EVALUATION OF SELECTED WHEAT GENOTYPES AT MULTI LOCATIONS FOR YIELD STABILITY, CLIMATE CHANGE AND FOOD SECURITY

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Abstract

Wheat is the staple food for most of the population, contributing to 60% of the dietary energy intake. The changing climatic conditions effect wheat grain yield drastically. To cope with the situation an experiment planned to evaluate newly developed high yielding wheat genotypes in multiple environment to check the yield stability and best-suited environment. Ten wheat genotypes sown at twelve locations. The experiment conducted in a randomized complete block design with three replications. The plot size was 5 m x 1.5 m during rabi season 2022-2023. Pooled (ANOVA) revealed significant variation in genotypes and environments. Maximum contribution in total variation was due to environments. AMMI and GGE Biplot indicated G5 was very sensitive and responsive across all the environments. CCRI Noshera found most suitable and best environment for wheat production. Genotypes G9 remained stable and high yielder across all environments.

Introduction

Wheat is one of the most important cereal crops in the world, providing food and income for billions of people. According to the Food and Agriculture Organization (FAO, 2023), wheat production reached 776 million tonnes in 2023, accounting for 19% of the global cereal production. Wheat is grown in more than 130 countries, covering about 220 million hectares of land. The major wheat-producing regions are Europe, Asia, North America and Australia. Pakistan is the eighth largest wheat producer in the world, with an annual production of about 27 million tonnes in 2022-23. Wheat is the staple food for most of the population, contributing to 60% of the dietary energy intake. Wheat is also a major source of income for farmers, as well as a key input for the flour milling, baking and other food processing industries. Wheat accounts for 10% of the value added in agriculture and 2% of the GDP

(PBS, 2023). Wheat accounts for about 40 percent of the total cropped area and 36 percent of the value added in agriculture. Wheat is an important source of income and food security for smallholder farmers, who produce about 80 percent of the total output. Wheat is also a key ingredient for livestock feed, especially for the poultry sector, which consumes about 10 percent of the total wheat supply. Wheat output is important for food security, poverty alleviation, and economic stability in Pakistan.

The yield and quality of wheat depend on various environmental factors, such as temperature, rainfall, soil, pests and diseases. Wheat is a cool-season crop that requires low temperatures during germination and flowering, and moderate temperatures during grain filling. Wheat is sensitive to water stress, especially during the reproductive stage. Wheat requires fertile soils with good drainage and aeration, as well as adequate nutrients, especially nitrogen and phosphorus. Wheat is susceptible to various biotic stresses, such as insects, fungi, bacteria, viruses and weeds, which can reduce yield and quality (Zhao *et al*., 2015). Among these biotic and abiotic factors, fluctuation and sudden change in climate is considered to be one of the most serious challenges for wheat production in the future (Smith *et al*., 1990). Climate change can alter the temperature, rainfall, and CO_2 levels, which can have both positive and negative impacts on wheat growth and yield. For instance, higher temperatures can reduce the length of the growing season and increase water stress, while higher CO_2 levels can enhance photosynthesis and water use efficiency. Climate change can also increase the frequency and intensity of extreme weather events, such as droughts, floods, heat waves, and frost, which can damage wheat crops and reduce yields (Anonymous, 2023). Moreover, climate change can affect the distribution and severity of pests and diseases, such as wheat rusts, aphids, and nematodes. According to a recent study by FAO, global wheat production could decline by 6 percent by 2050 due to climate change. The study also projected that wheat production in Asia could decrease by 8 percent by 2050, with South Asia being the most affected subregion. The study suggested that adaptation measures are needed to cope with the impacts of climate change by developing new wheat genotypes, which are less effected by changing climate, could perform in multi environments and have stable yield (Ginkel and Ortiz, 2018). A study was planned to evaluate elite lines of wheat at multiple locations to identify genotype which produce stable yield in different environments. Biplot and stability analysis are two important tools in plant breeding and genetics, especially for wheat (Yang *et al*., 2009). Biplot analysis can help visualize the relationships among genotypes, environments, and

traits, and identify superior genotypes for different environments or target traits (Gauch and Zobel, 1996a; Sareen *et al*., 2012; Tyagi *et al*., 2016). Stability analysis can measure the consistency of genotype performance across environments, and rank genotypes based on their stability parameters. Both biplot and stability analysis can provide useful information for genotype selection and recommendation in wheat breeding programs.

Material and Methods

Ten wheat genotypes with diverse genetic backgrounds evaluated under rain-fed conditions at twelve different locations. The experiment was conducted in a randomized complete block design with three replications. Each genotype was allotted to six rows with a spacing of 25 cm apart. The size of the plot was 5 m x 1.5 m. Genotypes were grown during the Rabi season of 2022-2023 to assess their stability for grain yield across different environments. Seeds of these genotypes were procured from the National Agricultural Research Centre Islamabad. The experiment was conducted in a randomized complete block design with three replications. A pooled analysis of variance (ANOVA) was conducted on the grain yield data of wheat to assess the effects of genotype (G), environment (E), and their interactions.

PB tools 2014 (Version 1.4, http://bbi.irri.org/products) and R (R CoreTeam, 2012) were used to visually evaluate the data. The mean square of error used to evaluate the significance of all effects. The Additive Main Effects and Multiplicative Interaction (AMMI) (Gauch and Zobel, 1997) and GGE Biplot or Site Regression (Yan and Kang, 2003) stability models used to evaluate the performance of wheat genotypes. While only the interaction component (GEI) of the AMMI model is employed for the analysis, the genotypic effect (G) and its interaction with the environment (GEI) are both included in the GGE biplot analysis. The AMMI analysis is based on two models. AMMI model first analyze main effect with analyzing the residual from this model (specifically the interaction), AMMI first uses analysis of variance (ANOVA) to examine the genotypes and environmental main effects (additive). Below is a model for AMMI analysis.

$Y_{ij} = \mu + \delta_i + \beta_j + \Sigma\lambda_k\delta_{ik}\beta_{jk} + \varepsilon_{ij}$

Where,

Y_{ij}: average yield of ith variety in the jth environment,

μ: general mean,

δ_i: genotypic effect of ith cultivar, β_j is jthenvironment effect,

λk : eigen value of the Principal Component Axis k,

δik: is the genotype eigen vector value for PC axis n,

βjk: is the environment eigen vector value for PC axis k and

εij: is the residual error.

The genotype and genotype environment variation by the GGE biplot, which is based on the site regression linear (SREG) bilinear model (Crossa and Cornelius, 1997; Crossa *et al*., 2002). The graph produced by GGE biplot shows (i) the polygon view of GGE biplot analysis (ii) genotype performance across environments, (iii) ranking of genotypes relative to ideal genotype, (iv) relationships between test environments, and (v) the representativeness of test environments. List of wheat genotypes and different location given in Table 1.

Table 1: Ten Wheat Genotypes and Twelve Environments

Genotypes		Environment	
G-1	301	E1	NARC, Islamabad
G-2	302	E2	ARS Swabi
G-3	303	E3	BAARI Chakwal
G-4	304	E4	ARI Quetta
G-5	305	E5	ARS BAFA Mansehra
G-6	306	E6	BARS Kohat
G-7	307	E7	CCRI Noshera
G-8	308	E8	Bahawalpur
G-9	309	E9	Dera Ismail Khan
G-10	310	E10	Tandojam
		E11	Larkana
		E12	WRI FSD

Results and discussion

Both genotype and environment mean sum of squares were significant for grain yield, according to a combined analysis of variance (Table 2). This demonstrated the presence of variation among genotype and environment. For grain yield in all environments, the AMMI analysis of variance revealed that variation due to genotypic effects accounted for 25.2% of the total variation, environmental effects for 67.6%, and genotype environment interaction effects for 7.2%. The AMMI model made it very evident that GEI existed, highlighting the significant variations in genotypic response in all environments.

The interaction between the ten wheat genotypes and twelve environments was predicted by the first two components of genotypes and environments. The G x E interaction was

partitioned among the first two interaction principal component axes (PCAI) and (PCAII), which accounted for 42.4% and 22.6% of the total variance, respectively. The cumulative variance explained by PCA I and PCA II was approximately 65.0% .

Table 2. Analysis of variance of ten wheat genotypes tested across twelve environments

SOV	Df	SS	MS	F value	%explained	Cumulative
Trials	119	1034102.75	8689.939	11.48		
Genotype	9	191024.24	21224.92	14.25	25.2	18.47
Environment	11	776034.64	70548.6	81.02	67.6	92.8
G*E Interaction	99	67043.87	677.2108	23.81	7.2	100.0
PCA I	19	18342172.9	965377.5	14.61	42.4	42.1
PCA II	17	9779063.2	575239	7.27	22.6	65.0

According to the mean performance of different genotypes in twelve different environments revealed that mean grain yield kgha^{-1} of genotype G-9 was highest among all other genotypes 4225.3 kgha^{-1} followed by G-8 and G-10. Among the environments at E7 (CCRI Noshera) produced highest mean grain yield 5964.5 kgha^{-1}.

Table 3. Mean performance of wheat genotypes across the environments for grain yield Kgha^{-1}

Genotypes	E-1 Kgha^{-1}	E-2 Kgha^{-1}	E-3 Kgha^{-1}	E-4 Kgha^{-1}	E-5 Kgha^{-1}	E-6 Kgha^{-1}	E-7 Kgha^{-1}	E-8 Kgha^{-1}	E-9 Kgha^{-1}	E-10 Kgha^{-1}	E-11 Kgha^{-1}	E-12 Kgha^{-1}	Means Kgha^{-1}
G-1	6680.0	4444.4	5291.7	1193.3	4666.7	2305.6	4677	666.7	943.3	4814.8	4200.0	3640.74	3626.9
G-2	6354.7	5000.0	4833.3	1126.7	4800.0	2527.8	5920	1666.7	817.8	4074.1	4239.6	4162.96	3793.6
G-3	5901.3	3333.3	4597.2	904.0	5066.7	3111.1	6447	1666.7	944.4	4444.4	5593.8	3866.67	3823
G-4	5504.0	5000.0	3972.2	920.0	5466.7	2683.3	6263	1666.7	735.6	5000.0	5475.0	2903.70	3799.2
G-5	5085.3	3333.3	4236.1	733.3	5600.0	3094.4	5000	2000.0	553.3	3703.7	5583.3	2961.73	3490.3
G-6	6052.0	3888.9	4680.6	813.3	4800.0	4433.3	5873	2000.0	916.7	4814.8	4229.2	2975.31	3789.7
G-7	5740.0	4444.4	4722.2	873.3	4933.3	5538.9	5730	1500.0	813.3	4074.1	5625.0	3160.49	3929.5
G-8	5949.3	5555.6	5027.8	410.7	4666.7	4950.0	6617	1833.3	1027.8	4444.4	4250.0	3296.30	4002.3
G-9	6041.3	6111.1	4569.4	273.3	4933.3	6005.6	6883	1666.7	800.0	5000.0	4333.3	4086.42	4225.3
G-10	5025.3	3888.9	6708.3	653.3	5200.0	5038.9	6237	1666.7	815.6	4814.8	4270.8	2979.01	3941.5
Means	5833.3	4500	4863.8	790.1	5013.3	3968.8	5964.6	1633.3	836.7	4518.5	4780	3403.3	

A biplot is a graphical method to display the mean yields and interactions of different genotypes or environments in a two-dimensional space. A biplot has a perpendicular line that divides the graph into two parts. Genotypes or environments that are close to this line have similar mean yields, while those that are far from it have different mean yields. Genotypes or environments that are near a horizontal line have similar interactions, while those that are far from it have different interactions. (Crossa *et al*., 1990). Results indicated that genotype G9 had high and stable yield, genotype G7 had high but unstable yield, and genotypes G8 and G10 had similar yield. These results shown in Figure 1.

The yield of genotypes G1 and G5 was lower than the others. Some environments (E4, E8 and E9) were not favorable for the most of wheat genotypes, while others (E7, E1, E5 and E3) were more suitable. The PCA1 score measures how much the genotypes interact with the environments. A high or low PCA1 score means a strong interaction, while a score close to zero means a weak interaction (Crossa *et al*., 1990). The genotypes G1, G2, G3, G4 and G5 had high PCA1 scores, highly affected by the environments. Among them, G6 had a good yield and a low PCA1 score, which reflects G6 was more stable and adaptable to different environments. The AMMI 2 bi-plot Figure 2 indicated that the environmental scores connected to the origin by lines. This helps to interpret the AMMI models.

The length of the vectors affects how much they interact with each other. Short vectors have weak interactions, while long vectors have strong interactions. This means that environments E3 and E9, which had short vectors, did not have much difference among them, but environments E6, E2, E11 and E1, which had long vectors, were more distinct from each other. The genotypes that are close to the origin of the graph are not affected by the environmental interactions, but the genotypes that are far from the origin are affected and show more variation due to the environment. Genotypes G6 and G4 were near the origin and did not change much across environments, but genotypes G5, G9, G8, G10, G7, G1, G2 and G3 changed a lot depending on the environment. The genotypes that performed best in environments E4, E3, E5 and E11 were genotypes G4, G6, G3 and G5 respectively.

Figure 1: AMMI 1 Biplot for grain yield of 10 wheat genotypes and twelve environments using genotypic and environmental scores
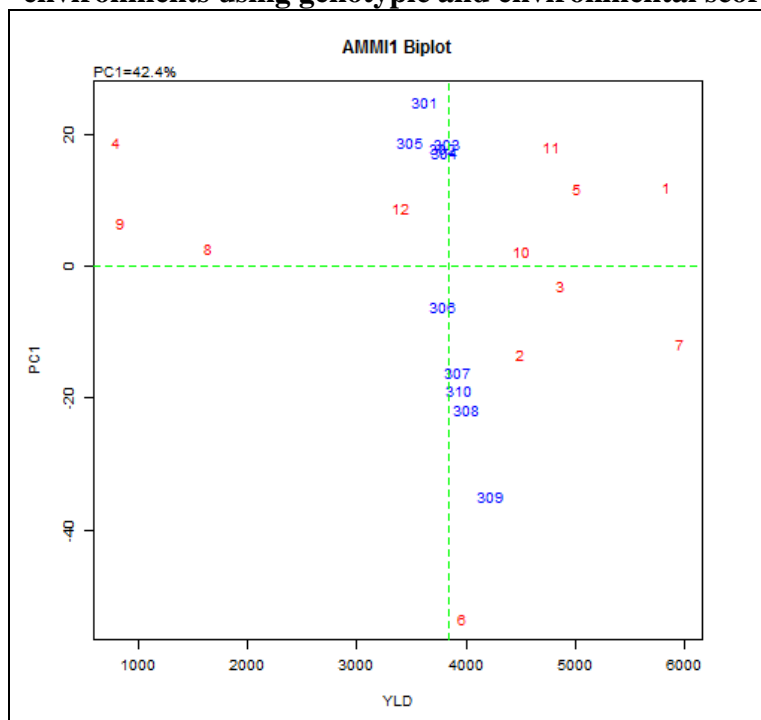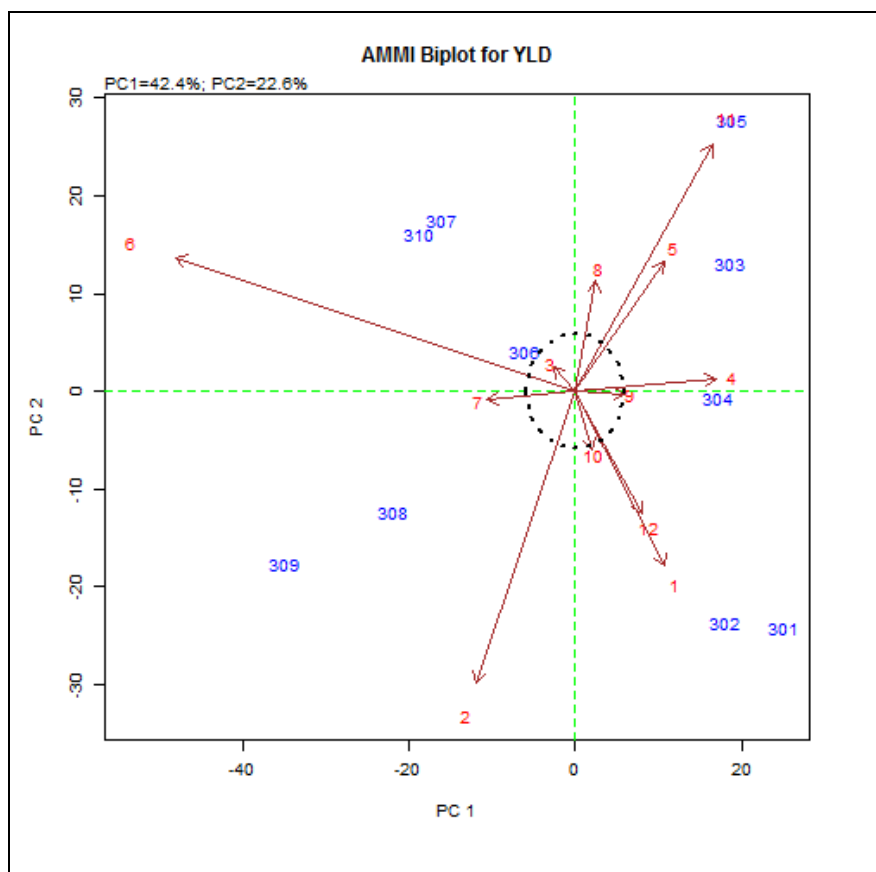
Figure 2: AMMI 2 Biplot for grain yield showing the interaction of IPCA2 against IPCA1 scores of ten wheat genotypes in twelve environments.

Wheat genotypes were compared in different environments by using vectors in Figure 3. The angle between the vectors of two genotypes reflects response in an environment. If the angle

is small (< 90°), the response is similar. If the angle is large (> 90°), they respond oppositely. If the angle is 90°, they are independent of each other (Yan and Tinker, 2006). In environments E3, E11 and E4, genotypes G1, G5, G3 and G4 had low yield, while genotype G9 had high yield in E2.

The vectors to use compare the performance of different genotypes in different environments. A vector is a line with a direction and a magnitude. The direction shows how the genotype responds to the environment and the magnitude shows how much it responds. If the angle was less than 90 degrees, it meant that the genotypes had similar responses, and behaved similarly in that environment. If the angle was more than 90 degrees, the genotypes had opposite responses, behaved differently in that environment. If the angle was exactly 90 degrees, genotypes had independent responses, been not related to each other in that environment. Results indicated that environments E3, E11 and E4, genotypes G1, G5, G3 and G4 had low yields, while genotype G9 had high yield in E2 Fig 3.

A model genotype is a type that can produce high yields in different conditions and does not change much in its performance (Yan and Kang, 2003). The figure 4 indicated a blue circle with an arrow that indicates the average of all the environments where the wheat genotypes were grown, and a dark blue dot that indicates the ideal genotype. The ideal genotype is the one that is closest to the blue circle and has the highest yield. Results indicated that genotype G9 was the best performer (Figure 4). Genotype G6 was also stable, but not as high yielding. Genotypes G1, G2 and G5 were very unstable and changed a lot in their performance. Genotype G3 was always low yielding. A stable genotype also had a high yield. Therefore, genotype G9 was the most desirable genotype in this study.

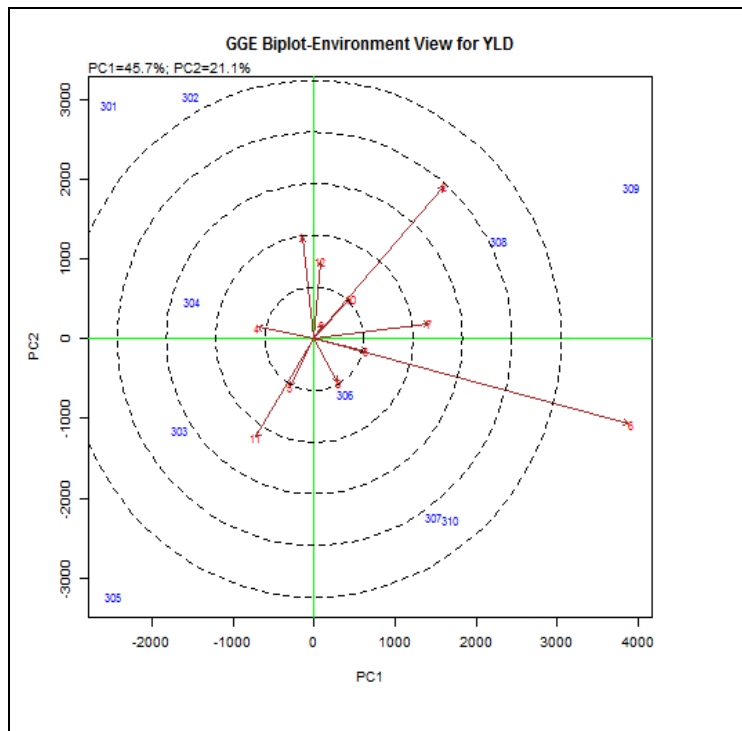**Figure 3: Ranking of genotype based on the performance across the environments**
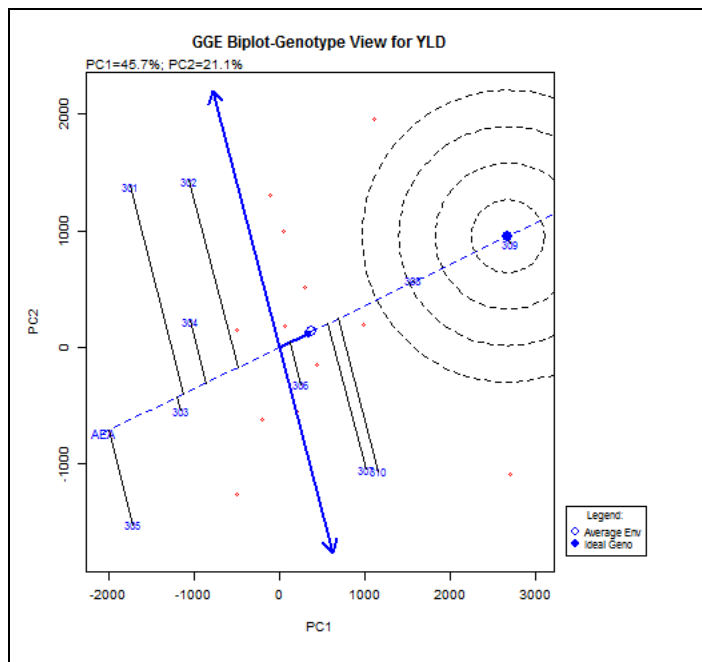
Figure 4: Average-environment coordination (AEC) view to rank genotypes relative to ideal genotypes

Polygon view of GGE biplot analysis of multi environment trial data

The GGE biplot indicates the best and the worst genotypes-environment combinations using a polygon view (Figure 5). The polygon connected the genotypes that are farthest from the centre of the biplot, and covers all the other genotypes inside it. Then, lines are drawn from the centre of the biplot to each side of the polygon, perpendicular to it. The genotypes at the corner of each sector were that had the highest yield in the environment that belongs to that sector (Yan et al., 2000). The genotypes G1, G5 and G9 are the most extreme ones, as they were farthest from the centre of the biplot. They had either very high or very low yield in some environments. The line between G9 and G5 showed that G9 had higher yield in E2 and E7, while G5 showed higher yield in E11 and E5. The line between G5 and G1 showed that G2, G3 and G4 had higher yield in E1, E4, E5, E11, E12.

Figure 5: Polygon view of genotype-environment interaction across twelve test environments
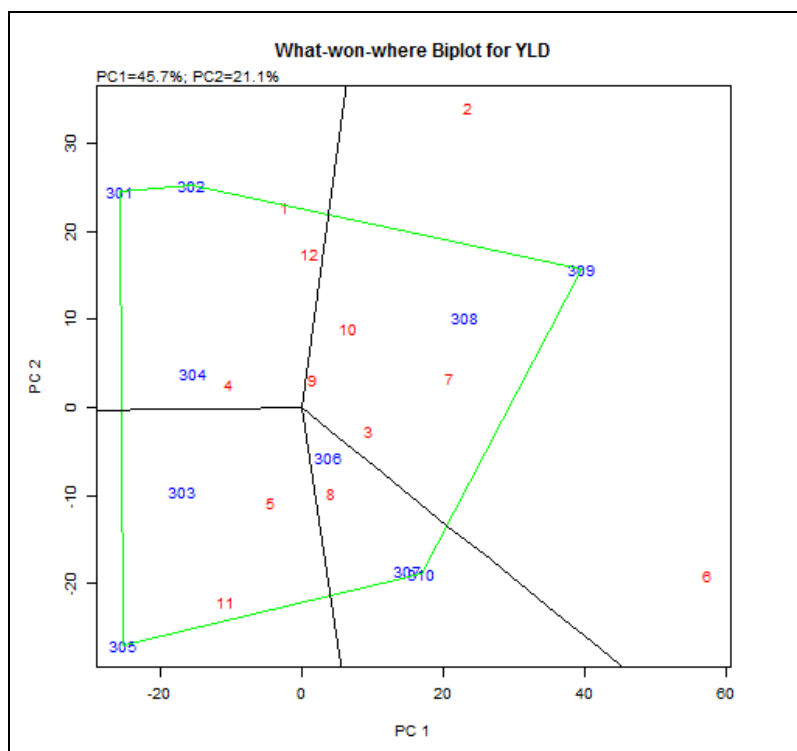
A vector that is on the AEC (Abscissa), had the highest discrimination and representation, and best way to measure the environment (Yan, 2001). This type of vector shown by blue dots in Figure 6. The red dotted line that goes through the centre of the biplot is called the average environment axis (AEA) and it shows how similar an environment is to the average of all environments. An environment with a long vector and a small angle with the AEC is more informative and representative than an environment with a short vector (Yan et al., 2007; Yan and Kang, 2003).

Comparison of different wheat genotypes and how they adapt to different environments vectors of each environment was measured, which indicated how much they differ from the average environmental conditions. Results indicated that environments E6 and E2 had long vectors, and very different from the average. These environments can help identify which genotypes more suited for specific conditions, but these vectors cannot help to select genotypes that can perform well in general. For that purpose, the environment E7, which had a medium vector length and a small angle with the average environmental condition (AEC) was more representative of the average environment. This is important because the global population is growing rapidly, but the wheat productivity is not keeping up due to changing environmental factors.

Figure 6: The discrimination and representativeness view of the GGE biplot to show the discriminating ability and representativeness the test environments
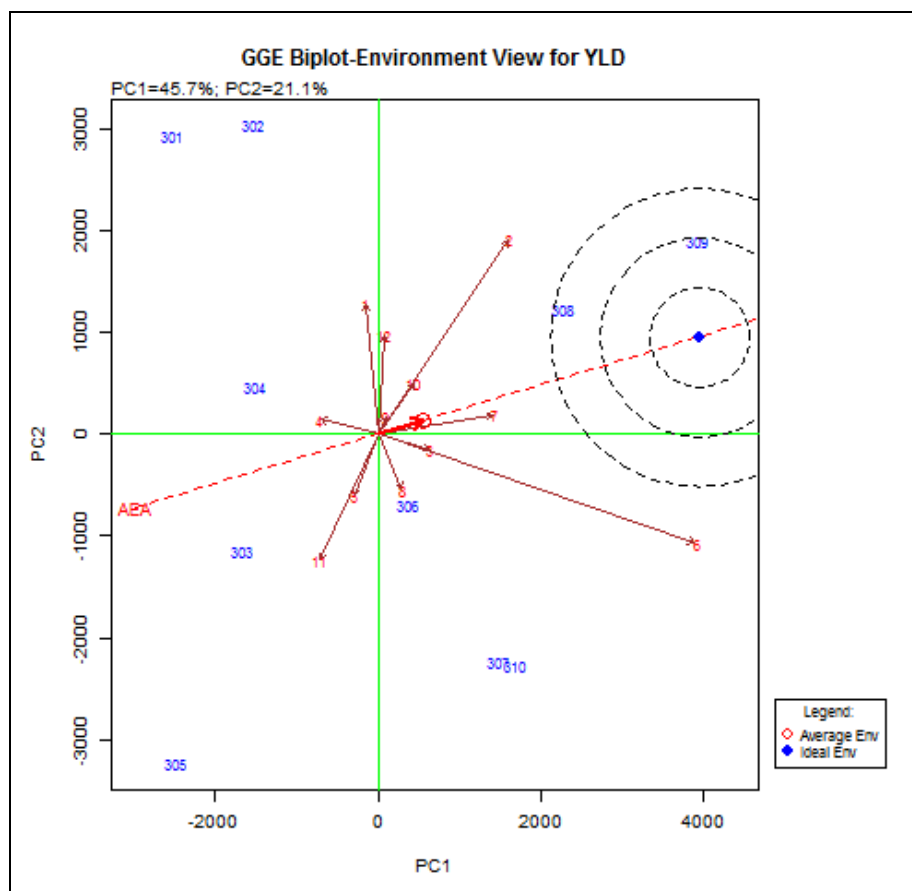
The main goal of this research was to find wheat varieties that can produce more and cope better with different environmental challenges (Crane *et al*., 2011; Parry *et al*., 2012; Macholdt *et al*., 2013; Mühleisen *et al*., 2014; Stratonovitsch *et al*., 2015). This is important for the current and future food security. However, finding such varieties is not easy because they may perform differently in different environments. This is called genotype by environment interaction (GxE). To deal with this problem, two statistical methods has been: AMMI and GGE biplot. These methods can help to compare the performance of different wheat varieties across multiple environments and to identify the ones that are stable and adaptable. AMMI can measure how much each variety interacts with its environment (Crossa *et al*., 1990). GGE biplot can show the relationship between varieties and environments and help to select the best ones for each situation (Yan, 2001). These methods have been used by many previous studies to evaluate wheat varieties in different regions (Farshadfar *et al*.,

2013; Rad *et al*., 2013; Hagos and Abay, 2013; Amiri *et al*., 2015; Ali *et al*., 2015; Kumar *et al*., 2016; Tekdal and Kendal, 2018).

The results of this study showed that genotypes, environments and GE interaction had significant effects on the traits measured (Table 2). This also indicated that the environments were very diverse, as they accounted for a large proportion of the variation. This is different from the findings of Farshadfar (2012), who found that environment, genotype and genotype by environment interaction explained 27.1 %, 15.6% and 57.3 % of the variation, respectively. Hagos and Abay (2013), Akcura *et al*., (2011) and Mohammadi *et al*., (2015) described how the GxE interaction was further analysed using principal component analysis (PCA), which is a statistical method to reduce the complexity of data. The first two principal components (PCs) explained most of the variation in grain yield. Stability analysis, which is another method to measure the performance of genotypes across environments, was only done when GxE interaction was significant. Comparison of the grain yield of different environments, and noting that E7 had the highest yield and E4 had the lowest yield.

The GGE and AMMI model were used to analyze the data. The AMMI analysis showed that the genotypes with lower yield than the average were grouped in low PCA1 scores and were on the left side of the AMMI-biplot (Gauch and Zobel,1996b). This means that they were less stable and more responsive to environmental changes. Genotype G9 was far from the origin and had high mean yield and stability. This agrees with previous studies by Ilker *et al*., (2011), Bavandpori *et al*., (2015), Tekdal and Kendal, (2018). An ideal genotype should have high mean yield and perform consistently across different environments (Yan and Kang, 2003). The AMMI biplot showed that the genotypes that were close to the mean environment and had small projections on AEC were ideal (Farshadfar *et al*., 2012; Yan and Tinker, 2006). To check the stability and adaptability GGE biplot used to visualize and interpret the data. This tool helps to see how the genotypes perform in different environments, and how similar or different the environments are and found that G9 and G6 were stable genotypes in different environments. However, G9 was the best genotype because of the highest yield potential. This agrees with what Farshadfar *et al*., (2013) reported in their study. Environments could be grouped into 4 clusters based on their similarity E2,E7,E9,E10 and E12 were similar to each other, and so were E3 and E11 in second cluster , E5, E6 and E8 in third and E1 and E4 were in fourth cluster. The environments can assessed on base of which one was more suitable for selecting genotypes that were either specifically adapted or

generally adapted. Specifically adapted genotypes perform well in some environments but not in others. Generally, adapted genotypes perform well in most environments E6 found good for selecting specifically adapted genotypes, while E7 was good for selecting generally adapted genotypes. This is based on the angle and length of the environmental vectors, which are lines that represent the environments on the biplot. The angle shows how different the environments are, and the length shows how discriminating they are. This method of analysing the data is useful for identifying different mega-environments in a region. A mega-environment is a place where the growing conditions are similar and some genotypes perform better than others. The GGE biplot showed which genotype won in which environment. G9 was found best genotype in E6 and while G1, G5, G3 and G4 was the best genotype in E12. Similar results were also reported by Kaya *et al.*, (2006), Mohammadi *et al.*, (2010), Akcura *et al.*, (2011), Rad *et al.*, (2013), Hagos and Abay (2013), Sabaghnia *et al.*, (2013), Amiri *et al.*, (2015), Kendal and Sener (2015),Abate *et al.*, (2015), Karimizadeh *et al.*, (2016) Alam *et al.*, (2017), Bacha *et al.*, (2017) and Kumar *et al.*, (2018) in wheat.

Conclusion

In conclusion, stable and high yielding genotypes can be identified using AMMI and GGE biplot. Based on the performance of genotypes 305 found very sensitive and responsive across the environments. CCRI Noshera found most suitable and best environment for wheat production. Genotypes 309 were found stable and high yielder across all environments.

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