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Generation Mean Analysis for Yield and Drought Related Traits in Barley (*Hordeum vulgare* L.)

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ABSTRACT

Six generations of two barley crosses were used for computation of generation mean analysis under rainfeed and irrigation conditions for yield and drought related traits. Epistasis was observed for all the traits studied in two crosses in both the conditions except for the proline content in irrigated condition, as it is apparent from the significance of one or more of the four scales (A, B, C and D scales). The dominance × dominance (l) interaction was larger than the additive × additive (i) and additive × dominance (j) effects put together, while for the main effects, the dominance component (h) was greater than the additive (d) component under both irrigated and rainfed conditions. The results of the present study confirmed that yield related traits like number of grains per spike, grain weight per spike, 100-grain weight and grain yield per plant along with stress related traits like stomatal conductance and proline content were predominantly influenced by dominance (h) and dominance × dominance (l) gene action. Therefore, selection of these traits will be difficult in the early generations.

Key words: *Gene action, Drought tolerance, Barley and Generation mean.*

INTRODUCTION

Hordeum, Triticum and Secale belong to the tribe Triticeae, the Poaceae family. Poaceae is considered to be monophyletic; therefore all grasses belonging to this family may have evolved from a single ancestor. The genus Hordeum consists of 32 species and 45 taxa including diploid (2n = 2x = 14), tetraploid (2n = 4x = 28) and hexaploid (2n = 6x = 42) cytotypes. Barley was considered to be the first ever cereal crop to be domesticated. Along with emmer wheat, low yielding awned wheat, barley was a staple cereal crop of ancient Egypt, dating back to as far as 5000 BC and even earlier than that. At that time the main use of barley was limited to making beer and bread. From eating, the importance of barley even extended to having religious significance in Europe and ritual significance in ancient Greece. It is fourth largest cereal crop after maize, wheat and rice in the world with a share of 7 per cent of the global cereal production. Overall India's barley production was estimated to be 1781.4 thousand tons spread over an area of 6.93 lakh ha for the year 2016-17.

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The average productivity was estimated to be 25.80 q/ha. The top three barley growing states with significant growth in production are Rajasthan (808 thousand tons), Uttar Pradesh (447 thousand tons) and Madhya Pradesh (261.6 thousand tons).

It is a major source of food for large population of cool and semi-arid areas of the world, where wheat and other cereals are less adapted. In European countries, it is used as the only breakfast food, whereas the people of Nepal, Tibet and Bhutan use it as a staple food. Barley is an annual cereal grain crop that is consumed as a major feed for the animals. The rest is used as malt in whiskey or sugar as well as health food. Barley is used for manufacturing of liquors in western countries. The crop resembles white berries and is believed to be excellent for drought-like conditions.

Drought is an important abiotic stress causing the major crop losses worldwide. Despite recent agricultural advances, climate play key role in today's agricultural production. In the light of climate changes and global warming, where some areas are expected to be more subjected to frequent severe drought, the development of drought-tolerant cultivars is the most efficient and cost-effective strategy for fighting drought stress in low-value cropping systems. Therefore, understanding the genetic control of drought tolerance is of a great importance for the application of breeding methods in the development of cultivars with improved tolerance. Since barley seems to be relatively well adapted to water deficit, it has proved to be good model to study and understand the genetic control and mechanisms of drought stress tolerance[4]. Drought tolerance is a complex polygenic trait involved powerful epistatic interactions among loci and powerful genotype × environment interactions. However, limited genetic, physiological, and biochemical studies have been carried out in the past two decades to explore the genetic control of drought tolerance and its mechanism in barley[4]. A significant yield improvement is possible through the development of high yielding cultivars, having wide genetic base and capable of producing higher under various agro-climatic conditions. For this purpose, basic knowledge of genetic architecture of yield and yield components and nature of gene action is required. Therefore, the present study is aimed to understand the gene action of quantitative traits related to yield and drought tolerance through generation mean analysis and to screen transgressive segregants for yield.

MATERIAL AND METHODS

The experiments for the present investigation were conducted during the *rabi* (winter) season of 2015-2016 and 2016-17 at the Agriculture Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. Off season trial for backcrosses and to develop fresh F_1s was conducted during *kharif* 2016-17 at IIWBR Summer Nursery Facility, Dalang Maidan, Lahaul-Spiti. The experimental area occupied was quite uniform in respect of topography and fertility. The soil of experimental site is sandy loam. The average annual rainfall is 1100 mm (44 inch) at BHU, Varanasi. The meteorological data during barley crop growth period from November to April 2016-17 has been represented in Fig. 1.

For the purpose of gene action study, crosses were made between diverse parents (Table 1.) i.e., HUB-113 (irrigated) was crossed with Azad (rainfed) and Geetanjali (hull-less). Six generations P_1, P_2, F_1, F_2, B_1 and B_2 from each of the cross were grown in Compact Family Randomized Block Design with three replications, under two environments i.e. moisture stress (rainfed) and moisture non- stress (irrigated) conditions. P_1, P_2 and F_1s were planted in two rows while, B_1s and B_2s were planted in three rows and F_2s in five row plots in each replication. The 3 meter rows were space planted 30 cm apart and a distance of 10 cm was maintained between the plants. Moisture non-stress plots were irrigated twice at tillering and flowering initiation stage to have full genetic yield potential. Ten competitive plants from each of the parents

and F_1s, 20 plants from backcrosses (B_1 and B_2) and 50 plants from each F_2 population from each replication were randomly selected and tagged for recording of data on 12 various yield and drought related quantitative traits (Table 2). The transgressive segregants which outperformed both the parents and standard check (K-603) were screened out in the F_2 generations of the same two crosses selected for generation mean analysis in both environments.

Table 1: Pedigree of the genotypes used for the study

Name of genotype	Pedigree	Sources	Remarks
Azad	K 12 / K 19	Kanpur, UP	Rainfed, alkaline & saline
Geetanjali	K 12 / K 572 // EB 410	Kanpur, UP	Rainfed, Hull-less
HUB-113	Karan 280 / C 138	BHU, Varanasi	Irrigated
K-603 (Check)	K257 / C138	Kanpur, UP	Rainfed

Generation mean analysis was performed using Mather and Jinks method[12]. In this method the mean of each character is indicated as follows:

$Y = m + \alpha\,[d] + \beta\,[h] + \alpha^2\,[i] + 2\,\alpha\,\beta\,[j] + \beta^2\,[l]$

Where:

Y = the mean of one generation.

m = the mean of all generation.

d = the sum of additive effects.

h = the sum of dominance effects.

i = the sum of additive × additive interaction (complementary).

1 = the sum of dominance × dominance interaction (duplicate).

j = sum of additive × dominance and α, 2αβ and β^2 are the coefficients of genetic parameters.

Simple scaling test

Adequacy of scale must satisfy two conditions namely, additivity of gene effects and independence of heritable components from non-heritable ones. The test of first condition provides information regarding absence or presence of gene interactions. The test of adequacy of scales is important because in most of the cases the estimation of additive and dominance components of variances are made assuming the absence of gene interaction. Mather[16] gave following four tests for scale effects:

$$A = 2.B_1 - P_1 - F_1; B = 2.B_2 - P_2 - F_1$$

$$C = 4.F_2 - 2.F_1 - P_1 - P_2; D = 2.F_2 - B_1 - B_2$$

When the scale is adequate, the values of A, B, C and D should be zero within the limit of their respective standard errors.

Variances of the above scales

$$V_A = 4.V_{B_1} + V_{P_1} + V_{F_1}; V_B = 4.V_{B_2} + V_{P_2} + V_{F_1}$$

$$V_C = 16.V_{F_2} + 4.V_{F_1} + V_{P_1} + V_{P_2}; V_D = 4.V_{F_2} + V_{B_1} + V_{B_2}$$

Standard errors of the above scale:

$$SE_A = V_A; SE_B = V_B; SE_C = V_C; SE_D = V_D$$

Now, the 't' values are calculated as follows:

$$t_A = \frac{A}{SE_A}; t_B = \frac{B}{SE_B}; t_C = \frac{C}{SE_C}; t_D = \frac{D}{SE_D}$$

The calculated value of 't' are to be compared with tabulated value of 't' at 5% level of significance. In each test, the degree of freedom is sum of the degrees of freedom of various generations (total number of observations - total number of replications) involved.

Joint scaling test

The main drawback of simple scale tests is that out of six populations only three or four are included in the test at a time. In order to overcome this problem, Cavalli[2] gave the method 'Joint scaling test' which includes any combination of families at a time. The 'weighted least square method' developed by Hayman[9] was used to estimate the parameters m, d and h. Here, the weights are defined as the reciprocal of standard error. From these estimates, the expected generation means were calculated and compared with the observed generation mean values using a χ^2 test. A significant χ^2 value indicates that the model is not adequate and the non-allelic interactions are added in the model.

Components of generation means

The results of scaling test showing inadequacy of additive-dominance model indicated presence of higher order interaction. Such

situation warranted the scope of analysis of data in six parameter model[9,12].

Six parameter model:

Estimates of various gene effects and non allelic interaction were computed following Jinks and Jones[9] and Hayman[12]. Formula for estimating both three and six parameter models were derived by solving the equations of expectation of means of generation by simple elimination method.

$$P_1 = m+(d)+(i);\ P_2 = m-(d)+(i);$$

$$F_1 = m+(h)+(l)\ F_2 = m+\frac{1}{2}(h)+\frac{1}{4}(l);$$

$$B_1 = m+\frac{1}{2}(d)+\frac{1}{2}(h)+\frac{1}{4}(i)+\frac{1}{4}(j)+\frac{1}{4}(l)$$

$$B_2 = m-\frac{1}{2}(d)+\frac{1}{2}(h)+\frac{1}{4}(i)+\frac{1}{4}(j)+\frac{1}{4}(l)$$

Where,

P_1 = Mean of higher parent

P_2 = Mean of lower parent

F_1 = Mean of progenies of first generation

F_2 = Mean of progenies of second generation

B_1 = Mean of backcrosses (F_1 × P_1) progenies

B_2 = Mean of backcrosses (F_1 × P_2) progenies

The perfect fit solution is given by formulae of Jinks and Jones[12].

$$m = \frac{1}{2}P_1 + \frac{1}{2}P_2 + 4F_2 - 2B_1 - 2B_2$$

$$d = \frac{1}{2}P_1 - \frac{1}{2}P_2$$

$$h = 6B_1 + 6B_2 - 8F_2 - F_1 - \frac{3}{2}P_1 - \frac{3}{2}P_2$$

$$i = 2B_1 + 2B_2 - 4F_2$$

$$j = B_1 - \frac{1}{2}P_1 - B_2 + \frac{1}{2}P_2$$

$$l = P_1 + P_2 + 2F_1 + 4F_2 - 4B_1 - 4B_2$$

Where,

M= Mean effect

d= additive gene effect

H= dominance gene effect

i= additive × additive interaction

j= additive × dominance interaction

l= dominance × dominance interaction

Variances of gene effects were computed using following formulae.

$$V_m = \frac{1}{4}VP_1 + \frac{1}{4}VP_2 + 16VF_2 - 4VB_1 - 4VB_2$$

$$V_d = \frac{1}{4}VP_1 - \frac{1}{4}VP_2$$

$$V_h = 36VB_1 + 36VB_2 + 64VF_2 + VF_1 + \frac{9}{4}VP_1 + \frac{9}{4}VP_2$$

$$V_i = 4VB_1 + 4VB_2 + 16VF_2$$

$$V_j = VB_1 + \frac{1}{4}VP_1 + VB_2 + \frac{1}{4}VP_2$$

$$V_l = VP_1 + VP_2 + 4VF_1 + 16VF_2 + 16VB_1 + 16VB_2$$

Where

Vm……Vl = Variances of respective gene effects and

VP_1…..VB_2 = Variance of respective means of generations.

The standard errors of these estimates were as follows:

$$S.E.(m) = \sqrt{(Vm)}$$

$$S.E.(d) = \sqrt{(Vd)}$$

$$S.E.(h) = \sqrt{(Vh)}$$

$$S.E.(i) = \sqrt{(Vi)}$$

$$S.E.(j) = \sqrt{(Vj)}$$

$$S.E.(l) = \sqrt{(Vl)}$$

The calculated value of 't' are to be compared with tabulated value of 't' at 5% level of significance. In each test, the degree of freedom is sum of the degrees of freedom of various generations (total number of observations - total number of replications) involved.

RESULTS AND DISCUSSION

The genetic studies have been conducted to understand the genetic control of grain yield and its component traits in barley. These studies have shown that both additive and non-additive genes control the grain yield in barley. The detection and estimation of epistasis would also enable the breeders to understand the genetic cause of heterosis with greater reliability. The presence or absence of epistasis can be detected by the analysis of generation means using the scaling test, which measures epistasis accurately whether it is

complementary (additive × additive) or duplicate (additive × dominance) at the digenic level reported by Sharmila *et al*[24]. The six parameter model of generation mean analysis provides information about all the six parameters (mean effects, additive, dominance, additive × additive gene interaction, additive × dominance gene interaction and dominance × dominance gene interaction) and thereby helps in formulating the guidelines for handling the segregating material in the subsequent generations by the exploitation of fixable component[23]. The genetic feature of the characters would have a direct bearing on the breeding programme for further advancement of the crop. A lot of information on nature and relative magnitude of genetic components of variation (additive and dominance) have been generated by generation mean analysis. However literature on barley in respect of fixable and non fixable gene effects is meager[21]. Therefore, the present study was planned to investigate genetics of 12 yield and its attributing traits by using the data of six-generations of four crosses under irrigated and rainfed conditions. The means of P_1, P_2, F_1, F_2, B_1 and B_2 of these four selected crosses were subjected to scaling tests of Mather[17] and Cavalli[2].

Scaling test and gene action

The additive, dominance and epistatic types of gene interaction in each cross for different traits were found to be different from each other. Epistasis was observed for all the traits studied in four crosses in both the conditions except for the proline content in irrigated condition, as it is apparent from the significance of one or more of the four scales (A, B, C and D scales) (Table 2). To validate the results of A, B, C and D scaling test, joint scaling test as suggested by Cavalli[2] was also performed. The joint scaling test also revealed presence of non-allelic interactions in all the four crosses for all the traits. The dominance × dominance (*l*) interaction was larger than the additive × additive (*i*) and additive × dominance (*j*) effects put together, while for the main effects, the dominance component (*h*) was greater than the additive (*d*) component under both irrigated and rainfed conditions. These findings were in line with earlier reports of Jatothu *et al*.[10], Said[22], Singh[26], Adriana *et al*.[1] and Raikwar[21].

Comparison of estimates of gene effect with respect to magnitude as well as significance reveled that additive (*d*) was of greater importance than to the dominance (*h*) gene effects for no. of effective tillers and 100-grain weight in the cross HUB-113×Azad; for proline content and plant height in HUB-113×Geetanjali. Thus, selection for no. of effective tillers, plant height and 100-grain weight will be effective in early segregating generations. The dominance (*h*) effect was more important than additive gene effects (*d*) in the inheritance of days to maturity and chlorophyll content in HUB-113×Geetanjali. The genetic effects for these characters suggested that selection for these characters will not be effective in segregating generations. Higher magnitude of dominance (*h*) component than the additive (*d*) component suggested that the parents involved in the crosses were in dispersion phase and dominance component was more important for these characters. Both additive (*d*) and dominance (*h*) effects were pronounced in crosses HUB-113×Geetanjali for chlorophyll content, no. of grains per spike and grain yield per plant in ; HUB-113×Azad for plant height. Additive × additive (i) epistatic effect was more important for days to maturity and chlorophyll content both in HUB-113×Azad and HUB-113×Geetanjali. However, dominance × dominance (*l*) epistatic effect was important for stomatal conductance proline content, no. of effective tillers, spike length, plant height, no. of grains per spike and grain yield per plant in HUB-113×Geetanjali ; no. of effective tillers, spike length, plant height, no. of grains per spike and grain yield per plant in HUB-113×Azad.

In the presence of epistasis, the dominance (*h*) and dominance × dominance (*l*) effects were in opposite direction, suggesting that duplicate-type epistasis occurred in most cases in both the conditions indicating predominantly dispersed alleles at the

interacting loci. This kind of epistasis generally hinders improvement through selection and hence, a higher magnitude of dominance and dominance×dominance type of interaction effects would not be expected. It also indicated that selection should be delayed after several generations of selection (single-seed descent) until a high level of gene fixation is attained. Subsequent intermatings between promising lines may be important in accumulating favorable genes[5]. Complementary type of gene interaction was found only for grain yield per plant in HUB-113×Geetanjali; in such situation additive component is often relatively underestimated while dominance effects tends to be overestimated[20].

The results of the present study confirmed that yield related traits like number of grains per spike, grain weight per spike, 100-grain weight and grain yield per plant along with stress related traits like stomatal conductance and proline content were predominantly influenced by dominance (*h*) and dominance × dominance (*l*) gene action. Therefore, selection of these traits will be difficult in the early generations. As selection based on progeny performance exploits only additive component of genetic variances, for these traits bi-parental mating followed by recurrent selection or diallel selective mating, which allows intermating among the selected segregates in the different cycles, would be useful to recover superior homozygote in later generations[5] normal breeding methods would not be fruitful and the methods which will exploit non-additive gene effect and take care of non-allelic interactions such as restricted recurrent selection by way of intermating the most desirable segregates, followed by selection[13] or diallel selective mating[11] or multiple crosses or biparental mating in early segregating generations[25] could be promising for genetic improvement of yield and associated traits. In addition, few cycles of recurrent selection, followed by pedigree method may also be useful for the effective utilization of all three types of gene effects simultaneously. It will lead towards an increased variability in later generations for effective selection by maintaining considerable heterozygosity through mating of selected plants in early segregating generations. These breeding approaches could be helpful in developing barley populations, which upon selection will result in the most desirable yield traits along with drought tolerant genotypes. Such genotypes could stand better under rainfed conditions to get maximum yield in barley.

Studies on transgressive segregants

The number of F_2 segregants showing grain yield per plant higher than both the parents as well as standard check K-603 were scored cross wise in the selected four crosses. The cross HUB-113×Azad had yielded good number of transgressive segregants under both irrigated and rainfed condition (10 and 7 respectively).

A striking difference among segregants with respect to check (K-603) can be observed for stomatal conductivity, spike length and grain weight per spike which were in general higher than check variety under irrigated condition (Table 3). Whereas, under rainfed condition, in general, stomatal conductivity was less than check in magnitude, while, proline content, spike length, grain weight per spike and number of grains per spike were higher in magnitude compared to check. To cope with drought stress, plants respond with complex physiological and biochemical changes that influence their growth and morphology. Relatively rapid physiological changes may be followed by alterations in shoot and root growth, morphology, and anatomy that affect plant functioning in a longer time scale[19].

Most of the promising segregants, irrespective of the parents involved, also showed an enhanced level of proline content as expected particularly under rainfed condition. Higher plants have developed different adaptive mechanisms to reduce oxidative damage resulting from stress, through the biosynthesis of a cascade of antioxidants. General metabolic adaptation which enables plants to cope with water or

osmotic stress, involves an increased synthesis of osmoprotectants, such as proline and soluble sugar[7]. Proline accumulation during drought is a typical plant response to water stress[15,18]. It allows adjusting many plant functions, i.e. cell turgor and stomatal opening, thereby increasing plant tolerance to drought. This increasing concentration of mineral nutrients, which is an effect of water deficit during seed development, is consistent with observations reported by Farahani *et al*.[6]. An estimate of proline accumulation potential in seedling plants could be useful selection screening test during cereal breeding for crop improvement in an environment in which water stress is a major field determination[14]. It is interesting that, crosses involving parents HUB-113 and Azad both with good level of gca ranking, for most of the traits yielded high number of transgressive segregants with respect to yield in irrigated as well as rainfed conditions. It is apparent from the present investigation that the parents HUB-113 coupled with Azad should be given due consideration while evaluating promising recombinants and best performing transgressive segregants under both the environments. These segregants might be continued by selfing for fixation of all genes responsible for trait of interest and developed promising genotypes.

Indeed, the current study showed a huge impact of pre-anthesis water deficit on barley productivity. In general, most of the genotypes were affected by stressed regimes. In addition, the early flowering and maturing genotypes had better enactment, as reflected in higher yield and its components when compared with late flowering ones. These results proved the essential importance of the early flowering behavior in barley to improve productivity in response to pre-anthesis water deficit conditions. The obtained results can be used as a guide for the selection of appropriate lines for future breeding purposes of barley varieties with improved elasticity and resilience to drought conditions under dry environments.

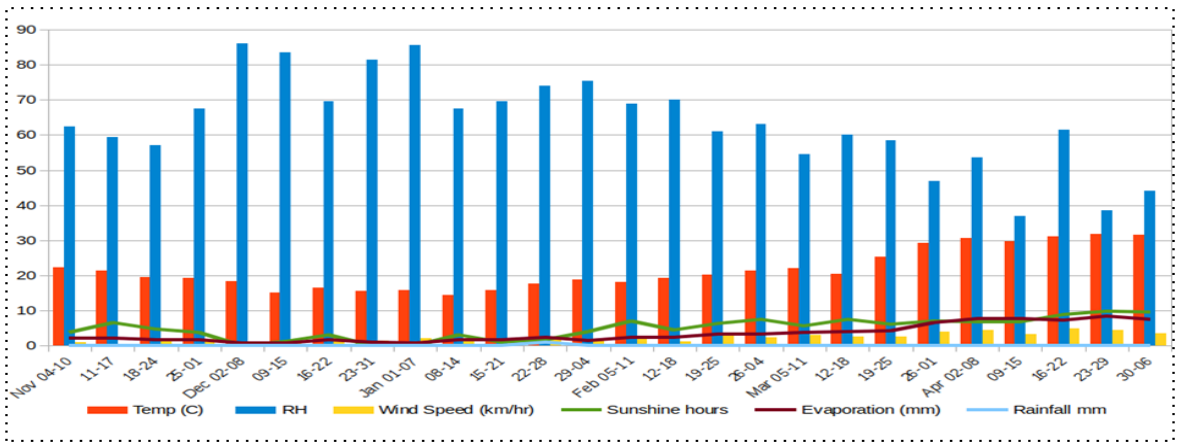

Fig. 1: Meteorological data during the crop growth

Table 2: Estimates of A, B, C and D scaling tests, joint scaling tests and estimates of six parameter *m, d, h, i, j* and *l* of the crosses for 12 traits of barley under irrigated and rainfed conditions

Environment	Cross	Simple Scaling test				Genetic components						Interaction
		A	B	C	D	*m*	*d*	*h*	*i*	*j*	*l*	
Days to 50% flowering												
Irrigated	HUB-113×Azad	-2.67	3.40*	-4.47	-2.60	77.3**	-3.2**	3.03	5.2	-6.07**	-5.93	-
	HUB-113×Geetanjali	-2.2	3.00	-9.60**	-5.20*	78.1**	-2.6	10.73*	10.4**	-5.2	-11.2	-
Rainfed	HUB-113×Azad	-1.60	1.87	17.07*	8.40*	82.1**	-5.4**	-23.13**	-16.8*	-3.47	16.53	-
	HUB-113×Geetanjali	-15.23**	5.51**	-8.77	0.48	72.1**	-6.92**	-8.88	-0.96	-20.74**	10.69	-
Days to maturity												
Irrigated	HUB-113×Azad	-3.13	-5.2	-22.33**	-7.01	107**	2.21	20.17*	14.22**	2.07	-5.67	-

	HUB-113×Geetanjali	2.47	0.87	-20.67*	-12.03*	114**	-3..32	31.67**	24.15**	1.61	-27.33	D
Rainfed	HUB-113×Azad	-8.9**	9.6	-11.3*	-6.06	106.8**	-5.23	8.02	12.13**	-18.5**	-12.70	-
	HUB-113×Geetanjali	2.02*	3.71**	-13.71**	-9.72**	107.94**	2.92**	19.71**	19.44**	-1.69	-25.17**	D
No. of effective tillers												
Irrigated	HUB-113×Azad	-7.01**	0.21	-0.24	3.28**	9.94**	-2.24**	-4.16	-6.56**	-7.21**	13.36**	-
	HUB-113×Geetanjali	-1.91**	-2.16**	1.85	2.96**	9.98**	1.36**	-5.29*	-5.92**	0.25	9.99**	D
Rainfed	HUB-113×Azad	-7.45**	0.21	0.52	3.88*	10.13**	-2.46**	-5.36	-7.76**	-7.65**	15.16**	-
	HUB-113×Geetanjali	-10.63**	-2.23	1.53	7.2**	9.12**	-2.2	-12.03**	-14.4**	-8.4**	27.27**	D
Chlorophyll content												
Irrigated	HUB-113×Azad	-8.43**	-3.97	-10.93	0.74	47.01**	-5.88**	1.5	-1.48	-4.46*	13.89	-
	HUB-113×Geetanjali	-13.44**	-1.87	-35.99**	-10.34**	44.46**	-4.5*	29.83**	20.68**	-11.57*	-5.37	-
Rainfed	HUB-113×Azad	8.37**	2.69	-5.98	-8.52	40.63**	0.82	19.26*	17.04**	5.67	-28.1*	D
	HUB-113×Geetanjali	-3.61*	-4.22*	16.19**	12.01**	48.33**	-6.53**	-21.19**	-24.02**	0.61	31.86**	D
Stomatal conductivity												
Irrigated	HUB-113×Azad	-18.62**	-36.81**	-19.59	17.92**	487.47**	13.26**	-26.77*	-35.84**	18.19*	91.27**	D
	HUB-113×Geetanjali	33.25**	-3.27	47.02**	8.52	476.23**	27.94**	-52.72**	-17.04	36.51**	-12.94	-
Rainfed	HUB-113×Azad	0.30	27.5**	44.13	8.17	154.27**	4.42*	8.29	-16.34	-27.22**	-11.46	-
	HUB-113×Geetanjali	-34.41**	-5.72	-6.63	16.75	167.76**	-26.71**	-17.77	-33.49	-28.69*	73.62*	-
Proline content												
Irrigated	HUB-113×Azad	0.04	1.17	1.39	0.09	12.81**	-1.98**	6.09	-	-	-	-
	HUB-113×Geetanjali	7.69**	5.42**	10.97**	-1.07	16.94**	-2.29**	1.27	2.14	2.27*	-15.25**	-
Rainfed	HUB-113×Azad	-0.32	-4.44**	-6.02	-0.63	40.91**	-3.7**	11.75	1.27	4.12	3.49	-
	HUB-113×Geetanjali	-4.55**	-4.83**	7.58**	8.48**	32.26**	4.78**	-11.51**	-16.96**	0.28	26.34**	D

Contd..

Environment	Cross	Simple Scaling test				Genetic components						Interaction
		A	B	C	D	*m*	*d*	*h*	*i*	*j*	*l*	
Spike length												
Irrigated	HUB-113×Azad	0.53	0.93	-3.93	-2.68*	12.9**	-0.12	7.93**	5.36**	-0.37	-6.79*	D
	HUB-113×Geetanjali	-0.73	5.03**	-1.72	-3*	11.7**	-1.8*	5.75*	6**	-5.77**	-10.3*	D
Rainfed	HUB-113×Azad	-1.65*	-5.36**	-0.93	3.04**	13.85**	3.42**	-2.78	-6.08**	3.71**	13.09**	-
	HUB-113×Geetanjali	-0.67	-5.16**	0.85	3.34**	14.03**	3.48**	-4.05**	-6.68**	4.49**	12.51**	D
Plant height												
Irrigated	HUB-113×Azad	-3.8*	-4	-23**	-7.6*	102**	-12.4**	13.03*	15.2*	0.2	-7.4	-
	HUB-113×Geetanjali	-3.53*	-10.27**	3.4	8.6**	101.6**	6.2**	-4.7	-17.2**	6.73**	31**	-
Rainfed	HUB-113×Azad	-13.6**	-7.07**	-46.67**	-13*	69**	11.4**	26.67*	26*	-6.53	-5.33	-
	HUB-113×Geetanjali	-10.6**	3.06*	-0.02	3.76**	75.92**	-9.68**	-0.77	-7.52**	-13.66**	15.06**	-
Grain weight per spike												
Irrigated	HUB-113×Azad	0.1	-0.7*	0.14	0.37	3.22**	0.08	-0.16	-0.75**	0.8	1.35	-
	HUB-113×Geetanjali	-1.01	1.52*	0.61	0.05	3.04**	-0.53	0.07	-0.11	-2.53*	-0.4	-
Rainfed	HUB-113×Azad	-0.35	-0.99**	1.18**	1.26**	2.65**	0.79**	-2.29**	-2.53**	0.64*	3.87**	D
	HUB-113×Geetanjali	0.56	-0.49**	1.23*	0.58	2.41**	0.56**	-1.47*	-1.16*	1.05**	1.09	-
No. of grains per spike												
Irrigated	HUB-113×Azad	-13.17**	-14.21**	-7.77*	9.8**	49.34**	3.52**	-19.3**	-19.6**	1.04	46.97**	D
	HUB-113×Geetanjali	-4.09*	-9.01**	7.66*	10.38**	48.14**	7.94**	-16.88**	-20.76**	4.91*	33.86**	D
Rainfed	HUB-113×Azad	-22.37**	-15.5*	-23.55*	7.16	50.43**	3.1	-12.22	-14.32	-6.87	52.19**	D
	HUB-113×Geetanjali	1.64	-6.64**	4.84**	4.92**	44.46**	6.04**	-6.67**	-9.84**	8.28**	14.84**	D
100-grain weight												
Irrigated	HUB-113×Azad	-0.55**	-0.7**	0.1	0.67**	4.65**	0.33**	-1.21**	-1.34**	0.15	2.58**	D
	HUB-113×Geetanjali	0.19	-1.23**	0.32	0.68**	4.62**	1.32**	-0.15	-1.36**	1.42**	2.4**	-
Rainfed	HUB-113×Azad	-0.57**	-1.6**	0.01	1.09**	4.31**	1.13**	-1.24	-2.18**	1.02**	4.36**	-
	HUB-113×Geetanjali	0.23	0.01	-1.56**	-0.9**	4.61**	-0.2	2.1**	1.8**	0.22	-2.04**	D
Grain yield per plant												
Irrigated	HUB-113×Azad	-13.32*	-22.57**	-23.01*	6.44**	42.49**	10.94**	-8.76	-12.88**	9.25*	48.77**	-
	HUB-113×Geetanjali	-1.58	3.9**	-8.65	-5.49*	24.34**	3.56**	9.84*	10.97*	-5.48**	-13.29*	D
Rainfed	HUB-113×Azad	-14.47**	2.86*	8.03**	9.82**	19.24**	-5.3**	-15.24**	-19.64**	-17.33**	31.25**	D
	HUB-113×Geetanjali	-6.63**	-5.6**	-17.15**	-2.46	11.13**	3.12**	7.55**	4.92*	-1.03	7.31*	C

Table 3: Performance of few promising transgressive segregants from HUB-113×Azad under rainfed and irrigated conditions

Segregant	No. of effective tillers	Chlorophyll content	Stomatal conductivity (m mol/m^2/s)	Proline content (mg/g)	Spike length (cm)	Grain wt per spike (g)	No. grains per spike	Grain yield per plant (g)	Per cent gain over check
Irrigated									
K-603(Check)	10.67	53.64	473.23	18.02	9.94	3.21	51.64	28.66	-
Segregant 37	12.10	49.40	476.30	12.39	14.50	3.25	46.50	32.40	13.07
Segregant 43	9.00	41.40	485.30	16.51	11.00	3.29	47.00	39.60	38.19
Segregant 8	8.70	48.80	481.70	17.89	12.50	2.60	51.60	37.40	30.52
Segregant 11	11.80	51.50	493.70	13.13	11.00	2.90	50.50	34.10	19.00
Segregant 28	10.00	49.70	497.60	15.66	11.00	3.31	51.50	39.20	36.80
Segregant 16	8.00	49.90	494.10	16.91	13.90	3.67	49.50	36.20	26.33
Segregant 39	10.00	49.40	463.40	16.40	15.00	2.60	42.50	33.70	17.60
Segregant 40	9.80	50.20	475.40	16.30	15.00	3.10	43.50	36.80	28.42
Segregant 22	10.60	49.50	468.60	17.10	13.50	2.80	40.80	32.50	13.42
Segregant 13	7.50	48.40	477.10	17.80	14.00	3.26	42.60	32.80	14.46
Rainfed									
K-603(Check)	8.27	45.97	164.87	42.43	6.70	1.83	49.89	10.13	-
Segregant 16	11.00	30.90	160.74	47.31	13.00	2.31	48.00	15.20	50.04
Segregant 37	9.00	42.70	157.29	43.97	13.00	2.76	46.20	13.70	35.23
Segregant 9	14.00	34.50	165.58	39.93	12.00	2.48	56.50	14.70	45.10
Segregant 46	9.00	40.40	135.86	48.51	13.00	2.73	42.50	12.83	26.65
Segregant 28	7.00	36.80	117.89	48.98	15.30	2.76	45.20	14.70	45.10
Segregant 21	13.00	38.00	178.96	32.01	14.00	2.43	64.40	15.20	50.04
Segregant 34	7.00	42.10	183.87	33.65	12.00	2.04	37.00	10.50	3.65

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REFERENCES

1. Adriana, C., Madosa, E., Giancarla, V. and Ciulca, S. Combining ability for some grains morphological traits in winter barley. *JOURNAL of Horticulture, Forestry and Biotechnology.* **19(3):** 67- 72 (2015).
2. Cavalli, L L. An analysis of linkage in quantitative inheritance. In *Quantitative Inheritance*, ed. E. C. R. Reeve, and C. H. Waddington. H.M.S.O., London (1952).
3. Ceccarelli, S. Drought and drought resistance. *Encycl. Biotechnol. Agric. Food* **1:** 205–207 (2010).
4. Ceccarelli, S. and Grando, S. Drought as a challenge for the plant breeder. *Plant Growth Regul.* **20:** 149–155 (1996).
5. Eshghi, R. and Akhundova, E. Genetic analysis of grain yield and some agronomic traits in hulless barley. *African Journal of Agricultural Research* **4(12):** 1464-1474 (2009).
6. Farahani, S.M., Chaichi, M.R., Mazaheri, D., Afshari, R.T., Savaghebi, G. Barley grain mineral analysis as affected by different fertilizing systems and by drought stress. *J. Agric. Sci. Technol.* **13:** 315–326 (2011).
7. Fayez, K.A. and Bazaid, S.A. Improving drought and salinity tolerance in barley by application of salicylic acid and potassium nitrate. *Journal of the Saudi Society of Agricultural Sciences* **13:** 45–55 (2014).
8. Hayman, B.I. The theory and analysis of diallel crosses II. *Genetics* **43:** 63-85 (1958).
9. Hayman, B.I. The theory and analysis of diallel crosses III. *Genetics*, **45:** 155–172 (1960).
10. Jatothu, J.L., Dangi, K.S., Sagi, S.K., Bhandari, H.R., Tripathi M.K. and Chaudhary, B. Estimation of Gene Effects Based on Joint Scaling Test and Sequential Model Fit Scheme for Quantitative Traits in Sesame (*Sesamum*

indicum L.). *Journal of Agricultural Science* **5(3):** 224–235 (2013).

11. Jensen, N.P. A diallel selective mating system for cereal breeding. *Crop Science*, **10:** 629–663 (1970).
12. Jinks, J.L. and Jones, R.M. Estimation of components of heterosis. *Genetics* **43:** 223-224 (1958).
13. Joshi, A.B. Breeding methodology for autogamous crops. *Indian J Genet*. **39:** 567–578 (1979).
14. Lal, J.P., Singh, H., Nandan, R., Prasad, L.C. and Kumar, H. Recombinants for enhanced productivity and drought tolerance in barley (*Hordeum vulgare* L.). *Journal of Agricultural Science and Technology* **1:** 550-555 (2011).
15. Man, D., Bao, Y.X. and Han, L.B. Drought tolerance associated with proline and hormone metabolism in two tall fescue cultivars. *Hortiscience* **46(7):** 1027–1032 (2011).
16. Mather, K, and Jinks, J.L. *Biometrical Genetics*, 3rd edition, Chapman and Hall, London (1982).
17. Mather, K. Biometrical Genetics-The Study of Continuous Variation, Methuen and Co Ltd, London pp-192 (1949).
18. Mohammadkhani, N., Heidari, R., Drought-induced accumulation of soluble sugars and proline in two maize varieties. *World Appl. Sci. J*. **3(3):** 448–453 (2008).
19. Nosalewicz, A., Siecin, J., Nosalewicz, Wiacek, M.D., Pecio, A. and Wach, D. Transgenerational effects of temporal drought stress on spring barley morphology and functioning. *Environmental and Experimental Botany* **131:** 120–127 (2016).
20. Pathak, R.S. and singh, R.B. Genetics of yield and characters in upland cotton. *Indian J. Gent. Breed.* **30:** 679-689 (1970).
21. Raikwar, R.S. Generation mean analysis of grain yield and its related traits in barley (*Hordeum vulgare* L.). *Electronic Journal of Plant Breeding* **6(1):** 37-42 (2015).
22. Said, A.A. Generation mean analysis in wheat (*Triticum aestivum* L.) under drought stress conditions. *Annals of Agricultural Science* **59(2):** , 177–184 (2014).
23. Sharma, A., Kapur, P. and Katoch, V. Generation mean analysis to estimate genetic parameters for desirable horticultural traits in garden pea (*Pisum sativum*) *Indian Journal of Agricultural Science*, **82(3):** 201–206 (2012).
24. Sharmila V., Ganesh S.K. and Gunasekaran M. Generation mean analysis for quantitative traits in sesame (*Sesamum indicum* L.) crosses. *Genetics and Molecular Biology* **30:** 80-84 (2007).
25. Singh, P., Bhadauria, A, and Singh, P.K. Combining ability and gene action for Alternaria blight and powdery mildew resistance in linseed. *Indian J Genet.* **68(1):** 65–70 (2008).
26. Singh, R.R. Estimation of Gene Effects for Grain Yield and its Related Traits Under Normal and Saline Sodic Soil in Barley (*Hordeum vulgare* L.). *Riticeae Genomics and Genetics* **5(1):** 1-6 (2014).