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GENOTYPIC VARIANCES AND INTERACTIONS WITH ENVIRONMENTS IN BARLEY GENOTYPES FOR GRAIN YIELD AND ITS ASSOCIATE CHARACTERS

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ABSTRACT
The experiments were conducted to study component of genetic variance in barley (*Hordeum vulgare L.*). Ten genotypes along with their 45 F_1's and 45 F_2's were evaluated in a randomized block design during *Rabi* 2015-16 at RARI Durgapura, Jaipur. The data obtained were subjected to statistical analysis to get information on significance of differences (Panse and Sukhatme, 1967), estimation of components of genetic variances. The results depicted significant differences for all the studied traits indicated the influence of environment on the expression of these characters. Further, the mean sum of squares due to parents' *vs* F_1 and F_2 displayed significant difference for days to heading(122.22**), days to maturity(2039.03**), flag leaf area(2570.70**), peduncle area(2563.22**), spike length(10.47**) and grain yield per plant(1355.66**). The G × E interaction was also found significant for days to heading (9.41**), days to maturity (49.00**), plant height (3.25**), peduncle area(6.90**), and grain yield per plant(3.30**) except tillers per plant, flag leaf area, spike length the analysis of variance was done for the individual environment separately.

INTRODUCTION

It occupies fourth position in acreage and third position in terms of crop production. This crop has potentials for growing under drought and saline conditions. Being an important food crop of India.Today barley is grown in 49781 thousand ha. The world production of barley is about 144755 thousand tons with Europe largest of producer, due to the highest yield (Anonymous 2014). Barley has also been very important winter cereal crop in India. In India it is grown on more than 671 thousand ha with the production of more than 1626 thousand tonnes with productivity of 2.5 q/ha (Anonymous 2014). In India is grown as rain fed crop or residual moisture. In many of these situations barley yields have not significantly increased and vary mostly in response to fluctuations in climate conditions. Barley is an important Rabi cereal next to wheat in acreage and production in Rajasthan. In Rajasthan it is grown over an area about 393 thousand ha with annual production of 942 thousand tonnes with an average yield of 30.00q/ha (Anonymous 2014). Barley cultivation in India is now becoming oriented towards industrial utilization. ultimate challenge to the breeders to breed varieties with high yield potential. High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters (Santosh *et al*., 2013). Therefore, it is necessary to estimate and study the genetic variation and mode of inheritance in different yield parameters and biotic stress resistance to initiate productive Barley breeding programs. The improved genotypes with early maturing and better tillering can further bridge the yield gap.

Genetic variability gives an idea of possible improvement of new population through selections, when compared to the original population. One of the main objectives of any breeding program is to produce high-yielding and better-quality lines for release as cultivars to farmers. The prerequisite to achieve this goal is to find sufficient amount of variability, in which desired lines are to be selected for further manipulation to useful as a general guide in the choice of parents for breeding hybrids. The adequate information on extent of variability parameters may be helpful to improve the yield by selecting the yield component traits because yield is a complex trait, whose manifestation depends on the component traits. Generally, the estimates of heritability (h2) of traits are environment specific (Shimelis and Rhandzu, 2010). These estimates should be incorporated and specifically applied only to the population and environment sampled (Dudley and Moll,1969). Thus, selection of traits based on h2 and genetic variability as percent of mean is of great importance to the breeder for making criteria for improvement in a complex character. Information on estimates of heritability and genetic variability in early segregating generations on seed yield and its components in barley is very limited, Hence, the present investigation was conducted to study the extent of variability of barley genotypes aimed at improving yield and provide better lines to develop the high yielding varieties to the farmers.

MATERIALS AND METHODS

The experiment was conducted at RARI Durgapura Jaipur is

situated at latitude of 26°49¹ N longitude of 75°48¹E and altitude of 450 meters above sea label in Jaipur district of Rajasthan This region falls under agro climatic zone - III a (semi-arid eastern plain) of the state. Weather parameters play an important role in affecting plant growth and development of crop. Ten genetically diverse parents namely RD 2786, RD 2832, RD 2878, BH 946, BH 902, RD 2715, RD 2035, RD 2592, PL 751 and JYOTI, were selected for present study. The ten parents and their resulting 45 F_1's and 45 F_2's were grown in a randomized block design with three replications under normal, late and very late sown conditions during *Rabi* 2015-2016. Each plot was consisting of 3 m long two rows for non-segregating material *i.e.* parents and F_1s and six rows in F_2's. Row to row and plant to plant distance were kept at 30 cm and 10 cm, respectively under all the three environments. Twenty competitive plants in parents and F_1's and 60 plants in F_2's progenies were selected randomly for recording observations for following characters *i.e.* days to heading, days to maturity, plant height, tillers per plant, flag leaf area, peduncle area, spike length and grain yield per plant under three environments separately.

Analysis of variance

The mean values of different parents, F_1's and F_2's for all the characters were subjected to analysis of variance separately for individual environment as well as for pooled data to determine the significance of differences among genotypes , environments and genotype x environment interaction effects (Panse and Sukhatme, 1967). The structure of analysis variance (ANOVA) is presented in

The data of each character were pooled over environments and the pooled analysis of variance was done. The structure of analysis of variance for pooled analysis is given in below Table 3.

For the combined analysis over environments, a pooled average effective mean square was calculated for each population by pooling the help of the following formula:

Pooled error (Me) = 1/er ($\tilde{A}^2$1 + $\tilde{A}^2$2 + ———————— $\tilde{A}^2$j)

Where,

$\tilde{A}^2$j is the error variance corresponding to j^{th} environment. The significance of genotype and environmental variance was tested against genotypes x environment interaction variance while the genotype x environment interaction variance was tested against the pooled error.

RESULTS AND DISCUSSION

The significant differences among all the three environments (showing dates) for all the studied traits *viz*., days to heading, days to maturity, plant height, tillers per plant, peduncle area, flag leaf area, spike length, and grain yield per plant. Pooled analysis of variance possessed diversified effects of environment on the expression of these traits (Table 3). The pooled analysis of variances also exhibited significant mean sum of squares due to genotypes including parents and generations (F_1's and F_2's) for all the characters under study. Further parents' *vs* generations (F_1's and F_2's) exhibited significant differences for all the studied characters (except plant height and tillers per plant) in all the three environments. The G x E interaction was also showed significant for most of the characters (except tillers per plant, flag leaf area and spike length), indicate a non-linear response of genotypes to the change in the environment (Table 3).This is in conformity with reports that G X E interactions is common in crop plant species (Allard and Bradshow, 1964 and Arati *et al*., 2015). In view of significant G × E interaction for most of the characters, the analysis of variance was done for the individual environment separately (Table 4). The analysis of variance in individual environment revealed that significant differences among the genotypes for all the characters, consequently established the circumstances that the characters manifested the presence of ample genetic diversity among the parents. Further analysis revealed significant mean squares due to generations and parents for all the characters in all the three environments. Mean squares due to F_1 and F_2 were found significant for all the characters in all the environments. Mean squares due to F_1 *vs* F_2 were found significant for all the characters except for days to heading in E_1 and E_2, plant height in E_3, flag leaf area in E_2 which supported the presence of inbreeding depression in all the three environments. Non-significant F_1*vs* F_2 for days to heading, plant height and flag leaf area was also observed by Singh *et al*.(2012). Likewise, Singh *et al*.(2003). The differences among parents *vs*

Table 1: ANOVA for individual environment

Source of Variance	d.f.	M.S.S.	Expected M.S.S.
Replication	(r-1)	Mr	$\tilde{A}^2$ e+ g $\tilde{A}^2$ r
Genotypes	(g-1)	Mg	$\tilde{A}^2$ e + r $\tilde{A}^2$ g
Error	(r-1) (g-1)	Me	$\tilde{A}^2$ e

Where,r and g are the number of replication and genotypes, respectively.
S.E. (Diff.) = (2 x error MSS/replication) $^{1/2}$ .The "F" values so obtained were tested at 5 percent level of probability

Table 2: ANOVA based on the data pooled over three environments

Source of variance	d.f.	M.S.S.	Expected M.S.S.
Environments	(e-1)	Me	$\tilde{A}^2$ e + rg $\tilde{A}^2$ r
Replication/Env.	(r-1) e	Mre	$\tilde{A}^2$ e + ge $\tilde{A}^2$
Genotypes	(g-1)	Mg	$\tilde{A}^2$ e +r(g/g-1) $\tilde{A}^2$ge + $\tilde{A}g^2$/(g-1)
Parents	(p-1)		
Generation	(Generation)-1		
Parents *vs* Generation	1		
Genotypes x Env.	(g-1) (e-1)	Mge	$\tilde{A}^2$ e + r(g/g-1) $\tilde{A}^2$ ge
Error	E(g-1) (r-1)	Me	$\tilde{A}^2$ e

Where, E = number of environments;$\tilde{A}^2$ ge = genotype x environmental interaction variance;$\tilde{A}^2$ re = replication x environment interaction variance;$\tilde{A}^2$ g = genotype variance and $\tilde{A}^2$ e = environment variance.

Table 3: Pooled analysis of variance showing mean squares of Parents, F_1's and F_2's for yield and its contributing attributes

source of variation	d.f.	Days to heading	Days to Maturity	Plant height(cm)	Tillers / plant	Flag leaf area(cm^2)	Peduncle area(cm^2)	Spike length (cm)	Grain yield/plant (g)
1	2	3	4	5	6	7	8	9	15
Env	2	1430.17**	11991.95**	477.66*	69.84**	82.17**	159.31**	11.99**	757.33**
reps/en	6	0.14	0.35	0.10	0.11	3.21	0.15	0.86	1.02
Genotype (F_1,F_2&P)	99	102.41**	286.37**	283.93**	69.49**	493.93**	216.84**	19.75**	1206.07**
parents	9	60.86**	18.44**	471.97**	56.72**	112.19**	265.17**	10.01**	272.87**
Generation (F_1&F_2)	89	106.32**	293.77**	268.10**	71.56**	509.20**	185.59**	20.83**	1298.75**
p *vs* Generation (F_1&F_2)	1	122.22**	2039.03**	0.20	0.11	2570.70**	2563.22**	10.47**	1355.66**
env x Genotype (F_1,F_2&P)	198	9.41**	49.00**	3.25**	0.73	9.06	6.90**	0.18	3.30**
error	594	2.64	2.64	1.49	1.35	7.55	0.44	0.49	1.77

*,** Significant at 5 per cent and 1 per cent levels, respectively

Table 4: Analysis of variance showing mean squares in individual environment of parents, F_1's and F_2's for yield and its contributing traits

S.No	Characters	Env.	Replications(2)	Treatment(99)	Parents(9)	Generation(89)	F_1's(44)	F_2's(44)	F_1vsF_2(1)	Pvs generation (1)	Error(198)
1	Days to heading	E_1	0.44	36.93**	20.09**	37.45**	47.06**	28.64**	2.90	141.45**	2.70
		E_2	0.06	25.82**	29.94**	21.03**	17.23**	25.17**	5.63	415.36**	2.54
		E_3	0.14	16.41**	13.96**	15.84**	16.07**	15.31**	28.68**	90.02**	2.68
2	Days to Maturity	E_1	0.01	100.74**	10.39*	68.61**	61.94**	43.84**	1451.39**	3773.65**	4.56
		E_2	0.09	58.02**	12.95**	45.18**	56.59**	34.07**	32.03**	1607.00**	3.07
		E_3	0.11	20.12**	16.87**	16.90**	19.42**	14.07**	30.00**	335.67**	2.70
3	Plant height (cm)	E_1	0.11	98.62**	180.77**	90.99**	91.31**	92.59**	6.19*	38.09**	1.25
		E_2	0.02	96.87**	178.72**	89.53**	86.91**	94.04**	6.05**	13.90**	0.80
		E_3	0.18	94.94**	129.66**	91.56**	91.21**	93.95**	1.61	83.15**	2.43
4	Tillers per plant	E_1	0.19	24.12**	18.73**	24.93**	28.82**	21.46**	6.77*	0.50	1.22
		E_2	0.11	24.19**	17.12**	25.18**	28.65**	21.75**	23.48*	0.23	1.23
		E_3	0.02	22.47**	21.21**	22.84**	25.43**	20.35**	18.83**	0.40	1.23
5	Flag leaf area (cm^2)	E_1	0.68	167.22**	50.31**	172.97**	186.32**	161.49**	90.56**	707.67**	0.22
		E_2	0.30	175.58**	35.69**	180.38**	204.38**	160.27**	9.34	1007.70**	21.96
		E_3	1.83	169.26**	40.08**	174.46**	185.38**	165.75**	77.15**	868.61**	0.45
6	Peduncle area(cm^2)	E_1	0.28	76.41**	87.22**	67.24**	67.52**	68.26**	9.94**	795.13**	0.67
		E_2	0.13	78.17**	91.01**	68.19**	66.48**	70.48**	42.51**	851.36**	0.26
		E_3	0.04	76.06**	87.26**	65.46**	67.58**	64.66**	7.37**	918.98**	0.39
7	Spike length (cm)	E_1	0.71	6.47**	3.46**	6.82**	6.96**	6.78**	1.96*	2.98*	0.50
		E_2	0.67	6.97**	3.43**	7.35**	7.79**	7.03**	2.09*	5.38**	0.50
		E_3	1.21	6.66**	3.40**	7.03**	7.61**	6.56**	2.37*	2.42*	0.48
8	Grain Yield per plant (g)	E_1	0.23	274.26**	89.30**	286.74**	253.18**	309.85**	746.00**	828.50**	2.29
		E_2	0.22	274.25**	88.13**	286.85**	253.09**	310.14**	747.24**	827.90**	3.12
		E_3	0.19	307.79**	97.13**	326.29**	286.33**	357.86**	696.04**	556.83**	2.59

*,** Significant at 5 per cent and 1 per cent levels, respectively

generations were significant for all the traits indicated the presence of heterosis in all the three environments except for tillers per plant, in three environments; (Table 4). Joshi *et al.* (2004) reported similar results (non-significant P *vs* F_1 or P *vs* F_2) for harvest index, number of tillers per plant and spike length, Pancholi *et al.* (2012) and Raikwar et al. (2014) for flag leaf area, while Singh *et al.* (2003) for plant height, number of tillers per plant, flag leaf area and harvest index.

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