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Genotype × Environment Interaction and Stability Analysis for Seed Yield in Desi Chickpea (*Cicer arietinum* L.) under Irrigated Condition

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ABSTRACT

Background: Chickpea is mainly grown on marginal lands and encounter the problem of erratic rainfall that causes lack of water availability especially at terminal growth stages. Exploration of yield stability and defining the adaptation domains of advance genotypes in different ecosystem is highly imperative for crop genetic improvement programs. Development of variety with high yield potential and stable under irrigated condition is one of the major objectives of chickpea improvement programme, which can be achieved by improving selection efficiency with estimating stability parameters. Ten chickpea genotypes as advance breeding lines and popular varieties were evaluated to assess seed yield stability under irrigated condition during *rabi* 2021-22.

Methods: Experiments were conducted in randomized block design with three replications at five different locations of Karnataka *i.e.* Bidar, Kalaburagi, Bheemarayanagudi, Raichur and Hagari. The interaction analysis (AMMI ANOVA) indicates large variations for seed yield due to highly significant ($p<0.01$) environment (65.42%) and significant ($p<0.05$) genotype (10.03%), thus the genotypes were diverse with large sum of squares for seed yield and environment.

Result: The differential response of chickpea genotypes for seed yield across the environments was observed. IPCA1 and IPCA2 together captured 12.97 per cent of the interaction mean squares RG-2016-134 and KCD-2019-05 showed higher mean yields and adaptable to favourable environments. Based on AMMI bi-plot analysis, genotypes (KCD-2019-05 and Super Annigeri-1) were stable and (DC-17-1111 and RG-2016-134) were unstable. Similarly, best performer genotypes and three mega environments were noticed through the analysis. Three environments *i.e.*, (Bidar, Kalaburagi and Raichur) were found with most selective for seed yield estimation. The genotypes (RGV-203, KCD-2019-02 and Super Annigeri-1) were the best among all the ten tested genotypes in terms of seed yield stability.

Key words: AMMI, Chickpea, Irrigated, Seed yield stability.

INTRODUCTION

Chickpea (*Cicer arietinum* L.), commonly known as Bengal gram, belongs to the family Leguminosae and is a major pulse crop that contributes ~20% of the world pulse production after dry beans and dry peas. There are two types of chickpeas: the desi type (mostly brown seeded), traditionally grown in warmer climates of Asia and Africa and the Kabuli type. Chickpea is an important *rabi* pulse crop of Karnataka and being grown in an area of 7.12 lakh ha with 4.91 lakh tonnes of production and 689 kg/ha of productivity (Anonymous, 2022-23). Chickpea is grown mainly in black soils of north Karnataka and now a days considerable large area is also found in red soils of southern Karnataka. In India, the desi type is used whole, shelled and split to produce *dhal* or *grind* into fine flour called *besan*. Being a winter crop, the yield stability under rainfed as well as irrigated ecosystem is a challenging task to increases the seed yield. Conversely, the effects of test environment on genotype performance through genotype by environment (GEI) interaction is of major importance, the additive main effects and multiplicative interaction (AMMI) model is a valuable tool (Gauch, 2006; Li *et al*., 2006). The assessment of genotype's performance to the specific environment is utmost important to understand their adoption to wide range of growing environments and contributes in enhancing not only its area and production, but also farmer's income and progress towards achieving self-sufficiency in chickpea.

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In the present investigation the advanced genotypes which are developed through conventional and modern approaches (molecular markers) and released varieties are subjected to stability analysis under irrigated condition at designated regions of Kalyan Karnataka. Further, AMMI analysis and biplot, has been utilized to estimate nature and magnitude of genotypes environment interaction (GEI) effects on seed yield in diverse production environments, to measure the yielding ability, genotypes stability to such environments.

MATERIALS AND METHODS

The experiment was conducted during the *rabi* 2020-21 main cropping season at five different locations representing various chickpea growing agro-ecologies of Kalyan Karnataka region in the Karnataka state of India. The environments were Bidar (E1), Kalaburagi (E2), Bheemarayanagudi (E3), Raichur (E4) and Hagari (E5) as details given in Table 1. Ten chickpea genotypes comprising elite crosses and popular varieties which were developed through collaboration effort including four checks varieties (A1, JG 11, Super Annigeri-1 and NBeG-49) (Table 2). Planting of the genotypes was done in cropping season using randomized complete block design with three replications at each site under irrigated conditions (Maximum three irrigations were given based on the crop critical stage (*i.e.*, initial seedling, branching and pod formation) and requirement). Each genotype was planted in in a plot size of 4.8 m^2 with four rows of 4m length each and at 1.2 m width, with spacing of 30 cm row to row and 10 cm plant to plants distance. The seed yield (kg/ha) for each replication was recorded for 4 rows of each entry at all the locations excluding boarder row, five random plants were selected for observation in each entry in each replication and further it was used for statistical analysis. The crop health has been maintained as per the package of practices released periodically from the university of agricultural sciences, Raichur.

The AMMI model referred is

$$Y_{ij} = \mu + g_i + e_j + \Sigma\, hk\, \alpha_{ij}\, \tau_{ik} + R_{ij}$$

Where,

Yij = Yield of ith genotype jth environment,

gi = Mean of the ith genotype as a deviation from the grand mean μ.

e_j = Mean of the jth environment minus the grand mean (μ),

hk = Eigen value of the PCA axis k.

α_{ij} and τ_{ik} = Principal component scores for K of the ith genotypes and the jth environment respectively.

R_{ij} = Residual.

The GE (genotype by environment) interaction sum of squares was subdivided into PCA axis, where axis k is regarded as having t + s-1-2K degrees of freedom and t and s are the number of the genotypes and environments respectively. The data was analysed using windostat (ver 9.2) statistical package at UAS Raichur.

RESULTS AND DISCUSSION

Performance of desi-type chickpea genotypes for yield under irrigated condition

Performance trials were conducted in multiple environments because of the presence of GE. For the same reason, the analysis of genotype by environment data must start with the examination of the magnitude and nature of genotype by environmental interaction (Ezatollah *et al*., 2011). Yield is a polygenic trait and is strongly influenced by environment in chickpea. Significant variation is observed for grain yield in chickpea genotypes, similar results also reported by Khan *et al*. (1987, 1988) and highly significant difference between genotypes and genotypes × irrigation noticed as earlier observed by Durga *et al*. (2005).

AMMI analysis of variance

The AMMI analysis of variance for seed yield of 10 genotypes tested in five environments showed that the main effects of genotypes, environments and G × E interaction. environment accounted maximum variation (65.42%) followed by G × E interaction (13.83%) and Genotypes (10.03%). The analysis revealed that variances due to environments, Genotype × environment interaction, PCA I and PCA II are highly significant (P<0.01) whereas, significant (p<0.05) for genotypes. The large sum of squares for environments indicated that the testing locations were diverse and large differences among environmental means causing most of the variation in seed yield, which is in harmony with the findings of Zobel *et al*., (1988). Further, genetic variability among the genotypes was indicated by large sum of squares for genotypes as reported by the Akter *et al*., (2014) and Jogendra *et al*. (2018). The presence of genotype × environment interaction (GEI) was clearly demonstrated by the AMMI model, when the interaction was partitioned among the first three

Table 1: Geographic and environmental conditions of experimental area.

Trial site	Agroclimatic zone of Karnataka	Soil type	Altitude (>MSL)	Geographical position	
				Latitude (N)	Longitude (E)
ARS, Bidar	1	Medium black and lateritic	710	17°55′N	770 39′E
ZARS, Kalaburagi	2	Medium black	443	17°20′N	760 49′E
AC, B’ Gudi	2	Deep black	411	16°15′N	760 47′E
MARS, Raichur	2	Deep black	389	16°15′N	17 20′E
ARS, Harari	3	Black	508	15°10′N	77-04′E

interaction principal component axis (IPCA), first two PCA axis declared significant by an F test and PCA III was statistically non-significant. The IPCA1 explained 10.13% of interaction sum of squares with 22% of the interaction degree of freedom (df). Similarly, the second and third principal component axis (IPCA 2 and 3) explained further 2.84 and 0.63% of the GEI sum of squares respectively (Table 3). This implied that the interaction of the chickpea genotypes with five environments was predicted by the two components of genotypes and environments. According to the findings of Zobel *et al.* (1988), accurate model for AMMI can be predicted using first two PCAs. But the best predictive model will be affected by diverse locations with respect to latitudes, altitudes, planting seasons, soil types, fertility and rainfall. According to the AMMI model, the genotypes which are characterized by means greater than grand mean and the IPCA score nearly zero are considered as generally adaptable to all environment (Ezatollah *et al*., 2013). However, the genotype with high mean performance and with large value of IPCA score are consider as having specific adaptability to the environments. The large sum of squares for environments showed that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield. This is in synchronization with the findings of Singh *et al*. (1990) in chickpea production.

Table 2: List of chickpea genotypes used in the experiment.

Genotypes	Checks
RVG-203 (G1)	A-1 (C) (G6)
KCD-2019-05 (G2)	JG11 (C) (G7)
DC-17-1111 (G3)	Super Annigeri-1 (C) (G8)
RG-2016-134 (G4)	NBeG-49 (c) (G9)
NBeG-857 (G5)	
BGD-111-1 (G10)	

G- Genotype; C- Check.

Stability analysis by AMMI model

The presence of GEI was realized when the interaction was partitioned into the first two interaction PC axis (IPCA) (Table 3). IPCA1 and IPCA2 scores were highly significant, explaining 73.22 and 20.52 per cent of the variability, respectively. These results are in agreement with Jogendra *et al*. (2018), Zobel *et al*. (1988) and Tilahun *et al*. (2015) in chickpea. In AMMI 1 biplot where the main effects (genotype mean and environment mean) and IPCA1 scores for both genotypes and environments are plotted against each other (Fig 1). On the other hand, the second biplot is AMMI 2 where scores for IPCA1 and IPCA2 are plotted (Fig 2). Different genotypes showed incoherent performance across all the environments (Table 4). The mean grain yield value of genotypes averaged over locations ranged between 1167 kg/ha (NBeG-49 (G9)) to 1465 kg/ha (RG-2016-134 (G4)). Whereas, environments mean grain yield ranged from 1731 (kg/ha) for E1 to 1043 (kg/ha) for E2. The averaged grain yield over environments and genotypes was 1641 (kg/ha).

Environmental index value revealed in terms of negative and positive, Kalaburagi (E2), Bheemarayanagudi (E3) and Raichur (E4) were impoverished and Bidar (E1) and Hagari (E5) were opulent environments. Among the genotypes RG-2016-134 (G4), KCD-2019-05 (G2), Super Annigeri-1 (G8) and RVG-203 (G1) recorded higher than average yields, while genotypes *viz*., NBeG-857 (G5), DC-17-1111 (G3), JG-11 (G7), BGD-111-1 (G10), A-1 (G6) and NBeG-49 (G9) showed less than average yield. The similar inconsistent performance and genotypic adaption to environment was also observed by Tilahun *et al*. (2015) in chickpea.

The AMMI I, biplot for grain yield of the 10 desi-type chickpea genotypes under irrigated condition at five

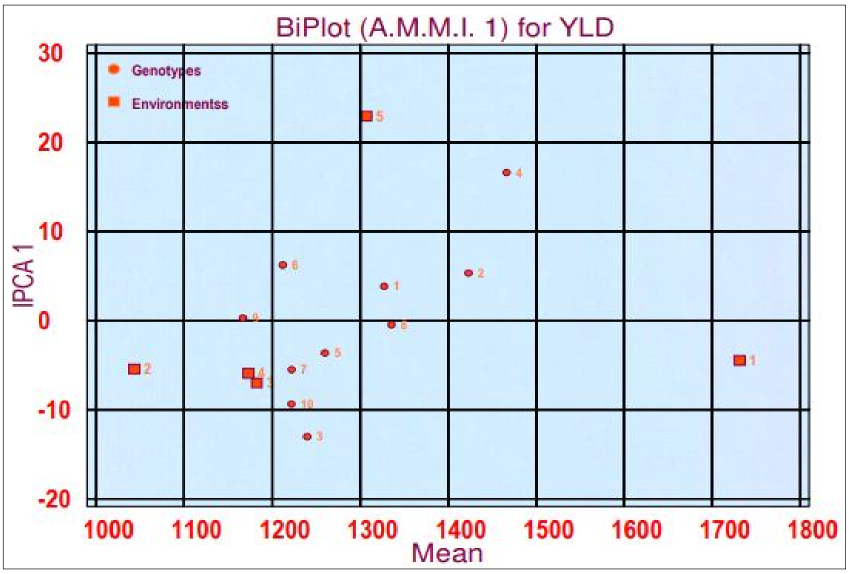


Fig 1: AMMI I bi-plot for average seed yield and PCA1 scores of 10 chickpea genotypes.

environmental locations is shown in Fig 1. The main effects (genotypes and environments) accounted for 75.45% of the total variation and IPCA 1 accounted for 10.13% of the total variation due to genotype by environment interaction alone. Environments showed high variation in both main effects and interactions (IPCA1) (Fig 1). Bidar (E1) and

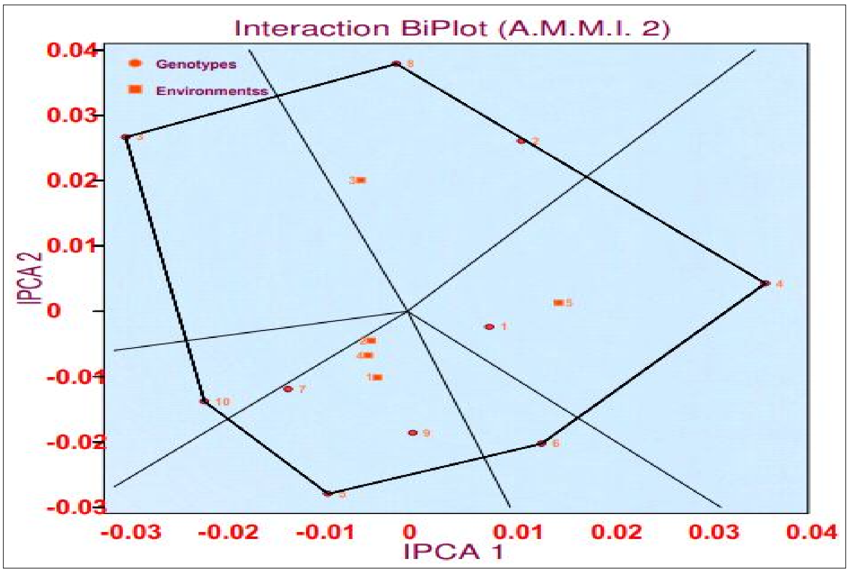
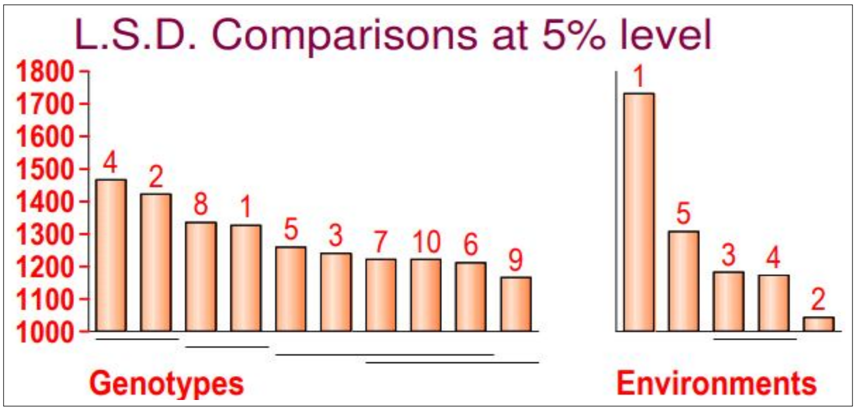


Fig 2: AMMI II biplot (IPCA 1 x IPCA 2) depicting genotype × environment interaction and stability of chickpea genotypes for seed yield across 5 environments.

Table 3: AMMI analysis of 10 Desi chickpea genotypes for seed yield over 5 environments.

Source of Variations	df	Sum of squares	Mean squares	Explained SS %	F ratio
Genotypes	9	431095.59	47899.51	10.03	2.90*
Environments	4	2811195.74	702798.94	65.42	42.57***
G*E Interaction	36	594286.92	16507.97	13.83	6.22***
PCA I	12	435111.41	36259.28	10.13	13.65***
PCA II	10	121964.79	12196.48	2.84	4.59**
PCA-III	8	27178.28	3397.28	0.63	0.738
Pooled residual	36	594286.92	2656.14		
Total	149	4297221.81	28840.42		
Comparison	S.E.D.	CD 5%		Variance	Variance %
Genotype Gi-Gj	42.93	87.0566	PCA I	35136.27	73.22
Environment Ei-Ej	30.35	60.2191	PCA II	121964.73	20.52
			Residual	10007.64	1.68

**Significant at *p*<0.05, ***Significant at *p*<0.01.



Hagari (E5) are the most favourable environments; Raichur (E4) and Bheemarayanagudi (E3) are the least favourable environments, while Kalaburagi (E2) is the average environment. Environments are classified into three main groups based on their IPCA 1 scores Hagari in quadrant I and have got large positive IPCA1 scores, which interact positively with genotypes that have positive IPCA1 scores and negatively with those genotypes having negative IPCA1 scores. Bidar is quadrants II and have got small negative IPCA1 and large positive environment index scores, which interact positively with genotypes that have positive IPCA1 scores and negatively with those genotypes having negative IPCA1 scores; Kalaburagi (E2), Bheemarayanagudi (E3) and Raichur (E4) in quadrant III and has got large negative IPCA1 scores which interact negatively with genotypes having negative IPCA1 scores and positively with genotypes having positive IPCA1 scores; and Akaki is in quadrant III and has got large negative IPCA1 scores which interacts negatively with genotypes that have negative IPCA1 scores and positively with those genotypes having positive IPCA1 scores (Table 4). The environments can be sub-grouped according to their average yield over the genotypes. According to environmental IPCA1 scores, Bidar (E1) and Hagari (E5) were more stable and had lower genotype by environment interaction and had high yield performance. According to IPCA1, these environments were also ideal environment for selecting genotypes with specific adaptation to high input and irrigated conditions.

The IPCA 1 and IPCA 2 components were significant ($P\leq0.01$) and accounted for 10.13 and 2.84 per cent of the total G × E interaction sum of squares, respectively (Table 3). which is in agreement with other studies (Zobel *et al*., 1988; Yan and Hunt, 2000). In Figure 1, the genotypes and locations that are located far away from the origin are more responsive. Kalaburagi (E2), Bheemarayanagudi (E3) and Raichur (E4) are the most differentiating environments, while Bidar (E1) and Hagari (E5) are more responsive environment than the other environments since it is far away from the origin. The AMMI 1 biplot expected yield clearly indicated for any genotype and environment combination can be calculated from Fig 1 as following standard procedures suggested by Zobel *et al*. (1988).

The genotype RG-2016-134 (G4) having highest mean yield, but recorded large IPCA 1 score indicating its environment sensitivity. The environments Hagari (E5) had positive IPCA 1 score, though Bidar (E1) has highest environment mean yield, negative IPCA 1 score were observed indicating the interaction effect on the genotype, among all environments. Bidar (E1) had smaller IPCA1 score (-4.50) hence had small interaction effects and which was favourable environment for the genotypes viz., RG-2016-134 (G4), KCD-2019-05 (G2), NBeG-857 (G5) and RGV-203 (G1). The genotype NBeG-49 showed poor mean yield but small IPCA1 (0.25) score close to zero, indicating that the variety was stable and less influenced by the environments. Similarly, the genotype KCD-2019-05 (G2) was stable across environments (low positive IPCA1 score) with high mean yield values. On the other hand, NBeG-857 (G5), JG-11 (G7) and Super Annigeri-1 (G8) and environments like, Kalaburagi (E2), Bheemarayanagudi (E3) and Raichur (E4) had below average yield with negative IPCA1 score indicating that these varieties were less influenced by the environments. The similar results of clustering of the genotypes and the different interaction effects were found in chickpea and (Funga *et al*., 2017) and wheat (Bishwas *et al*., 2021).

In AMMI 2 biplot, (Fig 2) the environmental scores are joined to the origin by side lines. Sites with short spokes do not exert strong interactive forces. Those with long spokes exert strong interaction. In Fig 2 where the points

Table 4: Additive main effects and multiplicative interaction (AMMI) analysis of variance for chickpea grain yield (per ha) of 10 genotypes across 5 environments.

Genotype	E1	E2	E3	E4	E5	Genotype mean	Var index	PCA I	G*E ResSS
RVG-203	1750	1107	1181	1165	1433	1327	39.60	3.81	2688.62
KCD-2019-05	1764	1153	1387	1240	1572	1423	135.67	5.30	1335.18
DC-17-1111	1717	1015	1347	1153	967	1240	-47.73	-13.06	1907.32
RG-2016-134	1826	1143	1262	1233	1867	1465	179.00	16.59	460.15
NBeG-857	1750	1058	1058	1244	1189	1260	-27.53	-3.67	2321.37
A-1 (C)	1729	910	989	1065	1367	1212	-75.47	6.22	5901.53
JG11 (C)	1705	1086	1099	1110	1111	1222	-65.47	-5.53	6933.94
Super Annigeri-1 (C)	1694	1026	1398	1206	1356	1336	48.20	-0.50	2369.76
NBeG-49 (c)	1646	861	987	1153	1189	1167	-120.67	0.25	11767.22
BGD-111-1	1732	1073	1121	1161	1022	1222	-65.60	-9.40	1509.58
Env.Mean	1731	1043	1183	1173	1307	1287			
Env.Index	443.83	-244.27	-104.77	-114.47	19.67				
PCAI	-4.50	-5.47	-7.01	-5.93	22.91				
G*ERes.SS	6117.59	17957.08	328.15	127890.59	11.26	37194.66			

GM= Grand mean, Var= Variety, Env= Environment. E1; Bidar, E2; Kalaburagi E3; Bheemarayanagudi, E4; Raichur, E5; Hagari, GM- Grand mean.

representing the environments E1, E2, E3, E4 and E5 are connected to the origin. The environments Bidar (E1), Kalaburagi (E2) and Raichur (E4) had short spokes and they do not exert strong interactive forces. The genotypes occurring close together on the plot will tend to have similar yields in all environments, while genotypes far apart may either differ in mean yield or show a different pattern of response over the environments. Hence, the genotypes near the origin are not sensitive to environmental interaction and those distant from the origins are sensitive and have large interaction. In the present study BGD-111-1(G10), NBeG-857(G5), A-1 (C) (G6), RG-2016-134(G4), KCD-2019-05(G2), Super Annigeri-1 (C) (G8) and DC-17-1111(G3)were more responsive since they were away from the origin whereas the genotypes viz., RVG-203 (G1) JG11 (C) (G7) NBeG-49 (C) (G9) were close to the origin and hence they were non sensitive to environmental interactive forces. Among the environment Bidar (E1), Kalaburagi (E2) and Raichur (E4) were near to the origin and they do not exert strong interactive forces compared to Bheemarayanagudi (E3) and Hagari (E5). Similar results were obtained by Akter *et al*. (2014) and Jogendra *et al*. (2018).

CONCLUSION

AMMI biplot employed for assessment of grain yield stability across test environments revealed that G-2 (KCD-2019-05) was the most stable and high yielding strain across all the test environments followed by G-8 (Super Annigeri-1) and G-1 (RVG-203). AMMI biplot for mega-environment analysis showed that E1 (ARS, Bidar) and E5 (ARS, Hagari) were most discriminating environments for grain yield and better representative than other test environments for screening of genotypes under irrigated condition. On the basis of results, it may be concluded that G-2 (KCD-2019-05) was most superior and ideal genotype across the environments. Therefore, G-2 (KCD-2019-05) suitable for irrigated condition and may be released as commercial variety in future in chickpea crop.

Conflict of Interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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