LR-4911
[1-6]

RESEARCH ARTICLE Legume Research- An International Journal, Volume Issue : ()

Seed Yield Stability Assessment of Chickpea Genotypes Through AMMI and Bi Plot Analysis

Laxuman[1], H. Avinalappa[2], Sidramappa[3], P.H. Kuchanur[4],
K. Shiva Kumar[5], G. Ashok Kumar[6]

10.18805/LR-4911

ABSTRACT

Background: Development of variety with high yield potential is the major objective of crop improvement program, which can be achieved by improving selection efficiency with estimating stability parameters. An elite crosses and popular varieties of twelve chickpea genotypes were evaluated for assess seed yield stability under four designated locations (Kalaburagi, Bidar, Raichur, and Sirguppa) during 2019-20.

Methods: All the experiments were conducted in randomised complete block design with three replications. The interaction analysis (AMMI ANOVA) indicates large variations for seed yield due to highly significant ($p<0.01$) environment and genotype, thus the genotypes were diverse with large sum of squares for their seed yield and environment.

Result: The differential response of chickpea genotypes for seed yield across the environments was observed. IPCA1 and IPCA2 together captured 4.27 per cent of the interaction mean squares. JG11 × WR315 (F7)-57 and ICCV 191106 showed higher average yields and adaptable to favourable environments. Based on AMMI bi-plot analysis, genotypes (JG11 × WR315 (F7)-57, JG11) and (JAKI 9218, RGV 203) were stable and unstable respectively. Similarly, best performer genotypes and three mega environments were noticed through the analysis. Environments (Kalaburagi, Sirguppa) were found with most selective for seed yield estimation. In terms of seed yield stability, the genotypes (JG11 × WR315 (F7)-57, JG11 and JG11 × WR315 (F7)-49) were the best among all.

Key words: Chickpea, Environment, Phenotypic stability, Seed yield.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a predominately leguminous crop and serves as an important source of dietary protein (Jendoubi *et al.* 2017). Among pulses, chickpea alone contributes over more than 45 per cent to total pulses production, but its existing varieties are liable to heavy yield losses (>50 per cent) due to changing climate, mainly heat stress and drought (Sinha *et al.* 2019 and Shah *et al.* 2020) during reproductive period (Devasirvatham and Tan, 2018), while waterlogged, saline soils and cold stress during cropping period (Rani *et al.* 2020). In Karnataka, Kalaburagi occupies the first position in chickpea area (1.24 lakh ha), production (8.63 lakh tonnes) and productivity (730 kg/ha) followed by Bijapur, Bidar, Dharwad, Bellary and Raichur (Kiresur *et al.* 2009). However, the varied climatic conditions and lack of varietal adaptation leads to reduced average seed yield of existing varieties from 769 to 867 kg/acre to 607 to 650 kg/acre (Kiresur *et al.* 2009).

Being a winter crop, the yield stability under rainfed ecosystem is a challenging task for seed yield increase. 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) to estimate such importance. 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.

In order to meet the global market demand, climate resilience and replace existing obsolete varieties, ICRISAT, UAS, Raichur, NARS partners and ICAR-IIPR have made collaboration in developing new chickpea varieties. The breeding lines which are developed through collaboration,

---

[1] Zonal Agricultural Research Station, Kalaburagi-585101, Karnataka, India.
[2] Crop Improvement-Chickpea Breeding, International Crops Research Institute for the Semi-Arid Tropics, Hyderabad- 502 324, Telangana, India.
[3] Agricultural Research Station, Bidar-585 401, Karnataka, India.
[4] Collage of Agriculture, Bheemarayanagudi-585 287, Karnataka, India.
[5] Main Agricultural Research station, Rachur-584 104, Karnataka, India.
[6] Agricultural Research Station, Sirguppa-583 121, Karnataka, India.

Corresponding Author: Laxuman, Zonal Agricultural Research Station, Kalaburagi-585 101, Karnataka, India.
Email: laxumanp@gmail.com

How to cite this article: Laxuman, Avinalappa, H., Sidramappa, Kuchanur, P.H., Kumar, K.S. and Kumar, G.A. (2022). Seed Yield Stability Assessment of Chickpea Genotypes Through AMMI and Bi Plot Analysis. Legume Research. DOI: 10.18805/LR-4911.

Submitted: 06-03-2022 **Accepted:** 04-06-2022 **Online:** 05-07-2022

and found promising among them are subjected to stability analysis under designated regions of Karnataka in the present investigation. Further, AMMI analysis and biplot, has been utilised to estimate nature and magnitude of genotypes environment interaction (GEI) effects on seed yield in diverse production environment, to measure the yielding ability, genotypes stability to such environments.

MATERIALS AND METHODS

The experiment was conducted to test the yielding stability of twelve chickpea genotypes (Table 1) (elite crosses, popular varieties) which are developed through collaboration effort including two checks (A1, JG 11) under designated locations (Kalaburagi-A/L1, Bidar-B/L2, Raichur-C/L3, Sirguppa-D/L4) of Karnataka in order to assess their performance over changing environment. A1 is being used as local check, due to its quality and well adaptation in northern Karnataka, while JG 11 is designated as national check due to its wider adaptation and nominated to south zone as well, henceforth used as recurrent parent in the crossing of present experiment. In all the locations, the planting was done during 1st week of October 2019-20. The locations were diverse with respect to weather conditions and nature of soil, hence are the designated regions for the evaluation of AICRP (All India Coordinated Research project) breeding lines. All the locations are belonging to North Eastern Karnataka. Where the agro-climatic zones is categorised as Eastern dry zone, North Eastern Transitional zone and Northern dry zone. Each entry at each location was sown in randomised block design with three replications. All the entries were accommodated in 4 rows with 4 meter length, spacing of 30 and 10 cm followed in-between rows and plants respectively. The seed yield (Kg/ha) for each replication was recorded for each entry at all the locations 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.

The AMMI model referred is

$$Y_{ij}=U+g_i+e_j+\sum hk\ \alpha_{ij}\ \tau_{ik}+R_{ij}$$

where, Y_{ij} is the yield of i^{th} genotype j^{th} environment, gi is the mean of the i^{th} genotype as a deviation from the grand mean μ; e_j is the mean of the j^{th} environment minus the grand mean (μ), hk is the eigen value of the PCA axis k, α_{ij} and τ_{ik} are the principal component scores for K of the i^{th} genotypes and the j^{th} environment respectively and R_{ij} is the 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

ANOVA for AMMI

The AMMI analysis of variance for seed yield (kg/ha) of twelve chickpea genotypes tested in four environments (locations) is presented in Table 2. Interaction analysis indicates large variations for seed yield due to highly significant (p<0.01) environment and genotype, further the genotypes were diverse with large sum of squares for their seed yield and environment, thus the genotypes were found stable for the tested locations, while percent variations for the genotypes accounted was 6.17 and 83 respectively. The similar results were recorded by Jagdish *et al.* (1996), Sellami *et al.* (2021), Yadav, *et al.* (2014) in *desi* and *Kabuli* chickpea. The presence of GEI was specified by the AMMI model when the interaction was categorised among two principal component axis (PCA). The mean squares for the PCA I and PCA II were significant at P = 0.01 and collectively contributed to 4.2 per cent of the total interactions sum of squares. Therefore, the postdictive assessment suggested that two principal component axes were significant for the model with 24 per cent of the interaction degrees of freedom (DF). Of the two significant IPCA axes muchof the interaction variance was explained by the PCA-I (49.99%). This entails that the interaction of the chickpea genotypes with four environments was predicted by the two components of

Table 1: List of chickpea genotypes used in the experiment.

Genotype name	Parentage	Target trait
JG11 × WR315(F7)-57 (G1)	JG11 and WR315	Yield, *Fusarium* wilt resistance
JG11 × WR315(F7)-49 (G2)	JG11 and WR315	Yield, *Fusarium* wilt resistance
ICCV 191106 (G3)	Genesis 836/JAKI 9218	ICRISAT bred lines identified for different target traits
ICCV 191114 (G4)	JG 11/ICCV 05103	like mechanical harvest, nutritional, herbicide tolerance *etc*.
ICCV 191112 (G5)	JG 11/ICCV 05103	
ICCV 191107 (G6)	Genesis 836/ICCV 97105	
ICCV 191108 (G7)	ICC 4958 TM/JAKI 9218	
A1 (G8) (C1)	Selection	Seed quality, high yield
JG11 (G9) (C2)	-	Early maturity, Mega variety, Superior Yield
Super Annigeri 1 (G10)	-	*Fusarium* wilt, superior yield than A1,
JAKI 9218 (G11)	-	Bold seeds, resistant to wilt, collar rot
RGV 203 (G12)	-	Early maturity

G-genotype; C-check.

Table 2. AMMI analysis of 12 desi chickpea genotypes for seed yield over 4 environments.

Source of variations	df	Sum of squares	Mean squares	Explained SS %	F ratio
Genotypes	11	1153760.44	104887.31	6.17	3.57**
Environments	3	15532521.48	5177507.16	83	176.48***
G*E Interaction	33	968134.08	29337.40	5.17	
PCA I	13	483991.39	37230.11	2.59	3.37**
PCA II	11	313576.61	28506.96	1.68	2.58**
Pooled residual	20	484142.69	24207.13		
Total	143	18713669.56	130864.82		
Comparison	S.E.D.	CD 5%		Variance	Variance %
Genotype Gi - Gj	74.28	151.12	PCA I	483991.39	49.99
Environment Ei - Ej	42.88	85.12	PCA II	313576.61	32.39
			Residual	170566.08	17.62

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

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.

Stability analysis by AMMI model

The mean performance of PCA scores for both the genotypes and environments used to construct the bioplot (Fig 1 and 2) are presented in Table 3. Due to the significance of IPCA I and IPCA II scores, the relative magnitude of interaction effects of each genotype and environment and identification of favourable environments was done through AMMI I and AMMI II biplot (Rao *et al.* 2011). ICCV 191106 (1854 kg/ha) (G3), JG11 × WR315 (F7)-57 (1811 kg/ha) (G1) and ICCV 191114 (1324kg/ha) (G4) were recorded the highest and lowest mean seed yield (kg/ha) value of the genotypes averaged over environments respectively. It is therefore, the differential range of mean seed yield across the environments was noticed in chickpea (Funga *et al.* 2017).

As a result, an inconsistent performance of the genotypes across the environments was recorded. Further, the environment's mean seed yield was ranged between 977.17 (kg/ha) for L3 to 2315.39 (kg/ha) for L4, while average seed yield over environments and genotypes was 1641.07 kg/ha. Such that the locations, L2 and L3 are poor, while L1 and L4 were found to be rich according to the environmental index value. Among the genotypes, JG11 × WR315 (F7)-57, and ICCV 191106 have higher average yields and adaptable to favourable environments, while remaining grouping to poor environments. The similar inconsistent performance and genotypic adaption to environment was observed by Tilahun *et al.* (2015) in chickpea.

Therefore, according to the AMMI model, the genotypes (JG11 × WR315 (F7)-57, JG11 × WR315(F7)-49, Super Annigeri-1, JAKI-9218), which are characterized by mean greater than the grand mean and the positive PCA scores are considered as generally adaptable to all the environments. However, the genotypes (Super Annigeri-1, JAKI-9218) with moderate to high mean performance and large value of IPCA scores are considered as having specific adaptability to the environments. The results are inconsistent with Shinde *et al.* 2002.

In AMMI I biplot (Fig 1), the IPCA scores of twelve chickpea genotypes and four different environments were plotted against their respective means. As per the plot analysis, three genotypes (JG11 × WR315 (F7)-57, ICCV 191106 and Super Annigeri 1) and two environments (Kalaburagi, Sirguppa) located on right side of the perpendicular vertical line, revealed high yielding genotypes and environments. While, JG11 × WR315 (F7)-57 and JG11 recorded lowest IPCA1 scores, thus indicates that these were least involved with interaction, and are therefore the most stable. But, only the yield of JG11 × WR315 (F7)-57 genotype was above-average.

Conversely, JAKI 9218 and RGV 203 were considers most unstable genotypes. Erdemci (2018) observed similar results while investigating interaction component for seed yield in chickpea. ICCV 191108 and A1 were on par with the same vertical line, hence they have similar yield performance across the environments, but they have different interaction effectssince they are not lies on same horizontal line.

While, the best entries namely ICCV 191112, ICCV 191107 and JG11 × WR315 (F7)-49, Super Annigeri 1 were grouped together, thus their performance is similar across all 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).

Cross over and non-cross over genotype-by-environment interaction and possible mega environments under multiple-location yield trials was detected through polygon view of the GGE-biplot analysis (Yan *et al.* 2007). In order to demonstrate the stability of genotype as well as the relative magnitude of interaction effects of each genotype and environment, AMMI II biplot was drawn using IPCA 1 and IPCA 2 scores (Fig 2). As per the Fig 2, ICCV 191114 (G4), A1 (G8), JG11 (G9), Super Annigeri 1 (G10), JAKI 9218 (G11), RGV 203 (G12) are located in the edge of the polygon and indicates the best performer genotypes, while

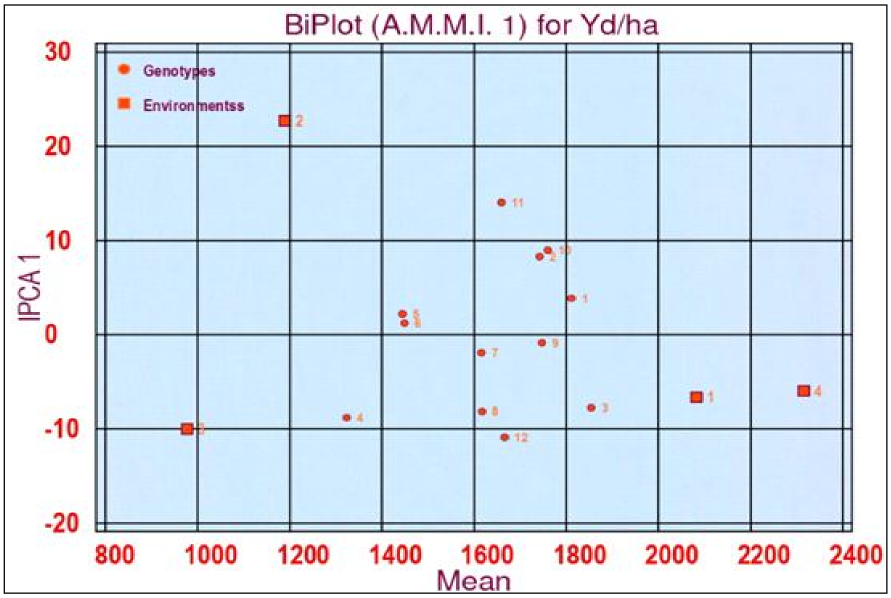

Fig 1: AMMI Ibi-plot for average seed yield and PCA1 scores of 12 chickpea genotypes.

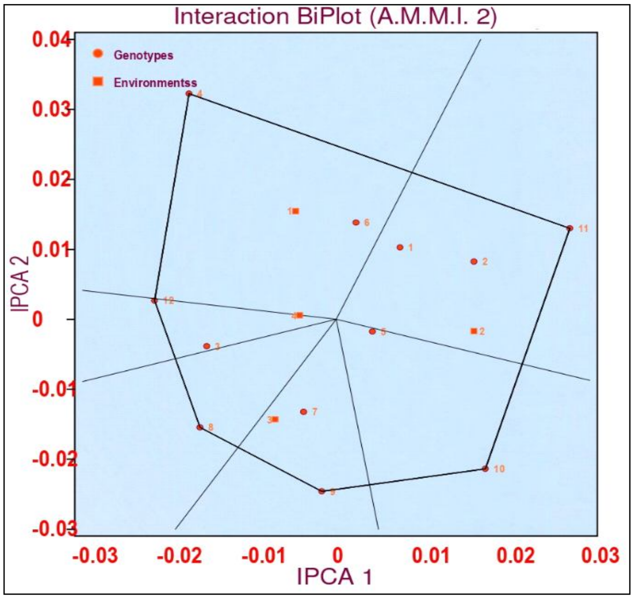

Fig 2: AMMI II biplot (IPCA 1 × IPCA 2) depicting genotype × environment interaction and stability of chickpea genotypes for seed yield across 4 environments.

six lines divided the bi-plot into six sectors and the environments fell into three of them, and are considered as three mega-environments.

Two environments (Kalaburagi-A; Sirguppa-D) are located in first sector and the vertex genotypes for this sector was ICCV 191114 (G4) and RGV 203 (G12). Whereas rest of the environments (Bidar-B, Raichur-C) fell into the second and fourth sector, and their vertex genotypes were JG11 (G9) and JAKI 9218 (G11) respectively. However, A1 (G8) and Super Annigeri 1 (G10) are the other vertex genotypes, which have not included any environment in their sectors, and were not listed with highest yielding genotypes at any environment, or might be poorest genotypes of all or some environments.

Hence, ICCV 191114 (G4), RGV 203 (G12), JG11 (G9), JAKI 9218 (G11), A1 (G8) and Super Annigeri 1 (G10) are specifically adaptable to an environment. Alternatively, ICCV 191112 (G5) was located very close to the centre of origin, and thus it would possess low genotype environment interaction variation (Erdemci, 2018).

Table 3: Additive main effects and multiplicative interaction (AMMI) analysis of variance for chickpea grain yield (per ha) of 12 genotypes across 4 environments. GM=Grand mean, Var=Variety, Env=Environment.

Genotype	L1	L2	L3	L4	Genotype mean	Var Index	PCA I	G*E ResSS
JG11 × WR315(F7)-57	2176.67	1458.67	1204.33	2405.33	1811.25	170.19	3.84	15073.27
JG11 × WR315(F7)-49	2077.67	1486.33	1062.33	2343.00	1742.33	101.27	8.28	7710.21
ICCV 191106	2351.67	1219.00	1217.67	2627.67	1854.00	212.94	-7.77	5380.70
ICCV 191114	1624.67	702.33	1006.33	1961.67	1323.75	-317.31	-8.84	115140.44
ICCV 191112	1759.33	1021.00	625.00	2372.67	1444.50	-196.56	2.18	102135.64
ICCV 191107	1759.33	1032.00	847.33	2158.33	1449.25	-191.81	1.20	22492.13
ICCV 191108	2141.67	1105.67	855.00	2362.33	1616.17	-24.90	-1.95	22539.20
A-1	2217.00	966.67	919.00	2367.67	1617.58	-23.48	-8.18	25258.45
JG11	2447.00	1268.67	993.00	2281.67	1747.58	106.52	-0.86	94740.38
Super Annigeri-1	2326.67	1500.00	887.33	2328.00	1760.50	119.44	8.96	51226.32
JAKI-9218	1924.00	1538.33	957.33	2218.33	1659.50	18.44	14.04	18594.31
RGV-203	2183.33	972.67	1151.33	2358.00	1666.33	25.27	-10.91	3921.10
Env.Mean	2082.42	1189.28	977.17	2315.39	GM-1641.07			
Env.Index	441.35	-451.78	-663.90	674.33				
PCAI	-6.65	22.69	-10.03	-6.01				
G*E Res.SS	193074.93	2490.25	169431.64	119215.33	484212.16			

L1; Kalaburagi, L2; Bidar, L3; Raichur, L4; Sirguppa, GM- Grand Mean.

CONCLUSION

Stability analysis using AMMI bi plot analysis provides a good understanding in estimation of adaptation level of chickpea genotypes. The present study indicates large variations for seed yield of chickpea genotypes tested across diverse environments. PCA-I revealed a greater interaction variance, thus the interaction of the chickpea genotypes with four environments was predicted by the two components of genotype and environment. The differential range of mean seed yield across the environments was noticed in chickpea genotypes due to significant interaction effect. Among the genotypes, JG11 × WR315 (F7)-57, and ICCV 191106 have higher average yields and adaptable to favourable environments, while remaining grouping to poor environments. Based on AMMI bi-plot analysis, genotypes [JG11 × WR315 (F7)-57, JG11] and (JAKI 9218, RGV 203) were stable and unstable respectively. Similarly, best performer genotypes and three mega environments were noticed through bi-plot analysis. Environments (Kalaburagi, Sirguppa) were found with most selective for seed yield estimation. Considering seed yield stability of genotypes [JG11 × WR315 (F7)-57, JG11 and JG11 × WR315 (F7)-49] were the best among all.

Conflict of interest: None.

REFERENCES

Bishwas, K.C., Poudel, M.R and Regmi, D. (2021). AMMI and GGE biplot analysis of yield of different elite wheat line under terminal heat stress and irrigated environments. Heliyon. 7(6): e07206. Doi.org/10.1016/j.heliyon.2021.e07206.

Devasirvatham, V. and D. Tan. (2018). Impact of high temperature and drought stresses on chickpea production. Agronomy. 8: 145.

Erdemci, Ý (2018). Investigation of genotype × environment interaction in chickpea genotypes using AMMI and GGE biplot analysis. Turkish Journal of Field Crops. 23: 20-26. Doi: 10.17557/tjfc.414846.

Funga, A., Bekele, D., Monyo, E., Tadesse, M., Mohamed, R., Gaur, P., Eshete, M., Ojiewo, C., Bishaw, Z., Fikre, A., Rao, G., Korbu, L., Girma, N., Siambi, M. (2017). Genotype by environment interaction on yield stability of desi type chickpea (*Cicer arietinum* L.) at major chickpea producing areas of Ethiopia. Australian Journal of Crop Science. 11(02): 212-219.

Gauch, H.G. (2006). Statistical analysis of yield trials by AMMI and GGE. Crop Science 46: 1488-1500.

Jendoubi, W., Bouhadida, M., Boukteb, A., Béji, M., Kharrat, M., (2017). *Fusarium wilt* affecting chickpea crop. Agriculture 7: 23

Kiresur, V.R., Kulkarni, G.N. and Kulkarni, V.S. (2009). Baseline Assessment of Chickpea for Karnataka State in India. Baseline research report for Tropical Legumes-II. ICRISAT, pp 150.

kumar, J., Singh, K.B., Malhotra, R.S., Miranda, J.H. and Gupta, T. D. (1996). Genotype x environment interaction for seed yield in chickpea. Indian Journal of Genetics. 56 (1): 69-78.

Li, W., Yan, Z.H., Wei, Y.M., Lan, X.J. and Zheng, Y.L. (2006). Evaluation of genotype × environment interactions in Chinese Spring wheat by the AMMI model, correlation and path analysis. Journal of Agronomy and Crop Science. 192: 221-227.

Rani, A., Devi, P., Jha, U.C., Sharma, K.D., Siddique, K., and Nayyar, H. (2020). Developing climate-resilient chickpea involving physiological and molecular approaches with a focus on temperature and drought stresses. Frontiers in plant science. 10: 1759. Doi.org/10.3389/fpls.2019.01759.

Rao, S., Reddy, S., Abhishek, R., Reddy, B.V. and Panwar, S. (2011). Application GGE biplot and AMMI model to evaluate sweet sorghum (*Sorghum bicolor*) hybrids for genotype x environment interaction and seasonal adaptation. Indian Journal of Agricultural Sciences. 81(5): 438- 444.

Sellami, M.H., Lavini, A.. Pulvento, C. (2021). Phenotypic and quality traits of chickpea genotypes under rainfed conditions in south italy. Agronomy. 11: 962.

Shah, T.M., Imran, M., Atta, B.M., Ashraf, M.Y., Hameed, A., Waqar, I., Shafiq, M., Hussain, K., Naveed, M., Aslam, M. and Maqbool, M.A. (2020). Selection and screening of drought tolerant high yielding chickpea genotypes based on physio-biochemical indices and multi-environmental yield trials. BMC Plant Biology. 20(1). Doi.org/10.1186/s12870-020-02381-9.

Shinde, G.C, Bhingarde, M.T., Khairnar, M.N. and Mehetre, S.S. (2002). AMMI analysis for stability of grain yield of pearl millet (*Pennisetum typhoides* L.) hybrids. Indian Journal of Genetics. 62(3): 215-217.

Sinha, R., Irulappan, V., Mohan-Raju, B., Suganthi, A. and Senthil-Kumar, M. (2019). Impact of drought stress on simultaneously occurring pathogen infection in field-grown chickpea. Scientific Reports. 9(1): 5577. https://doi.org/10.1038/s41598-019-41463-z.

Tilahun, G., Mekbib, F., Fikre, A. and Eshete, M. (2015). Genotype x environment interaction and stability analysis for yield and yield related traits of Kabuli-type chickpea (*Cicer arietinum* L.) in Ethiopia. African Journal of Biotechnology, 14(18): 1564-1575.

Yadav, A., Yadav I.S. and Yadav, C.K. (2014). Stability analysis of yield and related traits in chickpea (*Cicer arietinum* L.). Legume Research. 37: 641-645.

Yan, W., Kang, M.S., Ma, B., Woods, S. and Cornelius, P.L. (2007). GGE bi-plot vs. AMMI analysis of genotype-by-environment data. Crop Science. 47: 643-655.

Zobel, R.W., Wright, M.S. and Gauch, H.G. (1988). Statistical analysis of a yield trial. Agronomy. J. 80: 388-393.