



G × E models for yield adaptation and target environment analysis in barley (*Hordeum vulgare*)

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ABSTRACT

The present study was conducted to find out the best stability models out of methods, viz. Eberhart and Russell regression (ER model), yield stability index (YSI), AMMI, unscaled GGE and heritability adjusted GGE (HA-GGE) with target environment delineation in multi-location barley yield trials conducted at 08 locations during *rabi*, 2016–17. The pooled analysis revealed significant mean squares and large variations were attributed by the location effect (56.38%) followed by G × E (21.06%) and genotypes (7.77%), respectively. The initial two PCs exhibited 30.14 and 20.51 % variations in HA- GGE, which was slightly lower for PC1 and was marginally higher for PC2 than unscaled GGE. The which won where and mean vs. stability of GGE biplots model were useful to judge crossover G × E and in selecting specifically adapted genotypes easily. The YSI concluded based on grain yield and stability value simultaneously, hence found reliable than AMMI stability value. The locations Pantnagar and Modipuram were discriminating for genotypic differences, while the environments Durgapura and Ludhiana were found representative and discriminative for future barley yield trials. The genotype DWRB160 and two-row malt barley checks DWRB123 and RD2849 were found consistent and promising. Therefore, we suggest applying HA-GGE in coordinated barley yield trials to identify representative locations and thereby curtailing evaluation cost.

Key words: ER regression, G × E, HA-GGE, Unscaled GGE, YSI

The performance of a genotype in multi-location trials is unpredictable and even response may be at lower rank of a superior genotype over a wide range of environments (Comstock and Moll 1963, Lins *et al.* 1986). This inconsistent performance and differential response warranted plant breeders to study buffering capacity and adaptability of genotypes by any quick, relevant and easy statistical method (Kumar *et al.* 2018). Therefore, a genotype with well buffering capacity and capability of dynamic stability is required for yield maximization and wider acceptance (Becker and Leon 1988).

Genotype by environment interactions (G × E) result change in relative ranking of genotypes across varying locations, increase differences between genetic and phenotypic values, affect selection efficiency and often mislead plant breeders in breeding process (Kumar *et al.*

2018). Allard and Bradshaw 1964 classified environmental variation into predictable and unpredictable parts and reported that even the stratification of environments is not enough to deal with G × E. Therefore, G × E needs to be studied by any robust method like regression based Eberhart Russell model (1966) (ER model), multivariate graphical additive main effect and multiplicative interaction-AMMI (Zobel *et al.* 1988, Gauch *et al.* 2008) and genotype + G × E--GGE (Yan *et al.* 2000, Yan and Tinker 2006) biplot models. Rank based non-parametric stability models were also proposed and similarly, Kang (1988) elaborated non-parametric and rank based yield stability index (YSI) for the selection of consistent and high yielding genotypes. In addition to genotypic stability, breeders are also interested in selecting specifically adapted genotypes and finding information for discriminating and representativeness test environments. The AMMI and GGE biplot models are such graphical approaches and provide insight to evaluate target environments and general and specific consistent genotypes in turn helpful to drop out redundant environments without losing much information and saving resources.

Both the above biplot models have been extensively used in G × E analysis and well elaborated in Gauch (2006), Yan *et al.* (2007), Gauch *et al.* (2008). The use of GGE biplots has been also extended for diallel analysis,

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host pathogen interaction, microarray data and QTL by environment analysis (Yan and Hunt 2002, Shahriari *et al.* 2018). For the elimination of heterogeneity among environments by giving weight to the environments proportional to their heritability ($\sqrt{H}$) GGE biplots have been further modified and evolved to heritability adjusted (HA-GGE) biplots (Yan and Holland 2010). Therefore, we applied widely accepted ER model, YSI, AMMI, unscaled GGE and HA-GGE methods for cultivar evaluation and test environment analysis in multi-location barley yield trials to see the best method available.

MATERIALS AND METHODS

To perform $G \times E$ analysis using different stability models, viz. ER model, YSI, AMMI, GGE and HA-GGE, multi-location yield trials were conducted at 8 hi-input locations of north western plains zone (NWPZ) during *rabi*, 2016–17. The multi-location yield trials were conducted at Bawal (E1), Durgapura (E2), Hisar (E3), Ludhiana (E4), Bathinda (E5), Pantnagar (E6), Karnal (E7) and Modipuram (E8). The experimental materials comprised 20 barley genotypes, viz. BH1017 (G1), BH1018 (G2), DWRB136 (G3), DWRB160 (G4), DWRB161 (G5), DWRB162 (G6), KB1523 (G7), KB1535 (G8), PL895 (G9), PL896 (G10), PL899 (G11), RD2962 (G12), RD2963 (G13), RD2964 (G14), RD2965 (G15), UPB1065 (G16), DWRUB52 (G17), DWRB101 (G18), DWRB123 (G19) and RD2849 (G20). Out of the above experimental materials, the four genotypes, viz. G17, G18, G19 and G20 were commercial cultivars and rest of the lines were advanced fixed pure lines. The multi-location yield trials were conducted in randomized complete block design (RCBD) of four replicates in 6-row plots with 5 m row length and spaced 18 cm apart in each environment. Standard agronomic package and practices were followed to raise the good barley crop. The combined analysis of variance, YSI and all the biplots of AMMI1, AMMI2, unscaled GGE and HA-GGE were computed and constructed using R 3.4.3.

In GGE biplots the cosine angle between two environments described relationship between them and acute angles indicated positive relationship. The vector length described the discriminating ability in GGE biplots. The data were not transformed (“Transformation=0”), not scaled (“Scaling=0”) environment centred (“Centring=2”) and environment-focused (“SVP=2”) to obtain polygon view and test environment evaluation in GGE, while genotype focused (SVP=1) biplots were considered for mean vs. stability view, respectively. In AMMI1 and AMMI2 biplots the genotypes with low interaction effects and located at biplot origin were desirable, whereas the environments with long vectors were representative. Gauch (2006) summarized the equations of GGE (1) and AMMI (2) biplot models as presented below.

$$(Y_{ger} - \beta_e)/s_j = \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger} \quad (1)$$

$$Y_{ger} - \alpha_g - \beta_e + \mu = \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger} \quad (2)$$

where, Y_{ger} is the yield of genotype (g) in environment

(e) for replicate r , μ is the grand mean, α_g denotes genotype deviation, β_e represents environment deviation, λ_n is singular value for component n , γ_{gn} is the eigenvector value for g , δ_{en} is the eigen vector value for e , the residual is ρ_{ge} and ε_{ger} is the error for genotype g , environment e and replicate r . Here s_j is scaling factor and $s_j=1$ in unscaled GGE biplots. In heritability adjusted (HA-GGE) biplot model (3a and 3b) the scaling factor (s_j) was used as follows:

$$s_j = SD/\sqrt{H} \quad (3a)$$

$$(Y_{ger} - \beta_e)/(SD/\sqrt{H}) = \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger} \quad (3b)$$

AMMI stability value (ASV): AMMI stability value (ASV) were obtained from R software version 3.4.3 and formulae for the ASV was (Abakemal *et al.* 2016).

$$ASV = \sqrt{[(SSIPCA1/SSIPCA2)(IPCA1)]^2 + (IPCA2)^2} \quad (4)$$

Here in equation (4), SSIPCA1 and SSIPCA2 are sum of squares of principal components (PC) 1 and 2, respectively and IPCA1 and IPCA2 denotes the genotype scores in the AMMI biplot. A genotype with the low ASV was regarded consistent and adaptable.

Yield stability index (YSI): Yield stability index was calculated (5) as sum of overall yield (R_y) ranks and AMMI stability value (RASV) rank and a genotype with low YSI was considered desirable (Kumar *et al.* 2018).

$$YSI = RASV + R_y \quad (5)$$

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) revealed significant genotype mean squares across the locations in the individual site analysis (Table 1). The highest average grain yield was exhibited at Durgapura (61.20 q/ha) followed by Ludhiana (52.30 q/ha) and Bathinda (46.10 q/ha), whereas the mean site grain yield for 08 locations was estimated 45.90 q/ha. The genotype DWRB160 (G4) was highly responsive and showed significantly superior mean grain yield to the best two-row malt barley check DWRB123 (48.45 q/ha) and the genotype DWRB136 (49.39 q/ha) was numerically higher to the above best check.

The combined analysis of variance revealed significant $G \times E$ mean squares and the maximum variations were attributed by the location effect (56.38%) followed by $G \times E$ (21.06 %) and genotypes (7.77 %), respectively (Table 2). The large variations accounted by $G \times E$ and locations indicated possibility of different mega environments with in the locations, crossover $G \times E$ and differential buffering capacity of the genotypes. Yan and Hunt (2002), Abakemal *et al.* (2017) also reported high proportions for location and $G \times E$ variations and proposed possibilities of mega environments with in locations and delineated need to identify location specific genotypes. These possibilities were further substantiated in unscaled GGE, HA-GGE and AMMI2 biplots, where eight environments were categorised into 03 mega environments. This finding emphasized to review the coordinated varietal release zonation in NWPZ due to the possibilities of different mega environments. Thus,

Table 1 Location-wise analysis of variance and statistical parameters in barley

Parameter	Location							
	Bawal	Durgapura	Hisar	Ludhiana	Bathinda	Pantnagar	Karnal	Modipuram
Genotype (g)	20	20	20	20	20	20	20	20
Replication (r)	4	4	4	4	4	4	4	4
σ^2_g	31.51**	49.48**	14.06**	44.14**	23.66**	27.49**	38.91**	18.73**
σ^2_e	23.97	27.43	10.27	32.70	33.30	13.81	13.78	20.43
σ^2_p	55.48	76.91	24.33	76.85	56.96	41.31	52.69	39.16
μ =Mean (q/ha)	49.00	61.20	36.50	52.30	46.10	43.60	33.10	45.40
SE	4.90	5.24	3.20	5.72	5.77	3.72	3.71	4.52
SE _(m)	2.45	2.62	1.60	2.86	2.89	1.86	1.86	2.26
SD	7.45	8.77	4.93	8.77	7.55	6.43	7.26	6.26
CV (%)	9.99	8.56	8.78	10.93	12.52	8.52	11.21	9.95
H=1-(SE/SD) ² /r	0.89	0.91	0.89	0.89	0.85	0.92	0.93	0.87

modification in the existing zonation system may lead into the release of more fruitful niche specific climate resilient genotypes for grain yield maximization.

Eberhart and Russell model: The $E + G \times E$ mean squares were further partitioned into environment (linear), $G \times E$ (linear) and pooled deviation effects and all of these effects indicated to further study regression and deviation from the regression components. In this direction, the genotype DWRB 160 (G4) was most stable across the locations ($\mu=53.31$ q/ha, $bi=0.87$ and $S^2di=1.01$) followed by DWRB 136 (G3: $\mu=49.40$ q/ha, $bi=0.85$ and $S^2di=15.59$), DWRB 123 (G19: $\mu=48.45$ q/ha, $bi=0.90$ and $S^2di=18.93$) and DWRB 162 (G6: $\mu=47.25$ q/ha, $bi=1.05$ and $S^2di=4.60$) etc. The genotypes BH1018 and checks DWRB101, DWRUB52 and RD2849 depicted higher grain yield, regression coefficient more than unity and non-significant deviations from the regression and may be recommended for favourable environments. Further, the genotype RD2964 (G14) was observed with significant deviations from the regression and regarded as inconsistent, less responsive and undesirable. As the limitation, the ER regression model could not be ascertained information on mega environments, environmental relationship and genotype specific adaptability and these aspects were further studied by widely popular multivariate stability models.

Additive main effects and multiplicative interactions (AMMI) analysis: In AMMI analysis the genotype by environment interactions were partitioned into principal

components (PCs) and initial three PCs showed 26.65 %, 21.14 % and 17.94 % variations, respectively. The initial three PCs were plotted in triangular view to evaluate real picture of interactions and the locations Ludhiana, Durgapura, Pantnagar and Bathinda were observed with differential response than rest of the locations. The main effects and interactions were further refined in AMMI1 biplot by depicting grain yield on abscissa with PC1 on the ordinate to identify adaptable cultivars (Fig 1). The AMMI1 biplot revealed that the genotype G4 (DWRB160) was the most promising followed by the genotypes namely G3 (DWRB136), G6 (DWRB162), G9 (PL895) and G17 (DWRUB52), G19 (DWRB123) and G20 (RD2849), respectively. The AMMI2 biplot between PC1 and PC2 revealed that the locations Ludhiana and Durgapura were responsive with high PC1 and PC2 scores. The locations Bawal, Hisar and Karnal were grouped together, whereas the locations Modipuram and Bathinda shared same sector.

To substantiate AMMI analysis the ASV and YSI were also computed. Based on ASV and YSI, the genotypes namely DWRB160 (G4: 0.32 & 2), DWRB136 (G3: 1.30 & 12), DWRB162 (G6: 0.97 & 11), DWRUB52 (G17: 1.05 & 13) and DWRB123 (G19: 1.19 & 10), respectively were found adaptable and high yielding across different environments. Conversely, the genotypes, viz. RD2964 (G14), RD2965 (G15) and UPB1065 (G16) were inconsistent and poor yielding at different locations.

Unscaled-GGE biplot analysis: GGE biplot is one of

Table 2 Pooled analysis of variance and principal components of AMMI

Source	DF	SS	MS	F	Pr(>F)	%SS
Rep (environ.)	24	1365	56.9	2.59	<0.001	1.77
Environment	7	43381	6197.3**	108.96	<0.001	56.38
Genotype	19	5979	314.7**	2.58	<0.001	7.77
Genotype $\times$ Environ.	133	16207	121.9**	5.55	<0.001	21.06
PC1	25	4319.16	172.77**	7.85	<0.001	26.65
PC2	23	3426.16	148.96**	6.77	<0.001	21.14
PC3	21	2907.53	138.45**	6.29	<0.001	17.94
Residuals	64	5554.15	86.78**	3.94	<0.001	34.27
Error	456	10014.01	21.96	-	-	-

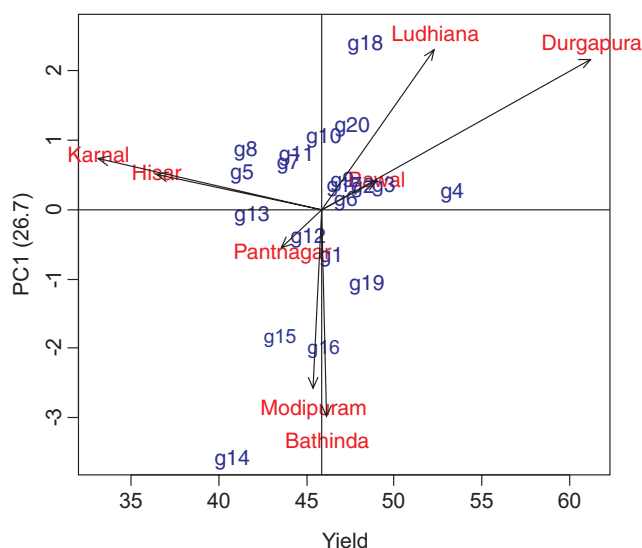


Fig 1 AMMI1 biplot for main effect and PC1.

the popular multiplicative models to identify stable and adaptable genotypes with explanation of “which won where” pattern and to select discriminating and representative environments. Here, initial two PCs showed 33.71% and 17.8 % of variations, respectively. The eight locations were grouped into three sectors and the locations Bawal, Hisar and Karnal were found similar and the environments Durgapura and Ludhiana were portrayed into same sector. The locations Bathinda and Modipuram were found similar, whereas Pantnagar revealed different niche from rest of the environments. The genotypes BH1018 (G2), DWRB160 (G4), KB1535 (G8), RD2964 (G14), UPB1065 (G16) and DWRB101 (G18) were observed as vertex genotypes on the equality lines. The genotypes G16 (UPB1065) was favourable for Bathinda (E5) and Modipuram (E8), while the genotypes G7 (KB1523), G9 (PL895) and G11 (PL899) performed better at Pantnagar (E6) location. In average environment coordination view the genotype DWRB160 (G4) was high yielding and most stable followed by the genotypes BH1018 (G2), DWRB136 (G3), DWRB162 (G6) and check cultivars, viz. DWRUB52 (G17), DWRB123 (G19) and RD2849 (G20), respectively. Contrary, the genotypes RD2964 (G14) and UPB1065 (G16) were less stable, lower adaptable and inconsistent performers. Based on vector length and cosine angles the locations Durgapura (E2) and Ludhiana (E4) were most discriminating and representative for genotype evaluation over the years.

HA-GGE analysis: Yan and Holland 2010 reported that the HA-GGE biplots are more suitable to judge the environmental relationship than unscaled GGE, when heritability estimates and error variances are heterogeneous across the environments. Here, the initial two PCs exhibited 30.14 and 20.51 % variations of the total variations, which was slightly lower for PC1 and marginally higher for PC2 than unscaled GGE (Fig 2). The genotypes namely G2 (BH1018), G4 (DWRB160), G6 (DWRB162), G9 (PL895) and G14 (RD2964) were selected form polygon as vertex genotypes. In AEC view of biplots obtained for mean

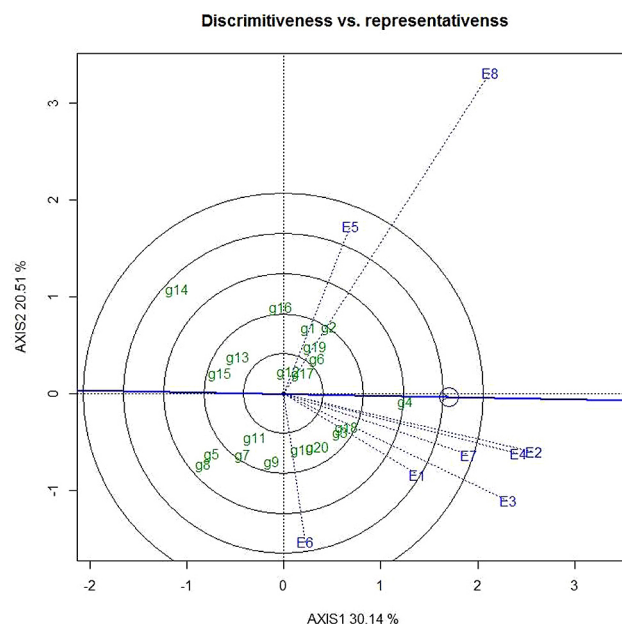


Fig 2 Heritability adjusted GGE biplot for test sites evaluation.

vs. stability, the genotype G4 (DWRB160) was on the extreme right with high mean grain yield and showed less deviation on AEC ordinate followed by G18 (DWRB101), G3 (DWRB136) and G20 (RD2849). The environmental relationship was quite clear in HA-GGE biplots than unscaled GGE and the environment Durgapura was most discriminating and representative followed by Ludhiana, Hisar and Karnal. The locations Pantnagar and Modipuram were discriminating for genotypic differences but could not be regarded representative due to obtuse angles with target environment axis.

Pragmatically, all the biplots namely AMMI2, unscaled GGE and HAGGE provided similar information for mega environment categorization, where the locations Bawal (E1), Durgapura (E2), Hisar (E3), Ludhiana (E4) and Karnal (E7) were found correlated and the location Pantnagar (E6) revealed separate environment. However, the information of similar kind was obtained from AMMI2 and GGE biplots but “which won where” polygons with intersecting lines in GGE biplots were easy and quick to judge mega environments. Yan *et al.* (2000) reported similar findings and elaborated that the “which won where” is a unique property of the GGE model in which an irregular shaped polygon is drawn and lines originating from the biplot origin intersect it and divide into mega environments (Akinwale *et al.* 2014). Yan and Tinker (2006) also mentioned that “which won where” option is an intrinsic property of the GGE biplot rendered by the inner product property and helpful in analysing crossover $G \times E$ and location specific genotypes.

Yan and Holland (2010) reported that different kind of GGE biplots can be generated by scaling based on standard deviation (SD), standard error (SE) and heritability (H) parameters prior to the singular value decomposition (SVD). They further described that two parameters, i.e. heritability in each environment (H) and its genetic correlation (r)

with test environment should be taken under consideration during test environment evaluation (Krishnamurthy *et al.* 2017). In our study we experienced that the heritability adjusted HA-GGE biplot was most suitable to judge target environment and to see environmental discriminating power and representativeness. In the unscaled GGE biplot the locations E1, E3 and E7 were clubbed nearby and vector lengths were not easy to manifest discriminating power. HA-GGE biplots are good approximation for test environment evaluation, where vector length proportionate square root heritability and angles between test and target environments describes genetic correlations (Yan and Holland 2010, Akinwale *et al.* 2014). The HA-GGE biplots visualized environmental relationship emphatically and the locations, viz. Bawal, Bathinda and Karnal were found redundant and may be dropped without losing much information after validation over two-three years to save resources. The test environment evaluation was not possible with conventional ER model and even not better portrayed in unscaled GGE but we found HA-GGE as better methodology for saving resources.

In accordance to the concept of dynamic stability the genotype DWRB160 was responsive and promising across the locations (Becker and Leon 1988) The ER model was most popular regression based approach but its assumption of linear response of genotypes to environments and inability of environmental delineation makes it cumbersome than the visual graphical multivariate models. While considering AMMI1 and GGE biplots the Average Environment Coordinate (AEC) view with projected ordinates scores depicted GGE biplots favourable in selecting high yielding and consistent genotypes. An ideal genotype delineates high AEC abscissa scores which are directly proportional to the main genotype effect and has low AEC ordinate scores representing stability or less deviation for G x E interactions in GGE biplot (Yan 2001, Yan *et al.* 2007, Kumar *et al.* 2016). Moreover, the Yield Stability Index (YSI) in consensus of AMMI Stability Value (ASV) was more helpful in identifying consistent genotypes coupled with high mean grain yield. Here, after considering application of different stability models the HA-GGE model was found easy for genotypic selection and mega environment delineation.

In conclusion, the GGE biplots were more easy, quick and informative for which won where and mean vs. stability view. Further, the HA-GGE biplot was most useful in identifying discriminating and representative environments. In light of the above findings the genotype DWRB160 and environments Durgapura and Ludhiana were found promising in barley. Here, we suggest applying HA-GGE in the AICRP system to identify representative locations and further cost effective evaluation in future.

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