

COMPARISON OF YIELD PERFORMANCE OF WHEAT GENOTYPES OVER ENVIRONMENTS BY GGE-BIPLLOT ANALYSIS

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ABSTRACT

Plant breeders perform multi-environment yield trials to identify superior genotypes for a specific region and to partition the target region into different mega-environments. In this investigation, the GGE-biplot was used to evaluate 15 bread wheat advanced lines for yield performance across five locations of Sindh, Pakistan. The results of the combined analysis of variance revealed that the genotypes, locations, and their interaction significantly affected the grain yield. The polygon view of GGE-biplot indicated that G4, G6, G8, G9, G13, and G2 were the vertexed genotypes while three rays divided the five locations into two mega-environments. First mega-environment comprised of only one location E1 for which G6 and G4 were the winner genotypes. The second mega-environment consisted of four locations *viz.* E2, E3, E4, and E5 which contained G8 and G9 as the winner genotype. The ranking biplot designated G6 as an ideal genotype followed by G8 and G11. The least average yield across all the environments was observed in genotypes G13 and G2. Comparison biplot based on ideal genotypes ranked the other favorable genotypes as G4 > G11 > G8. The environment ranking biplot revealed that E2 was an ideal location since it had excellent power to discriminate all the genotypes based on of grain yield and was more appropriate to represent the overall environments. Among five test locations, the discrimination power of three locations E2, E4, and E5 was very similar in ranking the wheat genotypes as the environmental vectors of these locations overlapped another. Overall, the maximum average yield was recorded for G11 (5925.0 kg ha⁻¹) followed by G6 (5852.5 kg ha⁻¹) and G8 (5831.0 kg ha⁻¹). Taken together, the wheat advanced lines G6, G8, and G11 showed good yield potential to become the candidate wheat lines for cultivation in Sindh province, Pakistan.

Keywords: Wheat, genotype × environment interaction, GGE-biplot, Multi-environment yield trial (MET), Sindh Pakistan

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INTRODUCTION

The spring bread wheat is the main staple crop of Pakistan which is cultivated in almost all the agro-climatic conditions of the country. According to FAO (2019), Pakistan ranks eighth in the world in terms of global wheat production, with a total wheat grain production of 24.35 million metric tons (MT) from the cultivated area of 8.678 million hectares (Mha) @ 2.80 tonnes per hectare. Overall, the average per unit area wheat production is low in Pakistan as compared to the rest of wheat producing countries. In this regard, wheat breeders are striving hard to evolve superior genotypes specific for each ecological zone to increase per unit area production.

It is well-established fact that a genotype shows significant variation in yield performance under different agro-climatic conditions due to variable environmental factors and, hence, can be referred as genotype × environment interaction (GEI) (Farshadfar *et al.*, 2012). Therefore, plant breeders have to conduct yield trials in diverse environments prior to finalize the superior genotype for the farmer's field (Abate *et al.*, 2015). These

multi-environment yield trials (METs) not only allow the breeders to identify superior genotype for a specific region but also assist in portioning the target region into different mega-environments (Yan *et al.*, 2000). However, this is not an easy task as the complexities of GE interaction hinder the selection of the best performing and the most stable genotypes, thus, reducing the efficiency of the breeding program (Kaya *et al.*, 2006). Like other crops, the grain yield in wheat is also the result of genotype, environment, and their interaction (GE), among which genotype and GE interaction are most relevant to evaluate the genotype and to identify mega-environment in METs (Sabaghnia *et al.*, 2013). This strategy has been adopted by most of the wheat breeders to evaluate genotypes for stability across different environments and also to recommend a genotype for a specific environment (Mohammadi *et al.*, 2010; El-Ameen, 2012; Sareen *et al.*, 2012; Rad *et al.*, 2013; Abate *et al.*, 2015; Bavandpori *et al.*, 2015; Mehari *et al.*, 2015; Karimizadeh *et al.*, 2016; Singh *et al.*, 2019; Singh *et al.*, 2020).

Numerous parametric and non-parametric statistical procedures such as regression coefficient (Finlay and Wilkinson, 1963), stability variance (Shukla,

1972), coefficient of determination (Pinthus, 1973), coefficient of variability (Francis and Kanneberg, 1978), additive main effects and multiplicative interaction (AMMI) (Gauch and Zobel, 1988) and the genotype main effect (G), and GE interaction effect (GGE) model (Yan *et al.*, 2000) have been proposed to estimate the genotypes and GE interactions for METs. Among these statistical approaches, the AMMI and GGE are frequently used in METs due to better diagnostics of G and GE variations, high accuracy, mega-environment delineation, and graphical presentation (Yan *et al.*, 2007; Gauch, 2013). Yan *et al.* (2000) proposed GGE-biplot method to graphically display the genotype and GE interaction of METs efficiently using the singular value decomposition (SVD) of environment-centered or within environment standardized data. The first principal component score of genotypes and that of environments are plotted against their respective scores of second principal component to construct which-won-where, mean performance versus stability of the genotypes, and the environmental evaluation biplots (Yan *et al.*, 2007). The analysis also defines the ideal test environment of all the studied environments having the longest vector length and is located on the 'average tester coordination' (ATC) abscissa. Additionally, the test environments can be ranked according to distance between the test environment markers and the marker of the ideal environment on the GGE biplot as well as based on identification of superior genotypes in a given environment (Yan *et al.*, 2001). Based on these advantages, GGE-biplot analysis has been extensively utilized in METs to discriminate mega-environments and to identify the most stable and outstanding genotypes not only in wheat (Mohammadi *et al.*, 2010; Farshadfar *et al.* 2012; Rad *et al.*, 2013; Kendal and Senser, 2015; Karimizadeh *et al.*, 2016; Singh *et al.*, 2019; Singh *et al.*,

2020) but also in other crops like rice (Akhter *et al.*, 2015), barley (Vaezi *et al.*, 2017), maize (Botovic *et al.*, 2018; Oliveira *et al.*, 2019), lentil (Karimizadeh *et al.*, 2013), soybean (Atnaf *et al.*, 2013) and medicinal plants (Shahriari *et al.*, 2018). Farshadfar *et al.* (2012) applied GGE-biplot analysis to identify the most stable and best performing wheat-barley addition lines. Similarly, Rad *et al.* (2013) opted for the combination of AMMI and GGE-biplot analysis approach to select the stable and the best performing wheat genotypes under drought conditions. Hence the study aimed to apply GGE-biplot procedure to evaluate 12 bread wheat advanced lines along with three checks for yield performance across five locations of Sindh province, Pakistan to determine the ideal mega-environment and to identify the winner genotypes for each tested environment (location).

MATERIALS AND METHODS

Plant material and experimental design: Fifteen bread wheat genotypes, including twelve advanced breeding lines and three check cultivars *viz.* Kiran-95, TD-1, and Benazir-2013 were used as the plant material for this multi-location yield trial. The advanced wheat breeding lines were developed by the wheat program at the Nuclear Institute of Agriculture, Tando Jam, Sindh, Pakistan. The detail of each entry regarding parentage and code followed in this study is given in Table 1. The field experiments were conducted during the year 2019-20 at five districts (locations) *i.e.* Hyderabad, Badin, Sanghar, Naushahro Feroz, and Dadu representing the mega agro-climatic zones for wheat production of Sindh province, Pakistan. The details of geographical coordinates, soil characteristics, and code of each site are provided in Table 2.

Table 1: Name and parentage/pedigree of wheat genotypes of multi-location yield trial.

Entry Name	Parentage/Pedigree
G1	ALTAR84/AE.SQUARROSA(219)//SERI*2/3/VEE'S/NAC
G2	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/4KAUZ/FLOR/WA-1/5 P.186/RESG/NAAMA
G3	CHEN/AE.SQUARROSA//2*WEAVER/3/BAV/92/4/JARU/5/OLI2/SALMEJA/6
G4	CHEN/AE.SQ//2*WEAVER/3/BAV92/4/JARU/5/OLI2/SALMEJA/6/CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2
G5	NR-234/PFAU/VEE#9//URES
G6	NR-234/PFAU/VEE#9//URES
G7	KAUZ//ALTAR84/AOS3/KAUZ/3/ATTILA/SOY1/ATTILA/BCN/4/PASTOR-6
G8	6006/TD-1//6095
G9	YAYE/4/WAXWING/3/PFAU/WEAVER//BRAMBLING/5/KACHU/SAUAL
G10	SAUAL/YANAC//SAUAL*2/3/TACUPETO F2001
G11	Bokota/3/UP2338*/KKTS*2//YANAC
G12	CROC-1/AE.SQUARROSA(224)//OPATA/3/PASTOR/4/2*SOKOLL/3
G13	TD-1
G14	Kiran-95
G15	Benazir-13

A randomized complete block design (RCBD) with three replications was used as experimental design at each location. The field plot at each location comprised of six rows (30 cm apart), having a row length of six meters. A uniform seed rate of 120 kg per hectare was used at all the locations. Recommended full dose of

phosphorous fertilizer and half dose of the nitrogenous fertilizer was applied at sowing while the remaining half dose of nitrogenous fertilizer was provided at booting and grain filling stages. Irrigation was applied as per requirement while other standard cultural practices were followed according to location.

Table 2: Description of experimental locations of multi-location yield trial.

Environment Code	Location	Longitude	Latitude	Soil type
E1	Shadi Large, Badin	69°10'47"E	24°37'38"N	Sandy clay loam
E2	Kandiaro, Naushahro Feroz	68°12'60"E	27°03'60"N	Clay loam
E3	Sita Road, Dadu	67°50'52"E	27°02'18" N	Clay loam
E4	Nuclear Institute of Agriculture, Tando Jam, Hyderabad	68°31'50"E	25°25'41"N	Sandy clay loam
E5	Tando Adam, Sanghar	68°33'48"E	24°45'13"N	Sandy clay loam

Data collection and statistical analysis: At maturity, the data of grain yield were recorded from each location. To determine the grain yield, four central rows of each field plot were harvested, threshed, and weighed. The grain yield was recorded in kg per hectare (kg ha⁻¹). At first, the data of grain yield were analyzed for combined analysis of variance to determine the significance of genotypic main effect and genotype into environment interaction using computer software GenStat V.12. Thereafter, the same dataset of grain yield was used for GGE-biplot analysis based on the sites regression linear-bilinear model proposed by Yan *et al.* (2000) using the PBTtools V1.3 software (PBTtools, 2014). This analysis graphically displays the G and GE interaction of MET data by plotting the first two symmetrically scaled principal components required for the evaluation of genotypes and environments. Five different biplots were generated among which “which-won-where” biplot identified the superior genotype in different mega-environments, ranking biplot ranked the genotypes based on stability and yield. Genotype-based biplot helped to visualize the performance of genotype in comparison with an ideal genotype and environment based biplots depicted the evaluation of environments related to ideal environment and represented the relationship among different environments.

RESULTS

Grain yield performance of genotypes across different environments: The yield performance of 15 wheat genotypes across five locations is given in Table 3. Overall, the maximum average grain yield across all the locations was recorded for G11 (5925.0 kg ha⁻¹) followed by G6 (5852.5 kg ha⁻¹). The results showed that

genotypes performed differently at each location, for instance, G6 outclassed other genotypes in E1 and E2; G5 produced maximum grain yield in E3 while G11 had the highest grain yield in E4 and E5 (Table 3). It is noteworthy that most of the advanced lines except G2 (5182.7 kg ha⁻¹) produced significantly higher average grain yield than other three checks i.e. G13 (TD-1; 4883.8 kg ha⁻¹), G14 (Kiran-95; 5020.1 kg ha⁻¹) and G15 (Benazir-13; 5206.4 kg ha⁻¹). Among the five test locations, all the genotypes performed relatively quite well at E1 whereas low yield performance of all the genotypes was recorded at E2 (Table 3).

The same data set of MET was then subjected to the combined analysis of variance analysis to partition the total variation of grain yield into different components along with interactions among different experimental factors (Table 4). Significant variation was recorded among all the genotypes for grain yield at different locations. The present results also revealed that the genotypes (G), locations (E), and their interactions significantly affected the grain yield. The relative contribution of G, E, and G × E towards total variation (total sum of the square) was 5.93%, 73.83%, and 10.85%, respectively (Table 4). The maximum variation explained by the environment suggested that the locations significantly affected the grain yield and the existence of mega-environments. Similarly, the significant interaction of the environment with genotypes also indicates the presence of crossover of GE interaction as some genotypes outclassed other genotypes at different test locations. Besides, the GGE-biplot analysis partitioned the entire observed variation into the first two main principal components (PC) which significantly explained 60.5% (PC1) and 16.5% (PC2) variation. Together these two components explained 77% of the total variation.

Table 3: Grain yield performance of 15 wheat genotypes across five locations.

Geno- types	Testing locations					Mean
	E1	E2	E3	E4	E5	
G1	7067.4 b-f	4428.9 l-t	5200.0 i-p	4920.0 j-s	5577.0 f-o	5438.7 ABCD
G2	7360.0 a-d	3252.2 t	5750.0 e-m	4740.0 j-t	4811.1 j-s	5182.7 Cd
G3	7233.3 b-e	4230.0 m-t	5241.7 i-p	5514.4 g-o	5521.5 g-o	5548.2 ABC
G4	8229.6 ab	4468.9 k-t	4791.7 j-s	5071.1 j-p	5288.9 h-p	5570.0 ABC
G5	7408.1 a-c	4128.9 o-t	5991.7 c-k	4924.4 j-s	5232.6 i-p	5537.1 ABC
G6	8783.0 a	5243.3 i-p	4525.0 k-t	5044.4 j-p	5666.7 f-n	5852.5 AB
G7	7486.7 a-c	3848.9 p-t	5450.0 g-o	4125.6 o-t	5155.6 j-p	5213.3 CD
G8	7294.1 a-d	5210.0 i-p	5966.7 c-k	5106.7 j-p	5577.0 f-o	5830.9 AB
G9	6803.7 b-h	4571.1 k-t	5833.3 d-l	4968.9 j-r	5365.9 h-p	5508.6 ABC
G10	7074.1 b-f	4108.9 o-t	4633.3 j-t	5433.3 g-o	5710.4 e-m	5392.0 ABCD
G11	8177.8 ab	4677.8 j-t	5291.7 h-p	5744.4 e-m	5732.6 e-m	5924.8 A
G12	6920.7 b-g	3494.4 q-t	5741.7 e-m	5022.2 j-q	5443.7 g-o	5324.6 CD
G13	6150.4 c-j	3423.3 st	5275.0 h-p	4393.3 l-t	5177.0 i-p	4883.8 D
G14	6698.5 b-i	3485.6 r-t	5283.3 h-p	4633.3 j-t	5000.0 j-r	5020.1 CD
G15	6807.4 b-h	4164.4 n-t	5066.7 j-p	4926.7 j-s	5065.9 j-p	5206.2 CD
Mean	7299.6A	4182.4D	5336.1B	4971.2C	5355.1B	5428.9

Table 4: Combined analysis of variance of grain yield of 15 wheat genotypes in 5 environments (locations).

Source	Df	SS	MS	F-value	p-value	%TSS
Replication	2	2.10E+05	1.05E+05			
Genotype	14	1.91E+07	1.36E+06	6.71	0.00	5.93
Location	4	2.38E+08	5.94E+07	292.12	0.00	73.83
Genotype × locations	56	3.49E+07	6.23E+05	3.07	0.00	10.85
Error	148	3.01E+07	2.03E+05			9.35
Total	224	3.22E+08				

df = degree of freedom; SS = sum of squares; MS = mean sum of square; % TSS = Percentage of total sum of square; p-value = 0.00 highly significant

Which-won-where view of MET data: In this study, the GGE biplot analysis of 15 genotypes across five different locations revealed that the first two principal components i.e. PC1 (60.5 %) and PC2 (16.5 %) explained a total of 77 % of the total variation (Fig. 1). The radiating rays distributed the which-won-where biplot into three sectors and allocated the test locations to only two sectors. Six genotypes i.e. G4, G6, G8, G9, G13, and G2 were found at the vertices of the polygon (Fig. 1). These vertex genotypes were the most responsive as these lie far from the biplot origin. The first sector represented the first mega-environment which had only one location i.e. E1 and contained four genotypes G4, G6, G10, and G11. The genotypes G4 and G6 were found at the vertex of the polygon of this sector hence declared as the best performing genotypes of this mega-environment (Fig. 1). The second mega-environment represented four locations i.e. E2, E3, E4, and E5 which contained five genotypes viz. G1, G3, G5, G8, and G9. Among these genotypes, the genotypes G8 and G9 were the winner genotypes of these locations as these performed well in this mega-environment and were present as the vortexed genotypes of this sector.

Mean grain yield and stability performance of wheat genotype: The ranking biplot represents the average grain yield and stability performance of 15 genotypes across five different ecological locations (Fig. 2). The average environment coordination (AEC) method was used to evaluate the stability of wheat genotypes. The ranking biplot showed that the genotypes G1, G3, G4, G5, G6, G8, G9, G10, and G11 were projected on the right side of the AEA hence showed a high average grain yield as compared to the overall average yield of all the genotypes. However, the genotypes G2, G7, G12, G13, G14, and G15 were found on the left side of AEA and characterized by low mean grain yield than the overall average yield of all the genotypes (Fig. 2). Among high yielding genotypes, G6, G8, and G11 were found at the top three positions. However, the G6 present at the position of ideal genotype in ranking biplot has less stability as compared to G11 and G8 due to longer projection to the AEA. On the other hand, the ranking biplot revealed that the G13 was the most unstable with low grain yield as compared to rest of the genotypes.

Evaluation of genotypes in comparison with ideal genotype: In this investigation, the GGE-biplot analysis revealed the presence of genotypes G6 right in the center of the concentric circles hence could be regarded as the ideal genotype (Fig. 2). However, the other biplot shown in Figure 3 represents the relative performance of other genotypes in comparison with G6. It can be observed that the G6 had the longest vector length (PC1) as compared to the rest of the genotypes and was located in the fourth quadrant of the biplot which had the characteristics of high adaptability and yield performance. Hence, G6 was the most favorable genotype followed by G4 which was closer to G6 compared to the rest of the genotypes (Fig. 3). Based on the ideal genotype the rank of other favorable genotypes was $G4 > G11 > G8$. It is interesting to note that the genotypes G12 and G13 showed good stability (PC2 score near to zero) but had very low PC1 values (Fig. 3). Therefore, this GGE biplot model can help plant breeders to visualize the comparative performance of candidate lines in context to GE interaction and allow to select genotype for further improvement. This procedure defines the GE interaction more simply by just measuring the distance from the ideal genotype thus delineating the complex aspects of

GE interaction to make final selection easier for breeders (Karimizadeh *et al.*, 2016).

Discriminating power and representativeness of locations: Discriminating power versus representativeness view of GGE-biplot refers to AEC which identifies the ideal environment that can effectively discriminate the genotypes and represents the mega-environment (Yan *et al.*, 2007). Based on five locations the wheat genotypes were grouped into two mega-environments. The first mega-environment included only one location i.e. E1 whereas four other locations *viz.* E2, E3, E4, and E5 constituted the second mega-environment in which the E3 laid far away from other locations (E2, E4, and E5) (Fig 4). Based on GGE-biplot analysis, the location E2 could be regarded as an ideal location since it had a long vector length and a very acute angle with AEA. Therefore, this location had excellent power to discriminate all the genotypes in terms of grain yield and was more appropriate to represent the overall environments. No correlation was observed between E3 with any other tested locations while the same characteristic feature was also observed for the most highly favorable location (E1) in terms of grain yield production (Fig. 4).

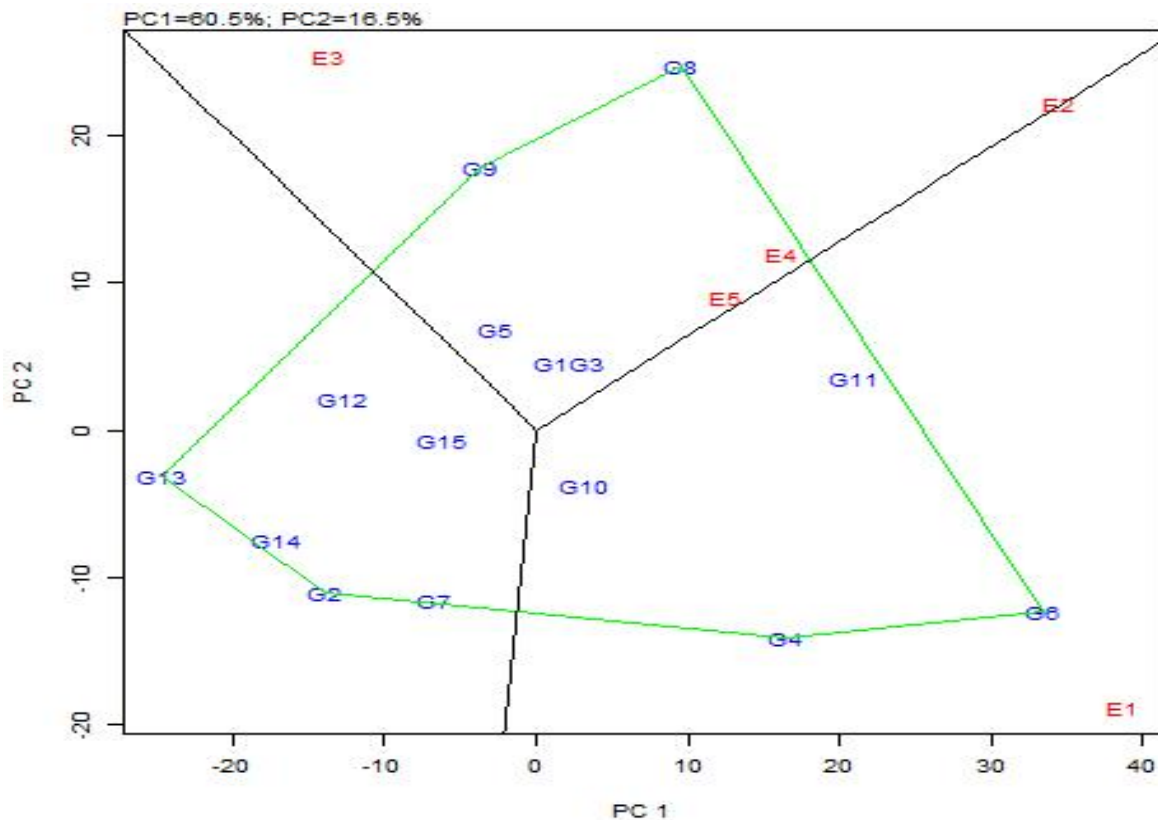


Figure 1: Polygon view of the GGE-biplot based on multi-location yield data of 15 wheat genotypes to illustrate which-won-where pattern. G, E, and PC represent the genotype, location, and principal component, respectively.

Among five test locations, the environment vectors of two locations i.e. E4, and E5 were almost equal in length, overlapped one another, and also had an acute angle with AEA, hence, possessed the same power to discriminate the genotypes and provided a good option to evaluate the genotypes (Fig. 4). On the other hand, the locations E1 had the maximum vector length but the angle between the AEA and E1 was obtuse which suggested that this location had the potential to discriminate the genotypes efficiently but it was not a good representative of the test locations. The GGE biplot analysis also denoted the ideal environment and draw concentric rings around the ideal environment to depict the distance between the test locations and the ideal location or environment (Yan and Rajcan, 2002). As

Figure 4 shows that E2 was an ideal test location as it was found within the concentric rings. Therefore, another biplot was also portrayed for five locations of this investigation to evaluate the test locations in comparison with the ideal environment. Based on the ideal environment, the E4 and E5 constituted a group that was relatively favorable test locations and was found close to E2 (Fig. 5). However, the location E3, a member of the second mega-environment was the poorest test location of the group as compared to the ideal environment while E1 also showed less discriminating power to distinguish among the genotypes (Fig. 5). Thus, E2 had the maximum ability to provide unbiased information about the yield performance of tested genotypes.

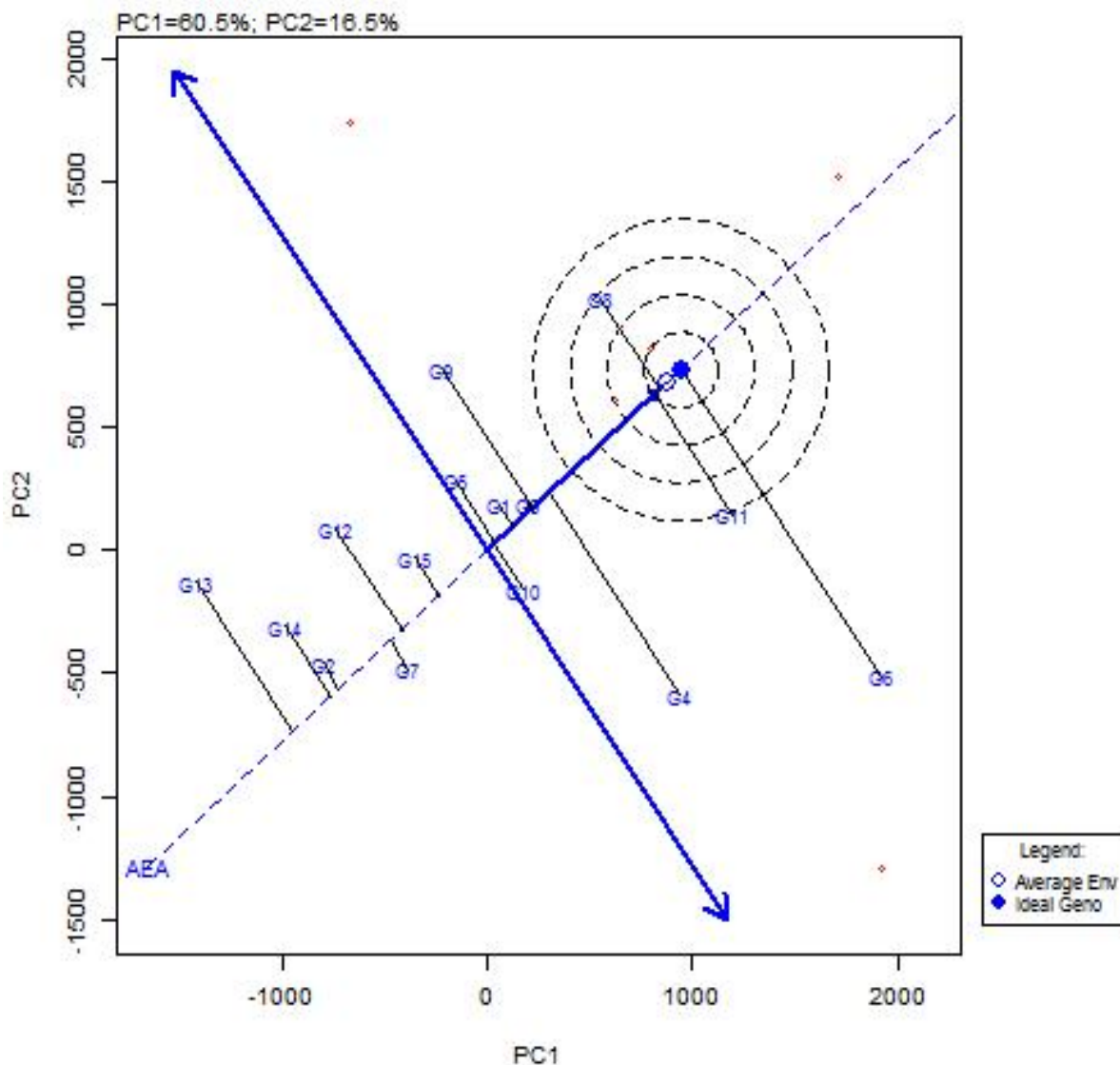


Figure 2: GGE-biplot view of “mean vs. stability” of 15 wheat genotypes based on average environment coordination (AEC). G, E, and PC represent the genotype, location, and principal component, respectively.

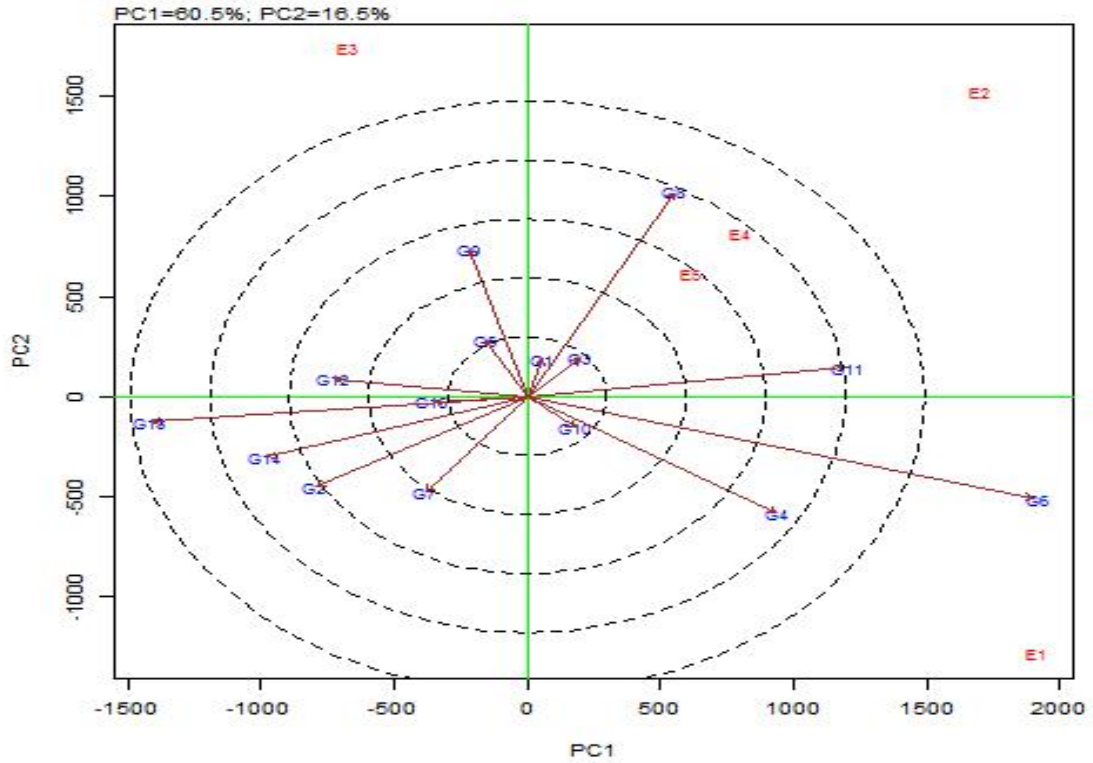


Figure 3: Comparison GGE-biplot based on an ideal genotype. G, E, and PC represent the genotype, location, and principal component, respectively.

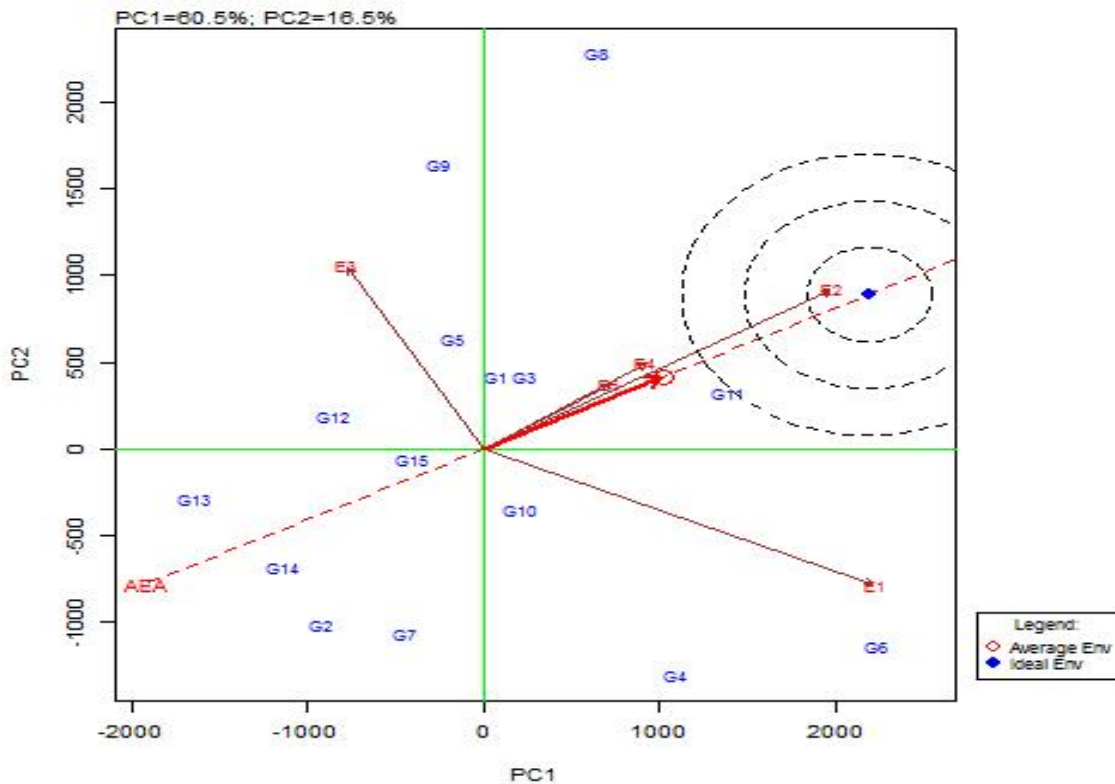


Figure 4: Discriminating power vs. representativeness view of GGE biplot to illustrate the relationship among different locations. G, E, and PC represent the genotype, location, and principal component, respectively.

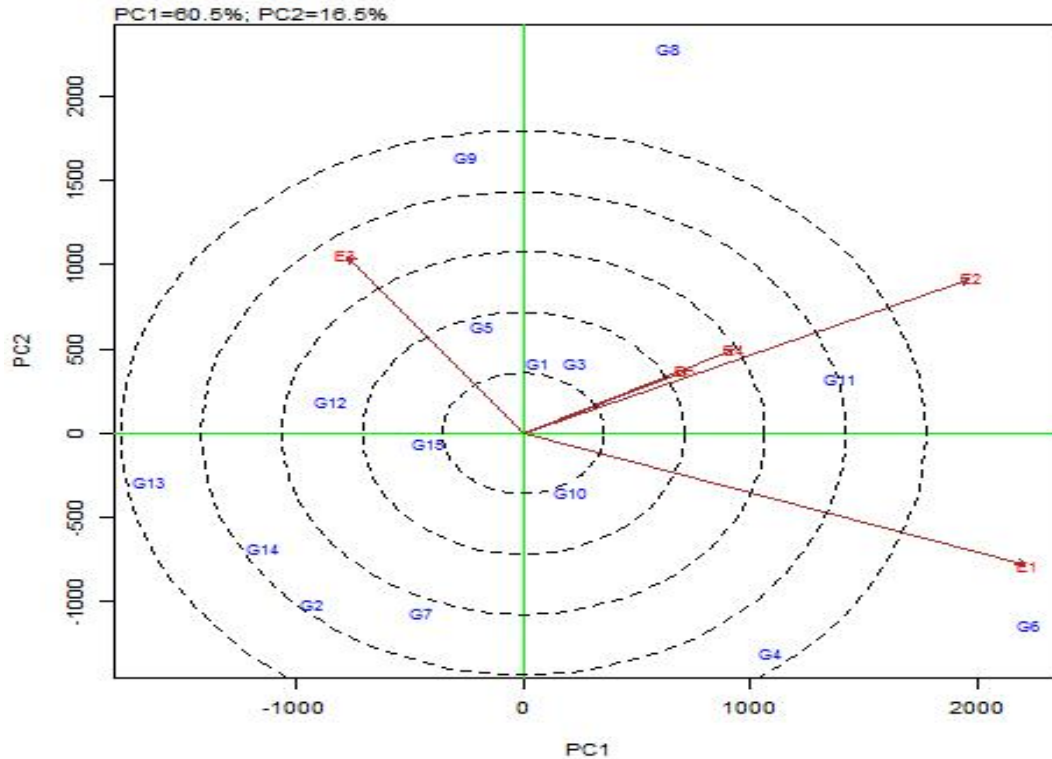


Figure 5: Comparison GGE-biplot based on an ideal location. G, E, and PC represent the genotype, location, and principal component, respectively.

DISCUSSION

The genotype main effect plus genotype-by-environment interaction (G+GEI) biplot analysis is a multivariate analysis tool that displays the relationship between genotypes and the test locations representing different environmental conditions. The which-won-where GGE biplot provides the best graphical view to visualize the G×E interaction (GEI) pattern, presence, and absence of cross over GEI and the presence of any mega-environments in the target or tested locations (Yan *et al.*, 2000; Yan and Tinker, 2006). This biplot represents a polygon that is drawn by joining the mark-points of those genotypes, lying at the farthest area from the origin of the biplot in such a way that the remaining genotypes are enclosed within the polygon (Yan *et al.*, 2002; Kaya *et al.*, 2006). The genotypes placed at the vertices of this polygon are considered as the poorest or the best genotypes depending upon the presence of environments in a given sector (Yan *et al.*, 2007). In this study, the GGE biplot allocated the test locations to only two sectors (mega-environments) of the polygon, for which six vertex genotypes *viz.* G4, G6, G8, G9, G13, and G2 were the winning genotypes. However, the genotypes G2, and G13 were the poorest genotypes in respect to grain yield in most of the tested locations as these genotypes were located farthest from the biplot origins in the sectors where no mega-environment was

found. The analysis of variance and mean genotype performance also designated these genotypes as poor performers due to the minimum grain yield as compared to other genotypes. These results further demonstrated that the genotype G4, G6, and G11 performed quite well specifically in lower Sindh (represented by E1) as well as also in other areas of Sindh. However, the genotypes G8 showed good stability coupled with good yield performance in lower (E4), middle (E5) and upper Sindh (E2 and E3). Hence, these genotypes could be the potential high yielding cultivars of the area.

Another view of GGE biplot named as ranking biplot used the average environment coordination (AEC) method to evaluate the stability of given genotypes. According to this method, a line known as average environment coordination abscissa (AEA) representing the average scores of the first two PC (PC1 and PC2) of all the tested environments is drawn through the biplot origin. The genotypes found closer to AEA indicate higher average yield. This AEA has only one direction and ranks the high-yielding genotypes accordingly in the direction of the arrow (Yan *et al.*, 2002; Abate *et al.*, 2015). Additionally, to estimate the stability performance of each genotype another double arrowhead line perpendicular to AEA is drawn which also passes through the origin of the biplot. The length of the projection vector of any genotype perpendicular to AEA to either side represents the strength of stability. Shorter the

projection more stable the genotype with minimum GEI. According to this description the genotypes G1, G3, G4, G5, G6, G8, G9, G10, and G11 found on the right side of AEA had good performance while the genotypes G2, G7, G12, G13, G14, and G15 appended on the left side of AEA had low mean grain yield than the overall average yield of all the genotypes. It is noteworthy that the genotype G8 showed the maximum stability across different environments and ranked second in grain yield production according to the ranking biplot, hence can also be designated as the most suitable candidate line for the target environments. In addition to this, the GGE biplot analysis also offers a unique and very useful tool to evaluate genotypes in comparison with the ideal or virtual genotype having the highest average yield and stability. Such an ideal genotype possesses a large PC1 score representing the highest value of trait of interest and low PC2 scores representing the stability performance of that genotype for a given trait at multi-locations (Yan and Kang, 2003; Farshadfar *et al.*, 2012). Our study revealed that G6 was an ideal genotype as found in the center of concentric rings. Based on the ideal genotype the rank of other favorable genotypes was $G4 > G11 > G8$.

The discriminating power versus representativeness biplot is another effective tool of GGE biplot analysis to identify the best environment that can discriminate the genotypes. The line joining the location or environment markers with the biplot origin is known as an environmental vector which is directly proportional to the standard deviation of the test location, thus, indicated the discrimination power of an environment (Abate *et al.*, 2015). While the angle between any two given environmental vectors defines the magnitude of the association between them. The correlation will be positive if the angle between vectors is acute while obtuse and right angles between vectors indicate negative and no correlation, respectively (Yan and Kang, 2003). Based on this biplot, the five test locations were classified into two mega-environments having E1 in the first mega-environment and E2, E3, E4, and E5 in the second mega-environment. The biplot also suggested that the locations E2 was an ideal location that grouped with E4, and E5 which were very similar in ranking the genotypes as the environment vectors of these locations overlapped another. Between these locations, E4 ranked better than E5 and anyone can be selected to evaluate wheat genotypes if the same pattern persists over the years. Therefore, among these three locations, anyone could be used in the future to evaluate the genotypes.

Conclusion: The results of this study demonstrated that the grain yield of 15 wheat genotypes across five different locations was significantly influenced by genotypes, locations (environments), and their interaction ($G \times E$). The GGE-biplot analysis revealed that the test locations could be grouped into two mega-environments

in which genotypes G4 and G6 were the winner genotypes in the first mega-environment while G11 also performed quite well across all the locations while in the second mega-environment, G8 was the winner genotype which showed good stability coupled with better grain yield as compared to rest of the genotypes. Additionally, GGE-biplot analysis designated G6 as an ideal genotype while E2 as an ideal test location which showed the maximum discriminating power to evaluate the wheat genotypes. The test locations E4 and E5 had the same ability to distinguish genotypes based on grain yield. Taken together, the wheat advanced lines G6, G8, and G11 showed good yield potential to become the candidate wheat lines for further evaluation in national trials and cultivation in Sindh province of Pakistan.

Author's Contribution: MF executed the experiment and wrote the manuscript. MAS supervised the experiment; MF, SA and KAL developed the experimental material.

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