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Genotype-by-Environment (G × E) Interaction and Grain Yield Stability Analysis for Selected Genotypes of Desi Chickpea (*Cicer arietinum* L.) by using AMMI Model

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ABSTRACT

Background: The present investigation was carried out with eight chickpea genotypes under six environments to study the stability performance of the genotypes for grain yield and other yield related traits to select the best stable high yield genotypes for the suitable environments.

Methods: The experiment was performed using a randomized complete block design (RCBD) with three replications and all the statistical analysis was done by using the software R-studio 4.1.0 with the help of package Metan 1.15.0.

Result: The genotypes ICCV14102 (1220.57 kg/ha), ICCV 15115 (1125.40 kg/ha) and ICCV14108 (1110.01 kg/ha) have their mean grain yield above the grand mean yield (1054.48 kg/ha) whereas five genotypes have yield lower than the grand mean yield. Based on the yield stability index and WAAS ranking, the most stable genotypes were, ICCV 14102 (YSI = 4) and ICCV 15115 (YSI = 8) across the environment and can be suggested for release of these genotypes after critical evaluation.

Key words: AMMI model, Chickpea, Genotype-by-Environment interaction, Stability.

INTRODUCTION

Chickpea (*Cicer arietinum* L.; 2n = 2x = 16) is the second most important food legume in the world next to dry bean (Funga *et al*., 2017; Koskosidis *et al*., 2021). This is also a premier pulse crop in Indian subcontinent and cultivated under both rainfed and irrigated conditions. The productivity of chickpea remained incompetent due to the lack of improved varieties with specific characteristics such as early maturity, biotic and abiotic stress tolerant and poor soil fertility (Irfan, 2018). Differential performance of chickpea under diverse environmental conditions decreases yield stability. The observed yield difference between actual and prospective chickpea yields may be owing in part to genotype and environmental variability (Funga *et al*., 2017). G × E analysis is important to identify superior varieties and their adaptation to and stability in diverse agroecological conditions (Kanouni *et al*., 2015). The stability of a variety is refers to the consistent high performance across a sets of environments. Inefficiency in the G × E analysis of variance may result in wrong selection of genotypes for yield. As a result, multi-environment experiments are necessary to find the best and most productive cultivar (Ebdon and Gauch, 2002). However, because of the existence of genotype-environment interaction, selecting an ideal genotype is difficult. Based on the experimental data, the number of environments and the accuracy of the data gathered and environmental information, there are several models for conducting GE interaction (GEI) research. When analysing yield stability, we employed the AMMI model (additive main effects and multiplicative interactions). Amplitudes on the x-axis represent major (additive) effects, while those on the y-axis represent changes in interdependencies between variables (Yan and Kang, 2003). Genotypes that group together have similar adaptation while environments which group together influence the genotypes in the same way. If a genotype or an environment has an IPCA1 score of close to zero, this implies that its interaction effects are minimal and therefore, it is stable (Carbonell *et al*., 2004). Therefore, the goal of this study is to investigate the yield stability and adaptability of different chickpea genotypes in Odisha's unique climatic circumstances.

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MATERIALS AND METHODS

Study site and experimental materials

The study was conducted at three locations; R.R.T.T.S., Bhawanipatna, R.R.T.T.S., Keonjhar and K.V.K., Shama khunta under Odisha University of Agriculture and

Technology, Odisha during *rabi* (2016-17) and *rabi* (2017-18) cropping seasons. The details of testing environment and its climatic condition during the crop growth are mentioned in Table 1. The present study was comprised of six elite genotypes (G1: ICCV 14106, G2: ICCV 15114, G3: ICCV 15115, G4: ICCV 15118, G5: ICCV14102; and G6: ICCV14108) along with two standard checks (G7: JAKI 9218 and G8: JG-14) and the materials were provided by ICRISAT, Hyderabad.

Experimental design and data collection

The experiment was performed using a randomized complete block design (RCBD) with three replications. The experimental unit was consists of 6 rows of 4 m length with spacing of 30 cm × 10 cm. All the agronomical practices were followed dung the cropping season to raise a healthy crop. The observations were recorded on the following parameters *viz*., days to 50% flowering, plant height (cm), no. of pods per plant, 100 seed weight (g) and grain yield (kg/ha). The individual plot yield was harvested separately and later it converted to grain yield per hectare (kg/ha).

Statistical data analysis

The grain yield was subjected to combined analysis of variance (ANOVA). All the statistical analysis was done by using the software R-studio 4.1.0 with the help of package Metan 1.15.0 (Olivoto and Lucio, 2020). The AMMI analysis first fits additive effects for the genotypes and environments by the usual additive ANOVA procedure and then fits multiplicative effects for genotype-by-environment interactions (G × E) by principal component analysis (PCA). The following mathematical AMMI model was used to study the G × E interaction and yield stability analysis based on the principal component analysis (PCA) (Gauch, 1992):

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{N} \lambda k + \alpha_{ik} y_{jk} + R_{ij}$$

Where,

Y_{ij} = Yield of i^{th} genotypes in j^{th} environment.

ì = Overall mean.

g_i= Effect of the i^{th} genotype.

e_j = Effect of the j^{th} enviroment.

$\Sigma\lambda k$ = Square root of the Eigen value of the PCA axis k.

Then α_{ik} and y_{jk} are the principle components scores for PCA axis k of the i^{th} genotype and j^{th} environment, respectively and R_{ij} is the residual. The GE interaction sum of squares was subdivided into PCA axis SS, 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 AMMI stability value (ASV) was calculated by using the following formula as described by Purchase (2000).

$$ASV = \sqrt{\left[\frac{SSIPCA1}{SSIPCA2}\,(IPCA\ Score)\right]^2 + [IPCA\ Score2]^2}$$

Where,

SS = Sum of square of the IPCAs and IPCA1 and IPCA2 are the 1st and 2nd interaction component axes respectively. Smaller the ASV scores indicates a genotype is more stable the across environments, whereas larger the IPCA score either positive or negative, the genotype is more specifically adapted to a certain environments.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA)

The pooled analysis of variance (ANOVA) for grain yield and other yield attributes (Table 2 and Table 3) of eight genotypes of chickpea were tested under six environmental conditions and showed significant variation ($p<0.001$) for genotypes (G), environments (E) and genotype-by-environment interactions (G × E). The main effect and its interaction effect showed significant variance, indicating that genotype performance fluctuates from environment to environment and confirming the absence of stable genotypes across environments. Grain yield variance among genotypes can be explained by a higher percentage of variation explained by environmental factors. This suggests that, in Odisha, the environment has a significant impact on chickpea grain yield. The presence of G × E interaction was clearly demonstrated by the AMMI model in which five of the principal component axes (IPCA1, IPCA2, IPCA3, IPCA4 and IPCA5) were significant (Table 3). Significant G × E interaction also reported by Balapure *et al*. (2016) and Kumar *et al*. (2020) for grain yield by using AMMI model.

AMMI-1 Biplot analysis for additive and interaction effects

There is a considerable G × E interaction that affects grain production in different growing environments. AMMI-1 biplot quadrats I and II contain the genotypes of the four ICCVs (ICCV 14108, ICCV 15115, ICCV 14102 and ICCV 15114), as well as the two environments (E4 and E5) that have the same positive sign of IPCA1 score (Fig 1). Furthermore, genotypes (JAKI 9218, ICCV 15118, JG 14 and ICCV 14105), as well as environments (E1–E6 of the AMMI-1

Table 1: Description of the test environment and the climatic variables during the cropping season.

Environment code	Location	Season	Total rainfall (mm)	Average temperature (°C)	Soil type
E1	R.R.T.T.S., Bhawanipatna	*Rabi* (2016-17)	82.96	24.50	Black soil
E2	R.R.T.T.S., Keonjhar	*Rabi* (2016-17)	80.05	24.00	Red lateritic
E3	K.V.K., Shamakhunta	*Rabi* (2016-17)	90.26	24.75	Sandy loam
E4	R.R.T.T.S., Bhawanipatna	*Rabi* (2017-18)	111.32	25.25	Black soil
E5	R.R.T.T.S., Keonjhar	*Rabi* (2017-18)	133.36	24.25	Red lateritic
E6	K.V.K., Shamakhunta	*Rabi* (2017-18)	125.00	24.75	Sandy loam

biplot), exhibit a positive interaction since they share the same negative sign of IPCA1 score in the AMMI-1 biplot quadrats III and IV. Surroundings with long arrows exert more interaction force than environments with short arrows. As a result, the environments E4, E1, E2, E3, E5, E6 have a lower contact force than the other environments. Quadrant I of the AMMI 1 biplot contains genotypes (ICCV 14108, ICCV 15115 and ICCV 1402) that are less impacted by the genotype-environment interaction. The genotypes and environments on the right side of the midpoint of the axis in the graph give more than those on the left side of the axis. To put it another way, the genotypes of the I. cruzi strains with the highest yield are ICCV 14102, ICCV 15115 and ICCV 14108. E4 and E5 were characterised as high yielding environments, while E1, E2, E3 and E6 were categorised as low yielding. However, there were no closely linked genotypes for the environment E4 that were readily available. All the findings of Funga *et al*. in the present analysis are in agreement with the findings of Kumar *et al*. (2020) and Dhuria and Babbar (2021).

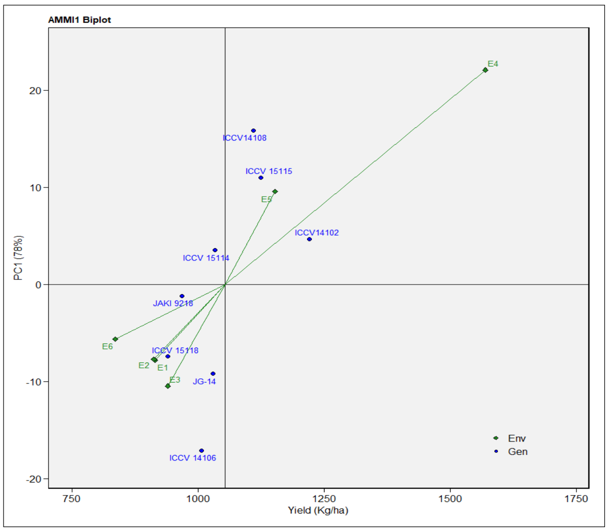

Fig 1: AMMI-1 biplot analysis of IPCA 1 score versus grain yield of eight chickpea genotypes under six environmental conditions (E1, E2, … and E6).

Table 2: AMMI analysis of variance (ANOVA) for yield related traits of eight test entries across three different environments during *Rabi* (2016-17) and Rabi (2017-18).

Source	DF	Mean sum squares (MSS)				
		Days to 50% flowering	Plant height (cm)	No. of pods per plant	100 seed weight (g)	Grain yield (kg/ha)
Environment	5	701.61***	346.84***	1540.20***	20.86***	1804888***
Replication (Environment)	12	4.03	36.70	8.99	1.31	6020.225
Genotype	7	41.41***	118.23***	282.38***	159.33***	152953.3***
Genotype: Environment	35	19.53***	43.11***	114.32***	5.76***	77669.58***
PC1	11	51.88	100.52	225.36	18.19	192879.9
PC2	9	10.58	38.39	95.71	0.10	36831.94
PC3	7	2.34	6.52	54.58	0.09	33779.18
PC4	5	0.16	1.67	48.66	0.02	5641.931
PC5	3	0.11	1.19	11.83	0	201.6502
Residuals	84	1.83	13.25	28.46	0.73	12344.37
Total	178	30.15	40.07	113.37	9.55	93489.64

***, ** and * represents the level of significance at <0.001, 0.05 and 0.5 respectively.

Table 3: AMMI analysis of variance (ANOVA) for seed yield of eight test entries across three different environments during Rabi (2016-17) and *Rabi* (2017-18).

Source	DF	SS	MSS	F-value	Pr (>F)	Proportion	Accumulated
Environment	5	9024442	1804888***	299.80	3.64	-	-
Replication (Environment)	12	72242.7	6020.22	0.48	0.91	-	-
Genotype	7	1070673	152953.30***	12.39	8.56	-	-
Genotype: Environment	35	2718435	77669.58***	6.29	2.84	-	-
PC1	11	2121679	192879.9***	15.62	0	78	78
PC2	9	331487.4	36831.94***	2.98	0.004	12.2	90.2
PC3	7	236454.2	33779.18***	2.74	0.01	8.7	98.9
PC4	5	28209.65	5641.93***	0.46	0.80	1	100
PC5	3	604.9505	201.65***	0.02	0.99	0	100
Residuals	84	1036927	12344.37			-	-
Total	178	16641156	93489.64			-	-

Where, DF = Degree of freedom, SS = Sum of squares, MSS= Mean sum of squares, ***, ** and * represents the level of significance at <0.001, 0.05 and 0.5 respectively.

AMMI-2 biplot analysis and which-won-where polygon view of biplot

Using an AMMI2 biplot, the amplitude of the G × E interaction is shown. The IPCA1 score was plotted against the IPCA2 score in order to better understand the adaptation of the IPCA1. The IPCA1 score accounts for 78.00%, whereas the IPCA2 score accounts for 12.20%. More interaction occurs between genotypes and surroundings that are far from the origin. There are beneficial interactions between genotypes and surroundings from the same sector. On the contrary, oppositely polarised genes and environments interact negatively. Genes (ICCV 15114 and JAKI 9215) closer to the AMMI-1 biplot's centre indicated that they were stable across the environment (general adaptability) and were not affected by environmental interactions (Fig 2). The environments (E2, E4 and E5) were least responsive or interactive based on their far distance from the origin in AMMI-2 biplot. The quadrant I and IV environments (E4 and E5) have a higher potential than the quadrant II and III settings (E1, E2, E3 and E6) (low potential environment). These three genotypes have similar yield performance in the same environment because they have the same genetic background. Mean yield and environmental responsiveness may differ between genotypes that were isolated from each other. Genes and environments are shown as polygons in the 'which won where' or 'which is better for what' perspective of genotypes and environments (Fig 3). The polygon is formed by combining the PC1 (78%) and PC2 (12%) components and connecting the farthest genotypes. Genetic variants found at the polygon's corners are the greatest or worst performers in specific situations, whereas the variant found at the polygon's centre is the top performer across all of this sector's environmental contexts and circumstances (Yan and Tinker, 2006). For the stability analysis of chickpea using the AMMI model, Funga *et al*. (2017) and Tiwari *et al*. (2018) similarly reported similar results. As a result, the polygon in this study has four vertexes and an equality line that divides the biplot for seed yield into five sectors, of which all the environments are spread in two of them. In E4 and E5, ICCV 14102 and ICCV 14108 are the vertex genotypes, respectively, while ICCV 15118 is the vertex genotype in E6. These vertex genotypes were shown to be the highest performers in their respective contexts.

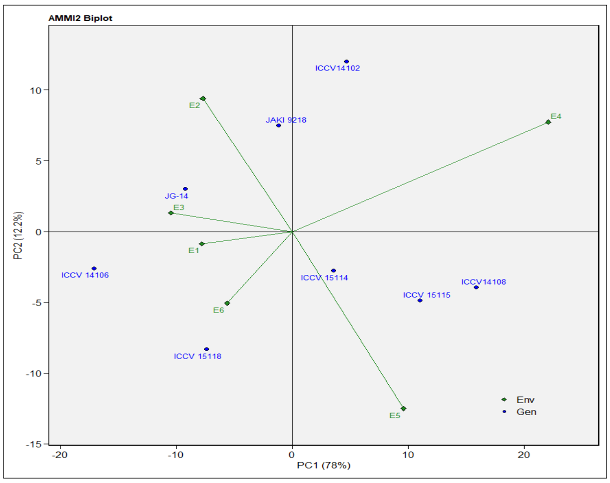

Fig 2: AMMI-2 biplot analysis of IPCA 1 score versus IPCA 2 score of eight chickpea genotypes under six environmental conditions (E1, E2, … and E6).

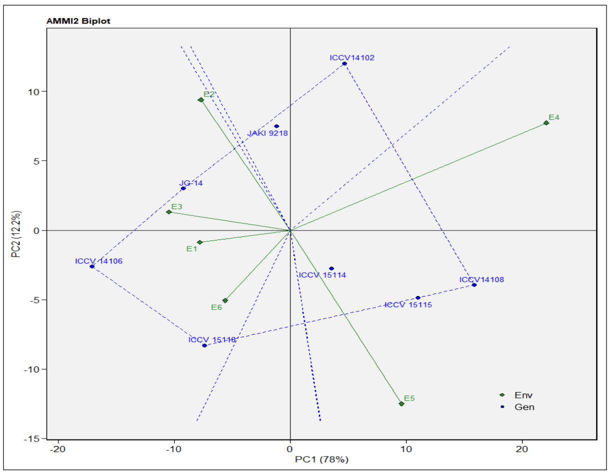

Fig 3: Polygon view of AMMI-2 biplot based on symmetrical scaling for which-won-where pattern of eight chickpea genotypes under six environments (E1, E2, … and E6).

AMMI stability value (ASV) and identification of stable high yielding genotypes

Average grain yields were calculated for all eight genotypes using a linear mixed effect model that included additive main effects and multiplicative interactions (ASV), IPCA scores and weighted averages of absolute grain yields from the singular value decomposition of the matrices of best linear unbiased predictions for genotype environment interaction effects (WAAS) were depicted in Table 4. Genotype ICCV 15118 had the lowest mean grain yield of 940.09 kg/ha, whereas genotype ICCV14102 had the highest mean grain yield of 1220.57 kg/h. The genotypes ICCV14102 (1220.57 kg/ha), ICCV 15115 (1125.40 kg/ha) and ICCV14108 (1110.01 kg/ha) have their mean grain yield above the grand mean yield (1054.48 kg/ha), whereas five genotypes have yield lower than the grand mean yield. Ordering genotypes by yield stability can be done with the help of the AMMI stabilisation value (ASV), which was first introduced by Purchase and colleagues (2000). When IPCA1 (interaction principal component analysis axis 1) scores are shown against IPCA2 (interaction principal component analysis axis 2), the ASV is the distance from zero. In order to account for the relative contribution of IPCA1 and IPCA2 to the total GE sum of squares, the IPCA1 score must be weighted by the proportionate difference between IPCA1 and IPCA2 scores (Table 4). Once the distance to zero has been calculated, the Pythagorean Theorem is applied (Purchase *et al*., 2000). A genotype with the lowest ASV score is the most stable and vice versa, according to

Table 4: Yield performance and stability of 8 chickpea genotypes based on mean grain yield (kg/ha) and measures of AMMI stability value (ASV).

Genotype	Y	Y-R	ASV	ASV-R	YSI	SIPC	SIPC-R	EV	EV-R	ZA	ZA-R	WAAS	WAAS-R
ICCV 14106	1006.66	6	109.71	8	14	27.09	8	0.18	6	0.51	8	14.48	8
ICCV 15114	1034.36	4	22.64	2	6	7.694	1	0.01	1	0.12	1	3.23	2
ICCV 15115	1125.40	2	70.44	6	8	19.63	3	0.08	3	0.34	6	9.59	6
ICCV 15118	940.09	8	48.29	4	12	20.80	6	0.12	5	0.28	5	7.33	4
ICCV14102	1220.57	1	32.21	3	4	23.45	7	0.20	7	0.24	3	5.76	3
ICCV14108	1110.01	3	101.44	7	10	20.16	4	0.11	4	0.45	7	13.01	7
JAKI 9218	968.28	7	10.73	1	8	20.47	5	0.22	8	0.14	2	2.90	1
JG-14	1030.43	5	59.12	5	10	12.24	2	0.04	2	0.26	4	7.64	5
Mean	1054.48		56.82			18.94		0.12		0.29		7.99	

Where, Y = Yield, R = Rank, ASV = AMMI stability value, YSI = Yield stability index (YSI=Y-R + ASV-R), SIPC = Sums of the absolute value of the IPCA scores, EV = Averages of the square eigenvector values, ZA = Absolute value the relative contribution IPCs to the interaction, WAAS = weighted average of absolute scores from the singular value decomposition of the matrix of best linear unbiased predictions for the genotype × environment interaction effects generated by an linear mixed-effect model.

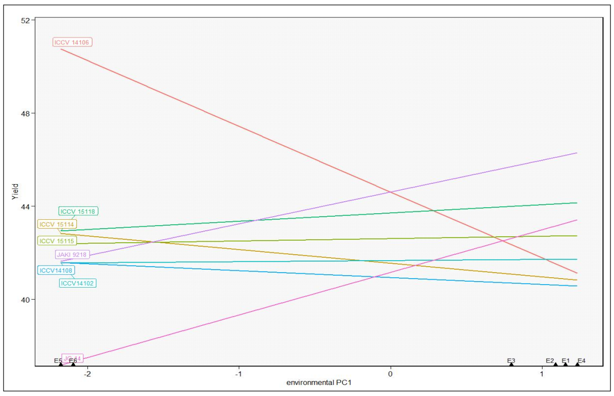

Fig 4: Crossover yield performance of chickpea genotypes across six growing environments.

the ASV technique. As a result, JAKI 9218 (ASV = 1) and ICCV 15114 (ASV = 2) are the most environmentally stable genotypes, although their mean grain yields are low, at 968.28 and 1034.36 kg/ha, respectively. Singular value decomposition (SVD) of best linear unbiased predictions for genotype-environment interaction effects derived by a linear mixed-effect model (WAAS) from this study also yielded a similar ranking in terms of absolute scores. With the use of the WAAS index, the best genotypes for any given situation can be found (Olivoto *et al*., 2019). High-yielding and stable genotypes can be identified using a yield stability index (YSI). The genotypes with the lowest YSI values are deemed the most stable and have a greater mean grain yield, according to the YSI technique. These genotypes have the greatest environmental stability, as measured by the genotype stability index (YSI) (Table 4). There was a significant difference in yield between the genotypes JAKI 9218, JG 14 and ICCV 15118 in environment E4 and ICCV 14106 in environment E5 when comparing their crossover performance across these six test conditions (Fig 4). There are parallels between our results and those described in the literature on chickpea by Funga and Bhardwaj (2017), Irfan (2018) and Dhuria and Babbar (2021).

CONCLUSION

In order to choose high-yielding stable genotypes, plant breeders must conduct GEI studies, which examine the effects of genotype on environment. Genetic and phenotypic values are reduced as a result of GEI, so both yield and stability performance should be taken into account while selecting genotypes. An AMMI model was used to analyse the yield stability of eight chickpea genotypes across six environmental factors to determine the best high yield stable genotype for Odisha's growing circumstances. The genotypes JAKI 9218 (ASV=1) and ICCV 15114 (ASV=2) were determined to be the most stable across environments based on the AMMI stability value (ASV), although their yield is poor. A combination of WAAS and the yield stability index (YSI) was used to find stable genotypes with high yields. ICCV 14102 and ICCV 15115 are the most stable genotypes across the higher yielding settings, according to the above methodologies. We can confidently suggest releasing these candidate genotypes in appropriate contexts for additional stability testing.

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