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RESEARCH ARTICLE

Unravelling chickpea (*Cicer arietinum* L.) genotype stability through univariate and multivariate approaches under varying soil types and water regimes

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Abstract

Chickpea (*Cicer arietinum* L.) is a vital protein-rich crop predominantly cultivated in rainfed conditions, making it vulnerable to environmental challenges like drought. Understanding genotype-by-environment interaction is crucial for developing cultivars that are adaptable to diverse climatic conditions. To identify promising genotypes for drought resilience, a multi-environment trial was conducted across 10 distinct environments varying in soil type and moisture, involving 21 chickpea genotypes. The study observed significant variation in seed yield among the genotypes, with genotype BGD103 (G4) consistently achieving the highest yields under drought-stress conditions. Combined variance analysis revealed that the environment accounted for 73.59% of the total variation in grain yield, while GEI contributed 13.95% and genotypes contributed 12.44%. GGE and AMMI biplots further illustrated the relationships between environments and genotypes, identifying environments E5, E1, and E3 (characterized by medium black soil) as favourable for chickpea cultivation. Genotypes (G1), (G4), and JG16 (G11) were recognized as stable and high-yielding across these environments. Additionally, genotypes BDG75, BGD103, Digvijay (G5), GNG1581 (G7), Pusa1003 (G14) and RSG896 (G18) demonstrated broad adaptability across all environments. Parametric and non-parametric stability models pinpointed genotypes BDG75, BGD103, GNG1581, and RSG896 as the most stable. Further, genotypes G1, G4, and G18 showing consistent genetic stability and high yields across diverse conditions. These findings provide valuable insights for chickpea breeding programs focused on enhancing yield resilience under water stress conditions, contributing to the development of robust, water stress resilient cultivars.

Keywords: Chickpea, AMMI, GGE, parametric models, biplots, GEI.

Introduction

Chickpea is the most extensively grown pulse crop around the worldwith diverse uses and specific consumer preferences in the global market.Asia accounts for most of its production, contributing 90.6% of the total output, followed by America, Africa, and Europe. Globally, ~15.8 mt of chickpea is produced from 15 m ha (FAOSTAT 2021). Of the total produce, ~70% of the global output is produced from India (Kushwah et al. 2021), with approximately 10.91 m ha dedicated to chickpea cultivation, yielding 13.75 million tonnes in 2021-22 (DES 2023, MOAF&W, GoI). Chickpea is an essential dietary protein source, containing protein levels ranging from 16 to 28% (Liu et al. 2008). Whole chickpeas are particularly rich source of leucine, lysine cysteine and methionine amino acids (Wang et al. 2010). The crop is also known to improve soil quality by fixing nitrogen through a symbiotic relationship with rhizobacteria upon nodulation (Arif et al. 2021). However, a significant challenge in the improvement of chickpea varieties has been the limited genetic diversity and susceptibility to various stresses.

The area under chickpea may not be enhanced after a certain point in time without affecting other crops, as cultivable land is a constraint. It is noticed that the chickpea yield has not improved to a satisfactory level. Presently, the global chickpea average yield is approximately 1.2 t/ha, although chickpea yield potential is reported to be between 2 to 5 t/ha under optimal growing conditions. To feed the ever growing world population, tapping the yield potential and enhancing the genetic gains is desired to attain the required chickpea production (Gayacharan et al. 2025). Despite its resilience to drought, chickpea productivity is on decline significantly under drought stress conditions during maturity and seed filling with rising temperatures and decreased rainfall (Jha et al. 2014; Rani et al. 2020; Shah et al. 2020). Drought stress results in yield loss of up to 50% with a reduction in growth, chlorophyll, and enzymes (Dencic et

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al. 2000; Varshney et al. 2014); however, it varies with variety grown, soil type, time, and extent of occurrence of stress. Thus, developing and deploying resilient crop cultivars becomes imperative to withstand periods of water scarcity and ensure sustained productivity (Massawe et al. 2015; Arif et al. 2021). Nevertheless, the slow progress in developing drought-tolerant chickpea varieties can be attributed to its scarce genomic resources, highlighting the need to enhance its genetic potential (Jaganathan et al. 2015). Achieving sustainable crop production under drought stress requires the utilization of techniques that offer adaptability and stability to select the best genotypes across varying environmental conditions.

Multi-environment trials (MET) are widely used to evaluate the effects of drought stress on crops (Ebdon and Gauch 2002). Since yield is a complex trait controlled by multiple genetic loci, genotype-by-environment interactions (GEI) can significantly affect the selection of high-yielding genotypes under stress conditions (Kushwah et al. 2021). Therefore, assessing GEI is crucial for identifying better performing and stable genotypes adapted to various situations (Yan and Hunt 2002; Kanouni et al. 2015; Khan et al. 2021; Rao et al. 2023). As GEI can elicit diverse responses contingent upon genotype capabilities and environmental conditions (Sharifi et al. 2017), it is paramount to prioritize the identification of genotypes that consistently excel across different environments. To pinpoint stable varieties, parametric univariate, non-parametric univariate, and multivariate approaches have been commonly used. The primary statistical methods crucial for evaluating yield stability across varied environments are the univariate stability parameters, categorized into parametric and nonparametric statistics. Parametric methods assume specific data distributions, while nonparametric methods do not, offering robustness against deviations from normality and improving the thorough evaluation of stability across different environments (Kebede et al. 2023). The Additive Main Effects and Multiplicative Interaction (AMMI) and Genotype and Genotype by Environment (GGE) biplot methodologies are multivariate tools highly regarded for their effectiveness in analysing and interpreting multi-environmental data within breeding programs (Yan et al. 2000; Samonte et al. 2005). They have been widely employed to elucidate genotype-by-environment interaction (GEI) and identify cultivars with both highyield potential and broad adaptability. These statistical techniques are particularly valuable for agricultural researchers, as they can be applied to various two-way data matrices from a range of experiments (Naroui et al. 2013; Erdemci, 2018). With this view, the current investigation was undertaken to determine the stability of chickpea genotypes under drought and control conditions using stability parameters for yield improvement. It was hypothesised that the genotypes perform distinctly in different environments, and some genotypes express adequate genotypic buffering capacity to perform well across varied environments. To support the hypothesis, a set of chickpea genotypes was evaluated across different environments conditioned with rainfed and irrigated situations. Different stability models were employed to identify the genotypes stable for drought conditions and stable across conditions.

Materials and methods

Plant material and experimental location

The study involved 21 chickpea varieties collected from different parts of the country. The list of materials and their details are presented in Table 1.The investigation was carried out at ICAR-National Institute of Abiotic Stress Management, Baramati, India, (18°09’30.62” N, 74°30’ 03.08”E) for two consecutive years (rabi seasons of 2020 and 2022) under rainfed and irrigated situations, respectively. There was no additional irrigation used for the rainfed situations. In an irrigated condition, supplemental irrigation was applied during the critical growth stage (the start of pod formation). Supplementary Figure 1 shows the average monthly rainfall, temperature, and relative humidity during the experiment.

Table 1. A list of chickpea cultivars used in the present study

S. No.	Genotypic ID	Genotype	Source of collection	Sr. No.	Genotypic ID	Genotype	Source of collection
1	G1	BDG75	IARI, Dharwad	12	G12	PG186	IIPR, Kanpur
2	G2	BG276	IARI, New Delhi	13	G13	PG5	IIPR, Kanpur
3	G3	BG396	IARI, New Delhi	14	G14	Pusa1003	IARI, New Delhi
4	G4	BGD103	IARI, New Delhi	15	G15	Pusa240	IARI, New Delhi
5	G5	Digvijay	MPKV, Rahuri	16	G16	Pusa244	IARI, New Delhi
6	G6	GG2	JAU, Junagadh	17	G17	Pusa362	IARI, New Delhi
7	G7	GNG1581	ARS, Sri Ganganagar	18	G18	RSG896	ARS, Durgapur
8	G8	ICC4958	ICRISAT, Hyderabad	19	G19	SAKI9516	JNKVV, Jabalpur
9	G9	ICCV92944	ICRISAT, Hyderabad	20	G20	Vijay	MPKV, Rahuri
10	G10	ICCV96030	ICRISAT, Hyderabad	21	G21	Vishal	MPKV, Rahuri
11	G11	JG16	JNKVV, Jabalpur				

Experimental design and layout

The study utilized a split-plot design arranged in randomized complete blocks to evaluate two distinct irrigation levels. The experiment involved two factors: Factor «A» encompassed 21 chickpea genotypes, while Factor «B» represented water treatment (Irrigated and Rainfed environment). The mainplot factor was the water treatment, with genotypes serving as the sub-plot factor. The 21 chickpea genotypes were randomly allocated to each plot and replicated thrice in each treatment. Each genotype was sown in five rows of 2-meter row lengths with a spacing of 30 cm between rows and 10 cm between plants. The standard recommended agronomic practices, including the application of fertilizers, manual weeding and need-based plant protection measures, were followed during the experiment. The experimentation was repeated in two seasons. The experiment was conducted in two different soil conditions; details are provided in Table 2.

Data collection and statistical analysis

Five randomly chosen plants from each plot in each field replication were used to gather data on grain yield. With the assumption that the impacts of the environment were random and the effects of genotype remained constant, a combined analysis of variance was carried out. Using the GGE biplot and AMMI approaches in R Studio, a condensed version of the R statistical program created by the R Core Team, a graphical multivariate stability analysis was carried out to get better insights into the GEI (RStudio 2014).AMMI model is expressed as:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{N} \lambda_n \gamma_{in} \alpha_{jn} + \rho_{ij} + \varepsilon_{ij}$$

Where, Y_{ij} represents the target trait response of the i^{th} genotype in the j^{th} environment; μ is the general mean;g_i is the main effect of the i^{th} genotype;e_j is the main effect of the j^{th} environment; N is the maximum of (G-1, E-1) (the number of principal axes preserved in the model to describe the interaction pattern between i^{th} genotype and j^{th} environment);λ_n is the singular value of the n^{th} principal interaction axis; γ_{in} is the i^{th}element of the singular column vector related to axis n; α_{jn} is the j^{th} element of the singular row vector associated with axis n; ρ_i and ε_{ij} are the AMMI residuesand pooled error respectively.

The GGE model is represented as

$$Yij - \mu - \beta j = \lambda 1 \xi\ i1 \eta 1j + \lambda 2 \xi i2 \eta 2j + \varepsilon ij$$

Where$Yij$is the corresponding variable of the i^{th} genotype in the j^{th} environment, $\mu$is the total mean, βj is the main effect of the j^{th} environment, $\lambda_1$and $\lambda_2$are singular values of principal components PC1 and PC2; ξi1 and ξi2 are eigenvectors in the j^{th} environment for PC1 and PC2 of i^{th}genotype in the j^{th}environment. "Which-won-where" plot (Gauch and Zobel 1997)was employed to select winning genotypes in different environments and delineate mega-environments. Relationships among test environments (Cooper et al. 1997) and genotypes (Yan 2001) were visualized using their respective GGE biplots. Additionally, an average environment coordinate (AEC) was incorporated into the genotype-focused biplot to illustrate the mean and stability of the hybrids (Yan and Kang 2003).The univariate stability statistics included Perkins and Jinks's (1968) model, Tai's (1971) statistic, Finlay and Wilkinson's model (1963).

Results

Variation in grain yield among the genotypes andcombined analysis of variance (ANOVA)

Under both rainfed and irrigated environments, a significant variation in seed yield was noted among chickpea genotypes (Table 3). Under irrigated conditions, the mean seed yield of all genotypes was higher than in the rainfed environment.

Table 2. A list of environments and their characteristics used in the present study

Environments	Season	Soil Type	Treatment	Soil Properties	Environments	Season	Soil Type	Treatment	Soil Properties
E1	*Rabi* 2020	Medium black	Irrigated	BD:1.3 Mg m^{-3} FC: 33.0% PWP: 17.0%, Sand: 11.8%, Silt (18.8%), and Clay (69.2%), pH: 8.2, EC: 0.2 dS m^{-1},OCC: 6.5 g kg−1, available N, P_2O_{5-}, and K_2O were 175.0, 7.9, and 180.0 kg ha^{-1}	E6	*Rabi* 2022	Medium black	Rainfed	Same as E1
E2	*Rabi* 2020	Medium black	Rainfed	Same as E1	E7	*Rabi* 2020	Shallow Basaltic soil	Irrigated	pH:8.4, EC: 0.13, dS m^{-1}, OCC: 0.35%, available N, P_2O_5, and K_2O were 158.0, 1.99, and 115.1 kg ha^{-1}
E3	*Rabi* 2021	Medium black	Irrigated	Same as E1	E8	*Rabi* 2020	Shallow Basaltic soil	Rainfed	pH:8.4, EC: 0.13, dS m^{-1}, OCC: 0.35%, available N, P_2O_5 and K_2O were 158.0, 1.99, and 115.1 kg ha^{-1}
E4	*Rabi* 2021	Medium black	Rainfed	Same as E1	E9	*Rabi* 2021	Shallow Basaltic soil	Irrigated	pH:8.4, EC: 0.13, dS m^{-1}, OCC: 0.35%, available N, P_2O_5 and K_2O were 158.0, 1.99, and 115.1 kg ha^{-1}
E5	*Rabi* 2022	Medium black	Irrigated	Same as E1	E10	*Rabi* 2021	Shallow Basaltic soil	Rainfed	pH:8.4, EC: 0.13, dS m^{-1}, OCC: 0.35%, available N, P_2O_5 and K_2O were 158.0, 1.99, and 115.1 kg ha^{-1}

Bulk Density = BD; Field Capacity =FC; Permanent Wilting Point= PWP; Organic Carbon Content=OCC;

Genotype G4 (BGD103) exhibited superior performance with the highest yield across all the rainfedenvironments, followed by G1 (BDG75).

Environment E6 (Rainfed conditions in black soil type) was found to be favourable compared to the remaining drought stress-related environments, with genotypes G1 (10.76g), G4 (10.02 g), and G11 (10.45 g) recording the highest yield. Underirrigated environmental conditions, G4 consistently achieved the highest yield in nearly all environments, while G12 (PG186) yielded the lowest. Certain genotypes, such as G13 (PG5) and G8 (ICC4958),displayed extreme variations, performing well in some environments but poorly in others. Among the irrigated environments, E5 (Irrigated conditions in shallow basaltic soil type) exhibited the highest yield for most of the genotypes*viz.*, G15 (Pusa240, 14.21 g), G11 (JG16, 14.55 g) and G5 (Digvijay, 13.47 g). The chickpea genotypes in ten environments were subjected to a combined analysis of variance (Table 4), which revealed very significant variations in grain yield based on genotype, environment, and interactions. The environment had the biggest impact on the trait, accounting for 73.59% of the variation, followed by genotypes (12.44%) and genotype × environment interactions (13.95%).

Additive main effects and multiplicative interaction

To study the adaptation of genotypes, the AMMI1 biplot was employed with horizontal and vertical axescorresponding to PC1 and the substantial impact of grain yield. Environments,E5 (0.85, 11.27), E3 (0.74, 10.05) and E1 (0.61, 0.18) coupled with genotypes G9 (ICCV92944, 0.78, 7.02) and G13 (PG5, 0.77, 7.40) had large PC scores along with high mean yield performance(Table 5). In contrast, the PCA1 scores of environments E2 (0.16), E4 (0.53), and E6 (0.46) were nearer zero than those of the other situations. Genotypes G1 (BDG75, 0.18), G4 (BGD103, 0.23), G5 (Digvijay, 0.25) and G7 (GNG1581, -0.21) had scores approximately close to zero on the first PCA1 axis, in addition to having a higher performance than the experimental mean (Fig.1a). Correspondingly, AMMI2 was employed to provide insights into GEI, which identified the principal components accounting for 76.06% of the G + G × E interaction variation for both traits (Fig.1b). As evident from the biplot, the environments were categorized into four sections. E2 and E3 exhibited relatively short vectors compared to other environments, while E1, E4, and E7 had longer spokes. Given their greater distance from the origin, the genotypes G6 (GG2), G8 (ICC4958), G9 (ICCV92944), G13 (PG5), and G21 (Vishal) were more responsive, with G8 being the optimal genotype for E5.On the other hand, because they were closer to the origin, the genotypes G4 (BGD103), G5 (Digvijay), G11 (JG16), G14 (Pusa1003), G17 (Pusa362), and G18 (RSG896) were thought to be the most stable because they displayed the lowest changes and were therefore less prone to environmental interactions. In terms of specific

Table 4. Mean performance of 21 chickpea genotypes under 10 environmental conditions

Sr. No.	Genotypic ID	Environments									
		E1	E2	E3	E4	E5	E6	E7	E8	E9	E10
1	G1	10.21	8.09	11.48	9.46	12.21	10.76	6.60	3.94	6.47	3.94
2	G2	9.35	4.96	10.79	5.72	10.63	6.91	5.58	5.41	5.89	5.41
3	G3	8.59	4.88	9.51	5.60	10.59	6.83	5.56	4.37	5.56	4.36
4	G4	11.14	8.95	12.88	9.52	11.85	10.03	6.37	4.52	6.37	4.52
5	G5	8.18	5.24	9.36	7.56	13.47	8.22	4.12	3.71	4.12	3.19
6	G6	7.21	4.99	6.09	4.61	9.26	5.21	5.33	4.55	5.33	4.55
7	G7	6.66	3.77	8.49	5.27	9.78	6.57	4.08	3.01	4.08	2.26
8	G8	11.86	8.86	12.06	7.42	13.15	9.56	3.13	2.44	3.13	2.02
9	G9	9.84	6.32	11.66	9.10	12.87	8.68	2.83	2.39	4.14	2.39
10	G10	7.74	5.15	7.58	5.72	8.26	7.30	4.43	2.69	4.43	2.69
11	G11	10.52	6.78	12.86	7.99	14.56	10.45	5.53	4.23	5.53	4.22
12	G12	4.74	3.31	7.43	5.25	8.70	6.31	3.63	2.94	3.63	2.13
13	G13	12.51	7.12	12.37	7.43	13.50	7.50	3.78	3.02	3.78	3.02
14	G14	8.51	4.75	8.67	4.39	10.38	6.59	3.23	2.56	3.23	2.56
15	G15	11.17	6.47	11.11	6.18	14.22	7.06	4.19	3.28	4.19	2.49
16	G16	8.59	4.71	10.13	3.95	10.51	6.62	5.82	4.22	5.82	4.22
17	G17	8.34	5.67	9.04	5.79	8.31	5.93	4.95	2.78	4.75	2.78
18	G18	10.16	7.34	10.71	7.01	12.00	8.86	7.41	4.75	7.92	4.13
19	G19	6.66	5.09	8.16	5.63	8.62	5.65	5.56	2.83	5.47	2.83
20	G20	10.06	4.78	11.36	8.33	12.57	9.24	4.07	3.13	4.07	2.65
21	G21	10.95	8.66	9.45	5.08	11.29	6.87	7.99	4.58	7.19	4.58

Table 5. Combined analysis of variance for seed yield in 21 chickpea genotypes

	Mean Sum of Squares	Degrees of Freedom	Explained (%)	Cumulative value
Environments	464.97**	9	73.59	73.59
Genotypes	35.39**	20	12.44	86.04
G x E Interaction	4.40**	180	13.95	100
PC1	17.13	28	60.44	60.44
PC2	4.76	26	15.61	76.06
PC3	3.87	24	11.72	87.78
PC4	1.74	22	4.84	92.62
PC5	1.33	20	3.36	95.99
PC6	0.99	18	2.24	98.24
PC7	0.58	16	1.17	99.41
PC8	0.19	14	0.34	99.75
PC9	0.16	12	0.24	100
PC10	0.00	10	0	100
Residuals	2.29	420	0	0

**Significant at 1% level of significance

Table 6. Principal Component scores of the chickpea genotypes and environments for grain yield

S. No.	Genotype	Grain yield (g)	PC1	PC2	PC3
1	G1	8.32	0.185	-0.437	0.525
2	G2	7.06	-0.430	0.127	-0.447
3	G3	6.59	-0.404	0.032	-0.282
4	G4	8.62	0.236	-0.149	0.585
5	G5	6.72	0.259	-0.400	-0.468
6	G6	5.71	-0.877	0.095	-0.162
7	G7	5.40	-0.216	-0.309	-0.195
8	G8	7.36	1.000	0.355	0.411
9	G9	7.02	0.785	-0.345	0.054
10	G10	5.60	-0.320	-0.230	0.420
11	G11	8.27	0.483	-0.168	-0.341
12	G12	4.81	-0.391	-0.656	-0.139
13	G13	7.40	0.773	0.568	-0.099
14	G14	5.49	0.051	0.207	-0.181
15	G15	7.04	0.546	0.560	-0.387
16	G16	6.46	-0.480	0.306	-0.386
17	G17	5.83	-0.317	0.081	0.445
18	G18	8.03	-0.313	0.081	0.197
19	G19	5.65	-0.574	-0.164	0.290
20	G20	7.03	0.563	-0.385	-0.216
21	G21	7.66	-0.559	0.831	0.376
22	E1	9.19	0.618	0.940	0.133
23	E2	5.99	0.167	0.504	0.897
24	E3	10.06	0.750	0.066	-0.135
25	E4	6.52	0.538	-0.944	0.349
26	E5	11.27	0.852	0.170	-0.879
27	E6	7.67	0.466	-0.726	0.198
28	E7	4.96	-1.000	0.104	0.213
29	E8	3.59	-0.722	-0.075	-0.508
30	E9	5.00	-0.904	-0.041	0.136
31	E10	3.38	-0.765	0.002	-0.403

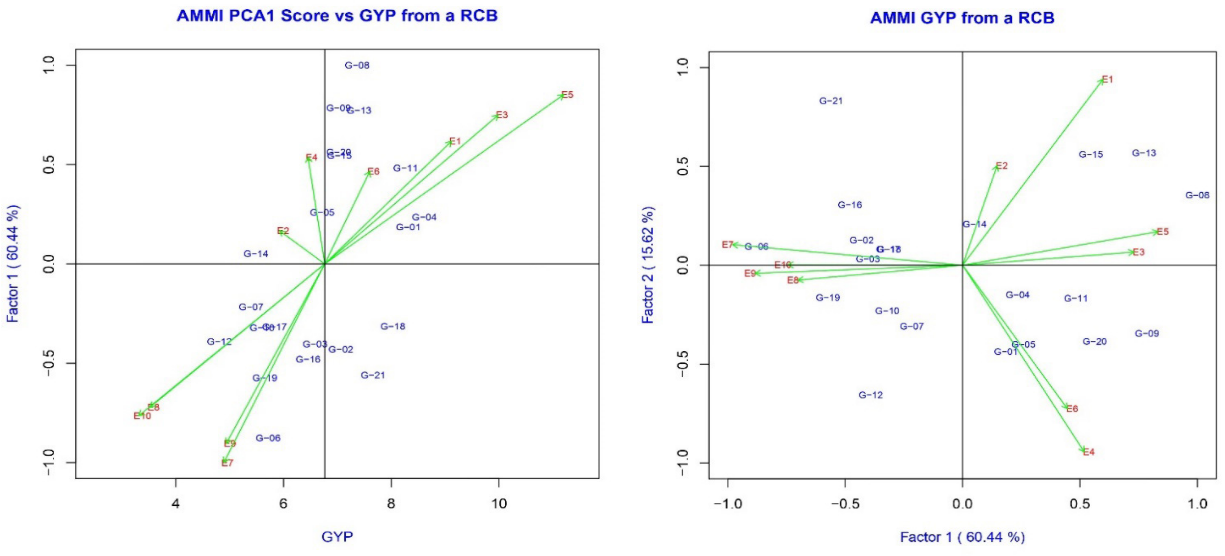
adaptation, genotype G2 (BG276) exhibited suitability for E4 (Rainfed situation of medium black soil), while genotypes G8 (ICC4958), G13 (PG5), and G15 (Pusa240) were explicitly adapted to environments E1 and E5 (Irrigated conditions of medium black soil). Genotypes G6 (GG2) and G3 (BG396) showed specificity for E7 (Irrigated conditions of shallow basaltic soil), whereas genotypes G7 (GNG1581), G10 (ICCV96030), G19 (SAKI9516) and G12 (PG186) displayed suitable specific adaptabilities for E8 (Rainfed conditions of shallow basaltic soil).

GGE biplot of environment-view for yield through multivariate analysis

The interrelationships between various environmental situations were investigated using the GGE biplot approach. To evaluate the pattern of environments, the environment-centered GGE biplot (Fig. 2) was utilised, where the angle between two environments indicates the degree of correlation. The first principal component (Axis1) and the second principal component (Axis2) each contributed 20.80% and 59.9%, respectively, to the total observed

Table 7. Missing Caption

S. No.	Model	Stability Parameters	Formula	Reference
1	Parametric	Wricke's ecovalence (W_i^2)	$W_i^2 = \sum_{i=1}^{n}(x_{ij} - \bar{x}_{i.} - \bar{x}_{.j} + \bar{x}_{..})^2$	Wricke (1962)
2	Parametric	Eberhart and Russell model	$Y_{ij} = m + b_i I_j + \delta_{ij}$ (i=1,2,..,t and j=1,2,…,s)	Eberhart and Russell (1966)
3	Parametric	Coefficient of variation (CV_i)	$CV_i = \left(\sqrt{S_i^2}/\bar{x}_{i.}\right) \times 100$	Francis and Kannenberg (1978)
4	Parametric	Superiority Index (P_i)	$P_i = \frac{\sum_{j=1}^{n}(x_{ij} - M_j)^2}{2E}$	Lin and Binns (1988)
5	Parametric	Shukla's stability variance (σ_i^2)	$\sigma_i^2 = [p/(p-2)(q-1)]W_i^2 - [SS(GE)/(p-1)(p-2)(q-1)]$ $SS(GE) = \sum_{I} W_i^2 = \sum_{i}\sum_{i}(x_{ij} - \bar{x}_{i.} - \bar{x}_{.j} + \bar{x}_{..})^2$	Shukla (1972)
6	Non-Parametric	Nassar and Huehn's parameter	$S_i^{(1)} = 2\sum_{j}^{m-1}\sum_{j'=j+1}^{m}\lvert r_{ij} - r_{ij'}\rvert/[m(m-1)]$ $S_i^{(2)} = \sum_{i=1}^{m}(r_{ij} - \bar{r}_{i.})^2/(m-1)$	Nassar and Huehn (1987)



(a) (b)

Fig. 1. (a) AMMI 1 biplot for grain yield and PC1 (b) AMMI 2 biplot for grain yield showing the interaction of IPCA1 against IPCA2 scores of 21 chickpea genotypes (G) in 10 environments (E)

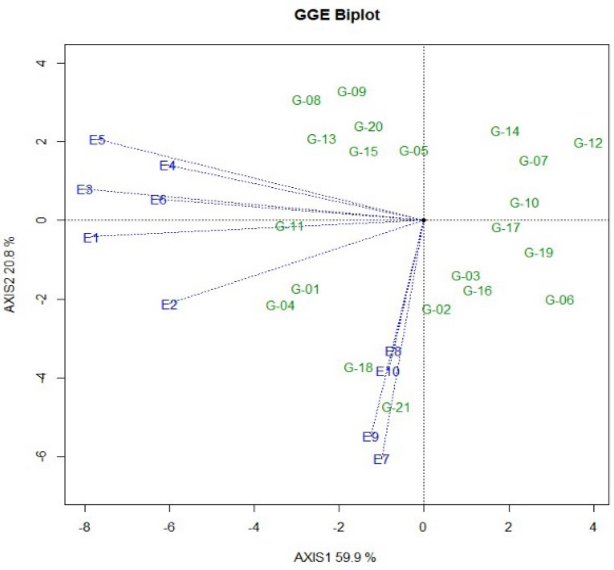


Fig. 2. Environment vector view of the GGE-biplot showing the relationship among 10 environments

variation. The environments E2and E4 show a positive correlation (Rainfed situations under black soil), as indicated by an acute angle between them. In contrast, environments E3 and E1 exhibit a negative correlation, characterized by an obtuse angle in the biplot. The angles of the environments E5 and E4 with E7, E9, E10, and E8 were greater than 90 degrees, suggesting a negative correlation. Also, the environments (E3 and E6), (E8 and E9) and (E9 and E10) had smaller angles between them.

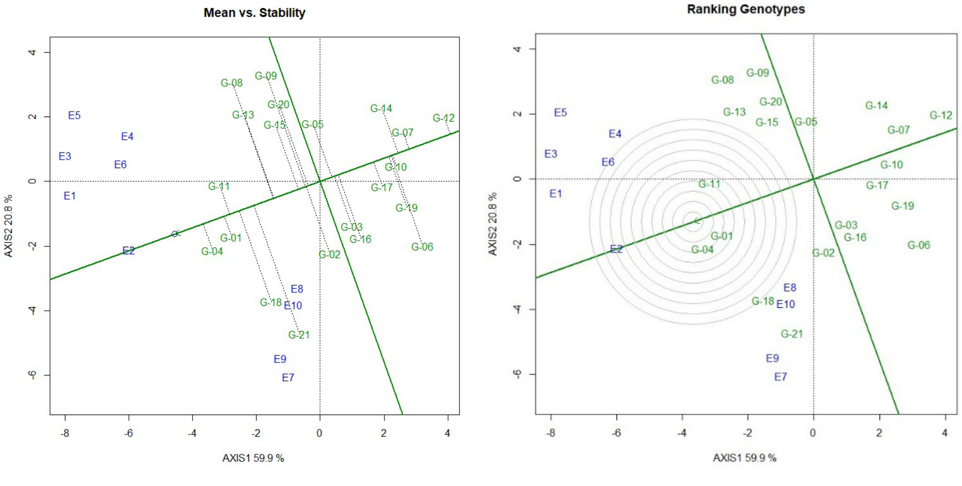
Identification of high-yielding stable genotypes and their ranking across environments

Genotypes ought to be assessed based on both their mean performance and stability across various environments within a particular mega-environment. Figure 3a depicts the AEC view in the GGE biplot, where the AEC abscissa (or AEA) indicates a higher mean yield across environments. Concurrently, G4 had the highest mean yield, followed by G1, G11, G18 and G21, while G12 and G7 had the lowest mean yield.Also, a larger projection onto the AEA ordinate, irrespective of direction, indicates greater stability across environments. The genotypes G1, G4, and G11, which had shorter projections, were deemed stable across environments and exhibited higher yields.

In contrast, the genotypes G7, G12, and G17 were also stable but had lower seed yields. Conversely, Environment E7 recorded the most extended projections from the axis, making it discriminating. Regarding the ranking of genotypes (Fig.3b), G1 was ranked highly in terms of performance, followed by G4 and G11 by being at the centre of the concentric circle. Additionally, the proximity of environments E2 and E6 to the centre of the concentric circle represent them as ideal environments.

Identification of winning genotypes through the "Which-Won-Where" pattern

The polygonal view of the GGE biplot, which is instrumental in illustrating the «which won where» pattern, revealed distinct winning genotypes across various environments (Fig. 4). The equity lines divided the polygon into seven sectors, with all environments falling into four sectors, thus delineating four mega-environments. Genotypes G9, G8, G4, G21, G6, and G12 were located at the corner of the polygon, making them the desirable vertex genotypes with the longest vectors. Genotypes G8 (ICC4958) and G9 (ICCV92944) won in first mega-environment (E4, E5,), while G4 genotype performed best in second mega-environment (E1, E2). Similarly, G21 was found to be winning in E7, E8, E9 and E10 environments.



(a) (b)

Fig. 3. AEC for assessing stability of chickpea genotypes (a) across the environments (b) ranking relative to an ideal genotype located at the center

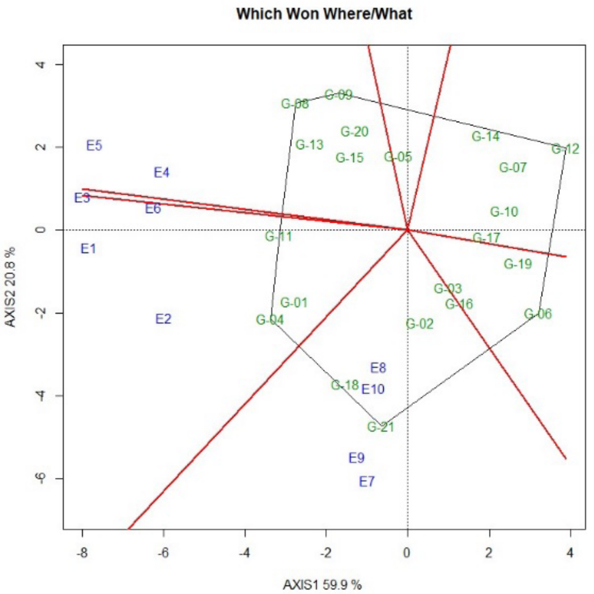


Fig. 4. Which won where the pattern for chickpea genotypes and environments in polygon view

Parametric and non-parametric stability models

According to the Eberhart and Russell model, genotypes with a high-yielding regression coefficient approximating unity (b_i= 1) and a sum of squares of regression deviation close to zero (S^2d_i = 0) are considered stable. The results indicated the existence of variation among the chickpea genotypes with Regression coefficient (b_i) values of genotypes varying from 0.45 (G6) to 1.53 (G8), as presented in Table 4 and in accordance with this model, G1, G4, G7, G14and G18 had bi-values near unity. The deviation from regression (S^2d_i) value among the genotypes ranged from -0.44 (G14) to 1.49(G21). Of the total 21 genotypes, seven genotypes (G1, G4, G6, G12, G15, G18, G20) had S^2d_i value nearly equal to zero.Overall, when the combination of parameters with high mean yield, regression coefficient and deviation mean square was examined,G1 (BDG75), G4(BGD103) and G18 (RSG896) emergedas stable for displaying yields surpassing the environmental mean yield and demonstrated adaptability in all environments (Table 6).

Meanwhile, according to the Finlay and Wilkinson model, genotypes G1, G4, and G18 were identified as stable, with a regression coefficient (b_i) near 1 and a mean yield surpassing the overall mean. It is noteworthy that the most stable genotypes were consistent across both the Eberhart and Russell models and Finlay and Wilkinson's models. Perkins and Jinks employed a statistical method to assess the non-linear responsiveness to environmental shifts, factoring in the GEI alongside the additive environmental aspect. In this framework, a cultivar with a Bi value nearing zero is termed stable, and consequently, genotypes G1, G4, G5, G7, G14, and G18 were identified.

Wricke's ecovalence statistic serves as a stability measure, indicating the cultivar's relative contribution to the overall GEI by utilizing mean squares as the basis for stability assessment.Genotypes with the lowest ecovalence values (W_i^2) exhibit fewer fluctuations across environmental conditions and are, therefore, considered stable. The ecovalence values for 21 chickpea genotypes over 10 environments were worked out as presented in Table6, which ranged from 2.02(G14) to 33.66 (G8). Since genotypes with the smallest ecovalence values are considered stable, G14 was highly stable, followed by G7 (3.33), G18 (5.79), G3(5.83) and G17(6.63). The cultivar deemed most promising is characterized by low superiority value among the cultivars exhibiting high responsiveness to specific environmental conditions. According to the stability parameter, genotype G4 (0.81) emerges as the top-ranked promising cultivar, having the lowest Pi values, followed by G1 (1.09), G11 (1.29), G18 (1.58) and G21 (3.09).Tai's stability statistic divided the G × E interaction into α and λ components and genotypes with α = 0, and λ = 1, *viz*., G1, G4, G13 and G20 were considered as medium stable. As per Shukla's variance, stable genotypes exhibit minimum stability variance (σ_i^2), which revealedG14 (0.17), G7 (0.33), G18 (0.63), G3 (0.63) and G17 (0.73) as highly stable.According to Francis and Kannenberg, genotypes with a combination of low CV_i values and high mean yield are considered as stable. A close pursual of Table6 showcased G18 (31.092), G21 (32.20), G2 (32.37) and G4 (34.93), G1 (36.00) as stable and adaptable genotypes, owing to their relatively low CV_i values and high mean yield. Conversely, genotypes G-13 (55.66), G9 (56.17), and G8 (59.26) were identified as unstable due to their higher CV_i values. With regard to the non-parametric stability measures, genotypes G7 (0.24), G12 (0.31), G18 (0.38), G14 (0.44) and G4 (0.49) were identified as the most stable. At the same time, G16 (1.31), G6 (1.42) and G8 (1.44) were unstable as per the $S_i^{(1)}$stability model proposed by Nassar and Huehn. Likewise, the $S_i^{(2)}$stability measure pointed G7 (3.67), G12 (3.67), G14 (4.78), G4 (7.22), and G11 (7.67) to be exhibiting the lowest values, indicating stability. Conversely, G6 (44.56), G9 (44.89) and G8 (74.11) were identified as unstable based on this measure.

On the whole, the comparative stability analysis of chickpea genotypes across various models revealed a thorough understanding of genotype performance under different environmental conditions. Genotypes G1, G4, and G18 consistently emerged as stable across multiple stability models, including Eberhart and Russell, Finlay and Wilkinson, and Perkins and Jinks models. Specifically, G1 and G4 show high stability in all three models, demonstrating a high mean yield, a regression coefficient (b_i) near unity, and minimal deviation from regression (S^2d_i). Wricke's ecovalence statistic further supported the stability of G14, G7, and G18, with G14 exhibiting the lowest ecovalence value, indicating minimal fluctuations across environments. Shukla's variance and non-parametric stability measures also identified G7,

Table 8. Univariate stability parameters and mean grain yield across ten environments in chickpea genotypes

S. No.	Genotype	Y_i	CV_i	b_i	S^2d_i	σ_i^2	B_i	W_i^2	P_i	λ	α	$S_i^{(1)}$	$S_i^{(2)}$
1	G1	8.32	36.01	1.05	0.25	0.87	0.05	7.68	1.09	1.27	0.05	0.89	8.89
2	G2	7.06	32.38	0.77	0.25	1.27	-0.23	10.98	4.25	1.26	-0.23	1.07	24.22
3	G3	6.59	33.80	0.79	-0.32	0.64	-0.21	5.83	5.18	0.49	-0.21	0.82	15.78
4	G4	8.62	34.94	1.06	0.18	0.80	0.06	7.16	0.82	1.17	0.06	0.49	7.22
5	G5	6.72	48.32	1.14	0.37	1.12	0.14	9.79	4.69	1.43	0.14	0.87	16.00
6	G6	5.71	26.08	0.46	0.09	3.11	-0.54	25.93	9.42	1.00	-0.55	1.42	44.56
7	G7	5.40	45.12	0.88	-0.40	0.33	-0.12	3.34	9.23	0.39	-0.13	0.24	3.67
8	G8	7.36	59.26	1.54	1.12	4.06	0.54	33.66	3.79	2.40	0.55	1.44	74.11
9	G9	7.02	56.18	1.40	0.52	2.42	0.40	20.33	4.11	1.61	0.41	1.07	44.89
10	G10	5.60	36.89	0.74	-0.38	0.79	-0.26	7.10	8.56	0.40	-0.27	1.13	13.56
11	G11	8.27	44.26	1.33	-0.34	1.16	0.33	10.06	1.29	0.45	0.34	0.53	7.67
12	G12	4.81	43.93	0.72	0.06	1.32	-0.28	11.35	12.43	1.00	-0.29	0.31	3.67
13	G13	7.40	55.67	1.48	0.25	2.72	0.48	22.76	3.31	1.23	0.49	1.09	34.89
14	G14	5.49	52.06	1.04	-0.45	0.17	0.04	2.02	8.68	0.33	0.04	0.44	4.78
15	G15	7.04	55.50	1.41	-0.14	1.87	0.41	15.82	3.88	0.72	0.42	1.07	21.11
16	G16	6.46	38.13	0.82	0.53	1.38	-0.18	11.89	5.88	1.65	-0.18	1.31	30.11
17	G17	5.83	37.61	0.78	-0.28	0.74	-0.22	6.64	7.62	0.55	-0.23	0.98	12.89
18	G18	8.03	31.09	0.88	-0.09	0.63	-0.12	5.79	1.59	0.81	-0.12	0.38	11.11
19	G19	5.65	33.60	0.66	-0.20	1.37	-0.34	11.78	8.66	0.64	-0.35	1.18	21.11
20	G20	7.03	52.45	1.32	0.08	1.53	0.32	13.06	3.83	1.03	0.33	1.02	26.11
21	G21	7.66	32.21	0.75	1.49	2.58	-0.25	21.61	3.09	2.94	-0.25	0.96	36.78

Y_i= Overall mean of yield; CV_i= Coefficient of variability (Francis and Kannenberg); b_i= Coefficient of regression to index the environment (Finlay and Wilkinson; Eberhart and Russel); S^2d_i = deviation of regression (Eberhart and Russell); σ_i^2= Shukla's variance; B_i= Adjusted linear regression coefficient (Perkins and Jinks); W_i^2= Wricke's ecovalence; P_i= Superiority Index; λ, α= Tai's stability measures; $S_i^{(1)}$ and $S_i^{(2)}$= Nassar and Huehn's parameter

G14, and G18 as highly stable genotypes. Genotype G4, consistently ranked highly stable, showed the lowest Pi value and notable stability across Tai's stability statistic and Francis and Kannenberg's measures. On the other hand, G8 was consistently ranked as unstable across various models, highlighting the robustness of these models in identifying stable genotypes. By integrating stability rankings across all models, G4, G1, and G18 emerge as the most stable and promising chickpea genotypes, providing a comprehensive view of their adaptability and performance.

Discussion

The primary source of variation in genotype assessment within multi-environment trials is the combined effect of genotype and G×E interactions (Yan et al. 2000). As chickpea is cultivated across various agro-ecological environments, assessing genotype performance and stability is essential for sustainable agriculture and food security (Bakhsh et al. 2011). In the present study, combined analysis of variance showed the environment, GEI and genotype as highly significant for yield, signifying the extensive genetic background and diversity of experimental material and locations across different environmental conditions. The environment was shown to be largely responsible for most of the yield variation, indicating a wide variety of environmental variables with notable variations in the mean genotype, which essentially causes the variation in grain yield. Considering that GEI can potentially diminish improvements resulting from selection, the choice of cultivars with stability in combination with seed yield had been prioritized for favourable outcomes, as suggested by Yan et al. (2001). Many other studies (Pouresmael et al. 2018; Azam et al. 2020; Karimizadeh et al. 2023) have also highlighted the significant impact of environmental factors on the overall variation in chickpea seed yield. As a stability statistic, AMMI provides insights into complex GEI, especially in scenarios involving multiple environments with the identification of genotypes having adaptability (Crossa 1990), while aiding breeders in making informed decisions in crop improvement. High mean performance and a sizable

PCA score (positive or negative) indicate that the genotypes have a high degree of environmental adaptability. On the other hand, broader adaptability is implied by a high mean performance and an IPCA score around zero (Crossa 1990). Accordingly, the control environments E1, E3 and E5, along with genotypes G9 and G13, exhibited significantly high principal component scores and high mean yield performance denoting specific adaptation. The PCA1 vectors of AMMI1 observed in rainfed environments E2, E4 and E6 exhibited notable proximity to zero compared to other environments, indicating diminished interaction effects and potentially superior performance of all genotypes in rainfed conditions. Concerning specific genotypes, the PCA1 scores for G1, G4, G5 and G7 were also closely aligned with zero, suggesting a reduced environmental influence on their performance. Such genotypes could be valuable in breeding programs aiming for stability as these tend to possess inherent characteristics that enable them to wide adaptation. Likewise, the first two PCs of AMMI2 accounted for 76.06% of the variation for yield, indicating their projection of the interaction among 21 chickpea genotypes tested in 10 environments. Our outcomes supported the conclusions of Karimizadeh et al. (2023), who found that the first two PCs were adequate for accurately projecting the AMMI model. Environments E2 and E3 exhibited shorter vectors, pointing to weaker interactive forces, making them ideal for selecting genotypes with mean performance and adaptability. Conversely, environments E1, E4 and E7 displayed longer spokes, indicating their role as the most discriminating environments, as suggested by Murphy et al. (2009). The genotypes *viz*., BGD103 (G4), Digvijay (G5), JG16(G11), Pusa1003 (G14), Pusa362 (G17) andRSG896 (G18) were positioned near the origin, indicating lower sensitivity and variations across environments, rendering them the most stable genotypes.

Applied plant breeding considers the GGE biplot, with its graphical representation, to be a novel methodology (Yan et al. 2000). The utilisation of this technique for examining genotype by environment interaction data in the breeding of chickpeas has been progressively growing (Rao et al. 2023). Subsequently, the angle between the two environments was utilized to elucidate the degree of correlation, following the methodology proposed by Dehghani et al. (2010). Environments E2 and E4 exhibited a positive correlation, as evidenced by an acute angle between them. In contrast, a wide, obtuse angle was observed between E3 and E1, indicating high cross-over GXE interaction with negative correlation (Yan and Tinker 2006). The angles of the environments E4 and E5 with E7, E9, E10, and E8 were greater than 90 degrees, pointing to an opposite ranking of accessions and a negative correlation between these environments. Small angles were observed between environments (E3 and E6), (E8 and E9), and (E9 and E10), implying their ability to offer comparable insights within genotypes.

The genotype that is positioned at the centre of the concentric circles on the AEC biplot and exhibits high mean performance and stability across environments is considered desirable (Yan and Hunt 2000; Yan 2001). Genotypes located closer to this ideal point are considered more desirable. Furthermore, the ranking of genotypes is based on their desirability from a line drawn from the biplot origin through the specific environment of interest. Thus, according to the interpretation of the present study, genotype G1 exhibited the highest desirability in terms of performance, followed by G4 and G11, as they were positioned closer to the ideal genotype and the line drawn through the relevant environment. This ranking provides valuable insights for genotype selection and breeding efforts aimed at improving crop performance and stability across diverse environments. Environments that are closer to the ideal point are considered more favourable for cultivation and are likely to support higher mean performance and greater stability across different genotypes. Concurrently, E7 was the most discriminating environment, helpful in understanding GEI and providing better assessment to researchers for finding the adaptability of genotypes across diverse conditions. Environments E2 and E6 were closer to the centre of the concentric circle as the ideal environments. They served as reliable benchmarks for evaluating the genotype's ability to withstand varying weather conditions, making it crucial for selection purposes. These findings align with previous studies by Tiwari et al. (2022), which also suggest that the environment closest to the axis or concentric point is optimal for selecting stable genotypes. On the other hand, E7 recorded the longest projections from the AEC axis, indicating its suitability for selecting high-yielding genotypes. However, it's important to note that while genotypes chosen in this environment may exhibit high yield, it does not necessarily imply stability.

Nonetheless, genotypes selected for high yield in such environments can still be valuable for breeding programs aimed at developing high-yielding varieties. Overall, G1, G4 and G11 stand out as stable and high-yielding across environments. In a similar study, Rao et al. (2023) employed the GGE biplot methods for testing 50 chickpea genotypes in five multi-environmental conditions for high yield and drought tolerance.

The GGE biplot's potential to illustrate the «which-won-where» pattern is another important feature that helps identify the genotypes that perform well in particular contexts (Yan et al. 2000). The genotypes at the polygon's vertices are the ones that are most suitable for the environment in the related sector (Yan 2002; Yan and Tinker 2006). Using this procedure, the genotypes G9, G8, G4, G21, G6, and G12 that were found at the polygon's corners with the longest vectors were identified, indicating their superior performance in specific environments.Genotypes G8 and G9 stand out as winners in the first mega-environment encompassing E4 and E5, suggesting their adaptability and high yield potential in these conditions. Similarly, genotype G4 demonstrated exceptional performance in the second mega-environment covering E1 and E2, making it promising for cultivation in those environments. Notably, G18 and G21 emerge as versatile genotypes, winning across multiple environments (E7, E8, E9 and E10), indicating their broad adaptability and stability across diverse conditions. Conversely, environments E4 and E5 appear to be well-suited for genotypes G8, G9, G15, G13 and G20, suggesting a potential GEI where these genotypes thrived optimally in these specific conditions.

Univariate stability parameters, categorized as parametric and nonparametric, are vital statistical tools for assessing yield stability across different environments (Annicchiarico 2002; Kebede et al. 2023). Eberhart and Russell (1966) presented a revised method of joint regression analysis, which has since been widely embraced as the most appropriate for interpreting crop stability data. Varieties with a regression coefficient close to one and minimal deviation from the regression value are perceived to have both high average yield and stability. Six genotypes (G8, G9, G11, G13, G15 and G20) exhibited b_i-values greater than unity (>1.0) alongside higher yields, suggesting their superior adaptability to environments conducive to growth. Consequently, these genotypes are likely to exhibit below-average responses when cultivated in unfavourable conditions but might achieve maximum responses when grown in ideal environments. Overall, a comprehensive analysis of various parameters, including mean yield, regression coefficientand deviation mean square, pinpointed G1, G4 and G18 as potentially stable genotypes. Their consistent performance, characterized by yields surpassing the environmental mean across all environments, suggests robust adaptability. This indicated the utility of these genotypes as reliable options for cultivation across diverse conditions, contributing to agricultural sustainability and productivity. Finlay and Wilkinson (1963) suggested that a genotype exhibiting a regression coefficient of 1 and a mean yield surpassing the overall mean is considered stable, indicating high adaptability across various environments. Based on this criterion, genotypes G-01, G-04 and G-18 were identified as stable, implying that they possess desirable characteristics for consistent performance across different conditions. Likewise, the utilization of statistical methodologies by Perkins and Jinks (1968) to evaluate the response of cultivars to environmental changes, incorporating both GEI and additive environmental factors, provides valuable insights into the stability of different cultivars. Accordingly, G1, G4, G5, G7, G18 and G14 emerged as stable from this parameter.

The significant variability in ecovalence values among the genotypes underscores the diverse responses exhibited across different environments (Wricke 1962). G14 was identified as highly stable, along with G-03, G-07, G-18,and G-17. It is noteworthy that while stability is a desirable trait, it does not necessarily correlate positively with grain yield. As observed in this study, genotypes characterized by lower ecovalence values, and thus greater stability, often exhibited lower mean yields compared to the overall mean yield, as has been highlighted in learlier reports. This negative correlation between stability and grain yield underscores the complex interplay between these two traits in chickpea genotypes. Overall, the identification of stable genotypes, as indicated by their ecovalence values, provides valuable insights for chickpea breeding programs.

The concept of superiority value, coupled with responsiveness to environmental factors, provides valuable insights into cultivar stability and adaptability, crucial factors for sustainable agriculture (Lin and Binns 1988). Genotype G4 stands out as the most promising cultivar in this investigation, characterized by its exceptionally low superiority value and high responsiveness to specific environmental conditions. This combination suggests that G4 exhibits consistent performance across diverse environments, making it robust for cultivation across different regions or under fluctuating climatic conditions. Following G4, genotypes G1, G11, G18, and G1 also demonstrated promise as stable cultivars with smaller P_i values. This parameter was found to be highly correlated with yield since genotypes with higher yield were also found to be highly stable, according to this parameter, as corroborated by Satturuet al. (2024). The stability statistic proposed by Tai (1971) partitions the G × E interaction effect into two distinct components: α and λ. The α value, measured on the vertical axis, represents the linear response to environmental effects. In contrast, λ, on the horizontal axis, quantifies the deviation from this linear response, as indicated by error variance. According to this model, genotypes characterized by $\alpha = -1$ and $\lambda = 1$ exhibit the highest stability, indicating a consistent response across diverse environments.

Conversely, genotypes with $\alpha = 0$ and $\lambda = 1$ demonstrate an average stability, showing moderate variation in their responses to environmental changes. In the Alpha-Lambda space, the region between the α-axis and $\lambda = 1$ indicated G1, G4, G13and G20 as average stable cultivars with $\alpha = 0$ and $\lambda = 1$. These cultivars display a reliable and consistent performance across different environmental conditions. Another parametric stability measure where the GEI sum of squares is partitioned into variance components (σ_i^2) with a higher value of σi indicating greater instability is Sukla's variance (Shukla 1972). In the current study, the most stable genotypes were identified as G3, G7, G14, G17 and G18,with low σi values. For this statistic, the stable genotypes had lower mean yieldssimilar toWricke's ecovalence model. The coefficient of variation serves as a valuable metric for identifying desirable genotypes based on their combination of low CV_ivalues and high mean yield (Francis and Kannenberg 1978). G18, G21, G2, and G4, characterized by their relatively low CV_i values and high mean yield were declared as stable. This observation underscores the importance of considering both stability and yield when evaluating genotype performance.

Regarding the non-parametric stability assessment, Nassar and Huhn (1987) rank stability method ($S_i^{(1)}$,$S_i^{(2)}$) is widely used and relies on comparing the ranks of genotypes across various environments, assigning equal importance to each environment. Genotypes exhibiting fewer fluctuations in ranking are deemed more stable, according to Becker and Leon (1988). As per the stability measure, genotypes G4, G7, G12 and G14 were identified as the most stable from both $S_i^{(1)}$ and$S_i^{(2)}$ measures, indicating that these genotypes are less affected by environmental fluctuations, making them reliable choices for cultivation across diverse conditions. A similar study on univariate stability parameters for assessing stability in chickpeas was performed by Farshadfar et al. (2012); and Kumar et al. (2023). Overall, the integration of both parametric and non-parametric measures identified genotypes G1, G4, G7 and G-18 as the most stable from the study.

Considering mean yield together with AMMI, GGE and univariate stability statistics, G1, G4 and G18 emerged as the most promising and stable genotypes, underscoring their potential for broader adaption and utilization in breeding programs aimed at improving crop productivity and stability across diverse environmental conditions. Further validation through field trials and multi-location testing would provide additional confirmation of their stability and performance.

Supplementary materials

The Supplementary Figs. 1 and 2 are provided, which can be accessed at www.isgpb.org

Authors' contribution

Conceptualization of research (BPS, JR); Designing of the experiments (BPS, JR); Contribution of experimental materials (BPS, JR, BKM, MK); Execution of field/lab experiments and data collection (RB, AG, SS); Analysis of data and interpretation (IV, AC, HCB, BKM, HMH, SRK); Preparation of the manuscript (BPS, DS, AC, JR, IV).

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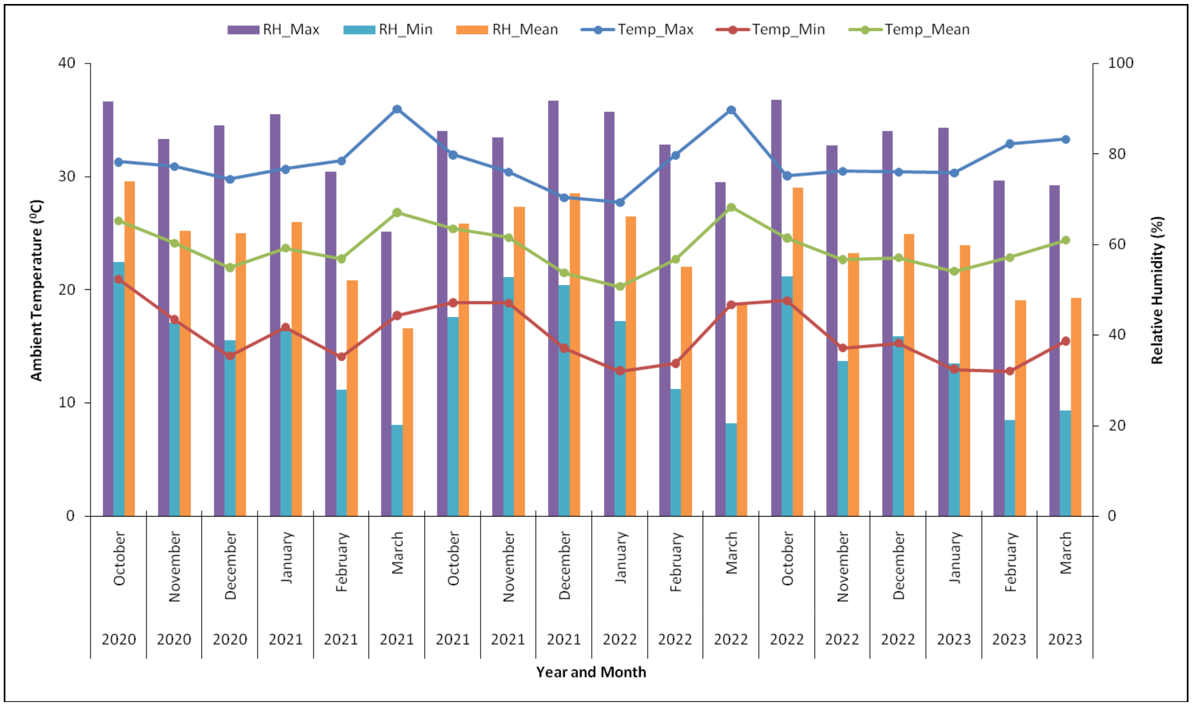
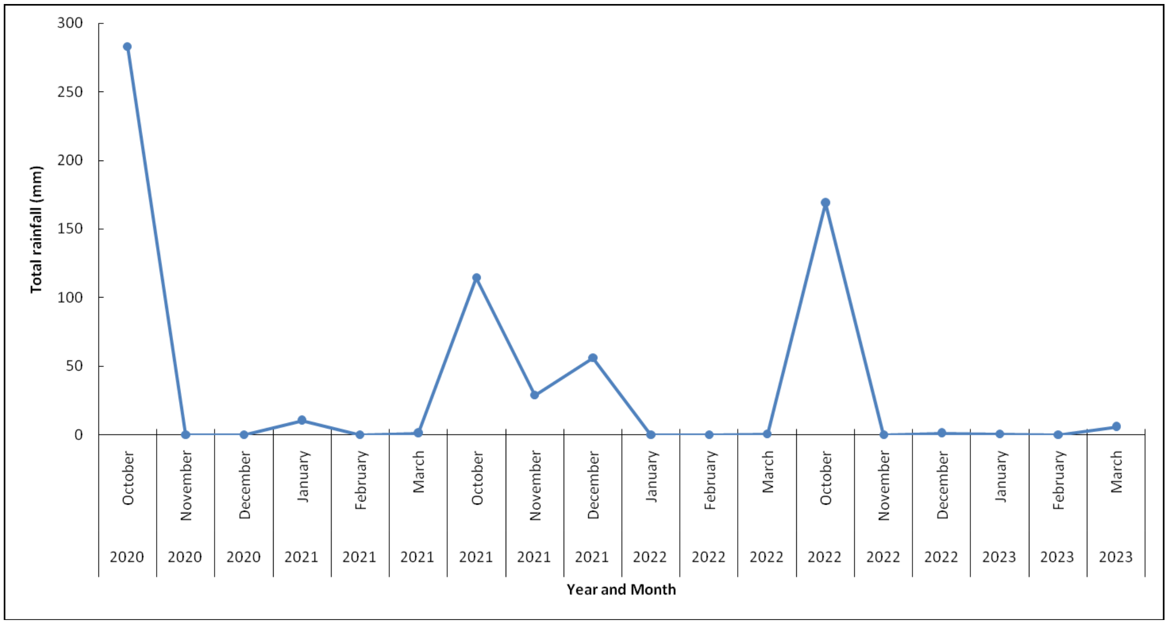


SupplementaryFig. 1. Weather parameters (Temperature, Relative humidity) of the experimental site during (2020-2022)



Supplementary Fig. 2. Rainfall received at the experimental site during (2020-2022).