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Research Article

Exploration of Grain Yield Stability of Advanced Chickpea Strains Across Environments

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Abstract | Exploration of yield stability and defining the adaptation domains of advance strains is highly imperative for crop genetic improvement programs. The research aimed to determine the yield stability of sixteen advance chickpea strains was carried out at eleven diversified locations across the Punjab province of Pakistan during cropping season 2019-20. GGE biplot and mega environment analysis were employed to identify the most stable and high yielding chickpea advance strains. GGE biplot among PC1 and PC2 illustrated that G-10 (K-15019) was ideal genotype performing best across the environments. Higher yield potential coupled with more yield stability across all test environments was recorded in G-10 (K-15019) followed by G-2 (CH47/12), G-12 (K-15001), G-15(CH66/10) and G-16(CH53/12). Mega environment analysis revealed that E8 (Adaptive Research Farm, Karor) and E2 (Nuclear Institute for Agriculture and Biology, Faisalabad) were most discriminating environments for grain yield and most useful for screening of genotypes. Result for yield stability indicated that G-10 (K-15019), G-2 (CH47/12), G-12 (K-15001), G-15 (CH66/10) and G-16 (CH53/12) were higher yielding and more stable across environments, therefore these genotypes may be utilized in chickpea breeding program for development of widely adapted chickpea cultivars. Moreover, G-10 (K-15019) identified as ideal genotype in terms of stability and yield potential may be released as commercial variety for general cultivation in future.

Introduction

Chickpea (*Cicer arietinum*), an important member of family Fabaceae sub-family Faboideae with diploid chromosome (2n = 16) is a versatile pulse legume crop and self-pollinating in nature (Kumar *et al*., 2021). Chickpea is a winter season crop generally grown for its edible grains and consumed across the world (Foyer *et al*., 2016). The importance of this legume cannot be overstated because of its major role

in balancing the ecosystem, generating revenue and sustaining food security (Moreno *et al*., 2003; Kaloki *et al*., 2019). Chickpea occupies very important place in rain-fed agriculture system of Pakistan. In Pakistan, average annual productivity of this legume is unstable and declining due to the scarcity of improved climatic resilient varieties (Jan *et al*., 2020). Development of high yielding, stable and climate-ready cultivars is direly needed for substantial improvement in chickpea productivity and to ensure the global food security. To

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achieve these objectives, continuous scientific efforts are required for characterization, screening and exploration of chickpea germplasm for development of high yielding cultivars with wider adaptability.

The genotypes selected from a single specific environment when used in other environments are generally vulnerable and less adaptable to other climates (Ebdon and Gauch, 2002; Asfaw et al., 2009). Environmental conditions; soil type, average temperature, humidity and annual rainfall vary from location to location and year to year. To develop widely adaptable and high yielding chickpea cultivars, screening of advance strains for yield stability has been an imperative approach for all breeding programs (Annicchiarico, 1997; Farshadfar et al., 2011). Genotypes showing less degree of yield fluctuation under different environments are considered as stable and useful to obtain better yield (Arshad et al., 2003; Erdemci, 2018; Kaloki et al., 2019). Comparative performance of a genotype in different environments is referred as genotype(G) × environment(E) interactions. G × E interactions have been extensively utilized to identify the most stable and adaptable genotypes. Measured grain yield of a genotype in an ecological zone is obtained by the effect of environment (E), the genotype (G) and G × E interaction (Yan and Rajcan, 2002; Moreno et al., 2003; Gauch et al., 2008).

Grain yield stability coupled with high yield potential is highly desirable for development of widely adapted and climate resilient chickpea cultivars (Singh and Bejiga, 1990; Arshad et al., 2003). Stability analysis founded on genotype x location may be considered as a primary selection model for development of high yielding and widely adapted varieties (Gauch et al., 1992; Annicchiarico, 1997; Funga et al., 2017). For selection of superior and stable genotypes multi-environment evaluation of advance breeding material is essential to determine their genetic potential (Yaghoutipor and Farshadfar, 2007; Asfaw et al., 2009). G × E interactions have already been emphasized and employed by various researchers for screening of genotypes with wider adaptability (Yan et al., 2001; Ebdon and Gauch, 2002; Samonte et al., 2005; Farshadfar et al., 2012; Hasan and Deb, 2017; Erdemci, 2018; Kaloki et al., 2019).

Vulnerability of chickpea cultivars to a wide range of environments have resulted in serious yield penalty.

Therefore, to explore and recommend superior cultivars with more stability is essential to improve the chickpea yields. The present study was planned to screen out the advance breeding lines and to identify the most stable and higher yielding genotypes for inclusion in chickpea varietal development program.

Materials and Methods

For exploration of yield stability of advance chickpea strains, a provincial coordinated yield trial (CYT) was carried out at eleven diversified locations of Punjab, province of Pakistan during the rabi season of 2019-20 under the umbrella of Ayub Agricultural Research Institute, Faisalabad. The experimental material consisting of 16 elite chickpea strains developed by different research organizations were coded, packed and sent to eleven different research institutes/stations (Table 1). Experimental layout, fertilizer recommendations, data recording sheets and other necessary guidelines were sent to all experimental sites in hard form to ensure uniform conduction of trial. Trial was laid down following tri-replicate randomized complete block design. Sowing of all targeted experimental sites was completed during last week of October by dibbler keeping 10 cm plant-plant and 30 cm row-row distance. All the recommended agronomic operations were undertaken. Insecticide, Emamectin Benzoate @ 700 ml ha^{-1} was sprayed twice during pod bearing stage to avoid pod borer attack.

Grain yield data was recorded at all experimental sites, compiled and subjected to plant breeding tools (version 1.3) for graphical illustration of GGE biplot analysis and GEI (Genotype by environment interaction).

Results and Discussion

The GGE biplot was made for estimation of yield stability through graphical illustration of data by plotting scores of first principle component against the respective second principle component as outlined by (Yan et al., 2000, 2007). For mega-environment analysis irregular polygon view has been illustrated in Figure 1 presenting "which won where for yield". The polygon biplot view is best way to investigate the interaction among genotypes and environments (Yan et al., 2001). The genotypes connected in the vertex were winning genotypes in different mega environments. The connected genotypes forming an irregular polygon were G-10, G-11, G-9, G-6, G-13

and G-8. The polygon of genotypes also depicted the grouping pattern of different environments to form the mega environment (Bakhsh *et al.*, 2011; Kaloki *et al.*, 2019). The first mega environment was formed by grouping of six environments i.e. E2 (Nuclear Institute for Agriculture and Biology, Faisalabad), E4 (Gram Breeding Research Sub-Station, Kallurkot), E5 (Farmer Field, Awan wala, Kallurkot), E10 (Arid Zone Research Institute, Bhakkar), E8 (Adaptive Research Farm, Karor) and E11 (Arid Zone Research Institute, Bhakkar, Location 2) with G-10 (K-15019) as winning genotype. G-11 (CH48/12) was winning genotypes present in second mega environment which was formed by E9 (Barani Agricultural Research Institute, Chakwal). Likewise, E6 (Gram Breeding Research Sub-Station, Kallurkot, Location 2) and E7 (Gram Breeding Research Sub-Station, Rakhutra, Khushab) formed third mega environment with G-9 (CH51/12) as winner. E3 (Barani Agricultural Research Station, Fateh Jung) formed another mega environment with G-8 (K-15012) as winner. Our results were in line to the previous findings of (Bakhsh *et al.*, 2011; Naroui *et al.*, 2013; Getachew *et al.*, 2015).

(Gram Breeding Research Sub-Station, Kallurkot), E9 (Barani Agricultural Research Institute, Chakwal), E5 (Farmer Field, Awan wala, Kallurkot) and E1 (Pulses Research Institute, AARI, Faisalabad, Pakistan) have small vector length have no considerable effect on genotype performance. Type-2 environments have comparatively more length forming smaller angle with AEA abscissa are most useful environments. E8 (Adaptive Research Farm, Karor) and E2 (Nuclear Institute for Agriculture and Biology, Faisalabad) are most influential and ideal for selection genotypes. Type-3 environments have long vectors of with relatively larger angle. These environments are not useful having no worth in performance of genotypes like E3 (Barani Agricultural Research Station, Fateh Jung), E10 (Arid Zone Research Institute, Bhakkar, Location 1) and E6 (Gram Breeding Research Sub-Station, Kallurkot, Location 2). Former findings of (Singh and Bejiga, 1990; Yan *et al.*, 2000; Funga *et al.*, 2017; Kaloki *et al.*, 2019) agree to the results of this study who concluded that certain environments were discriminating having representative effects and the others are worthless for selection of genotypes.
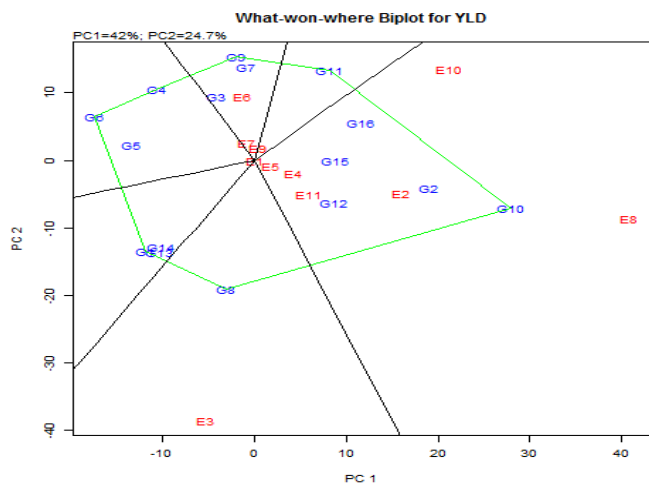

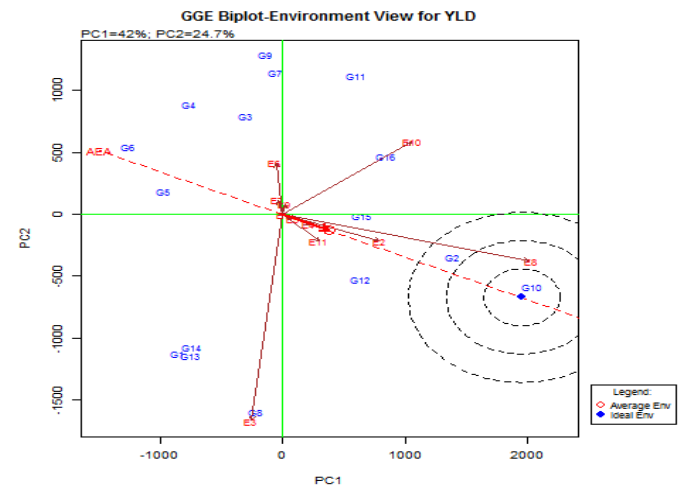**Figure 1:** *What won where Biplot for yield.*

Figure 2: *GGE Biplot for environment view for yield.*

GGE biplot for environment view was made by plotting the vectors for determination of most useful environments which ultimately diagnosed the superior genotypes (Figure 2). In GGE biplot for environment, angles formed by different environments with AEA abscissa and the length of vectors indicate the power of environments (Yan *et al.*, 2000; Erdemci, 2018). Based on vector lengths environments are divided into three types. Type-1 environments have shorter vector length having limited effect on determination of performance of genotypes. E7 (Gram Breeding Research Sub-Station, Rakhutra, Khushab), E4

GGE biplot for yield was constructed for illustration of genotype view for yield as given in Figure 3. The average tester coordinate AEA was constructed following the outlines of (Yan *et al.*, 2001; Yan and Rajcan, 2002). AEA perpendicular axis with double arrow was drawn which passes through the average environment and the origin of biplot. AEA abscissa illustrates the respective yield performances of chickpea genotypes. The genotype G-10 (K-15019) showed the highest yield and identified as ideal genotype across the mean environment. The genotypes with higher yield means and stable within

environments ranked to "G" were in following order G10>G2>G12>G16>G15>G3>G11>G14>G7>G1> G13>G3>G9>G5>G4>G6.

Figure 3: *GGE Biplot for genotype view for yield.*

Mean yield performances of included chickpea advance lines (Table 2) indicated that G-9, G-4, G-6, G-13 and G-8were comparatively stable but had less average yield potential. Low yield potential of genotypes is undesirable in breeding programs therefore such genotypes have no worth and may be discarded (Bakhsh *et al.*, 2011; Farshadfar *et al.*, 2011; Funga *et al.*, 2017; Erdemci, 2018; Kaloki *et al.*, 2019). On the other hand G-10 (K-15019), G-2 (CH47/12), G-12 (K-15001), G-15 (CH66/10) and G-16 (CH53/12) showed high yield potential coupled with more stability across environments. The genotypes with high yield means and stablility across environments are of high value for chickpea breeding program and development of superior high yielding cultivars.
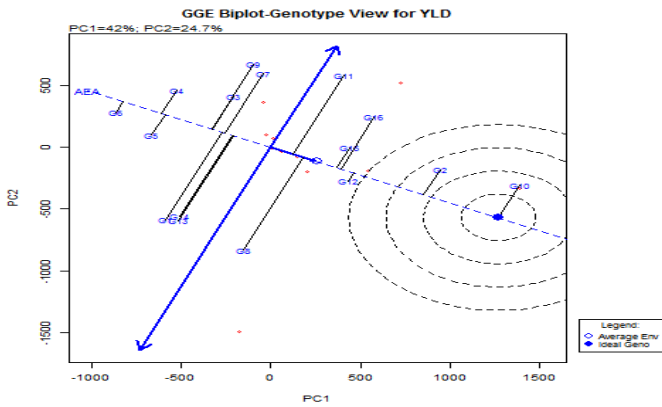
Table 1: *List of experimental stations/ test environments.*

S. No	Environment code	Location /Environment Name
1	E1	Pulses Research Institute, AARI, Faisalabad, Pakistan.
2	E2	Nuclear Institute for Agriculture and Biology, Faisalabad, Pakistan.
3	E3	Barani Agricultural Research Station, Fateh Jung, Pakistan.
4	E4	Gram Breeding Research Sub-Station, Kallurkot, Location 1, Pakistan.
5	E5	Farmer Field, Awan wala, Kallurkot, Pakistan.
6	E6	Gram Breeding Research Sub-Station, Kallurkot, Location 2, Pakistan.
7	E7	Gram Breeding Research Sub-Station, Rakhutra, Khushab, Pakistan.
8	E8	Adaptive Research Farm, Karor, Pakistan.
9	E9	Barani Agricultural Research Institute, Chakwal, Pakistan.
10	E10	Arid Zone Research Institute, Bhakkar, Location 1, Pakistan.
11	E11	Arid Zone Research Institute, Bhakkar, Location 2, Pakistan.

Table 2: *Mean performance of chickpea advance strains.*

Entry code	Genotype	Breeding center	Type/Status	Mean yield	PC1	PC2
G1	K-15014	PRI	K/Advance line	1289	-592.697	-588.886
G2	CH47/12	NIAB	K/Advance line	1478	942.3578	-182.076
G3	K-15018	PRI	K/Advance line	1275	-207.222	411.676
G4	K-15010	PRI	K/Advance line	1191	-527.528	461.037
G5	CH54/12	NIAB	K/Advance line	1181	-664.935	97.18294
G6	NOOR 2013	Check	K/ Variety	1135	-868.792	281.1151
G7	CH56/12	NIAB	K/Advance line	1300	-45.2657	598.0616
G8	K-15012	PRI	K/Advance line	1341	-155.23	-832.987
G9	CH51/12	NIAB	K/Advance line	1213	-98.0057	671.5627
G10	K-15019	PRI	K/Advance line	1546	1387.084	-307.849
G11	CH48/12	NIAB	K/Advance line	1362	408.3947	583.1787
G12	K-15001	PRI	K/Advance line	1458	429.2103	-275.508
G13	CH69/09	NIAB	K/Advance line	1355	-515.54	-595.523
G14	TGM12K01	AZRI	K/Advance line	1275	-509.93	-559.281
G15	CH66/10	NIAB	K/Advance line	1447	440.2993	-5.10916
G16	CH53/12	NIAB	K/Advance line	1377	577.8001	243.4056

PRI: Pulses Research Institute; AARI, Faisalabad, Pakistan, NIAB: Nuclear Institute for Agriculture and Biology, Faisalabad, Pakistan; AZRI: Arid Zone Research Institute, Bhakkar, Pakistan.

Conclusions and Recommendations

GGE biplot employed for assessment of grain yield stability across eleven test environments revealed that G-10 (K-15019) was the most stable and high yielding strain across all the test environments followed by G-2 (CH47/12), G-12 (K-15001), G-15 (CH66/10) and G-16 (CH53/12). GGE biplot for mega-environment analysis showed that E8 (Adaptive research farm, Karor) and E2 (Nuclear institute for agriculture and biology, Faisalabad) were most discriminating environments for grain yield and better representative than other test environments for screening of genotypes. On the basis of results, it may be concluded that G-10 (K-15019) was most superior and ideal genotype across the environments. Therefore, G-10 (K-15019) may be released as commercial variety in future.

Novelty Statement

Exploration of advance chickpea strains rather than varieties is a novel research study to identify the most stable and high yielding chickpea strains. This novel study will provide a practicable way to researchers for selection of most stable genotypes.

Author's Contribution

MTM wrote abstract, methodology, did analysis and managed the whole preparation of article, MA conceived idea and gave technical inputs, KLC wrote conclusion and technically guided during writeup, MA data collection and helped in analysis, MJK wrote results and discussion, AZ collected and compiled data, MK checked plagiarism and made corrections, ZA prepared introduction and references section of the article.

Conflict of interest
The authors have declared no conflict of interest.

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