



Screening of Chickpea Genotypes for Yield Stability Across Environments

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Abstract: Yield stability of 24 elite chickpea genotypes was assessed through chickpea cooperative yield trials at nine diversified locations of Punjab, Pakistan, during 2017-18. Data were subjected to Genotype main effects and genotype \times environment interaction effects (GGE) biplot analysis and mega-environment analysis to identify the most stable and high yielding genotypes. Through GGE biplot, irregular polygon of genotypes connected the genotypes with each other representing the what-won-where for yield mean. Biplot illustrated that genotype G23 (TG1415) was ideal in performance, followed by G15 (D-15024), G17 (D-15033) and G16 (D-15030) and all the aforementioned genotypes were found more stable and high yielding across the environments. Mega environment analysis revealed that G23 (TG-1415) had higher yield in E1 (Pulses Research Institute, Faisalabad) and E3 (Gram Breeding Research Sub-Station, Kallurkot) environments. Similarly, G15 (D-15024) showed higher yield in E5 (Adaptive Research Station, Karor), G17 (D-15033) performed better in E2 (Nuclear Institute for Agriculture and Biology, Faisalabad) and G16 (D-15030) performed better in E4 (Arid Zone Research Institute, Bhakkar). Mega environment analysis also confirmed that E1 (Pulses Research Institute, Faisalabad, and E5 (Adaptive Research Station Karor) are most useful and ideal environments for the selection of genotypes. The genotypes G23 (TG1415), G15 (D-15024), G17 (D-15033) and G16 (D-15030) are more stable and better performing, therefore, these genotypes may be considered further for chickpea breeding program.

Key words: Chickpea, Yield stability, GGE biplot, Mega-environment analysis.

INTRODUCTION

Chickpea is one of the most important food legume crops and chief source of dietary protein thereby plays a vital role in mitigating protein malnutrition across the world (Choudhary *et al.*, 2018; Considine *et al.*, 2017). Present status of pulses production depicts a gloomy picture with an erratic harvest caused by certain manageable and non-manageable aspects (Fikre, 2016). In current scenario, United Nations initiated global efforts for promotion of legume crops through their development program on "Nutritious seeds for a sustainable future" (Foyer *et al.*, 2016; FAO, 2016). In Pakistan, chickpea is being cultivated on 2399 million hectare land and Punjab solely contributes 90% (2175 million hectare) of the national area under crop (Agricultural Statistics of Pakistan, 2016-17). In Pakistan, average yield of this legume per unit area is low and fluctuating annually, i.e., during 2012-13, 2013-14, 2014-15, 2015-16 and 2016-17, was recorded 751, 399, 379,

286 and 329 thousand tons, respectively (AMIS, 2016-17). The gap between production and consumption in the country is being bridged by importing a substantial quantity of chickpea. Despite the availability of high yielding varieties of chickpea, fluctuation in average production indicates vulnerability of genotypes to a wide range of environments (Bakhsh *et al.*, 2011; Sharifi *et al.*, 2018). Environmental conditions, such as, temperature, humidity, soil moisture and rainfall, vary from year to year and location to location to a great extent. Therefore, stability in chickpea production may only be attained through development of widely adapted chickpea varieties coupled with high yield potential.

Gap between potential yield and attained yield in chickpea is highly significant and needs to be addressed on priority basis (Malik *et al.*, 2014). Development of high yielding stable chickpea varieties having wide ecological adaptability across

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the environments may reduce this production gap. Stability in grain yield of cultivars under diversified environmental conditions is highly desirable to develop and release widely adapted chickpea varieties (Singh and Bejiga, 1990). Differential performance of a cultivar under variable environments is termed as genotype \times environment interactions ($G \times E$). Such performances are compared when two or more genotypes are evaluated in two or more diversified environments. Grain yield stability analysis founded on genotype \times location may be considered as a primary selection model for the development of high yielding and widely adapted varieties (Annicchiarico, 1997).

For selection of superior genotypes regarding yield and stability, evaluation of genotypes under diversified environmental conditions is essential (Yaghotipoor and Farshadfar, 2007). Grain yield stability has already been emphasized and employed by various researchers for screening of genotypes with wider adaptability and better yield potential (Gauch and Zobel, 1996; Yan *et al.*, 2001; Samonte *et al.*, 2005; Farshadfar *et al.*, 2012; Naroui Rad *et al.*, 2013).

Many statistical strategies are developed to check the yield stability of genotypes at distinctive environments, but one of the foremost utilized strategies is the multiplicative analysis, i.e., GGE Biplot (Gauch, 1992; Ebdon and Gauch, 2002; Moreno-Gonzalez *et al.*, 2003). This examination depicts the interaction of genotypes across different environments (GEI). The GGE Biplot has extraordinary significance for breeders and agriculture researchers because it contains two-way data and graphical representation. The GGE biplot analysis decides the interaction between the genotype and the environment (Zobel *et al.*, 1988). This method gives more information about the yield stability of genotype (Purchase *et al.*, 2000). The identification of high performance stable genotypes is essential for sustainable chickpea production. The present study was planned to identify the widely adapted chickpea genotypes capable of high yield potential across the environments.

MATERIALS AND METHODS

The experimental material consisting of 24 chickpea advance genotypes developed by various research institutes/stations were evaluated for higher yield potential coupled with stability through Chickpea Cooperative Yield Trial 2017-18. The trial was conducted at nine diversified locations of Punjab, Pakistan (Table 2). The experiment was laid down in tri-replicate randomized complete block design (RCBD). Sowing at all the targeted sites was done during the second fortnight of October with dibbler by planting two seeds in each hole. After germination, plant-to-plant and row-to-row distance was maintained as 10 cm and 30 cm, respectively, by thinning.

All the agronomic operations were carried out as per requirement of the crop. On maturity, yield data of all the genotypes were recorded from all sites and compiled.

The data were subjected to statistical software Plant Breeding Tools (PB Tools) version 1.3 for GGE Biplot analysis. The multi-environment analysis was done in order to check the genotype by environment interaction (GEI) through graphical methods.

RESULTS AND DISCUSSION

The GGE biplot was made by plotting the scores of genotypes and environments of first principal component (PC1) against their respective scores of the second PC (Yan *et al.*, 2007). The GGE biplot of mega-environment analysis consists of irregular polygon that connects the genotypes with each other and lines drawn from the origin of biplot intersect with polygon at right angles to illustrate what-won-where for yield mean. The polygon marks the better performing genotypes, which were located away from the biplot origin in different directions and join to form a polygon (Yan *et al.*, 2000; Yan *et al.*, 2007).

The 6 genotypes formed a polygon which is connected to each other as shown in Fig. 1. These genotypes located furthest away from the origin represent winning mean performance. These genotypes were G23 (TG-1415), G15 (D-15024), G9 (D-1505), G2 (BRC-446), G6 (CH-2/11) and G17 (D-15033). The lines started from the origin of biplot and intersected the polygon perpendicularly representing the winning environment with genotypes. These lines divide the polygon into different sectors and each sector having winning genotype/genotypes (Yan and Rajcan, 2002). If all environments fall within a single sector, it indicates that one genotype has higher yield in all environments. If environments fall into different sectors, it indicates that different genotypes have the highest yield in different environments. From Fig. 1, it is evident that G23 (TG-1415) has higher yield in E1 (Pulses Research Institute, Faisalabad) and E3 (Gram Breeding Research Sub-Station, Kallurkot) environments. Similarly, G15 (D-15024) showed higher yield in E5 (Adaptive Research Station, Karor), G9 (D-1505), G6 (CH-2/11) and G2 (BRC-446) had higher yield in E6 (Regional Agricultural Research Institute, Bahawalpur), G17 (D-15033) performed better in E2 (Nuclear Institute for Agriculture and Biology, Faisalabad), E7 (Gram Breeding Research Sub-Station, Kallurkot, location-2) and E9 (Arid Zone Research Institute, Bhakkar, location-2), as shown in Fig. 1.

Environment evaluation was also done to identify the most useful environment, which ultimately identifies the superior genotypes. For this purpose, vectors were plotted through GGE biplot for environment view (Fig. 2). Length of vectors of environments is directly proportional to the standard deviation of genotype mean in the given environment.

It also measures the selective power of environments. On the basis of length of vectors, environments are divided into three types. Type-1 environments, the length of the vector is short, it means that these environments have little or no useful information about the genotypes performance including E2, E3, E6, E7, E8, E9 (Nuclear Institute for Agriculture and Biology, Faisalabad, Gram Breeding Research Sub-station, Kallurkot-1, Regional Agricultural Research Institute, Bahawalpur, Gram Breeding Research Sub-Station, Kallurkot-2, Farmer field, Bhakkar, Arid Zone Research Institute, Bhakkar-2), while, Type-2 environment had vectors with long length as

compared to Type-1 and formed a small angle with the average environment coordination (AEC) abscissa including E1 and E5 (Pulses Research Institute, Faisalabad; Adaptive Research Station, Karor), which means that these environments are ideal for the selection of genotypes. Type-3 environments are those which have long vector and formed a large angle with AEC abscissa, i.e., E4 (Arid Zone Research Institute, Bhakkar-2), indicating it is worthless in selecting the genotypes (Fig. 2). The findings of this study are similar to the results of Yan *et al.*, 2001.

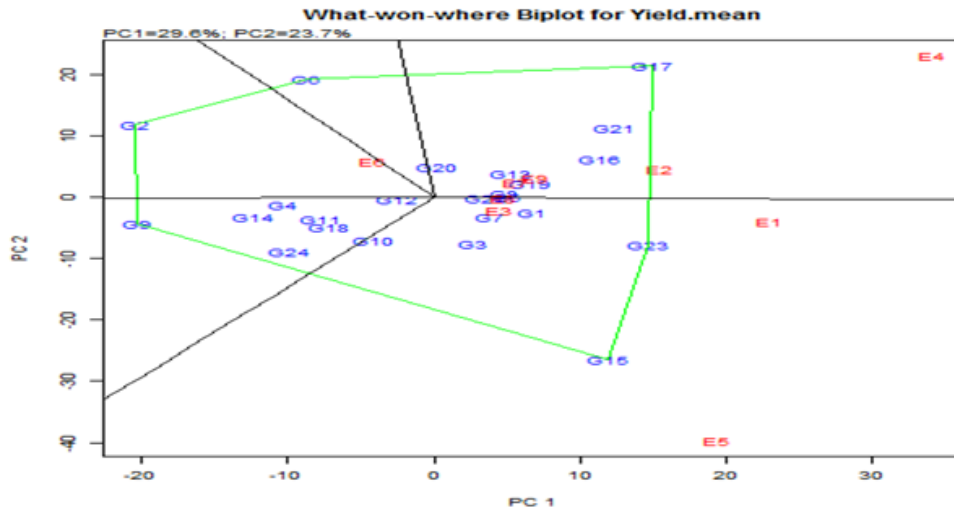


Fig. 1: GGE Biplot 'What-won-where biplot for yield mean'.

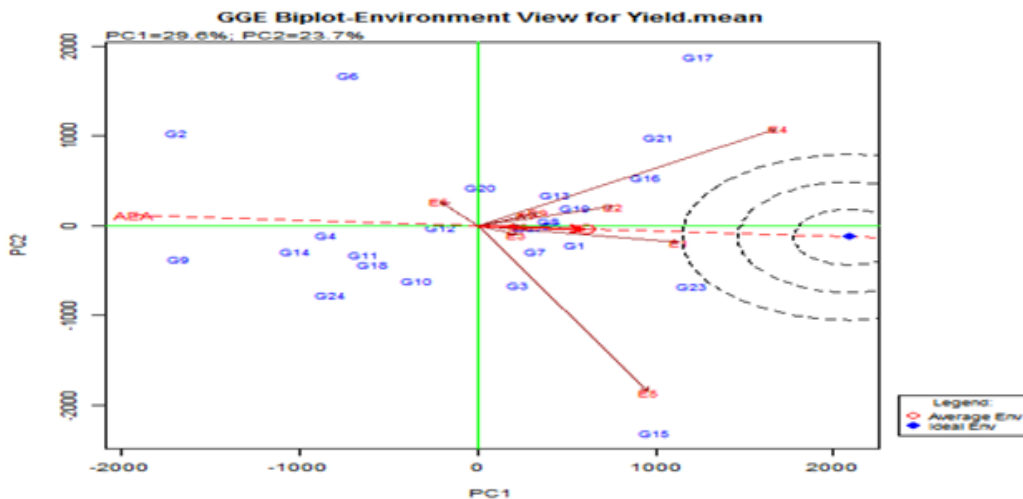


Fig. 2: GGE-Biplot for environment view for yield mean.

Genotype evaluation was carried out to identify the ideal genotypes stable across the environments and capable of exhibiting high yield potential. AEC was constructed following the study of Yan and Rajcan (2002), as shown in Fig. 2. The axis of AEC abscissa also known as average environment axis consists of single line headed with an arrow which passes through the origin of biplot and average

environment. Location of genotypes on average environment axis represents the main effect of genotypes called "G". The arrow towards the axis of AEC abscissa shows the direction of high performing genotypes (Yan *et al.*, 2001; Yan *et al.*, 2007). From GGE biplot-genotype view (Fig. 2) for illustration of superior genotypes, which are stable within environments and having high yield means ranked to

“G” are documented here as under:
 G23>G15>G17>G16>G21>G1>19>G8>G13>G7>
 G3>G12>G10>G18>G11>G24>G5>G4>G14>G9>
 G2 non-coded TG1415>D-15024>D-15033>D-15030
 >TG1305>Bittle-16>Punjab-2008>CH39/11>D-
 15019>CH-24/11>CH10/11>D-15015>15012>D-
 15036>D-15014>TG-220>CH19/10>GCH13/11>D-
 15020>D-15005>BRC-446. These results agree to the

previous findings of other scientists (Yan *et al.*, 2001; Yan *et al.*, 2007). It is obvious that G23 (TG1415) is ideal genotype because it occupied the closest place near to zero on axis. So, TG1415 is highly performing genotype in mean mega-environments, followed by G15 (D-15024), G17 (D-15033), G16 (D-15030) and so on (Fig. 3).

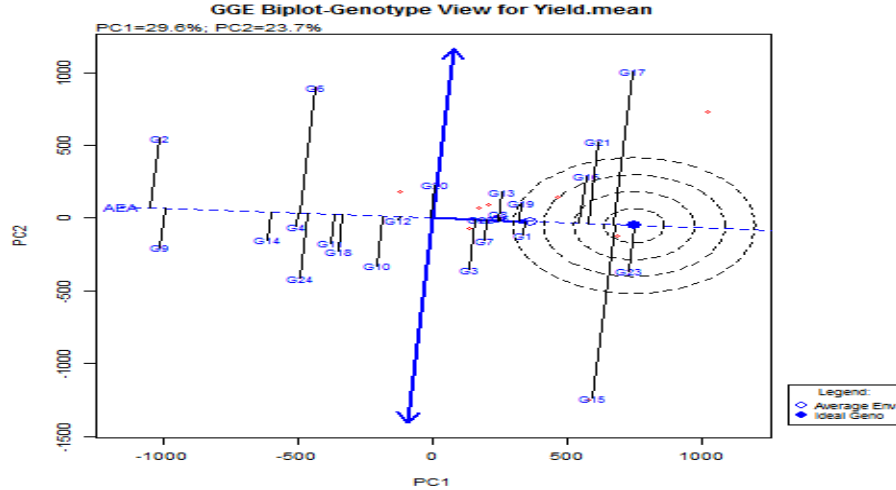


Fig. 3: GGE Biplot-Genotype view for yield mean.

Mean yield performance (Table 1) indicates that G9, G2, G6 showed lower mean yields but are stable. Low yield genotypes have no worth in chickpea breeding program, therefore, not useful for further retention in chickpea breeding program. Highly stable and better mean yield genotype is ideal and the other genotypes closer to the ideal genotype are

comparatively more stable and high yielding are also desirable (Yan and Tinker, 2006). The genotypes G15 (D-15024), G17 (D-15033) and G16 (D-15030) located closer to ideal genotype G23 (TG1415), also have more stability coupled with high yield potential. Therefore, these genotypes may also be preferred for further utilization in chickpea breeding program.

Table 1: Mean yield performance of chickpea genotypes.

Code	Genotype	Yield mean kg ha ⁻¹	PC1	PC2	S.D.
G1	Bittle-16	1762.78	-330.83	116.43	1126.02
G2	BRC-446	1480.44	1016.49	-552.04	780.53
G3	CH 10/11	1778.78	-134.82	354.29	1013.35
G4	CH 13/11	1656.44	510.03	59.35	812.35
G5	CH 19/10	1731.78	-249.53	-0.75	978.98
G6	CH 2/11	1621	436.19	-898.77	973.29
G7	CH/24/11	1795.11	-191.25	152.68	938.09
G8	CH39/11	1870.44	-241.7	-28.04	1049.02
G9	D-15005	1409.67	1010.71	202.25	916.68
G10	D-15012	1611.89	208.04	330.13	1055.33
G11	D-15014	1574.22	381.37	171.42	986.60
G12	D-15015	1568	127.48	14.26	1055.33
G13	D-15019	1778.22	-257.98	-180.9	1040.73
G14	D-15020	1539.67	611.43	152.38	929.44
G15	D-15024	1840.33	-592.94	1239.3	1269.07
G16	D-15030	1872.56	-566.05	-285.78	1010.57
G17	D-15033	1847.33	-740.4	-1006.34	1072.65
G18	D-15036	1779.67	353.01	229.57	1030.35
G19	Punjab-2008	1740.78	-325.82	-102.78	1074.39
G20	TG1218	1806.56	-7.85	-228.87	1010.55
G21	TG1305	1806.89	-611.98	-526.12	1036.86
G22	TG1410	1832.67	-174.97	8.53	1017.03
G23	TG1415	2010.33	-723.91	363.97	1023.77
G24	TG220	1636	495.26	415.82	920.12

Table 2: List of environments/locations.

S. No.	Name of location/Environment	Environment code used in the graph
1	Pulses Research Institute, Ayub Agricultural Research Institute, Faisalabad, Pakistan	E1
2	Nuclear Institute for Agriculture and Biology, Faisalabad, Pakistan	E2
3	Gram Breeding Research Sub-Station, Location-1, Kallurkot, Pakistan	E3
4	Arid Zone Research Institute, Location-1, Bhakkar, Pakistan	E4
5	Adaptive Research Station, Karor (Layyah), Pakistan	E5
6	Regional Agricultural Research Institute, Bahawalpur, Pakistan	E6
7	Gram Breeding Research Sub-Station Location-2, Kallurkot, Pakistan	E7
8	Farmer Field, Bhakkar, Pakistan	E8
9	Arid Zone Research Institute, Location-2, Bhakkar, Pakistan	E9

CONCLUSION

GGE biplot employed for exploration of yield stability identified G23 (TG1415) as most stable and high yielding chickpea genotype across the environments, followed by G15 (D-15024), G17 (D-15033) and G16 (D-15030). Mega environment analysis revealed that G23 (TG-1415) has higher yield in E1 (Pulses Research Institute, Faisalabad) and E3 (Gram Breeding Research Sub-Station, Kallurkot) environments. Similarly, G15 (D-15024) showed higher yield in E5 (Adaptive Research Station, Karor), G17 (D-15033) performed better in E2 (Nuclear Institute for Agriculture and Biology, Faisalabad) and G16 (D-15030) performed better in E4 (Arid Zone Research Institute, Bhakkar). Mega environment analysis confirmed that E1 and E5 (Pulses Research Institute, Faisalabad and Adaptive Research Station, Karor) are the most useful environments and ideal for the selection of genotypes.

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