



GGE bi-plot analysis for grain yield in chickpea (*Cicer arietinum*) under normal and heat stress conditions

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ABSTRACT:

Efficiency of genetic gain received through selection is seriously affected by genotype \times environment ($G \times E$) interaction, as $G \times E$ directly affects the stability and performance of genotype under multi environment. In the current study a total of 34 chickpea (*Cicer arietinum* L.) genotypes were evaluated at two locations (Kanpur and Bhopal) in two seasons (timely sown and late sown conditions) during 2016-17 to gain insights into the $G \times E$ effect and the stability of genotypes grown across the sites. Plot yield data recorded from the genotypes were analyzed by using GGE bi-plot method. The combined analysis of variance (ANOVA) revealed highly significant effects of environment on plot yield attribute among the genotypes, evaluated over the two seasons across the two locations. However, the most stable genotype across the two locations remained g 23 (JAKI 9218). Among the tested environments Bhopal timely sown (BL-T) and Bhopal late sown (BL-L) were the most representative, whereas Kanpur timely sown (KAN-T) was the least representative. Moreover, g 01 (HC 1) was the best cultivar under KAN-T and KAN-L environments whereas, g 23 (JAKI 9218) was the best cultivar under BL-T and BL-L environments.

Key words: Chickpea, Genotype \times environment interaction, GGE bi-plot, Heat stress

Chickpea (*Cicer arietinum* L.) is the second most important global grain legume next to common bean, producing 13.73 MT from 13.98 mha globally (FAO 2016). As an important member of legume family, it serves as cheap source of plant based dietary protein as well as essential micronutrients to the global human population (Graham and Vance 2003). Besides, it also remains instrumental in enriching soil nitrogen status by fixing atmospheric nitrogen through symbiotically active rhizobia (Graham and Vance 2003). In parallel, it also plays essential role in maintaining cereal –legume cropping system thus, helps in sustaining cropping ecosystem and ecology. Under the current global climate change, heat stress is becoming a great challenge that limits crop productivity including chickpea (Jha *et al.* 2014a,

2014b; 2017). Thus, heat tolerance and sustainable yield under the unpredicted global climate change in chickpea is of utmost importance. $G \times E$ interaction remains a persistent challenge to the plant breeders as it hampers selection of superior genotypes due to their variable response under different environments and years. Yield traits remain the crucial parameter that ultimately decides the selection of superior cultivar under crop breeding programme. As grain yield is quantitative in nature, and are controlled by minor gene(s) and QTLs, it showed high response to GE interaction effects (Fleury *et al.* 2010). Thus, based on evaluation of genotypes for yield trait under multiple environments could assist in selection of superior and stable genotypes across the environments. In order to partition the $G \times E$ interaction several statistical models, viz. regression analysis (Gauch 1988), multivariate analysis (Westcoff 1987), cluster analysis (Crossa *et al.* 1991) and additive main effect and multiplicative interaction (AMMI) model (Gauch 1992) have been employed. Likewise, genotype main effect plus genotype \times environment interaction (GGE) biplot (Yan *et al.* 2000) is an important statistical model that allows investigating $G \times E$ interaction of various multi-environment trials and assists in selection of superior genotypes. Thus this technique has been successfully employed for evaluating superior high yielding and stable genotypes in various crops like wheat (Crossa *et al.* 1991, Elbasyoni 2018), maize (Purchase *et al.* 2000, Badu *et al.* 2003), rice (Sharifi *et*

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al. 2017), chickpea (Farshadfar *et al.* 2011, Rashidi *et al.* 2013) and other grain legumes (Horn *et al.* 2018, Odeseye *et al.* 2018). Hence, the current study was intended to know the efficacy of test sites, stability performance of different chickpea genotypes and to determine ideal genotype under normal and heat stress via GGE-biplot analysis. Thus multi-location and multiyear testing of genotypes remains essential for identification of mega environment and identification of genotypes with wider adaptability and stability (Yan *et al.* 2000).

MATERIALS AND METHODS

A set of 34 chickpea genotypes (coded as g1 to g34) including three heat tolerant checks ICC 92944, ICC 4958 and ICC 1205 was selected (Table 1). These genotypes were evaluated along with the checks during 2016-2017 at Indian Institute of Pulses Research (IIPR), Kanpur and at Phanda farm, Bhopal under normal and late sown conditions. The timely sown genotypes were grown on 16.11.2016 at IIPR, Kanpur and on 10.11.2016 at Phanda farm in Bhopal. While, the genotypes were grown under late sown condition on 16.12.2016 at IIPR, Kanpur and on 14.12.2016 at Phanda farm in Bhopal. Same agronomics package and practices were followed in both normal and late sown trials at the both sites. The experiment was designed in randomized block design (RBD) with three replications. Data was analyzed using analysis of variance (ANOVA) to know the role of genotypes, environment and their interaction. Considering environment (E) and genotype (G) as fixed effects and replication (R) as random effects, this mixed additive model has been formulated. Estimates and significance of random effects were computed using RG×E program (Dia *et al.* 2017). The development of each genotype in each environment was plotted with analyzes by GGEBiplot using the package GGEBiplotGUI (Frutos *et al.* 2014) implemented in the software R (R CORE TEAM 2017).

RESULTS AND DISCUSSION

As grain yield is governed by multiple gene(s) and high influence of G×E interaction causes complexity in genotype evaluation (Elbasyoni 2018). Thus, G×E interaction analysis employing AMMI, GGE biplot could enable plant breeder to select suitable genotype adapted to specific environment and to investigate its higher stability and adaptability across various locations (Yan *et al.* 2000, Yan and Tinker 2006). Mean plot yield of all the genotypes grown across the environments given in Table 2. The combined analysis of

Table 1 List of chickpea genotypes

Genotype	Code	Status
HC1	g1	Released variety
RSG11	g2	Released variety
VISWAS	g3	Released variety
GG2	g4	Released variety
PDG3	g5	Released variety
RVG203	g6	Released variety
CSG8962	g7	Released variety
GCP101	g8	Released variety
RSG88	g9	Released variety
ICC1205(Ch)	g10	Accession
RSG931	g11	Released variety
GL769	g12	Released variety
BGM413	g13	Released variety
RVG202	g14	Released variety
GPF2	g15	Released variety
JG11	g16	Released variety
DIGVIJAY	g17	Released variety
PUSA372	g18	Released variety
PUSA547	g19	Released variety
ICC4958(Ch)	g20	Accession
RAU52	g21	Released variety
JG130	g22	Released variety
PUSA209	g23	Released variety
PUSA72	g24	Released variety
JAK19218	g25	Released variety
PDG4	g26	Released variety
PBG1	g27	Released variety
C235	g28	Released variety
PUSA261	g29	Released variety
ICC92944(Ch)	g30	Released variety
ICC10150	g31	Accession
ICC12907	g32	Accession
ICC15104	g33	Accession
K1085	g34	Accession

variance (ANOVA) revealed highly significant main effects ($P < 0.001$) of genotypes, environments and G×E interaction (Table 3). The first two principal components (PC1) and

Table 2 Analysis of variance for plot yield under different environments

Source of variation	Df	Sum of Square	Mean sum of Square	F value	Prob F
L	3	1805239	601746.5***	55.56524	<0.001
G	33	4516221	136855.2***	12.6372	<0.001
L×G	99	3289385	33226.11***	3.068097	<0.001
R			463.9276		
Pooled error	264		10829.55		

***P < 0.001

Table 3 Plot yield of genotypes grown under timely and late sown conditions at Kanpur and Bhopal locations

Genotype	KAN-T	KAN-L	BL-T	BL-L
HC1	999.3	324.3	683.3	669.0
RSG11	588.7	363.9	708.3	553.6
VISWAS	572.3	260.8	343	392.0
GG2	756.0	404.5	467.2	542.6
PDG3	541.3	368.7	805	571.7
RVG203	857.7	457.5	545	620.1
CSG8962	760.0	469.3	863.3	697.5
GCP101	695.0	437.8	600	577.6
RSG88	727.3	433.8	715	625.4
ICC1205	500.3	369.1	723.3	530.9
RSG931	870.7	341.9	523.3	578.6
GL769	329.7	275.3	540	381.7
BGM413	854.7	385.7	683.3	641.2
RVG202	891.0	534.3	661.7	695.7
GPF2	522.3	323	780	541.8
JG11	900.0	564.5	416.7	627.1
DIGVIJAY	565.0	379	425.8	456.6
PUSA372	546.7	342.5	443.3	444.2
PUSA547	684.7	478.9	521.3	561.6
ICC4958	695.7	520.5	690	635.4
RAU52	383.3	277.6	491.7	384.2
JG130	675.3	501.8	668.3	615.1
PUSA209	424.3	306.2	387.9	372.8
PUSA72	495.3	379.6	310	395.0
JAKI9218	746.3	551.5	991.7	763.2
PDG4	688.0	441.9	830	653.3
PBG1	705.7	581.2	580	622.3
C235	709.0	474.3	463.3	548.9
PUSA261	834.7	535.4	721.7	697.3
ICC92944	596.7	398.9	504.5	500.0
ICC10150	748.7	372.1	848.3	656.4
ICC12907	732.7	389.7	665	595.8
ICC15104	739.7	485.3	621.7	615.6
K1085	731.7	441.1	813.3	662.0
Mean	678.5	416.82059	618.7	571.4

(PC2) explained 90.2% of the total GGE variation, and the PC1 was responsible for 64.5% of the total variation. Likewise given the GGE biplot analysis, significant interaction of G × E was recorded under different sowing dates and multiple sites for yield trait in cowpea (Shiringani and Shimelis 2011, Horn *et al.* 2018, Odeseye *et al.* 2018, Sousa *et al.* 2018), in wheat under heat stress (Elbasyoni, 2018), for *Fusarium* wilt in pigeonpea (Sharma *et al.* 2016) and for drought stress in brassica (Zali *et al.* 2016).

Ranking of 34 genotypes based on mean yield and stability has been depicted in Fig 1. The line passing the

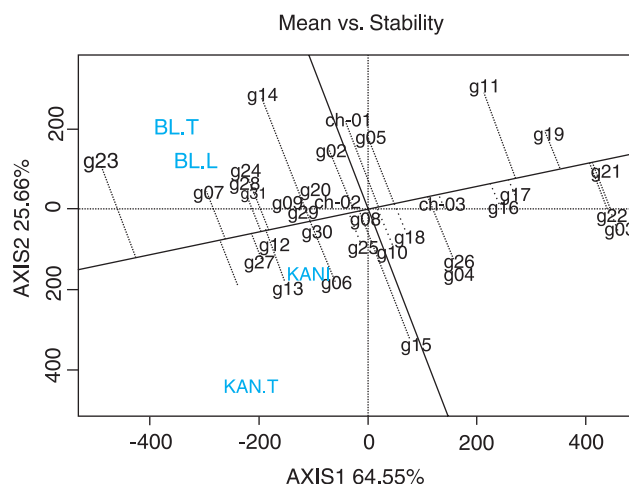


Fig 1 Results of the GGE-Biplot based on mean × stability. AXIS1 and AXIS2 refer to Principal component 1 (PC1) and principal component2 (PC2), respectively.

biplot origin from upper right to lower left is known as average environment axis (AEA). The line passing through the origin and perpendicular to AEA with double arrow denotes stability of genotype (Yan and Hunt 2002). The genotypes existing in either direction away from the origin on the axis indicate G×E interaction and low stability (Yan and Hunt 2002). Thus, g 23 (JAKI 9218) had the highest mean yield, whereas g 19 (RAU 52) had the lowest mean yield. Thus, g 14 (GPF 2) was highly unstable, whereas g 23 (JAKI 9218) was highly stable. An ideal genotype displays highest mean performance and remains stable across all the environments (Yan and Tinker 2006, Kaya *et al.* 2006). Thus, the g 23 (JAKI 9218) genotype appeared to the most stable in the current study.

GGE biplot analysis helps in ranking genotypes based on mean performance and stability. Average-environment coordination (AEC) comparing genotypes relative to an ideal genotypes is depicted in Fig 2. The arrow depicts the position where an ideal cultivar should be (Frutos *et al.* 2014). Therefore, genotypes located closer to the

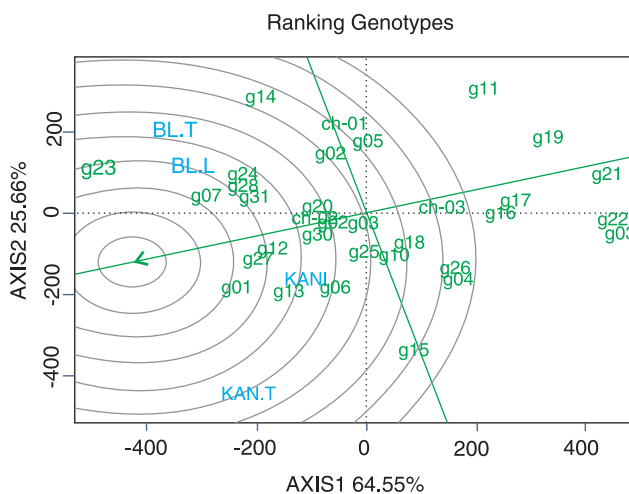


Fig 2 Results of the GGE-Biplot based on ideal genotype.

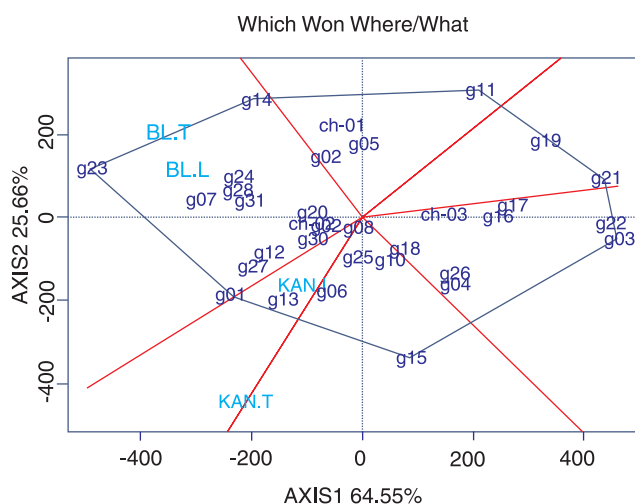


Fig 3 GGE biplot identification of winning cultivars across four environments KE, KL, BE and BL during the year 2016-2017. AXIS1 and AXIS2 refer to Principal component 1(PC1) and principal component 2(PC2), respectively.

ideal genotype are more desirable than others. Thus, g 23 (JAKI 9218), g 01 (HC1) and g 07 (CSG 8962) were more desirable and stable.

A “which won where” polygon view of the relationship between genotypes and environments is presented in Fig 3. Genotypes appeared on the vertices of the polygon suggest the best or the poorest in one or other environment (Yan and Hunt 2002). The genotypes g 23, g 14, g 11, g 19, g 21, g 22, g 03, g 15 and g 01 appeared on the corners of “which won where” polygon revealing that they were the best genotypes in specific environments. The genotype g 01 (HC 1) appeared on the corner of the polygon where KAN-L and KAN-T environments fell. This suggests that HC1 was the best cultivar for KAN-L and KAN-T. Likewise, the g 23 (JAKI 9218) genotype remained on the vertex of the polygon where the BL-L and BL-T environments fell; indicating g23 was the best cultivar for BL-L and BL-T environments. The genotypes g 15, g 03, g 21, g 19, g 22 and g11 located on the vertices did not fall in any environment, suggesting that these genotypes were not the best in any of the environments (Fig 3). The genotypes, viz. g 08, g 20, g 30 remained in the centre of origin showed stable performance across the environments. This result was in agreement with the result suggested in cowpea (Horn *et al.* 2018). Importantly, evaluation of test environment could help in identifying environments that could be utilized for selecting superior genotypes for mega environment (Rashidi *et al.* 2013, Sousa *et al.* 2018).

GGE biplot “discrimination-and-representativeness” facilitates representativeness and differentiating power of environments to be tested (Frutos *et al.* 2014). Among the four environments studied, BL-T and BL-L remained the most discriminating (informative) and KAN-T remained the least differentiating. The average environment (denoted by the small circle at the end of the arrow) has the “average coordinates” of all the four test. AEA is the line that passes through the average environment and the biplot origin. A

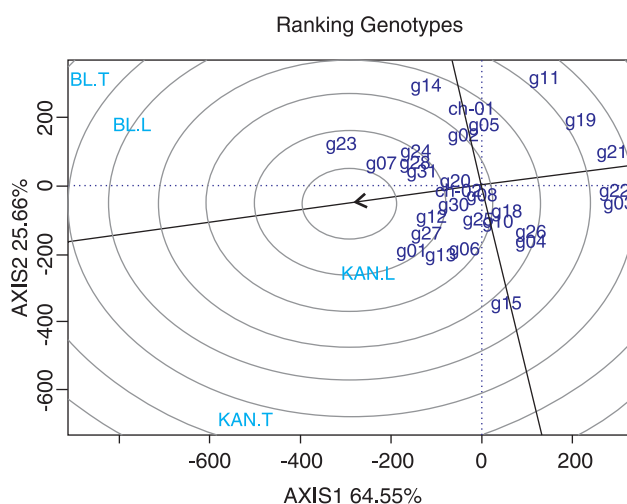


Fig 4 Vector view of GGE biplot for relationships among environments Kanpur early sown (KE), Kanpur late sown (KL), Bhopal early sown (BE), Bhopal late sown (BL).

test environment having smaller angle with the AEA is more representative of other test environments (Frutos *et al.* 2014). Thus, BL-T and BL-L were most representative, whereas KAN-T was least representative (Fig 4).

Conclusion

The result suggested that chickpea performance was significantly affected by various environments and $G \times E$ interaction. The late sown genotypes displayed significant yield loss. High $G \times E$ interaction was recorded for the genotypes and change in sowing date increased the interaction. Given the GGE biplot analysis, JAKI 9218 was identified to be the most stable genotypes across the two locations. Thus, GGE biplots analyses could be greatly implicated for identification of genotype best suited for specific environment or wider adaptable and stable across the multiple environments.

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