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GGE-Biplot Analysis on Seed Yield of Elite Drought-Tolerant Chickpea (*Cicer arietinum* L.) Genotypes in North-eastern Ethiopia

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ABSTRACT

Drought tolerance is an important objective in many plant breeding programs. Global annual yield losses due to drought stress may reach 50% depending on the crop's growth stage and extent of drought severity. The present study was conducted to examine the yield performance and stability of elite drought-tolerant chickpea genotypes under diverse environments and to identify a stable genotype that performs well in moisture deficit environments using fourteen high drought index genotypes, including *Fetenech* (commercial variety). GGE biplot methodology was used to analyze genotypic stability across the environments. Additive main effect and multiplicative interaction (AMMI) analyses revealed significant ($P < 0.01$) genotype (G) and environmental (E) effects as well as G×E interaction with respect to chickpea yield. As per the AMMI analysis, 66.1% of the total variation was attributed to the environment, while G and G×E interaction explained 8.2% and 11.5%, respectively. According to AMMI's stability value (ASV), the most stable genotypes were G9 and G1, considering both mean yield and ASV. The testing environments were clustered into two mega environments. The study clearly shows that G1 is near to the ideal genotype that does well under terminal moisture deficit environments with desirable and stable attributes with a yield advantage of 29.1% over standard cultivar (Fetenech). Further research on molecular and physiological analysis has to be conducted to identify gene/s conferring drought tolerance in chickpeas. Moreover, schematic hybridization should be designed to introgress novel gene/s conferring drought tolerance to high-yielding and adapted commercial chickpea varieties.

Keywords: Desi chickpea, Drought index, GEI, GGE-biplot, Stability.

INTRODUCTION

Ethiopia is the largest producer of chickpea in Africa, accounting for about 65.3% of production. It is the seventh largest producer worldwide and contributes about 3.1% to the total global chickpea production (FAO, 2020). Chickpea is the second most important pulse crop after faba bean in production and third in area coverage after faba bean and field pea with annual production of 322,838 tonness. The average productivity level of 1.7 tonness/ha (CSA, 2017) is among the highest recorded globally and double the global average (FAO, 2020). The varied climatic and diverse agro-ecological conditions of Ethiopia are very suitable for growing chickpeas (Fikru, 2017). The country is also considered as the secondary center of diversity for chickpea (Bejiga et al., 1996). Chickpea has become an important legume, accounting for more than 15% of Ethiopian legumes with about one million households engaged in its production (CSA, 2017). Chickpea serves as a multi-purpose crop where the whole seeds are eaten fresh, cooked, boiled or in the form of stew.

Despite the growing demands and high yield potential, chickpea yields are not increasing and productivity of chickpea remains stagnant. Drought is one of the major constraints affecting food security and livelihoods of more than two billion people that reside in dry areas, which constitute 41% of the world's land surface (Araus et al., 2002). Terminal moisture-stress is one of the limiting factors for chickpea production in its growing areas. It typically affects desi type of chickpea, which is grown with residual moisture; terminal moisture-stress caused by drought frequently occurs in Ethiopia (Fikru, 2017).

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Plants have developed various strategies to acquire stress tolerance. In genetic sense, the mechanisms of drought resistance can be grouped into three categories: drought escape, drought avoidance and drought tolerance. However, crop plants use more than one mechanism at a time to resist drought (Mitra, 2001). In chickpea, the focus of drought tolerance research is to sustain greater biomass production and crop yield under extreme drought shock (Serraj & Sinclair, 2002). This has led to the focus on escape and avoidance strategies such as early maturity (Kumar & Abbo, 2001) and large root biomass (Kashiwagi et al., 2006). Therefore, yield improvements in rain-fed environments could be achieved by identifying and selecting drought-resistance component traits in a breeding program (O'Toole & Change, 1979).

Due to the limited availability of genetic diversity to make crosses, attempts to improve this crop has, therefore, been mostly confined either to the examination of varietal differences or selection from the cultivars of improved stocks (Fikru, 2017). At the early stage of this study, 1200 genotypes of single seed descent pure lines were evaluated and selected in a single drought-stressed environment using preliminary observation and preliminary yield trial. Those genotypes were selected for drought tolerance from the core set by proper phenotyping and evaluation of agronomic performance, and adaptable traits were advanced for multi-environment variety trials. Multi-location trials were conducted to get improved genotypes in varietal developmental programs.

However, a variety of trial data are rarely utilized to their full capacity. Furthermore, analysis of genotype-by-environment data is often limited to genotype evaluation based on genotype main effect (G) while genotype-by-environment interactions (G×E) are treated as noise or a confounding factor. Besides, G×E limits yield estimates because it is associated with genotypes and environment interactions (Zobel et al., 1988). There remains a gap in how G×E is measured and addressed between biometricians and quantitative geneticists versus breeders and other practitioners. Despite breeders' strong interests in interactions and mega-environment analysis, the linear ANOVA technique is not of too much help in selection of cultivars because it does not consider the positivity and negativity of factors. At present GGE biplot data visualization tool (Yan et al., 2000) graphically displays a GxE interaction in a two-way table (Yan, 2000). The tool is effective for mega-environment analysis such as, "which-won-where" pattern, whereby specific genotypes can be recommended to specific mega-environments (Yan, 2003; Yan, 2006), genotype evaluation (the mean performance and stability), and environmental evaluation (the power to discriminate among genotypes in target environments). The additive main effect and multiplicative interaction (AMMI) model (Gauch, 1988) complements GGE biplot, provides meaningful interpretation of genotype by environment interactions of yield and yield component data (Gauch & Zobel, 1997). Models were effective in field pea, wheat, maize and chickpea. In light of this, the present study was aimed to develop and select drought resistant/tolerant genotypes that can do well in the drought and terminal moisture stress area of the region over multi-location sites using the aforementioned models.

MATERIALS AND METHODS

Description of the study area:

The experiment was conducted at three drought prone environments in major chickpea growing areas of eastern Amhara, Ethiopia. It included North Wollo zone (Kobo, which represented lowland altitude with sandy loam (brown) soil type, and Jari, which represented intermediate altitude with black soil type, and Oromia Zone (Chefa, representing sub-humid lowland with black soil type) (Table 1 and Fig. 1). The field experiments were conducted for three subsequent cropping seasons (2017-2019).

Table 1: Geographical, climatic and agro-ecological features of the experimental sites

Description parameter	Location		
	Jari	Chefa	Kobo
Major agro-ecology	M1-7	M1-3	SM1-3
Mean range of temperature (°C)	22-35	21-36	25-38
Mean rainfall (mm)	150	125	60
Latitude	11°21'N	10°57'N	12°12'N
Longitude	39°38'E	39°47'E	39°18'21''E
Altitude	1600	1680	1450
Soil type	Black soil	Alluvial /Black soil	Eutric Fluvisol Sandy loam (Brown)

Source=Natural Resource Management and Regulatory Department (MOA, 2008)

Experimental design and agronomic practices:

The experiment was carried out in randomized complete block design replicated three times. A plot size of 2.4 m wide and 4 m long, with an inter-row and intra-row spacing of 0.4 and 0.1m, respectively, was used. Seedbed preparation was done three times; the genotypes were sown in the

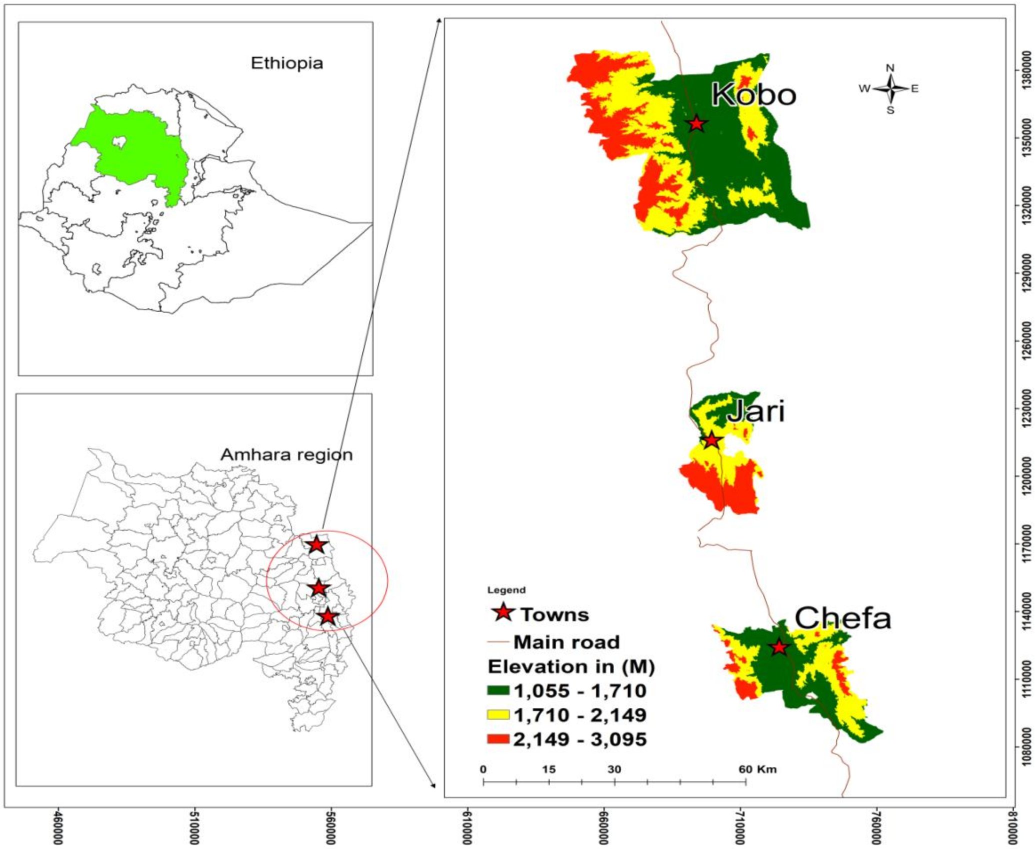


Fig. 1: Geographical position of the experimental sites

Table 2: Description of the 14 chickpea genotypes tested during 2017–2019 cropping season

No	Treatment (Genotype)	Genotype label	Genotype Source	Property
1	CH-Acc. 41053	G1	Amahara	High drought index
2	CH-Acc. 207612	G2	Amhara	High drought index
3	CH-Acc. 41034	G3	Oromiya	High drought index
4	CH-Acc. 215033	G4	Amhara	High drought index
5	CH-Acc. 41149	G5	Amhara	High drought index
6	CH-Acc. 41039	G6	Oromiya	High drought index
7	CH-Acc. 207647	G7	Amhara	High drought index
8	CH-Acc. 41056	G8	Amhara	High drought index
9	CH-Acc. 20077	G9	Unknown	Mild drought index
10	CH-Acc. 41279	G10	Amhara	High drought index
11	CH-Acc. 207666	G11	Oromiya	High drought index
12	CH-Acc. 41213	G12	Amhara	Mild drought index
13	CH-Acc. 41219	G13	Amhara	Mild drought index
14	*Fetenech*	G14	Commercial variety/SARC/	Commercial drought-tolerant variety

Source = Lijalem et al. (2021); SARC = Sirinka Agricultural Research Centre

first week of September in all the three cropping seasons. Fertilizer was not applied; hand weeding was carried out twice. Data on days to maturity and seed yield were recorded. For the sake of this paper, we have included only days to 90% maturity (DM), and seed yield (SY) in kg per hectare for analysis. Plot means were used to estimate the mean performance of the genotype.

Plant materials:

Thirteen advanced chickpea genotypes denoted as G1-G13 including drought tolerant (*Fetenech* variety) labeled as G14 were evaluated (Table 2). The genotypes were advanced from a previous preliminary yield trial from the drought tolerant core set of the Ethiopian germplasm. Before

Table 3: Combined analysis of days to maturity and seed yield in tonnes ha^{-1}across eight environments using additive main effect and multiplicative interaction (AMMI) model

Source	DM					SY			
	df	Sum Square	Mean square	% Total SS	%TRT	Sum Square	Mean square	% Total SS	%TRT
Total	377	23626	62.7			251424666	666909		
Treatments	125	21550	172.4**	91.2		215650989	1725208**	85.8	
Genotypes	13	1258	96.7**		5.8%	20581339	1583180**		8.2
Environments	8	18375	2296.9**		77.8%	166179050	20772381**		66.1
Block	18	203	11.3ns			4485395	249189*		
Interactions	104	1917	18.4**		8.9%	28890601	277794**		11.5
IPCA 1	20	969	48.5**		50.5%	15144165	707208**		52.4
IPCA 2	18	504	28**		26.3%	5532394	307355**		19.1
Residuals	66	444	6.7			9214042	139607		
Error	234	1874	8			31288281	133711	14.2	

DM = Days to Maturity; SY = seed yield; df = degree of freedom; SS = sum of squares

characterization and advanced trial the accession was collected from Ethiopian Biodiversity Institute (EBI) in 2010. In 2020 cropping season, three promising candidate genotypes were evaluated on both station and on-farmer's field with a plot size of 10 m by 10 m. Farmers' assessment and evaluation such as tolerance to drought, pod load, and earliness were included in the data and converted to rank.

Data Analysis:

The collected data were subjected to analysis of variance (ANOVA) using general linear model using two software programs: GenstatV.18 and R V1.4.1106. The AMMI model developed by Gauch (1986) was calculated as:

$$Yij = \mu + Gi + Ej + \sum \lambda \alpha iK\delta jK + Rij + \varepsilon$$

Where, Y_{ij} is the value of the ith genotype in the jth environment; μ is the grand mean; G_i is the deviation of the ith genotype from the grand mean; E_j is the deviation of the jth environment from the grand mean; λK is the singular value for PC axis K; α_{ik} and δ_{jk} are the PC scores for axis K of the ith genotype and jth environment, respectively; R_{ij} is the residual and ε is the error term (Gauch, 1992).

AMMI's stability value (ASV) was calculated following the formula proposed by Purchase et al. (2000) as follows:

$$\text{ASV} = \sqrt{[\text{SSIPCA1}/\text{SSIPCA2})(\text{IPCA1 SCORE})]2 + (\text{IPCASCORE2})2}$$

Where: SSIPCA1/SSIPCA2 is the weight given to the IPCA1 value by dividing the IPCA1 SS by the IPCA2 SS; and the IPCA1 and IPCA2 scores are the genotypic scores in the AMMI model.

The GGE-biplot methodology, which is composed of two concepts, the biplot concept (Gabriel, 1971) and the GGE concept (Yan et al., 2000), was used to visually analyze the multi-environment yield trial (MEYTs) data. This methodology uses a biplot to show the factors (G and G×E) that are important in genotype evaluation and that are also sources of variation in GEI analysis of MEYTs data (Yan, 2001; Yan et al., 2000).

RESULTS

Analysis of variance:

The analysis of variance of the data showing mean performance of day maturity and seed yield are presented in Table 3. The combined analysis of variance across nine environments revealed significant differences among the genotypes in days to 90% maturity and seed yield. The pooled analysis of variance revealed a significant interaction between genotypes, locations and year for both these traits (Table 3). The additive combined ANOVA showed that the earlier genotype matured within 83 days and the longest maturity for 90 days (data not shown). The lowest mean seed yield recorded genotype G8 (1.4 tons ha^{-1}) and the highest for genotype G1 (2.3 tons ha^{-1}) (Table 4).

Additive main effect and multiplicative interaction (AMMI) analysis:

The results of the AMMI analysis of variance are shown in Table 3. It showed highly significant differences for the environment, genotype and their interactions for both days to maturity and seed yield. The majority of the variation was contributed by environments (66.1%) followed by G×E interaction (11.5%) and genotypes (8.2%) (Table 3).

The observed G×E interactions in the AMMI model have been partitioned among the first and second Interaction Principal Components Axes (IPCA). The first principal component (PC1) was

Table 4: Mean seed yield (tons/ha) of chickpea genotypes, AMMI stability values across nine environments

Genotype	J8	C8	K8	J9	C9	K9	J10	C10	K10	GM	IPC1
G1	3.29	3.19	1.71	2.41	2.46	1.17	2.62	2.00	1.74	2.29	-1.38
G2	2.58	2.55	0.89	2.55	1.89	0.26	1.92	1.38	1.23	1.69	10.92
G3	2.64	2.54	0.91	2.20	1.83	0.33	1.90	1.33	1.14	1.65	4.70
G4	2.62	2.53	0.98	2.01	1.82	0.41	1.93	1.34	1.12	1.64	2.64
G5	2.51	2.46	0.95	1.98	1.77	0.36	1.90	1.30	1.07	1.59	3.84
G6	2.53	2.50	0.96	2.16	1.83	0.36	1.93	1.35	1.14	1.64	6.12
G7	2.42	2.39	1.07	1.45	1.69	0.52	1.93	1.28	0.96	1.52	-2.03
G8	2.56	2.39	1.01	1.01	1.59	0.54	1.83	1.16	0.81	1.43	-11.2
G9	2.64	2.51	0.98	1.79	1.77	0.44	1.91	1.30	1.05	1.60	-1.03
G10	2.62	2.60	1.24	1.82	1.91	0.67	2.13	1.49	1.19	1.74	0.40
G11	4.48	3.55	1.39	1.29	2.33	1.17	2.25	1.65	1.41	2.17	-39.3
G12	1.59	2.06	1.26	1.61	1.61	0.55	2.08	1.37	0.97	1.46	14.93
G13	2.62	2.58	1.02	2.31	1.91	0.42	2.00	1.43	1.23	1.72	6.88
G14	2.41	2.50	1.22	1.87	1.86	0.62	2.11	1.47	1.17	1.69	4.56
Grand Mean	2.68	2.60	1.11	1.89	1.88	0.56	2.03	1.42	1.16	1.70	

GN = genotype number; J8 = Jari in 2017; C8 = Chefa in 2017; K8 = Kobo in 2017; J9 = Jari in 2018; C9 = Chefa in 2018; K9 = Kobo in 2018; J10 = Jari in 2019; C10 = Chefa in 2019; K10 = Kobo in 2019; GM =Grand Mean; IPCA = interaction principal component axes value; AMMI = Additive main effect and multiplicative interaction; ASV = AMMI stability value.

Table 5: The first four additive main effect and multiplicative interaction (AMMI) selections per environment

Environment	Mean	Score	1	2	3
4	1.89	29.47	G2	G1	G13
9	1.16	5.57	G1	G11	G2
8	1.42	5.4	G1	G11	G10
7	2.03	5.2	G1	G11	G10
3	1.11	3.2	G1	G11	G12
5	1.886	0.43	G1	G11	G13
6	0.56	-5.28	G11	G1	G10
2	2.60	-11.76	G11	G1	G10
1	2.68	-32.24	G11	G1	G3

Table 6: The mean performance of the candidate chickpea genotype on verification trial for both research and farmers site across 12 environments

Genotype	DM	Seed yield (tonne ha^{-1})	Yield advantage (%)	Farmers' response and rank			
				Earliness	Seed Boldness	Pod yield score	Disease score
41053	90	2.12	29.1	1	1	1	1
41219	88	1.76	7.3	1	3	2	1
207666	90	1.48	-9.7	2	3	3	1
Fetenech	92	1.64		2	2	1	1

NVRC=National Variety Releasing Committee; DM=Days maturity

significant with p<0.001 according to Gollob's F test, as was the second (PC2) (Table 3). While PC1 explained 52.4% of the variability, the percentage attributed to PC2 was 19.1%. PC1 and PC2 together explain 71.5% of the variability, which is sufficient, since 70% is considered the minimum amount of variability for the model to be relatively reliable.

Mean performance and stability of chickpea Genotypes by GGE biplot:

The first two principal components explained 89.2% of the total GGE variation obtained through the SVD of the data converted into GGE data by extracting environments' main effect (Fig. 2a). The first principal component explained 66.8% of the variation while 22.4% of the variation was explained by the second principal component (Fig. 2a). The genotypes with the highest average seed yield were G1 >G11 >G10 >G13 >G2 >G14 >G3 >G4 >G6, in decreasing order (Table 4). According to ASV ranking, the most stable genotypes were G9, and G1, considering both mean yield and ASV (Table 5).

Evaluation of genotypes and similarity and dissimilarity based on GGE biplot were shown, by average environmental coordination (AEC), ordinate separates genotypes with below-average means from those with above-average means (Fig. 2a). Therefore, genotypes with above-average means were G1 (highest), G11, G10, G2 and G13 whereas those with below-average means were G12 (lowest), G7, G8, G9, with G5 (Fig. 2a and Table 4).

Mega-environments analysis ('Which one where' GGE Biplot):

The 'which one where' view of the GGE biplot is an effective tool for mega-environment analysis (Fig. 2b). The polygon is formed by connecting vertex genotypes (G1, G2, G8, G11 and G12). These genotypes have the largest vectors in their respective directions. These superior genotypes are called winner genotypes in respective regions. Depending on the mega environment definition, it appears that there exist two possible mega environments (Fig. 2b). The first mega environment (Mega-1) consisted of seven environments, J9, C9, K8, K9, J10, C10 and K10, which are found in sector 1 with the G1 being the best winner in these environments (Fig. 2a and Table 5) relative potential for chickpea production as compared to sector 2. And, the second mega environment (Mega-2) was small as compared to the first containing four environments, J8, C8, K8 and K9 (Fig. 2b). However, the environments K8 and K9 found in sector 2 were intentionally combined with sector 1 to constitute mega-1 as these environments were similar to each other except the difference in seasonal effects for the locations in sector 1 and had also strong positive correlation (Fig. 2a).

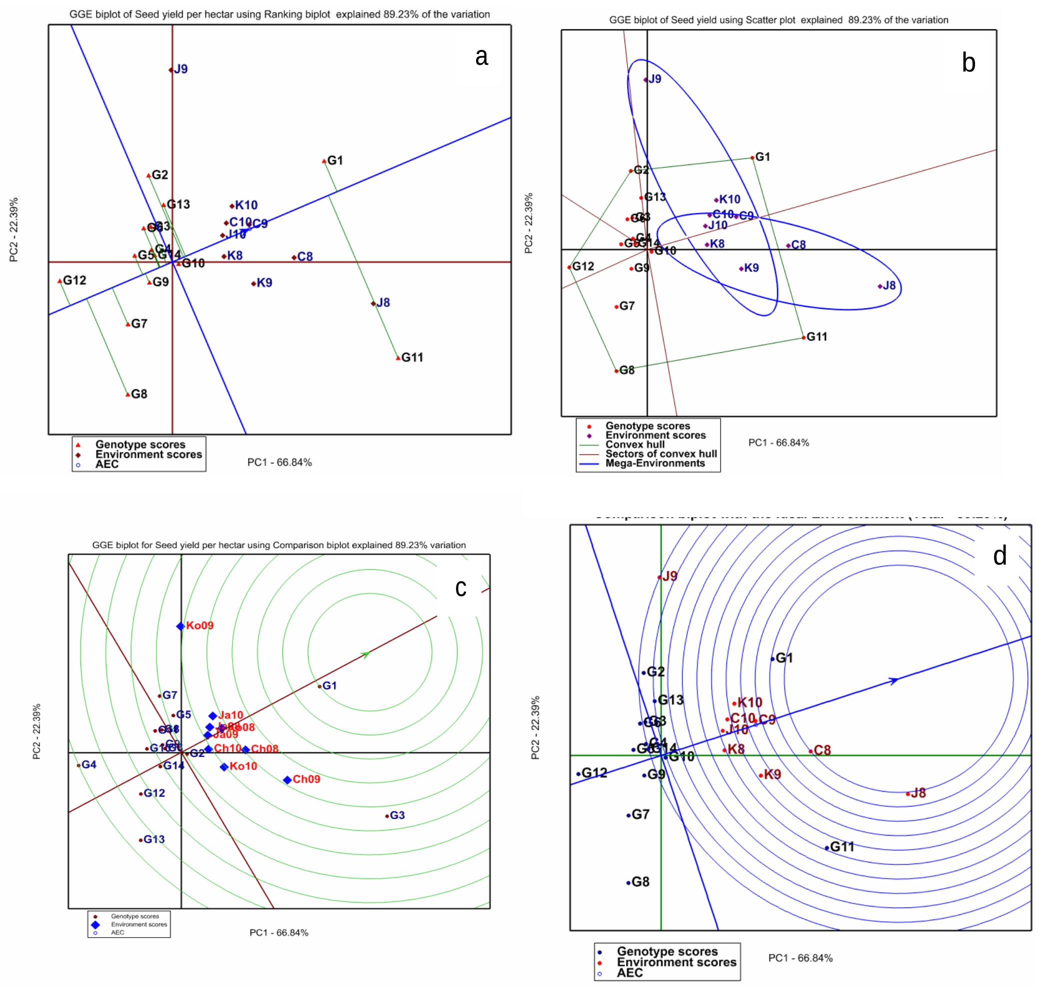
Ranking genotypic performance in reference to the ideal genotype and ideal environment:

Figures 4 and 5 show the ranks of genotypes based on their yield performance with reference to the ideal genotypes and ideal environment, respectively. From Fig. 2c, genotypes G4, G10, G12, and G13, which are found below the perpendicular line to the axis had far from the ideal genotypes than the average yield of the environment, while genotypes G2, G4, and G6 showed nearly average yield performance. The candidate genotype (G1) had the shortest vector length both with the ideal genotypes and ideal environment (Fig. 2c and d). As displayed in (Fig. 2c and d) the environmental evaluation of the power to discriminate among ideal genotypes in target environments, Chefa was more ideal to discriminate candidate and ideal genotype. According to the farmers' assessment, the candidate genotypes had better performances in earliness, boldness, and yield advantage over the standard check (Table 6).

DISCUSSION

The analysis of variance is an important preliminary analysis for confirming the presence of genotype environment interaction. The results of the AMMI analysis clearly showed the effect of environment, genotype and their interactions for both days to maturity and seed yield. The findings of maximum variation recorded for seed yield due to environments were in agreement with the findings of Yan and Tinker (2006), who reported that the major contributing factors for variation in multi-location trials came from changing environmental variables. This variation is useful when aiming to study the significant effects of G×E interaction, as well as to evaluate the phenotypic stability of the genotypes under different environments.

Thus, the large sum of squares and significant effect of environments proved that the experiments were carried out under divergent edaphic and climatic conditions. In agreement with report of Regis et al., (2018), the divergent environmental conditions were aggravated due to climate change, which brought difference for environmental means and thereby causing variation in chickpea yield. The observed G×E interactions in the AMMI model were in agreement with Mattos et al. (2013) and Regis et al. (2018) who suggested that G×E pattern is collected in the first principal components of analysis. Due to the fact that subsequent PC was less significant of the variability, it was omitted from further analysis so that the simplicity of two-dimensional analysis would be maintained. Besides, the magnitude of the GEI sum of squares was relatively similar with that of the genotypes, indicating that there was somehow similar response of some of the genotypes across environments.



G=genotypes; E=environment; G×E=interaction of genotype and environment; PC1=first principal components; PC2=second principal components; J8 = Jari in 2017; C8 = Chefa in 2017; K8 = Kobo in 2017; J9 = Jari in 2018; C9 = Chefa in 2018; K9 = Kobo in 2018; J10 = Jari in 2019; C10 = Chefa in 2019; K10 = Kobo in 2019

Fig. 2: (a) Average environment coordination views of the GGE: Ranking biplot based on environment-focused scaling for the means seed yield per hectare performance and stability of genotypes; (b) The "which-won-where" view of the GGE biplot based on the G×E data in Table 4. It explained 89.2% of the total G plus G×E. The genotypes are labeled with black and the environments are labeled blue; (c) GGE-biplot comparison of the genotype with the ideal genotype (genotypes are in blue, and environment are in red); (d) GGE-biplot based on genotype-focused scaling for comparison of the environment with the ideal environment (genotypes are in blue, and environments are in red)

The quantitative stability value called AMMI Stability Value (ASV), developed by Purchase et al. (2000) to rank genotypes was considered an appropriate method of describing the stability of genotypes (Equation 2). This model showed the significant interaction in genotype and environment for chickpea yield pointed out that each factor cannot independently explain all the variation observed. This necessitates a more detailed account of the study of this interaction to interpret it in order to recommend superior genotypes. This validates the need to take more seriously stability and adaptability trials (analysis results) for selection and recommendation of promising chickpea genotypes that do well in drought environments.

According to AMMI selection over environments, the three genotypes that performed the maximum seed yield in different environments include G1 in six environments and G11 in two environments and G2 in one environment. Thus, such inconsistent yield ranking from environment to environment indicates the presence of possible cross-over G×E as described by Baker (1988), Crossa (1990), Yan and Hunt (2001) and Kaya et al. (2006). Despite this fact, G9 has the lowest ASV value followed by G1 with lower value IPCA

1 and 2 score. This suggests that such kinds of interaction were possible in the case of non-cross-over GEI. Thus, according to ASV ranking, the most stable genotype, G1, does well under different moisture deficit and terminal drought environments.

The environments with the highest productivity on average were J8 (Jari 2017) followed by C8 (Chefa 2017), due to better moisture in these two environments, and it is the second candidate genotype (G11) that performs better in this moisture condition. Whereas Kobo over the three seasons positioned below the average mean performance of the environment; this being more due to the fact that the location was more frequently exposed to severe drought stress than the other six environments.

The test environment evaluation axis is useful for yield and stability within a mega-environment. The axis passing through this virtual environment is called average environment axis (AEA) while a perpendicular axis overlaid on the GGE biplot is called average coordination axis (ACA). According to Yan et al. (2000) AEA is highly correlated with genotypic performance and indicates genotypes average performance visualized by the projection of a genotype on this axis. Moving in either direction away from ACA ordinate and from the biplot origin indicates greater GEI effect and reduced stability. The ACA ordinate separates genotypes with below-average means from those with above-average means. The performance of the genotype in an environment is better than average if the angle between its vector and the environment’s vector is less than 90°, is less than average if the angle is greater than 90° and near average if the angle is about 90° (Yan & Tinker, 2006). In this regard, genotype G1 performed well in all environments over the others and has wide adaptability. Genotype G11, which performed specifically better in J8 and K10 has specific adaptability. Genotypes G7, G8, G9, and G12 had poor performance below average in most of the environments. Genotypes located near to the biplot origin had an average value in each of the environments, such as G10, G4, G5 and G14. Such genotypes had a very minimum contribution to both G and GE interaction.

To visualize the relationship between environments, lines are drawn to connect the test environments to the biplot origin known as environment vectors. Thus, all environments that are found in quadrant I were positively correlated to each other as the angle between them was less than 90° (i.e., acute angle); whereas, J8 and K9 were positively correlated at quadrant IV. However, since the angle between all environments is less than 90°, the correlation between them was strong and it more represents the drought nature of the environments and also it indicates the presence of close associations between most testing environments. This reveals that similar information about the genotype could be obtained from fewer test environments and hence there could be better potential to reduce testing cost under limited resources as per Yan & Tinker (2006) and Kaya et al. (2006) reports.

Imagining the polygon view of a biplot is the best way to visualize the interaction patterns between genotypes and environments (Yan & Kang, 2003). It shows the presence or absence of cross-over GEI which is helpful in estimating the possible existence of different mega environments (Gauch & Zobel, 1997; Yan & Rajcan, 2002; Yan & Tinker, 2006). The genotypes that are located on vertices of the polygon formed are either the best or poorest in one or more environments. The sectors formed by perpendicular lines enclose similar type environments that have specific performers; those environments that fall in this region are called mega-environment (Yan et al., 2000; Yan & Rajcan, 2002; Yan & Kang, 2003; Yan & Tinker, 2006).

The genotype on the vertex of the polygon, contained in a mega-environment, had the highest yield in at least one environment and was one of the best-performing genotypes in the other mega environments (Yan & Rajcan, 2002). Therefore, the candidate G1 was the highest yielder in all environments and coupled with additional worth, earliness that escaped terminal drought. It can be observed from Fig. 3, all of the test environments across all years except J8 and C8 were clustered into the same sector. There was inconsistency of genotypes performance in the two environments (J8, C8). The environment PC1 scores had positive scores in this sector, indicating that there was no difference in rankings of yield performance among genotypes across six environments leading to non-cross-over GEI. Unlike PC1, the environmental PC2 scores had positive and negative scores. This gives rise to cross-over GEI, leading to inconsistent genotypes in yield performance over J8 and K9. The environment PC1 and PC2 scores in this study showed G×E components in line with the reports of (Surinder et al., 2014; Regis et al., 2018; Yan & Hunt, 2001; Yan et al., 2000) that indicated PC1 for non-cross-over and PC2 for crossing over.

Simultaneous accounting of factors may not linearly associate together; in that case, visual identification of genotypes is difficult and complex. Solving this problem is accomplished by defining ideal genotypes. The ideal genotype is a virtual genotype that has the highest mean yield and zero in stability. The distance from the ideal genotype can decrease either mean yield or stability or both. Therefore, distance is considered as an indicator of ranks in evaluation of genotypes. The result depicts that G1 was near to the ideal genotype (the center of concentric circles) with desirable and stable attributes. In ranking genotypes based on their performance in an environment, a line is drawn that passes through the biplot origin and the environment. This line is called the axis for ideal environment (Yan &Tinker, 2006) and along it is the ranking of genotypes with reference to the ideal environment. In addition to that, C8, C9, C10, and J10 were near to the ideal environment, implying that they are potential environments for chickpea production. However, environments in their order 'K9, K10, and K8, J8' were far from the ideal environment, associated with poor potential and instability.

The main positive feature(s) of the candidate genotype included typically better performance in earliness, boldness, and yield advantage over the released standard check *Fetenech* as per the farmers' assessment. They may have genes conferring drought-stress and expressed under drought-prone environments. The candidate genotype belongs to extra early group than varieties released before.

In conclusion, the results of this study showed that chickpea seed yield performance was highly influenced by environmental effects followed by the magnitude of GEI and genotype. In this study, the candidate genotypes showed less cross-over GEI across the environment in terms of high mean yield. The stability and adaptability of GGE biplot and AMMI analysis identified G1 and G11 as the most productive genotypes in terms of seed yield (tonnes ha^{-1}). These two are recommendable as suitable genotypes across the environments. Regarding the testing environments, there exist two possible mega environments (Mega-1 and 2) with less non-cross-over interaction. The analysis result also indicated that more of the variance was contributed by the seasonal difference. GGE biplot clearly depicted G1 with shortest vector length was highly stable and high yielding in K8, C9, J10, C10, and K10 environments. Chefa was more ideal to discriminate the candidate and ideal genotype. In addition to this, the candidate genotype has a high drought index and early maturing across nine environments. It can complete grain filling phase before the onset of long dry season and has an advantage in its use of the scarce available moisture and the recurrent drought where other crops do not survive in the area.

The candidate genotypes were verified on both station and on-farmers' fields in the 2019/2020 cropping season and evaluated by the national variety releasing technical committee and host farmers. In spite of AMMI selection per environment, farmers evaluated genotypes based on their own selection and attribute criteria and ranked the genotypes. They considered earliness, pod size, pod load, seed boldness and seed yield as an important selection parameter. In the nine environments, farmers preferred G1 as the first rank. At the end, G1 (CH-Acc. 41053) was officially released in 2020 with the name "*Maritu*" for commercial production in eastern Amhara, where recurrent drought is common. G1 (*Maritu*) has shown 29.1% of yield advantage over standard variety G14 (*Fetenech*). Further study has to be supplemented with hybridization and introgression of such kinds of varietal genes with lines potential to high input conditions.

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