Stability Analysis in Six-row Barley Genotypes for Grain Yield in Multi-environmental Trails Using Eberhart and Russel (1966)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

The current study aimed to determine the phenotypic stability for grain yield per plant under three distinct environmental conditions using fifteen parental lines and three testers with 45 crosses (30 single crosses and 15 three-way crosses) of six-row barley in three replications using Randomized

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Block Design. Eberhart and Russell (1966) developed the modal to examine stability. The mean sum of squares due to genotype and environment wassquares due to genotype and environment were found to be significant for grain yield per plant, which showed the differential effect of environment on genotypes. For grain yield per plant, it was also observed that the mean sum square resulting from the climate + (G x E) interaction, E (linear), and G x E (linear) was significant. With a non-significant deviation from regression (S2di=0) and regression coefficient near unity (bi=1), the genotypes BG 959, BG 105 x RD 2508, PL 751 x RD 2508, DWRB 137 x RD 3005, and RD 2035 x F1 exhibited higher grain yield than the population mean. These genotypes were the most stable and desirable under variable environmental conditions. These genotypes could be used as donors in regular breeding programs to improve barley grain yield.

1. INTRODUCTION

Barley (*Hordeum vulgare* L. 2n =2x = 14) is a cleistogamous, self-pollinated, sexually propagated and important *rabi* cereal crop grown throughout the temperate and tropical regions of the world. After wheat, maize and rice, it is the fourth-most important cereal crop in the world. It is a highly important cereal crop and is regarded as the first cereal that was domesticated for human consumption [1]. Barley can be used as human food, animal feed and fodder. Barley grains are mostly used to produce malt, which is utilized by breweries to make vinegar, malted milk, industrial alcohol, beer, and syrups. In India, 6.17 lakh hectares area of barley were cultivated in 2022–2023 with an average grain productivity of 2733 kg per hectare and a total production of 16.88 lakh tonnes [2]. Barley is grown on 3.37 lakh hectares in Rajasthan, with an average grain productivity of 2815 kg per hectare and a total production of 9.48 lakh tonnes during 2022–23 [2]. The extent to which grain yield and yield parameters vary across different environments is a critical factor in identifying genotypes widely adapted in barley crops. Grain yield is a quantitatively inherited trait, and there is considerable interaction between genotypes and environments. The Genotype x environment interaction is a complex phenomenon which involves environmental conditions such as agroecological, climate, and agronomic factors, as well as genetic factors which determine plant growth and development [3]. Through genotype stability testing, plant breeders can determine a genotype's stability across various environments and its adaptability to a specific environment. The information on genotype × environment interaction is crucial for plant breeders as it helps them to develop improved stable variety. Different stability measures have been used by other workers; each has benefits and drawbacks. As a measure of stability, Eberhart and Russell's model

considered both linear (b_i) and non-linear (S^2d_i) components of G x E interaction for predicting the performance of a genotype. According to this model, the genotypes with high mean (μ) performance, a regression coefficient of unity ($b_i=1$), and minimum deviation from regression ($S^2d_i=0$) exhibit better general adaptability across environments and are considered stable ones.

2. MATERIALS AND METHODS

Crosses among the 15 parents and 3 testers were made according to ketata et al. [4] *rabi,* 2021-22. In *rabi* 2022–2023, at Research Farm, S.K.N. College of Agriculture, Jobner, fifteen parental lines and three testers with their 45 crosses (30 single crosses and 15 three-way crosses) of six row barley (*Hordeum vulgare* L.) were evaluated in Randomized Block Design in three environments created three date of sowing 21 October (early sown), 15 November (normal sown), and 12 December (late sown) with three replications. The row length was grown in a 4 m length plot with row to row distance of 30 cm and plant to plant distance of 10 cm. Observation was recorded on ten randomly selected plants in each replication in each environment for grain yield per plant. Mean values over selected plants will be used for statistical analysis. As the Eberhart and Russell [4] model recommended, stability parameters for grain yield per plant were calculated.

3. RESULTS AND DISCUSSION

Table 1 displays the findings of the pooled variance analysis for stability, developed by Eberhart and Russell [5]. The pooled analysis of variance across the environments revealed that the mean sum of squares due to genotypes and environments was found to be significant for grain yield per plant, indicating the differential effect of environment on the genotypes. The mean sum of squares due to G x E interaction

was also significant for grain yield per plant. Similar findings were also reported by Chand et al. [6], Kavitha et al. [7], Lodhi et al. [8] and Sharma et al. [9]. The E + (G x E) were observed to be significant for grain yield per plant under study, indicating significant genotype-environment interactions. Further partitioning of E+ (G x E) into linear [E (linear) and G x E (linear)] and non-linear (pooled deviation) components. For grain yield per plant, the mean square due to E (linear) and G x E (linear) were also found significant against pooled error, suggesting that macro-environmental differences existed in all three of the environments examined and were still predictable. The variation due to pooled deviation was non-significant for grain yield per plant, which indicated that genotypes differed with respect to their stability and prediction for this trait would be difficult. Similar trends of results were reported by Chand et al. [6], Kavitha et al. [7], Lodhi et al. [8], Megahed et al. [10] and Sharma et al. [9].

The range of mean value varied from 9.10g (NDB 1445) to 16.13g (DWRUB 64) for parents and 12.05g (NDB 1445 x RD 3005) to 22.50g (DWRUB 64 x RD 2508) for crosses with population mean of 14.71g. Parents and crosses had regression coefficients (bi) ranging from 0.33 (RD 2052) to 1.41 (PL 751) and 0.54 (JB 110 x RD 2508) to 1.46 (PL 751 x F1), respectively. Predicting performance was possible for 61 genotypes (18 parents and 43 crosses) out of 63 genotypes as they showed non-significant deviation from regression (Table 2).

Among the parents, only one parent, BG 959, displayed a regression coefficient that was nearly equal to unity (bi=1) and non-significant deviation from regression with a higher mean than the population mean, demonstrating its average stability across the environments. Regression coefficient greater than unity (b$_i$>1) and non-significant deviation from regression with higher

mean value than the population mean showed by one parent, PL 751, indicating below average stability in a favorable environment. Regression coefficient less than unity (b$_i$<1) and non-significant deviation from regression with a mean value higher than the population means were seen in three parents RD 2508, BG 105, and DWRUB 64, indicating above-average stability in an unfavorable environment.

Among the 45 crosses, 4 crosses BG 105 x RD 2508, PL 751 x RD 2508, DWRB 137 x RD 3005, and RD 2035 x F1 showed non-significant deviation from regression with higher mean than the population mean and regression coefficient close to unity (b$_i$=1) which indicates average stability and their suitability under various environments. As these twelve crosses BG 959 x RD 2508, DWRUB 64 x RD 2508, K 551 x RD 2508, RD 2552 x RD 2508, BG 959 x RD 3005, DWRUB 64 x RD 3005, PL 751 x RD 3005, RD 2552 x RD 3005, RD 2907 x RD 3005, PL 751 x F1, RD 2552 x F1 and RD 2660 x F1 had regression coefficient greater than unity (b$_i$>1) and non-significant deviation from regression with higher mean value than the population mean, it was determined that these crosses were suitable and showed below average stability for favorable environment. The nine crosses VLB 118 x RD 2508, RD 2035 x RD 2508, RD 2660 x RD 2508, RD 2907 x RD 2508, BG 105 x RD 3005, BG 105 x F1, BG 959 x F1, DWRUB 64 x F1 and DWRB 137 x F1 showed regression coefficient less than unity (b$_i$<1) and non-significant deviation from regression with higher mean performance than population mean which indicates above average stability and were appropriate for poor environmental conditions in terms of grain yield per plant. The present finding supported the results obtained by Pilania and Dhaka [11], Chand et al. [6], Kavitha et al. [7], Lodhi et al. [8], Yadav et al. [12], Baranda et al. [13], Kajla et al. [14] and Sharma et al. [9].

Table 1. Analysis of variance Eberhart and Russel [5]

Source of Variation	d.f.	MSS due to grain yield per plant
Genotypes	62	23.40**
Environment	2	1636.57**
E+(G x E)	126	9.40**
E (L)	1	1091.05**
G x E (L)	62	1.24**
Pool deviation	63	0.27
Pool error	372	0.31

*, ** Significant at 5% and 1% level, respectively*

Table 2. Stability parameters for grain yield per plant

S.No.	Genotype	Grain yield per plant (g)		
		μ_i	b_i	S^2d_i
Parents				
1.	RD 2508	15.66	0.72	-0.30
2.	RD 3005	12.23	0.96	-0.29
3.	F1(RD 2508 x RD 3005)	12.93	0.97	-0.01
4.	BG 105	14.97	0.56	-0.26
5.	BG 959	15.13	1.00	-0.21
6.	DWRUB 64	16.13	0.73	-0.11
7.	DWRB 137	14.50	0.66	0.19
8.	HUB 113	11.86	1.14	-0.28
9.	JB 110	11.77	0.98	0.11
10.	K 551	10.69	1.03	0.49
11.	NDB 1445	9.10	0.80	0.31
12.	PL 751	16.08	1.41	0.45
13.	VLB 118	10.22	0.72	-0.28
14.	RD 2035	11.30	0.38	-0.24
15.	RD 2052	9.59	0.33	0.24
16.	RD 2552	14.34	1.30	-0.25
17.	RD 2660	9.82	0.62	0.21
18.	RD 2907	10.84	0.86	-0.11
Crosses				
19.	BG 105 x RD 2508	19.93	1.03	0.37
20.	BG 959 x RD 2508	16.58	1.37	0.47
21.	DWRUB 64 x RD 2508	22.50	1.06	-0.16
22.	DWRB 137 x RD 2508	14.68	0.73	-0.29
23.	HUB 113 x RD 2508	14.37	1.19	-0.30
24.	JB 110 x RD 2508	14.57	0.54	0.90*
25.	K 551 x RD 2508	15.16	1.13	-0.27
26.	NDB 1445 x RD 2508	13.59	1.04	0.34
27.	PL 751 x RD 2508	19.79	1.05	-0.28
28.	VLB 118 x RD 2508	14.99	0.82	-0.19
29.	RD 2035 x RD 2508	19.22	0.58	-0.31
30.	RD 2052 x RD 2508	17.41	0.56	1.00*
31.	RD 2552 x RD 2508	20.66	1.12	-0.18
32.	RD 2660 x RD 2508	15.37	0.86	-0.15
33.	RD 2907 x RD 2508	15.10	0.91	-0.28
34.	BG 105 x RD 3005	15.36	0.73	-0.24
35.	BG 959 x RD 3005	17.33	1.23	-0.19
36.	DWRUB 64 x RD 3005	16.91	1.07	-0.31
37.	DWRB 137 x RD 3005	15.04	1.03	-0.02
38.	HUB 113 x RD 3005	13.70	1.03	-0.31
39.	JB 110 x RD 3005	13.87	1.16	0.29
40.	K 551 x RD 3005	12.89	1.06	-0.30
41.	NDB 1445 x RD 3005	12.05	1.15	0.21
42.	PL 751 x RD 3005	15.83	1.35	0.53
43.	VLB 118 x RD 3005	12.69	1.16	-0.27
44.	RD 2035 x RD 3005	13.48	1.03	-0.30
45.	RD 2052 x RD 3005	13.02	1.35	-0.28
46.	RD 2552 x RD 3005	16.00	1.37	-0.20
47.	RD 2660 x RD 3005	12.94	0.95	-0.29
48.	RD 2907 x RD 3005	15.07	1.18	-0.27
49.	BG 105 x F1	18.87	0.93	-0.30
50.	BG 959 x F1	16.59	0.75	0.40
51.	DWRUB 64 x F1	19.76	0.73	0.28

S.No.	Genotype	Grain yield per plant (g)		
		μ_i	b_i	S^2d_i
52.	DWRB 137 x F1	16.42	0.86	0.10
53.	HUB 113 x F1	14.20	1.21	-0.07
54.	JB 110 x F1	12.66	1.34	-0.29
55.	K 551 x F1	12.50	1.31	-0.25
56.	NDB 1445 x F1	12.64	1.12	0.27
57.	PL 751 x F1	16.80	1.46	-0.19
58.	VLB 118 x F1	12.63	1.17	-0.10
59.	RD 2035 x F1	16.38	0.98	-0.28
60.	RD 2052 x F1	13.03	1.45	0.08
61.	RD 2552 x F1	17.22	1.18	-0.25
62.	RD 2660 x F1	16.12	1.26	-0.23
63.	RD 2907 x F1	13.79	1.25	-0.21
Mean		14.71		

*,** and +, ++ significantly deviating from 0 and 1 at 5% and 1% respectively

4. CONCLUSION

Out of 63 genotypes, only one parent BG 959 and four crosses BG 105 x RD 2508, PL 751 x RD 2508, DWRB 137 x RD 3005, and RD 2035 x F1 exhibited non-significant deviation from regression with higher mean than the population mean and regression coefficient close to unity ($b_i=1$) in term of grain yield per plant. Therefore, compared to other stable genotypes; these genotypes can be said to be the most stable grain yield per plant and adapted to all environments. As a result, it might be included in the hybridization program to converge the grain yield stability characteristics with the purpose of producing stable cultivars that are ideal for various environmental conditions.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

ACKNOWLEDGEMENTS

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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Peer-review history:
The peer review history for this paper can be accessed here:
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