Research Article

Ekin
Journal of Crop Breeding and Genetics

8(1):41-52, 2022

www.ekinjournal.com

Ekin International biannual peer-reviewed journal

Deciphering Genotype×Environment Interaction by AMMI and GGE Biplot Analysis Among Elite Wheat (*Triticum aestivum* L.) Genotypes of Himalayan Region

Adil NAIK[1] Shabir Hussain WANI[2*] Sumira RAFIQEE[1] Mehrajuddin SOFI[2]

Najeebul Rehman SOFI[2] Asif Bashir SHIKARI[2] Ashaq HUSSAIN[2] Fayaz MOHIDDIN[2]

Intikhab Aalum JEHANGIR[2] Gazala Hassan KHAN[2] Muneer Ahmed SOFI[2] Farooq Ahmed SHEIKH[1]

Mohammad Ashraf BHAT[1] Mohammad Nisar KHAN[1] Zahoor Ahmed DAR[3] Mehdi RAHIMI[4]

[1] Division of Genetics and Plant Breeding, Faculty of Agriculture Wadoora, Sopore, Skuast-Kashmir
[2] Mountain Research Centre for Field Crops, Khudwani, Anantnag-192 101, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, J and K, India
[3] Dryland Agricultural Research Station, Rangreth, SKUAST-Kashmir
[4] Department of Biotechnology, Institute of Science and High Technology and Environmental Sciences, Graduate University of Advanced Technology, Kerman, Iran

[*] Corresponding author e-mail: shabirhussainwani@gmail.com

Citation:
Naik A., Wani SH., Rafiqee S., Sofi M., Sofi NR., Shikari AB., Hussain A., Mohiddin F., Jehangir IA., Khan GH., Sofi MA., Sheikh FA., Bhat MA., Khan MN., Dar ZA., Rahimi M., 2022. Deciphering genotype×Environment Interaction by AMMI and GGE Biplot Analysis Among Elite Wheat (*Triticum aestivum* L.) Genotypes of Himalayan Region. Ekin J. 8(1):41-52.

Received: 03.10.2021 ***Accepted: 10.11.2021*** ***Published Online: 30.01.2022*** ***Printed: 31.01.2022***

ABSTRACT

To determine yield stability and the effects of the interaction between the genotype and the environment, 101 wheat genotypes were assessed over 2 years (2018-2020). The experiments were performed at different diverse locations in Kashmir traversing a significant altitudinal range viz. Khudwani (34.38°N of latitude and 77.0°E of longitude) and Wadura (34.52°N of latitude and 74.52°E of longitude) following recommended agronomical practices. Analysis of the main additive effect and multiplicative interaction (AMMI) of the seed yield variance revealed a significant genotype, environmental and genotype × environment interaction effect at p< 0.01% probability level. Three main principal components based on AMMI explained most of the variation due to genotype × environment interaction at p<0.01% probability level. The GGE biplot indicated that two mega-environments were present. The first section (large environment) contains the KH18 and WA18 test environments with genotypes G2, G38, and G16 with the highest yield (winner), the second section (large environment) contains KH19 and genotypes G28, G19 and G3, KH19 and WA18 WA19 environment included. as a winner. Plots of mean versus stability show that the genotypes exhibiting both high mean yield and stability scores at the test sites are G2, G50, G26, G80, and G1. Hence, the above identified genotypes with superior yield and other desirable attributes can be recommended as generally adapted or niche specific genotypes for broad and specific areas, respectively.

***Keywords*:** Wheat germplasm, biplot, wheat yield stability, principal component, wheat screening

Introduction

Bread-making wheat (*Triticum aestivum*, L.) is a major cereal grown throughout the world as a basic food. In India, wheat is the second largest grain crop and the primary food crop in the north and northwest of the country. The crop is grown on 30.5 million hectares and yields an average of 3.51 tons per hectare (FAO 2021). The most important wheat-producing states are Punjab, Haryana, Utter Pradesh, Rajasthan and Madhya Pradesh. Global population in general and Indian population in specific has been increasing at an exponential rate which proportionally increases demand for food supply on daily basis. New benchmarks for food requirement are set as challenges for plant breeders across the globe to

enhance the sustainable food production for nutritional security. It is mandatory to explore interventions of vertical expansion rather than horizontal under scarce availability of land and other resources. Therefore, it is imperative to improve upon the productivity potential of the existing wheat germplasm using tools of crop improvement. The existence of genetic variability is pre-requisite for any successful breeding program (Kant et al. 2011). Therefore, before planning of any breeding program the variability parameters like coefficient of variation (COV), genotypic variation, critical difference, heritability and correlation is important to get efficient results (Abebe et al. 2017). There is significant level of genetic variability among various ecotypes of wheat in the existing regional and global wheat biodiversity and act as an important source of elite ness and disease resistance for breeding novel wheat varieties. It has been ascertained that novelty of eliteness or superior performance either gets masked up or performs poorly across diverse niche environments. This differentiated behavior of crop varieties in ecoregions is due to the interaction of genotype × environment, as reported for environmental-induced yields and other phenotypic traits (Ajay et al. 2018) and other biotic and abiotic factors. It is mainly due to gene × environment interaction that complicates the selection process for targeted trait due to change in response under varied environmental conditions affecting selection accuracy. The improvement is also limited due to the complex nature of trait (yield) being regulated by many genes (Sallam et al. 2019). For such conditions, stability analysis facilitates the best possible solution to assess the relative performance of genotypes with respect to specific and broad environmental evaluation (Kant et al. 2014). Large scale testing across multiple sites helps in delineating major mega-environments. Various statistical parameters were developed and used for efficiency in estimating the stability index of genotypes across environments, such as, coefficient of determination (Ri^2), regression coefficient (bi), coefficient of variability, deviation due to regression (S^2_{di}) linear regression, and pooled analysis of variance across the environments. Additive Main Effect and Multiplicative Interaction (AMMI) model and two-step GGE analysis have been observed and reported to accurately capture the majority of sum-of-squares interactions, isolate major and interacting components, and facilitate visualization of genotypic fitness in various environments (Shashikumara et al. 2020). The AMMI model mainly consists of the additive main effects of genotype and environment and the multiplier effect of the genotype × environment interaction, so it can obtain more information than other methods. It can also be viewed as a combination of ANOVA and principal component analysis (Ebdon and Gauch, 2002) and describes the genotype ×environment interaction in more than one dimension (Yan and Kang, 2003). The AMMI stability parameters allow examining yield stability after reduction of the noise from GE interaction effect (Ajay et al. 2020). This model interprets genotype × environmental interactions in terms of external environmental factors and genotypic variables in common wheat. Here, multi-media testing (MET) data can be used to predict phenotypic responses in an uncontrolled environment using explicit environmental information (Mohammadi et al. 2020). AMMI method has been used in several studies to select stable bread wheat cultivars (Katsenios et al. 2021; Ljubičić et al. 2021; Verma and Singh 2021a, 2021b). The present investigation was undertaken to explore available wheat diversity for genetic variability for yield superiority and other important attributing factors. To evaluate the stability of genotypes in different environments, experimental experiments were performed at multiple sites to identify a wide range of specifically suitable wheat germplasm. Good and stable genotypes were identified by evaluating yield and variation due to genotype, environment, and HE interactions for yield determinants.

Materials and Methods

Experimental wheat trials were conducted during the year 2018-19 and repeated in 2019-20 i.e. two years at two locations constituting four (4) environments. The evaluation of these experimental wheat genotypes was carried out during the Rabi season of these respective year at Mountain Research Centre for Field Crops (MRCFC) Khudwani (Anantnag- South Kashmir) and Research field of Division of Genetics and Plant Breeding, Faculty of Agriculture (FOA), Wadura, Sopore (North Kashmir). The experimental material comprised of 101 genotypes collected from CIMMYT, ICAR-IIWBR Karnal exotic nurseries and four check varieties Shalimar Wheat1, Shalimar Wheat 2, HS-562, VL 907. (Table 1.) Field trials were presented in a randomized block design (RCBD), each repeated twice over two years. Each genotype was represented by a plot size of 1×1 m with six rows. The row-to-row spacing kept at each block is 20 cm. Data was recorded from all the genotypes in each replication for yield and associated morphological traits. Observe to determine characteristics such as plant height (cm), days to maturity, number of tillers per meter, spike length (cm), number of spikelet's per spike, grains per spike, thousand grain weight, and yield per plot.

Statistical analyses

We calculated G × E interactions using the AMMI method. An integrated analysis of variance was performed and the mean was used as the basis for the AMMI analysis. The basis of the AMMI mathematical formula was as follows:

$$y_{ij} = \mu + g_i + e_j + \sum_{k}^{N} = 1\ \lambda_k Y_{ik} \alpha_{jk} + \varepsilon_{ij}$$

where y_{ij} is the yield of the i-th genotype in the j-th environment, N is the number of major components of the AMMI model, μ is the total mean value of the genotype, g_i and e_j are the overall mean value of the deviation between the genotype and the environment, λ_k is the k-axis eigenvalue of the PCA, Y_{ik} and α_{jk} are the estimates of principal components of the genotype and environment on the k-axis, and ε_{ij} is the remainder.

AMMI analysis results were interpreted based on two AMMI analysis plots. The first type of diagram was constructed based on the values of the first principal component, genotype, and mean overall fields for the environment, while the second type of diagram was constructed based on the values of the first and second principal components.

ANOVA pooled analysis and AMMI stability analyzes were performed using R package 'ammistability' (Ajay et al. 2018). The ranking of genotypes was based on the co-selection index for yield and stability (SSI).

The graphical analysis was carried out using the GGE biplot methodology (Yan, 2001; Yan and Kang, 2003) according to Equation below:

$$Yij - = \lambda 1 \xi i1 \eta j1 + \lambda 2 \xi i2 \eta j2 + \varepsilon ij$$

Yij: Mean yield of genotype i in medium j, $\overline{Y_j}$: Average yield of all genotypes in medium j, λ1 and λ2: Characteristic value for PC1 and PC2 (equivalent respectively), ξi1 and ξi2: scores PC1 and PC2 (respectively) for genotype i, ηj1 and ηj2: scores PC1 and PC2 (respectively) for environment j, εij are the remaining phenotypes of genotype i in environment j. GGE biplot analysis was carried out by using R package 'GGEBiplotGUI' (Frutos et al. 2014).

Results and Discussion

Combined Variance Analysis

The observed data for all the phenotypic traits recorded at different locations and over the years was processed for combined analysis of variance (ANOVA) and it was revealed that there were significant variations due to the interaction of environment, genotype and genotype × environment ($p < 0.01$) for plant height, spike length, spikelets per spike, grains per spike and grain yield (Table 2.)

The genotypes exhibited significant level of genotype by environment interaction (GEI), which is attributed to differential adaptation of diverse genotypes across the locations and years. The total variation exhibited by the genotypes with respect to measured traits was partitioned into variation due to genotypes (G), environment(E) and genotype x environment (GxE) interaction. The major proportion of variation was explained by genotypes for different traits as depicted in Table 2. Spikelet's per spike explained 54.92% of total sum of squares. Likewise, grains per spike and plant height also explained 52.11%) and 51.11% of total sum of squares, respectively. This implicates that maximum variation in studied traits is due to genotypic difference. However, significant quantum of phenotypic variation was observed from environments and GEI. This also signifies the role of both genotype and environmental factors. The observed data was also analyzed for AMMI effects and also visualized using GGE biplot analysis with an objective to identify desirable genotypes over environments based on their stability and higher mean yield. The current findings of this investigation are consistent with previous findings (Mwadzingeni et al. 2017).

Correlation

Genotypic and phenotypic correlation for 8 studied traits

Improvement of grain yield is a major objective of major wheat breeding programmes and also in other crops as reported in multiple studies. However, to improve yield its direct selection for yield trait is not an effective means (Kumar et al. 2016 and Nagar et al. 2018). Indirect selection for highly contributing traits to yield is more effectives in improving novelty of the developed/identified wheat genotypes. Correlated response of yield for indirect selection of effective attributing trait is mainly driven by the level of significant correlation between yield and yield component traits. The critical assessment of results demonstrated a positive and very significant correlation of yield (g/plot), with plant height, tillers per meter, spikelet's per spike, grains per spike and thousand grain weight. (Fig 1). Yield revealed a negative and highly significant correlation with maturity, these findings validate the earlier observations reported from other diverse studies (Baranwal et al. 2012, Nagar. et al. 2018 and Mansouri et al. 2018).

Yield AMMI analysis

Additive analysis of main effects and multiplicative interactions (AMMI) is an effective statistical method for analyzing proportional variation due to genotype-environmental interactions (GEI) as a

major component of the interaction between genotype-dependent variation in grain yield and environmental factors (Rad et al. 2013). This GEI significantly affects the attainment of genetic advance from phenotypic selection due to differential response of genotypes under the target test or productive environments (Mwadzingeni et al. 2017). AMMI analysis revealed that the grain yield is significantly affected by the genotype, environment, and GE interactions and explained 46.65%, 7.83% and 23.58% of variation, respectively. AMMI principal component I and II cumulatively explained 83.8% of genotype x environment variation (Table 3).

All the three interaction principal components (IPCA's) were significant at ($p< 0.01$), among which first IPCA captured 52.8% of interaction sum of square, second 31% and third one contributed 16.2% of interaction sum of squares.

The significant proportion of GEI assures the estimation of phenotypic stability of genotypes over environment (Ajay et al. 2020). A significant proportion of variation (sum of squares) was exhibited due to genotypes diverse nature of genotypes, with respect contrasting features among yield and yield attributing traits. GEI was identified as another significant factor along with environmental variation that attributes differential performance of genotypes for grain and other related traits across the environments.

Based on mean performance in grain yield and AMMI analysis, 10 best selections in terms of their relative performance across the environments were compared and few genotypes were identified that performed better in more than one tested environment as depicted in Table 4. G80 and G33 were best performers across 3 environments (except one) followed by G7, G20, G23, G2, G28, G31, G-19 and G34. The two-way data on grain yield from top performing genotypes and other wheat varieties was used to perform stability analysis using GGE biplot visualization method to precisely identify specific and broadly adapted stable wheat genotypes across different environment.

GGE biplot analysis for grain yield of wheat

Yan et al. (2001) proposed a procedure known as GGE-biplot to graph GE models of interactions with test data in different environments (MET) with different advantages. Two GGE chart analyses consider the influence of genotype (G) and GE interactions and graphically display GE interactions in a two-sided table (Yan et al. 2000). It permits graphical scrutiny of the relationships among the test environments, genotypes and the GE interactions.

Due to the different conditions of the experimental environment, GGE biplot graphic method was used to study the cultivars and obtain more information about their reaction in these environments. Based on the results of this method, the sum of the first and second main components (PC1 = 92.53 and PC2 = 3.06) explained 95.59% of the variation, which means that these two components were able to 95.59% of the variation. Explain the variation related to grain yield, which indicates the high validity of the biplot diagram obtained from this study in explaining the changes in G + GE.

When the bipolar diagram explains at least 60% of the variance of the data, it can be used to determine large environments (Yang et al. 2009). The details of this method are explained below.

Polygon view (Which-Won-Where Pattern) of GGE biplot analysis for grain yield of MET data

Polygonal 2D plots are the best way to display the presence or absence of GE crosstalk by expressing the interaction patterns between genotype and environment (Yan and Kang, 2003). It provides an efficient and elegant visualization tool for which-won-where patterns in MET datasets useful for evaluating the existence of various mega-tools (Gauch and Zobel, 1997; Yan and Rajcan, 2002; Yan and Tinker, 2006). Fig. 2 represents the polygon view of wheat genotypes for grain yield data in this investigation. In this biplot, a polygon was drawn by joining the genotypes that are located away from the biplot origin, so that all other genotypes are enclosed within the polygon. A genotype located at the edge of a polygon is called a vertex genotype. Separating the GE interactions by GGE biplot analysis revealed that PC1 and PC2 accounted for 92.53% and 3.06% of the GGE sum of squares, respectively, explaining a total variance of 95.59%. The vertex genotypes are G-2, G-38, G-16, G-28, G-19, G-3, G-56, G-57 and G-67. They have the longest vector in each direction, which is a measure of their response to the environment. Therefore, the upper genotype belongs to the most sensitive breeds. All other genotypes are less sensitive in their respective directions. These genotypes were the best or worst genotypes in some or all environments because they were the most distant from the origin of the biplot (Yan and Kang, 2003). The genotypes located at the beginning of the biplane have the same grade in all environments and do not respond at all.

The perpendicular lines are drawn to each side of the polygon, these lines are called equality lines. These lines divide the genotypes and the environments into sections. The polygon view of biplot shows that the genotypes fell in seven sections and the test environments fell in two sections. The first section contains test environments KH18 and WA18 with genotypes G-2, G-38 and G-16 as the best yielder.

And the second section contains environments KH19 and WA19 with genotypes G-28, G-19 and G-3 as the winner. This cross over GE suggests that the target environments may be divided in to two mega-environments. No environments fell in the sections with G-56, G-57 and G-67 as vertex genotypes. This specifies that these genotypes were not the best in any of the test environments, reflecting the fact that they yielded poorly at each environment (Rahmatollah et al. 2013).

Mean and stability performances of genotypes

The productivity and stability of genotypes were evaluated by the average coordinates of the environment (AEC) method (Yang, 2001; Yang, Hunt, 2002; Yang, 2002). In this method, the average environment is determined by the average PC1 and PC2 scores for all environments indicated by the small circles (Figure 3). The line passing through the origin of the two graphs and the average environment is the axis of the average environment. This is the abscissa AEC. The projection of the genotype markers on this axis roughly coincides with the average yield of the genotype. Thus, genotypes are ranked on the AEC abscissa, with arrows indicating higher average performance. Genotype G-2was clearly the highest yielding genotype, on average, followed by G-28 and G-80, followed by G-21, G-50, G-19, G-1, G-26, G-38, G-42, G-58, G-20, G-10, G-41, G-4, G-23, etc.

The AEC ordinate is a line passing through the origin of the two plots and perpendicular to the AEC abscissa (Figure 3). The transverse AEC estimates G and the longitudinal AEC approximates the GEI associated with each genotype, which measures the variability or instability of the genotype. This means that large projections on the AEC ordinate, regardless of orientation, exhibit significant instability. Therefore, G16 at the top and G3 at the bottom of the 2D plot are more variable and less stable than the other genotypes. Other genotypes with above-average yields include: G-2, G-28, G-80 etc and the genotypes with yield less than mean yield include G-57, G-56, G-67 etc. The ideal genotype for breeding is a genotype with high average yield and high stability. It is close to the origin on the 2D plot and has the shortest vector in ATC. Genotypes with high yield and stability are G2, G50, G26, G80, and G1. In addition, genotypes with high yield but low stability are G28, G7, and G19, which are similar to genotypes with low yield and stability. Low stability was G57 and G56. Genotypes G2 (relatively high yield) and G60 (lowest yield) were parallel in the GE interaction.

Yan and Kang (2003) reported that based on the grain yield and stability performance, genotypes can be classified into three categories: (1) generally adapted, genotypes with high yield and stability performance (G-2, followed by, G-50, G-26, G-80, G-1 etc.) (2) specifically adapted, genotypes with high mean yield but low stability performance (G-28, G-7 and G-19) and (3) adapted nowhere, genotypes with low grain yield and low stability performance (G-57 and G-56).

Scientists can also use mean vs stability to select the genotypes with best response to specific environments. The genotype G-28 had the highest yielding performance in environment WA18, genotypes G-2 and G-1 performed well in the environments KH-18 and the genotypes G-7 and G-19 performed better in WA19, whereas G-28 was poor in environment WA19 and genotypes G-2 and G-1 had low yield performance in KH19.

Evaluation of genotypes relative to an ideal genotype

The ranking of genotypes according to "ideal" genotypes is shown in the graph (Figure 4). The small circle on the AEC abscissa where the arrow points indicate the ideal class. It is defined by two criteria. 1) It has the highest income among the entire data set. 2) Absolutely stable as indicated by the AEC abscissa. Since such an ideal genotype hardly exists in reality, it can be used as a reference for genotype evaluation (Mitrovic et al. 2012). The closer the genotype is to the "ideal" genotype, the more desirable (Kaya et al. 2006 and Mitrovic et al. 2012). The genotype closer to the "ideal" genotype on this graph is G2. Rank other genotypes by ideal genotype: G50> G1> G80> G26> G21> G42> G38> G23, etc. That is, the low-yield genotypes (G56, G57) were bad because they were far from the ideal genotype.

Evaluation of environments relative to an ideal environment

An ideal environment can be defined based on the projection of the ideal environment on the same horizontal ATC axis as the longest vector of all environments (Figure 5). Environments closer to the hypothetical ideal environment showed that the environment was suitable for genotyping testing. Therefore, the WA18 environment is more suitable, followed by KH19, WA19 and KH18.

Relationship among test environments

Fig. 6 is referred to as a vector view of a 2D GGE plot in which the environment is associated with the origin of the binary plot by a line called a vector. Looking at the 2D graph in this way helps us understand the relationships between the environments. One interesting interpretation is that the angular cosine between the vectors in the two media is approximately equal to the correlation coefficient between the two

media. Acute angles indicate positive correlation, obtuse angles indicate negative correlations, and right angles indicate no correlation (Yan and Kang, 2003). Short vectors can indicate that the test environment is not connected to other environments. The cosine of the angle is not accurately converted to a correlation coefficient because the 2D plot does not account for all the variations in the data set. However, angles provide enough information to provide a complete picture of the relationship between the test environments. Based on the angle between the environment vectors, the environments KH19 and WA19 form an acute angle with each other, so the two environments show a strong positive correlation. Further, KH19 and WA18 and also, KH18 and WA18 made acute angles with each other, therefore these environments are also positively correlated. No negative correlation was found between any of the environments. The 2D vector images were also used to define environments that could be used for indirect selection. It also helps to identify matches between natural and artificial conditions for indirect selection.

Discriminating ability and representativeness of the test environments

Discriminating ability is an important criterion for a test environment. A test environment without discrimination is useless because it does not provide information on genotype (Yan and Kang, 2003). Another equally important indicator of a test environment is its representativeness to the target environment. If the test environment is not representative of the target environment, it is not only useless but also deceptive as it can provide biased information about the genotype tested (Yan and Kang, 2003). In the GGE biplot, genotype distinctness and representativeness of the target environment are important measures of the test environment. Concentric circles in the 2D plot as shown in Figure 1. 7 helps to visualize the length of the media vector, which is proportional to the standard deviation of each media and measures the distinctness of the media. Therefore, among the four test environments, KH19, WA18, and WA19 were the most discriminating (informative) and KH18 was least discriminated. A test environment that is not always indistinguishable (uninformed) should not be used as a test environment as it provides little information about genotype (Yan and Tinker, 2006). The average environment (indicated by the small circle at the end of the arrow) has the average coordinates of all test environments, and the Average Environment (AEA) axis is the average environment and two plots (Yan, 2002). A test environment with a smaller angle with the AEA better represents other test environments. Therefore, after WA18, KH19 and WA19 were the most representative media, and KH18 was the least representative (Figure 7). A differential and representative test environment (location) is generally a good test environment for selecting an adaptable genotype (Yan and Tinker, 2006). Therefore, KH19, WA18 and WA19 were good test environments for selecting widely adapted genotypes. According to Yan and Tinker (2006), when the target environment can be subdivided into mega-environments, a differential but non-representative test environment is useful for selecting especially adaptive genotypes, and when the target environment is a single mega-environment, it is useful to select unstable genotypes. Useful for sorting. environment. On the other hand, indiscriminate and representative environments are meaningless.

Conclusions

The most important goal in all crop breeding programs is to increase yield, and yield improvement requires the use of efficient statistical methods to identify superior genotypes. In determining the superiority of genotype, in addition to high yield, yield stability in different environments must also be considered. AMMI and biplot analyses are good tools for selecting superior genotypes and to increase efficiency in selection. It has been concluded that the combined analysis of variance for yield and yield-associated traits is the best tool for displaying the significance of components of variance among the studied traits. The correlation between the traits depicts the importance of traits related to target trait. The tools like AMMI Analysis and GGE biplot are very effective in order to study the GEI in multi-environments similarly GGE biplot facilitates the graphical representation of GEI pattern of multi-environment traits (MET). It also permits the graphical inspection of the relationship among the test environments and GE interactions. Based on the AMMI analysis and GGE biplot, many genotypes were identified (G-1, G-2, G-3, G-7, G-8, G-16, G-19, G-20, G-21, G-26, G-28, G-31, G-33, G-34, G-38, G-58, G-50, G-80,). Which are suggested to send for further field trails across the country, in order to understand and scrutinize their stability of these genotypes throughout the environments thereafter can be used under breeding programs aimed high yield as well as can be recommended as generally adapted varieties or varieties for specific areas.

Table 1. Experimental material of bread wheat (*Triticum aestivum* L.) used for present study.

Code	Pedigree	Code	Pedigree	Code	Pedigree
G1	CIM-KW-17-1	G35	CIM-KW-17-95	G69	CIM-KW-142-17-163
G2	CIM-KW-17-2	G36	CIM-KW-17-96	G70	CIM-KW-142-17-164
G3	CIM-KW-17-3	G37	CIM-KW-17-97	G71	CIM-KW-142-17-165
G4	CIM-KW-17-4	G38	CIM-KW-17-98	G72	CIM-KW-142-17-166
G5	CIM-KW-17-5	G39	CIM-KW-17-99	G73	CIM-KW-142-17-167
G6	CIM-KW-17-6	G40	CIM-KW-17-100	G74	CIM-KW-142-17-168
G7	CIM-KW-17-7	G41	CIM-KW-17-141	G75	CIM-KW-142-17-169
G8	CIM-KW-17-8	G42	CIM-KW-142-17-142	G76	CIM-KW-142-17-170
G9	CIM-KW-17-9	G43	CIM-KW-142-17-143	G77	CIM-KW-142-17-171
G10	CIM-KW-17-10	G44	CIM-KW-142-17-144	G78	CIM-KW-142-17-172
G11	CIM-KW-17-11	G45	CIM-KW-142-17-145	G79	CIM-KW-142-17-173
G12	CIM-KW-17-12	G46	CIM-KW-142-17-146	G80	CIM-KW-142-17-174
G13	CIM-KW-17-13	G47	CIM-KW-142-17-147	G81	CIM-KW-142-17-175
G14	CIM-KW-17-14	G48	CIM-KW-142-17-148	G82	CIM-KW-142-17-176
G15	CIM-KW-17-15	G49	CIM-KW-142-17-149	G83	CIM-KW-142-17-177
G16	CIM-KW-17-16	G50	CIM-KW-142-17-150	G84	CIM-KW-142-17-178
G17	CIM-KW-17-17	G51	KW-17-12	G85	CIM-KW-142-17-179
G18	CIM-KW-17-18	G52	KW-17-7	G86	CIM-KW-142-17-180
G19	CIM-KW-17-19	G53	KW-17-3	G87	CIM-KW-142-17-181
G20	CIM-KW-17-20	G54	KW-17-8	G88	CIM-KW-142-17-182
G21	CIM-KW-17-81	G55	KW-17-6	G89	CIM-KW-142-17-183
G22	CIM-KW-17-82	G56	KW-17-2	G90	CIM-KW-142-17-184
G23	CIM-KW-17-83	G57	CIM-KW-142-17-151	G91	CIM-KW-142-17-185
G24	CIM-KW-17-84	G58	CIM-KW-142-17-152	G92	CIM-KW-142-17-186
G25	CIM-KW-17-85	G59	CIM-KW-142-17-153	G93	CIM-KW-142-17-187
G26	CIM-KW-17-86	G60	CIM-KW-142-17-154	G94	CIM-KW-142-17-188
G27	CIM-KW-17-87	G61	CIM-KW-142-17-155	G95	CIM-KW-142-17-189
G28	CIM-KW-17-88	G62	CIM-KW-142-17-156	G96	CIM-KW-142-17-190
G29	CIM-KW-17-89	G63	CIM-KW-142-17-157	G97	CIM-KW-142-17-191
G30	CIM-KW-17-90	G64	CIM-KW-142-17-158	G98	**Shalimar Wheat-1**
G31	CIM-KW-17-91	G65	CIM-KW-142-17-159	G99	**Shalimar Wheat-2**
G32	CIM-KW-17-92	G66	CIM-KW-142-17-160	G100	**HS 562**
G33	CIM-KW-17-93	G67	CIM-KW-142-17-161	G101	**VL 907**
G34	CIM-KW-17-94	G68	CIM-KW-142-17-162		

Table 2. Combined analysis of variance for 8 yield contributing traits at 2 locations under 4 environments.

SV	Df	DM	%	PH	%	T/M	%	SL	%
E	3	180.4	3.61	88.80	5.77	1100	10.14	4.74	11.02
REP (ENV)	4	13.9	0.37	0.504	0.05	181.6	2.23	0.271	0.84
G	100	39.8	26.53	23.56	51.11	156.6	48.13	0.467	36.26
G×E	300	16.2	32.41	3.41	22.39	1.8	16.82	0.119	27.80
Residual	400	13.9	37.06	2.381	20.65	18.4	22.66	0.077	24.14
COV%		1.62		1.65		4.77		2.54	
SV	**S/S**	**%**	**G/S**	**%**	**TGW**	**%**	**YIELD**	**%**	
E	40.44	18.50	25.96	19.97	35.06	11.57	20440	7.83	
REP (ENV)	0.158	0.09	1.365	1.39	0.381	0.16	502	0.25	
G	3.6	54.92	2.034	52.11	4.415	48.59	3634	46.45	
G×E	0.479	21.93	0.275	21.11	0.566	18.67	615	23.58	
Residual	0.072	4.42	0.512	5.35	0.477	20.98	428	21.87	
COV%	1.92		2.02		2.33		4.87		

SV= Source of Variation, G= Genotype, E= Environment, Rep (Env) = Replications within Environments, G×E, Genotype × Environment Interaction, CoV= Coefficient of Variation, df= Degree of Freedom, DM= Days to Maturity, PH= Plant Height, T/M= Tillers per Meter, SL= Spike Length, S/E= Spikelet's per Spike, G/S= Grains per Spike and TW= test weight

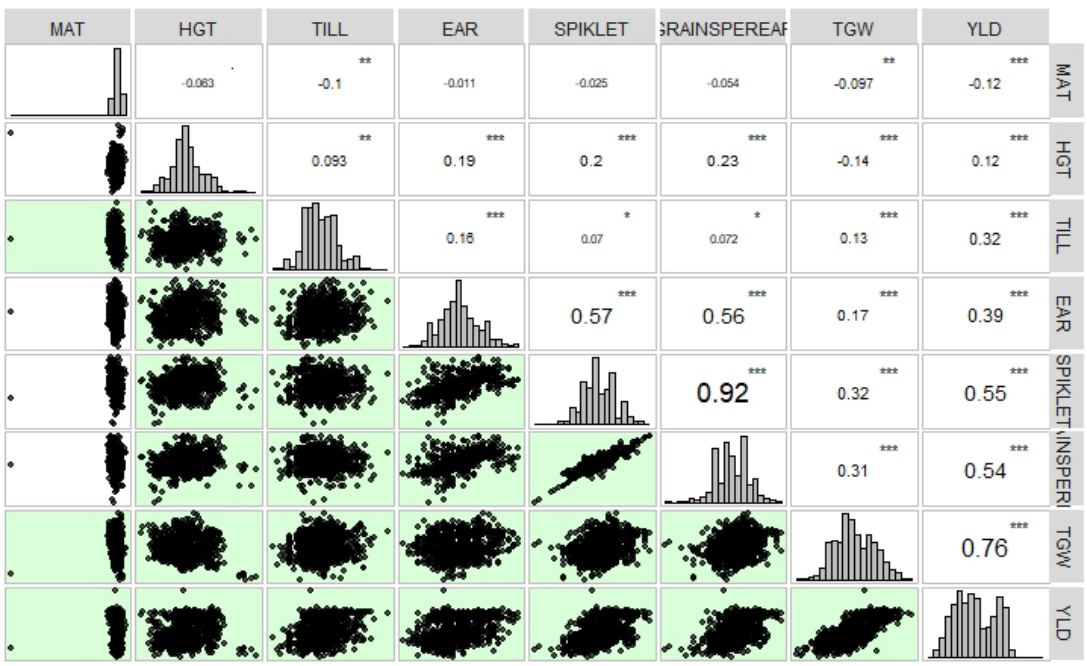
Table 3. Seed yield variance analysis of wheat promising lines by AMMI analysis.

Source	df	SS	M.S	Percentage Variance
Total	1107	966896	3778	
Environments	3	61320	20440**	7.83
Genotypes	100	363440	3634**	46.65
Rep (Env.)	4	2009	502	0.25
Interactions	300	184503	615**	23.58
IPCA1	102	97365	955**	52.8
IPCA2	100	57163	572**	31.0
IPCA3	98	29975	306**	16.2
Residuals	400	171121	428	21.87

** Significant at 0.01

Table 4. Mean of seed yield and amount of first four interaction principal component analysis of AMMI model in wheat promising lines.

	KH 18-19		WA 18-19		KH 19-20		WA 19-20	
No	**G**	**Y(g/p)**	**G**	**Y(g/p)**	**G**	**Y(g/p)**	**G**	**Y(g/p)**
1	G-80	546.17	G-33	540.68	G-31	540.76	G-7	557.22
2	G-20	542.65	G-41	538.92	G-28	540.58	G-1	538.53
3	G-23	541.12	G-34	538.65	G-8	534.81	G-19	536.42
4	G-2	538.44	G-42	536.19	G-80	534.6	G-3	533.6
5	G-50	537.32	G-3	535.61	G-58	530.79	G-21	533.07
6	G-26	531.65	G-26	534.85	G-7	529.79	G-2	531.93
7	G-38	530.95	G-28	534.73	G-21	527.41	G-50	523.74
8	G-31	528.51	G-23	534.72	G-22	525.91	G-28	517.86
9	G-33	528.49	G-20	532.32	G-20	520.72	G-33	517.73
10	G-1	528.12	G-38	526.06	G-34	520.37	G-58	517.72
Mean of Selected Individuals		535.34		535.273		530.57		532.78
Mean of All Individuals		420.99		433.79		446.81		427.71
Selection Differential		114.35		101.48		83.76		105.07
Mean GY (SW-1)		425.07		418.52		457.43		417.09
Mean GY (SW-2)		423.5		436.05		415.89		448.7
Mean HS-562		424.88		432.24		445.46		433.06
Mean VL-907		454.8		430.93		428.06		437.72
Percent Mean of Selected Individuals Over Checks		23.9		24.6		21.5		22.7



* Significance at 0.05 probability level, ** Significance at 0.01 probability level, *** Significance at 0.001 probability level. MAT= Maturity, HGT= Eight, Till= Tillers per meter, Spikelet= Spikelets per spike, grains per spike, TGW= Thousand grain weight, and YLD= Yield.

Figure 1. Correlation among yield and yield associated traits in wheat under four environments across two locations. Bigger size of the number is indicator of strong correlation while smaller number size depicts weak correlation between the traits.

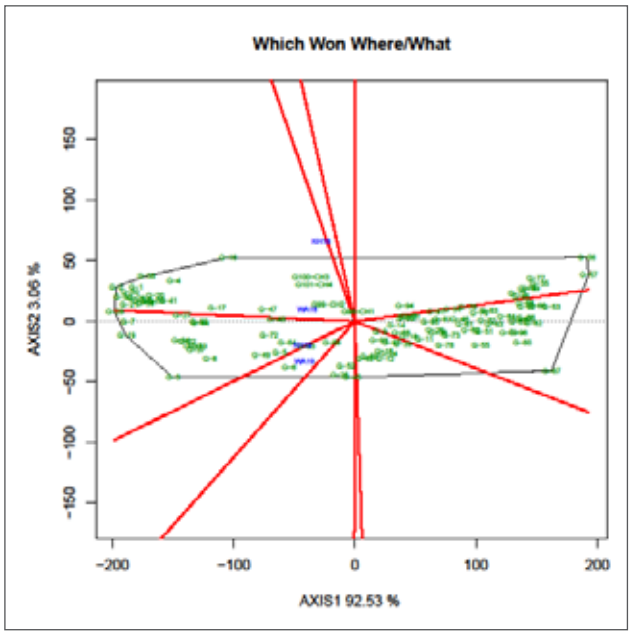


Figure 2. Polygon view of GGE biplot (which-won-where model) showing view of wheat genotypes and environments. Black and blue numbers represent genotypes and environments, respectively.

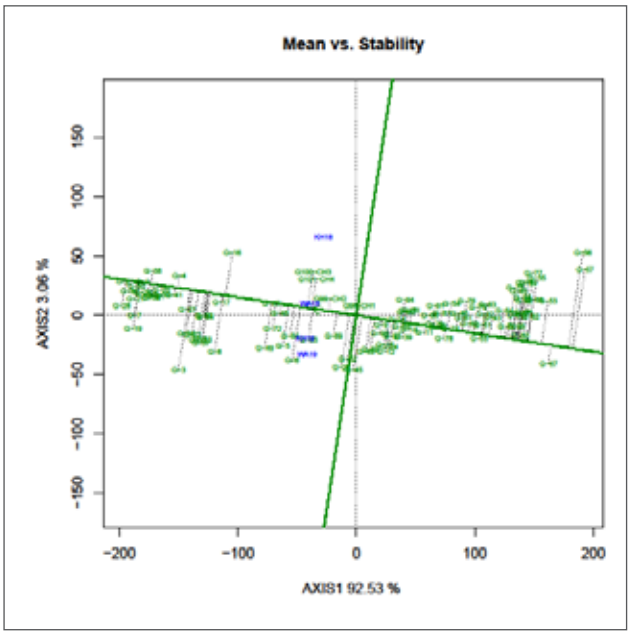


Figure 3. Average environment coordination (AEC) views of the GGE-biplot based on environment-focused scaling for the mean performance and stability of genotypes.

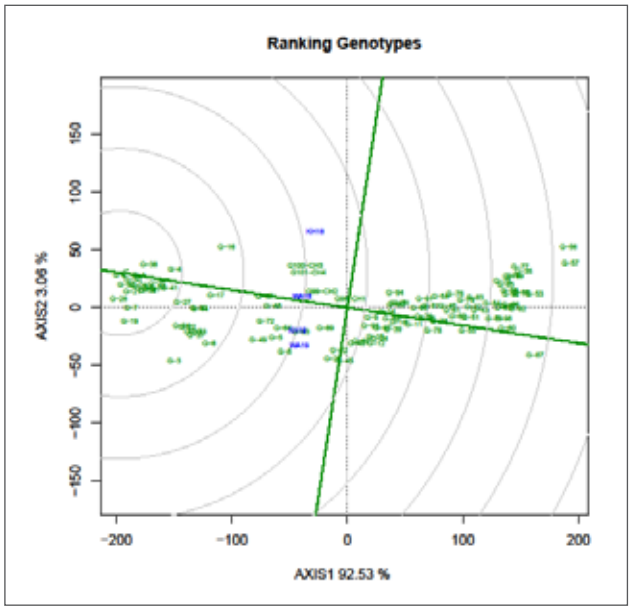


Figure 4. GGE-biplot based on genotype-focused scaling for comparing the genotypes with the ideal genotype.

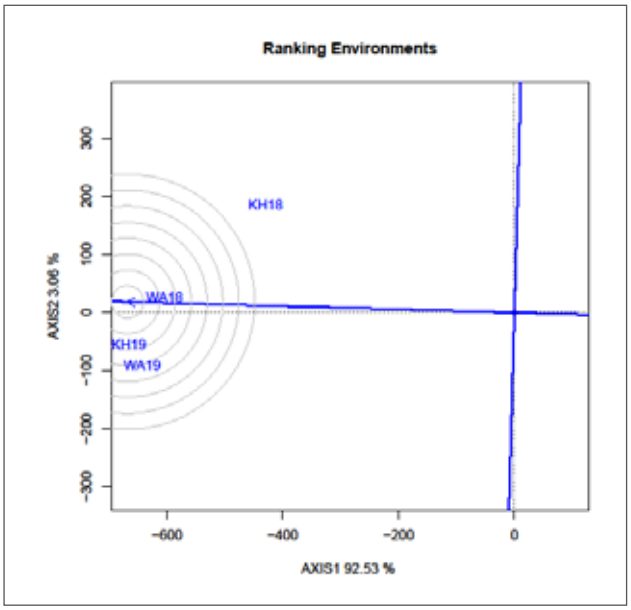


Figure 5. GGE-biplot based on environment-focused scaling for comparing the environments with the ideal environment.

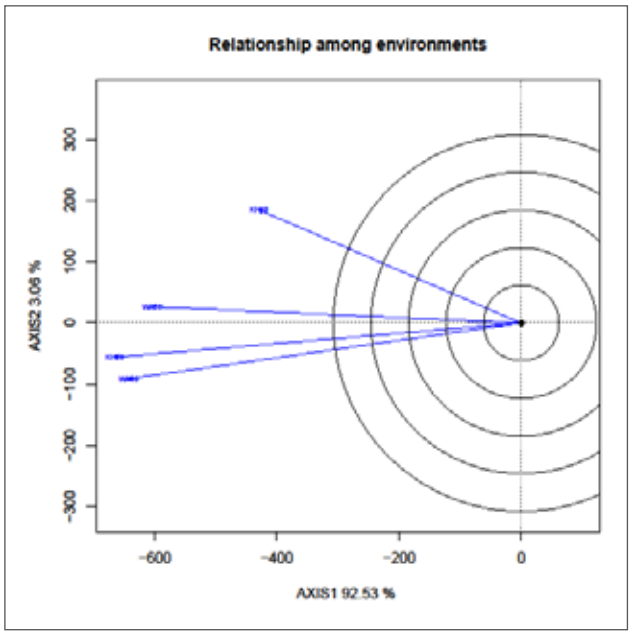


Figure 6. GGE-biplot based on environment-focused scaling for environments.

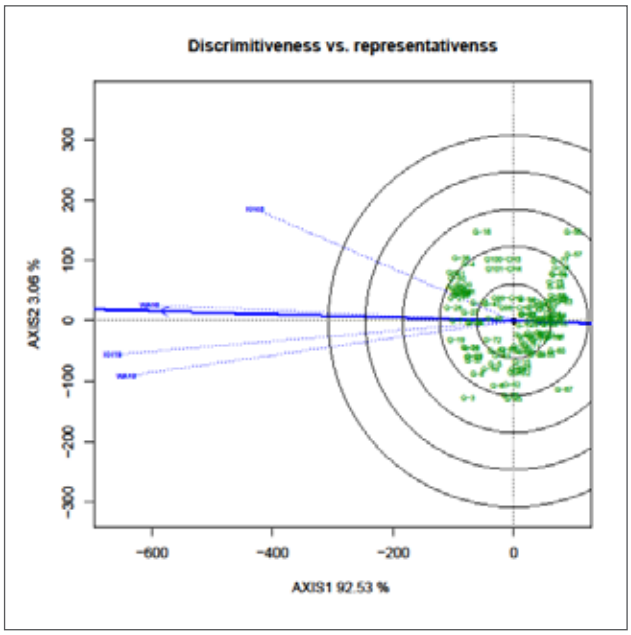


Figure 7. Vector view of the genotype main effect and GGE biplot showing the discriminating ability and representativeness of the test environments.

References

Abebe T, Alamerew S and Tulu L, (2017). Genetic variability, heritability and genetic advance for yield and its related traits in rainfed lowland rice (*Oryza sativa* L.*)* Genotypes at fogera and pawe, Ethiopia. Adv. Crop. Sci. Technol 5:270. DOI:10.4172/2329-8863.1000272.

Sallam A, Alqudah AM, Dawood MFA, Baenziger PS and Börner A, (2019). Drought stress tolerance in wheat and barley, Advances in Physiology, Breeding and Genetics Research. Int. J. Mol . Sci. 20:31-37.

Ajay BC, Aravind J, Bera SK, Singh AL, Narendra K, Gangadhar K and Kona P, (2020). Evaluation of GEI and yield stability Analysis in Peanut Under Phosphorus Stress Condition Using Stability Parameter of AMMI Model. Agric Res 9: 477-486.

Ajay BC, Aravind J and Abdul Fiyaz R, (2021). Ammistability: Additive main effects and multiplicative interaction Model Stability Parameters. R package version 0.1.1, https://ajaygpb.github.io/ammistability/https://CRAN.R-project.org/package=ammistability.

Baranwal DK, Mishra VK, Vishwakarma MK, Punam, Yadav S and Arun B, (2012). Studies on genetic variability, correlation and path Analysis for Yield and Yield Contributing Traits in Wheat (*T. aestivum* L. EmThell.). Plant Arch 12: 99-104.

Ebdon J S and Gauch H G (2002). Additive main effect and multiplicative interaction analysis of national turf grass performance trials: II. Cultivar recommendations. Crop. Sci. 42: 497-506.

FAOSTAT Statistics Division Online Database (2019-2021). http://faostat.fao.org.

Frutos E, Galindo MP and Leiva V, (2014). An interactive biplot implementation in R for modelling genotype-by-environment interaction. Stoch Environ Res Risk Assess 28:1629-1641.

Gauch HG Jr and Zobel RW, (1997). Identifying mega-environments and targeting genotypes. Crop. Sci. 37: 311-326.

Kant S, Lamba RAS, Arya RK and Panwar IS, (2014). Effect of terminal heat stress on stability of yield and quality parameters in bread wheat in south-west Haryana. J Wheat Res 6(1): 64-73.

Kant S, Lamba RAS, Panwar IS and Arya RK, (2011). Variability and inter-relationship among yield and quality parameters in bread wheat. J Wheat Res3(2): 50-55.

Katsenios N, Sparangis P, Leonidakis D, Katsaros G, Kakabouki I, Vlachakis D and Efthimiadou A, (2021). Effect of genotype×Environment interaction on yield of maize Hybrids in Greece Using AMMI Analysis. Agronomy 11(3): 479.

Kaya Y, Akcura M and Taner S, (2006). GGE-biplot analysis of multi-environment yield trials in bread wheat. Turk J Agric For 30: 325-337.

Kroonenberg PM, (1995). Introduction to biplots for G×E tables. Department of Mathematics, Research Report #51, University of Queensland, 22.

Kumar P, Singh G, Kumar S, Kumar A and Ojha A, (2016). Genetic analysis of grain yield and its contributing traits for their implication in improvement of bread wheat cultivars. J Appl Nat Sci8(1): 350-357.

Ljubičić N, Popović V, Ćirić V, Kostić M, Ivošević B, Popović D, Pandžić M, El Musafah S and Janković S, (2021). Multivariate interaction analysis of winter wheat grown in environment of limited soil conditions. Plants 10(3): 604.

Mansouri A, Oudjehih B, Benbelkacem A, Elabidine Fellahi Z and Bouzerzour H, (2018). Varation and relationships among agronomic traits in durum wheat (*Triticum turgidum* L.) thell ssp. under south mediterranean growth conditions, stepwise and path analysis. Int J Agron 2018: https://Doi.Org/10.1155/2018/8191749.

Mitrovic B, Stanisavljevi D, Treski S, Stojakovic M, Ivanovic M, Bekavac G and Rajkovic M, (2012). Evaluation of experimental maize hybrids tested in multi-location trials using AMMI and GGE biplot analysis. Turkish J Field Crops 17(1): 35-40.

Mohammadi R, Etminan A and Shooshtari L, (2019). Agro-physiological characterization of durum wheat genotypes under drought conditions. Exp Agric 55: 484-499.

Mohammadi R, Armion M, Zadhasan E, Ahamadi MM and Amri MM, (2018). The use of AMMI model for interpreting GEI in durum wheat. Exp Agric 54: 670-683.

Mwadzingeni L, Shimelis H and Tsilo TJ, (2017). Variance components and heritability of yield and yield components of wheat under drought-stressed and non-stressed conditions. Aust J Crop Sci 11(11): 1425-1430

Nagar SS, Kumar P, Vishwakarma SR, Gyanendra and Tyagi BS, (2018). Assessment of genetic variability and character association for grain yield and its component traits in bread wheat (*Triticum aestivum* L.). J Appl Nat Sci10(2): 797-804.

Rad MN, Kadir MA, Rafii M.Y, Jaafar HZ, Naghavi MR and Ahmadi F, (2013). Genotype environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (*Triticum aestivum* L.) under normal and drought stress conditions. Aust J Crop Sci, 7(7): 956.

Rahmatollah K, Mohtasham M, Naser S, Ali A, Barzo R, Faramarz S and Fariba A, (2013). GGE biplot analysis of yield stability in multi-environment Trials of Lentil Genotypes under Rainfed Condition. Int J Res Rev 4(12): 7-12.

Shashikumara P, Harikrishna, Jain N, Sinha N, Chauhan D, Rahul MP, Ambati D, Singh JB, Sai Prasad SV, Singh GP, Prabhu KV and Singh PK, (2020). Genetic variability, GEI for grain Yield of Wheat (*Triticum aestivum)* backcross inbreed lines population under different regimes. Indian J Agric Sci90(9): 1687-84.

Verma A and Singh GP, (2021a). GxE interactions analysis of wheat genotypes evaluated under peninsular zone of the country by AMMI model. Am J Agric For 9(1): 29-36.

Verma A and Singh GP, (2021b). Stability, adaptability analysis of wheat genotypes by AMMI with BLUP for restricted irrigated multi location trials in peninsular zone of India. Agric Sci 12(3): 198-212.

Yan W, (2002). Singular value partitioning in biplot analysis of multi-environment trial data. Agron J 94: 990-996.

Yan W and Tinker NA, (2006). Biplot analysis of multi-environment trial data: Principles and applications. Can J Plant Sci 86: 623-645

Yan W, (2001). GGE biplot-a windows application for graphical analysis of multienvironment trial data and other types of two-way data. Agron J 93: 1111-1118.

Yan W and Hunt LA, (2002). Biplot analysis of diallel data. Crop Sci 42: 21-30.

Yan W, Hunt LA, Sheng Q and Szlavnics Z, (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci 40(3): 597-605.

Yan W and Kang MS, (2003). GGE biplot analysis : A graphical tool for breeders, geneticist, and agronomists. CRS PRESS. Boca Raton, FL.

Yan W and Racjan I, (2002). Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Sci 42 : 11-20

Yang RC, Crossa J, Cornelius PL and Bugueno J, (2009). Biplot analysis of genotype× environment interaction: Proceed with caution. Crop Sci 49: 1564-1576