	0.00	69	1.58	19.03
6	Effective tillers per plant	0.65	0.00	0.65	0.00	0.00	62	1.31	15.30
7	Grains per spike	32.86	0.00	32.86	0.00	0.00	61	9.24	16.47
8	100-grain weight	0.05	0.00	0.05	0.00	0.00	72	0.39	10.86
9	Biological yield per plant	6.33	0.00	6.33	0.00	0.00	71	4.38	15.33
10	Harvest index	2.87	0.00	2.87	0.00	0.00	44	2.31	6.64
11	Grain yield per plant	0.54	0.00	0.54	0.00	0.00	65	1.23	12.42
12	Proline content	16.30	0.00	16.30	0.00	0.00	58	6.32	8.34
13	Phenol content	1156.3	0.00	1156.39	0.00	0.00	63	55.7	9.35
14	SPAD content	4.14	0.00	4.14	0.00	0.00	61	3.27	7.46
15	Relative water content	4.65	0.00	4.65	0.00	0.00	30	2.44	3.50
16	Membrane stability index	7.99	0.00	7.99	0.00	0.00	46	3.94	5.85

AV M= additive variance due to male; AV F= additive variance due to female; AV average of additive variance; DV= dominance variance; DV/AV= degree of dominance; h^2 = heritability, GA= genetic advance; GAM; genetic advance as percent of mean; $V<0$ was considered as 0.00

(71%), spike length (69%), Plant height (66%), grain yield per plant (65%), phenol content (63%), effective tillers per plant (62%), grains per spike and SPAD both showed 61 per cent. Medium heritability was observed for proline content (58%), membrane stability index (46%), harvest index (44%) and relative water content (30%) (Table 1).

As indicated in table no. 1, moderate magnitude of genetic advance as percent of mean under restricted environment was obtained for spike length (19.03%), grains per spike (16.47%), biological yield per plant (15.33%), effective tillers per plant (15.30%), days to reproductive phase (14.79%), grain yield per plant (12.42%), plant height (12.04%) and 100-grain weight (10.86%). While low magnitude of genetic advance as percent of mean was observed for phenol content (9.35%), days to heading (9.03%), proline content (8.34%), SPAD (7.46%), harvest index (6.34%), days to maturity (6.34%), membrane stability index (5.8 %) and relative water content (3.50%).

DISCUSSION

In population of cross 'RD 2715 x RD 3002' under drought environment (E_1), high heritabil-

ity estimates were recorded for twelve traits. Among these, the maximum was for days to maturity (88%) and the minimum was for SPAD (61%). For all of these high heritable traits additive genetic variance was found to be more important and selection will be effective. Moreover, genetic advance as percent of mean was moderate for most of these traits, suggesting the effectiveness of phenotypic selection (Table 1). Similar findings on different crops were reported by Nematullah and Jha, (1993) and Badran and Moustafa, (2015) in wheat. Patial *et al.* (2023) detected high heritability for 1000-grain weight, days to maturity and plant height in barley. Zewodu *et al.* (2025) discovered high heritability with high genetic advance for number of fertile tillers and days to heading in barley using lattice design.

Overall, these findings emphasize that traits exhibiting both high heritability and high genetic advance are governed primarily by additive gene action. Hence, the predominance of additive variance suggests that selection-based breeding approaches such as pedigree selection, mass selection, or recurrent selection would be highly effective for genetic improvement of these traits.

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