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Original Paper

Agronomic Performance and Stability of Kabuli-type Chickpea (Cicer arietinum) Genotypes in Northwestern Ethiopia

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Abstract*— Chickpea (Cicer arietinum) is a versatile pulse crop commonly grown in Ethiopia. The study aimed to develop a stable, high-yielding Kabuli chickpea variety with broad adaptability. The research was conducted over three years across eleven environments, testing thirteen genotypes using a randomized complete block design with three replications. GGE biplot analysis and a multi-trait stability index (MTSI) were used to identify genotypes that are both high-yielding and stable. The combined ANOVA showed significant differences among the genotypes for all traits except seed per pod (SPP). The highest grain yield, 1897.7 kg/ha, was recorded for genotype DZ-2012-CK-0291 (G12), followed by DZ-2012-CK-0306 (G13) with 1797.2 kg/ha. The lowest yield was observed in the variety Acosdubie, with 1023.3 kg/ha. Stability analysis comparing mean performance and stability indicated that genotypes DZ-2012-CK-0291 (G12) and ICCI449XEjerip6-14 (G1) were both high-yielding and stable. Conversely, Acosdubie (G4), Flip-09-76c (G6), and Arerti (G10) were stable but low-yielding. Meanwhile, DZ-2012-CK-0025 (G7), Flip-09-187c (G8), and DZ-2012-CK-0306 (G13) were high-yielding but unstable across environments. The results from the MTSI showed that DZ-2012-CK-0291 (G12) and Flip-93-146-c (G11) were stable across different environments. In conclusion, DZ-2012-CK-0291 (G12) proved to be the most suitable chickpea variety for cultivation in northwestern Ethiopia, based on both yield and stability.

***Keywords*— Chickpea, Dry root rot, Fusarium wilt, GGEbiplot, MTSI**

I. INTRODUCTION

Chickpea (Cicer arietinum) is an annual legume and belongs to the Fabaceae family in botanical classification [1]. It is a highly valuable crop, with multiple uses and wide adaptability. Ethiopia is recognized as a secondary origin of diversity for this crop [2]. It is prominent among legumes for its high protein content and nutritional value, contributing to its widespread popularity worldwide, both in terms of cooking versatility and health benefits. Additionally, it can be grown during the fall and rainy seasons [3]. Chickpeas have a positive impact on increasing soil organic matter and productivity, particularly for cereal crops [4]. In Ethiopia, chickpea is the most important pulse crop next to faba bean and field pea in terms of production and area coverage [5]. For example, in the 2022 cropping season, the total chickpea area harvested was 208, 015 hectares, with a total production of 322,987.1 tons [6]. The Amhara region covers over 49% of the country's chickpea production, with 70% of this being desi-type varieties [6].

Identification of high-yield and market-preferred varieties with adaptation to a wide range of environments is the major goal in crop breeding programs [7]. In Ethiopia, the initial chickpea breeding efforts introduced several varieties intended to benefit farmers, but these varieties were not well-suited to the current climatic conditions, which are affected by both biotic and abiotic factors [8]. Furthermore, the inconsistent performance of genotypes across different environments poses a significant challenge in breeding programs, particularly in crops like chickpeas, which are susceptible to varying environmental conditions. Stability analysis is fundamental for plant breeders, as it enables the identification of superior genotypes that consistently surpass diverse environments, demonstrating wider adaptability [9], [10], [11]. This analysis also mitigates the risks linked to crop failure due to unforeseen environmental shifts, allowing breeders to confidently recommend varieties to farmers [9]. Overall, stability analysis plays a pivotal role in aiding plant breeders to select ideal varieties that perform reliably across various conditions, thereby promoting sustainable and dependable agricultural practices.

In the previous studies, several stability analysis techniques have been employed, including best linear unbiased predictions (BLUP), additive main effects and multiplicative interaction (AMMI) in multi-environment trials, multi-trait stability index (MTSI), and GGE (Genotype Main Effect plus Genotype-by-Environment Interaction) biplot. Those techniques are best for evaluating plant genotypes in diverse environmental conditions and developing elastic genotypes across environments. AMMI is broadly utilized for analyzing genotype-by-environment interactions (GxE) and the stability of crop genotypes by using a single trait [12], [12], [13]. Furthermore, the GGE biplot serves as a better visual aid in analyzing the stability of crop performance across various environments, illustrating interactions between genotypes (G) and genotype × environment (GE) in multi-environment trials [14]. In addition to this, MTSI is used to identify stable genotypes across diverse environments by combining all measured agronomical traits of the genotypes [15], [16], and this method allows researchers to assess how well genotypes maintain desirable characteristics across various conditions, rather than focusing on single traits in isolation [16]. By examining multiple traits simultaneously, such as plant height, pod per plant, seed per pod, primary branch, hundred seed weight, and grain yield, breeders can gain a more comprehensive understanding of genotype stability and make informed decisions regarding breeding strategies or variety recommendations. In general, the graphical method helps researchers understand how different crop varieties perform across various environmental conditions, facilitating the identification of genotypes that exhibit stability and adaptability across diverse growing environments and classifying mega-environments [14]. This approach helps ensure that chickpea genotypes selected for cultivation are robust and reliable across diverse agricultural locations, contributing to sustainable and resilient crop production.

Numerous varieties have been released in Ethiopia through the national research system's efforts. Regional research centers are also working to adapt these varieties to local conditions using different approaches. As a result, only a few varieties have been successfully adopted in certain areas, while farmers, due to their poor performance, have not adopted most of the nationally released varieties. Furthermore, Kabuli-type chickpeas have not been released for the high-potential areas of the Amhara region, despite being suitable for all chickpea-growing regions. This study aimed to identify stable, high-yielding, bolded seed, and disease-resistant Kabuli chickpea genotypes in a high-potential area of the Amhara region, utilizing both GGE biplot analysis and a multi-trait stability index.

II. MATERIALS AND METHODS

A. *Description of the Study Area*

The trial was conducted over three consecutive years (2020-2022) across four locations (Table I), in the Dabat, Gondar Zuria, Dembia, and Takusa districts of Gondar (Fig. 1). The climatic conditions are described in detail and provided in (Fig. 2).

TABLE I. LOCATION

Environment	Location	Year
E1	Takusa Station	2021
E2	Takusa Station	2022
E3	Takusa, On-farm	2022
E4	Dembia	2022
E5	Dembia	2021
E6	Gondar Zuria	2022
E7	Gondar Zuria	2021
E8	Dabat	2022
E9	Dabat	2021
E10	Takusa Station	2020
E11	Takusa On farm	2020

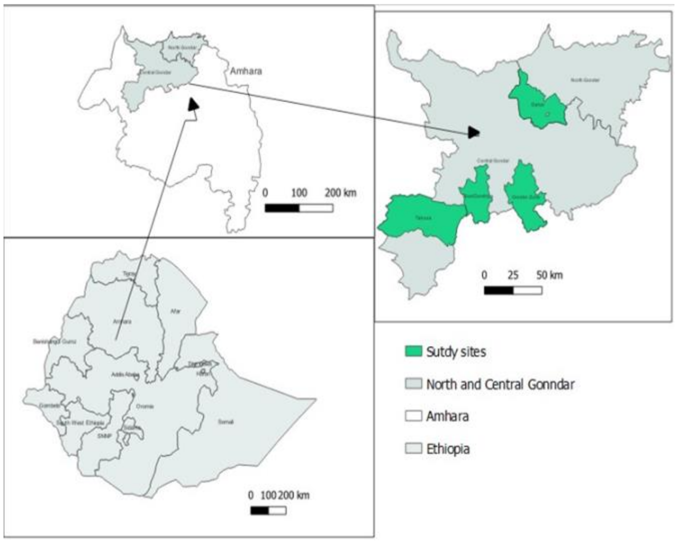


Fig. 1. The map of the study area

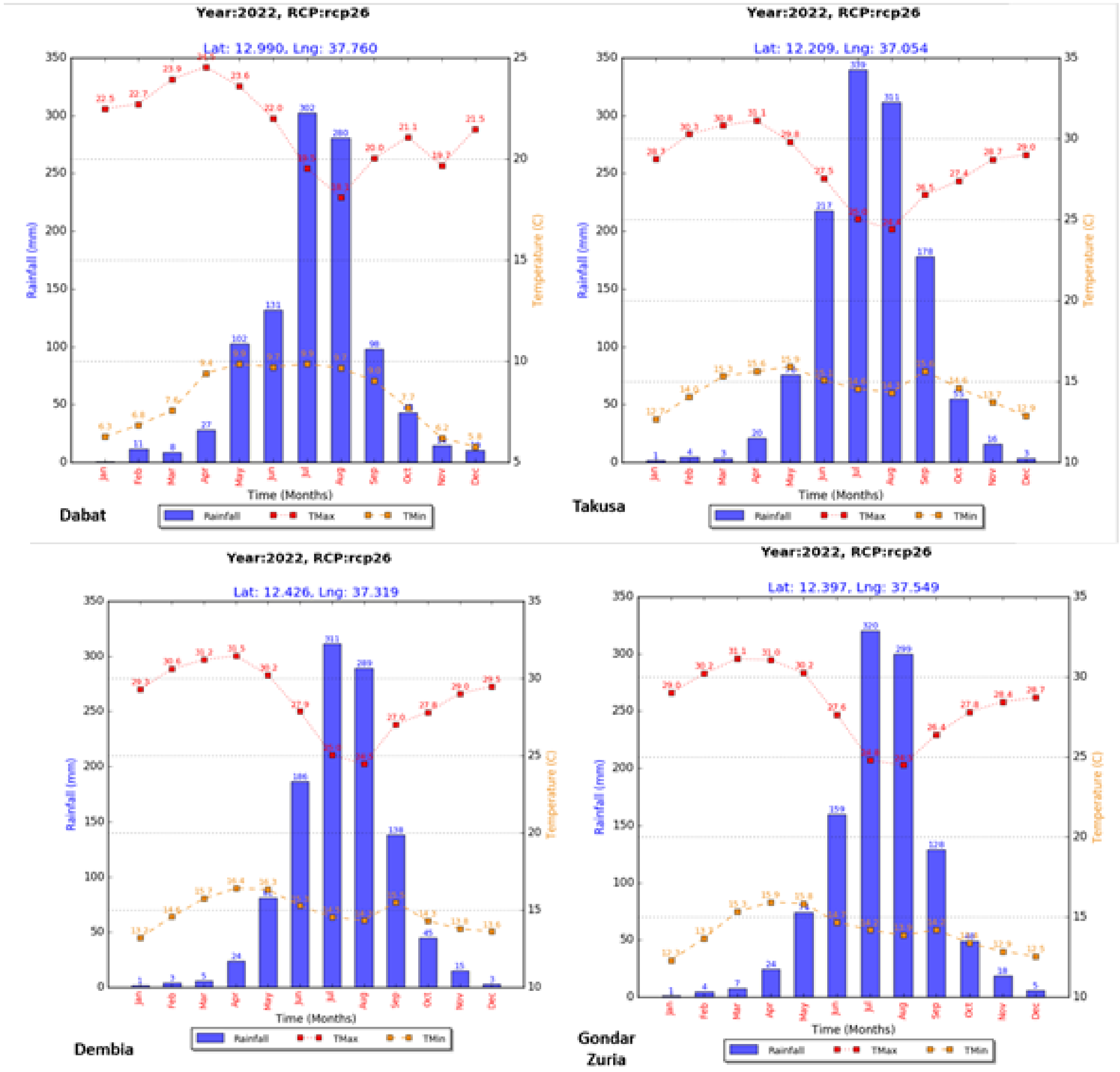


Fig. 2. The climatic conditions of the testing districts over one year, including rainfall, minimum and maximum temperatures, as well as latitude and longitud

B. Experimental Genotypes and Trial Management

The experiment was performed by using thirteen genotypes, including two standard checks (Arerti and Acosdubie), (Table II). It was carried out using a randomized complete block design (RCBD) with three replications. Each plot measured 1.5 m × 5 m (7.5 m²) and consisted of five rows, and all data were collected from the central three rows. Planting distances were set at 1.5 m between replications, 50 cm between plots, 30 cm between rows, and 10 cm between plants. Phonological traits such as days to flowering and days to maturity, as well as metric traits including plant height, pods per plant, seeds per pod, primary branches, hundred seed weight, and grain yield, were recorded. Disease scores for Fusarium wilt and dry root rot were documented during the experiment using a 1 to 9 scale according to [17]. The data were analyzed using R software. Mean separation among genotypes of agronomic performance was done using LSD at a 5% significance level. The stability analysis was conducted using the "metan" package, and correlation was analyzed by using the "corrplot" package.

TABLE II. THE DESCRIPTION OF THE TESTED GENOTYPES WITH THE PEDIGREE

Name of Genotypes	Code	Origin
ICCI449XEjerip6-14	G1	DZARC
DZ-2012-CK-0298	G2	DZARC
DZ-2012-CK-0288	G3	DZARC
Acosdubie	G4	DZARC
Flip-93-93c	G5	DZARC
Flip-09-76c	G6	DZARC
DZ-2012-CK--0025	G7	DZARC
Flip-09-187c	G8	DZARC
Flip-86-5c	G9	DZARC
Arerti	G10	DZARC
Flip-93-146-c	G11	DZARC
DZ-2012-CK-0291	G12	DZARC
DZ-2012-CK-0306	G13	DZARC

Note: * G: code of Genotypes, DZARC: Debrezeit Agricultural Research Center

III. RESULTS AND DISCUSSION

A. Combined Yield and Yield-related Traits of the Genotypes

The combined ANOVA (Table III) showed that there is a significant difference between the genotypes ($p<0.05$) on the measured traits except seed per pod (SPP). The ANOVA of genotype by environment interaction demonstrated that all measured traits were significantly different ($p<0.05$), excluding plant height (PH) and seed per pod (SPP). Among the tested genotypes, the highest grain yield was observed on genotypes DZ-2012-CK-0291 and DZ-2012-CK-0306 (1897.7 kg ha-1 and 1797.27 kg ha-1, respectively), while the lowest yield was observed on the variety Acosdubie (1023.3 kg ha-1). In addition to this, the standard check variety Arerti recorded 1540.3 kg ha-1. The result indicates that the superior genotype DZ-2012-CK-0291 has a 25% and 46% yield advantage over the standard check varieties Arerti and Acosdubie, respectively. In addition, genotype DZ-2012-CK-0306 was the second-best genotype and had 17.1% and 37.6% yield advantages over Arerti and Acosdubie, respectively. A recent study, similar to the findings of [18], revealed that the grain yield of the newly released chickpea varieties beats that of the oldest variety. The results suggested that genetic improvements increased each year.

The size of the seeds is another primary factor used to determine the ideal genotypes in chickpea. The current study demonstrated a significant difference among genotypes, environments, and their interaction for hundred-seed weight. Specifically, Acosdubie and DZ-2012-CK-0025 exhibited the largest seed sizes, weighing 50.6 g and 45.4 g, respectively, while the smallest seed size, 27.8 g, was found in the Arerti variety. In the current study, which is consistent with [19], the largest seed size was found in the Acosdubie variety, while the smallest seed size was observed in the Arerti variety. The number of pods per plant significantly varied among genotypes, across environments, and their interaction, as indicated by ANOVA. Genotype DZ-2012-CK-0291 (G12) recorded the highest number of pods per plant at 38.9, followed by genotype DZ-2012-CK-0306 (13) at 38.5, which is consistent with previous research reports [20], [21], [22], [23]. This result verified that the genotype exhibiting the highest yield also resulted in a greater number of pods per plant. However, the number of seeds per pod does not exhibit significant variation among genotypes, nor does the interaction between genotypes and environment. Additionally, significant differences in days to flowering and maturity were observed among genotypes, across environments, and in their interaction. The variety Arerti took the latest days to flower and maturity, whereas genotype DZ-2012-CK-0025(G7) showed the earliest days to flowering and maturity. According to previous studies, among the kabuli types of chickpea released varieties, Arerti is the late-maturing variety [19], [24], [25]

TABLE III. THE COMBINED RESULT OF YIELD AND YIELD-RELATED PARAMETERS IN ELEVEN ENVIRONMENTS

Genotypes	DF	DM	PH	PPP	SPP	PB	HSW(g)	GYD (kg/ha)
ICCI449XEjerip6-14	45	102	40.9	36.4	1.11	3.33	32.7	1663.4
DZ-2012-CK-0298	48	103	39.8	32.3	1.08	3.14	32.1	1568.7
DZ-2012-CK-0288	51	107	43	30.3	1.08	2.95	37.3	1379.7
Acosdubie	47	102	45.6	26.1	1.07	2.46	50.6	1023.3
Flip-93-93c	48	107	43.2	36	1.1	3.09	31.3	1590.5
Flip-09-76c	54	109	44	33.8	1.14	4.06	29.6	1396.6
DZ-2012-CK--0025	43	102	38.9	25.6	1.12	2.77	45.4	1640.4
Flip-09-187c	48	104	41.6	35.7	1.11	2.81	31.3	1741.1
Flip-86-5c	49	104	41.2	33.1	1.13	3.2	29.1	1323.1
Arerti	57	112	39.6	34.8	1.08	4.4	27.8	1458.9
Flip-93-146-c	49	105	41.7	35.2	1.13	2.97	30.7	1540.3
DZ-2012-CK-0291	47	103	42.2	38.9	1.15	3.02	32.2	1897.7
DZ-2012-CK-0306	48	105	42.5	38.5	1.1	3.13	32.2	1797.2
Mean	49	105	41.8	33.5	1.1	3.1	33.9	1538
CV	6.9	4.67	10.1	27.6	15.5	24	13	27
LSD	1.6	2	2	4.5	0.8	0.37	2.1	203
GEN	**	**	**	**	ns	**	**	**
ENV	**	**	**	**	**	**	**	**
GEN*ENV	**	**	ns	**	ns	**	**	**

Note: *DF-Days to flowering, DM- days to maturity, PH-plant height, PPP-pod per pod, SPP-seed per pod, PB-primary branch, HSW-hundred seed weight, GYD-grain yield, **-significant level at 99% confidence interval, ns-non significant

B. *The Response of the Genotypes for Economically Important Diseases*

Define abbreviations and acronyms the first time they are used in In Ethiopia, Fusarium wilt (Fusarium oxysporum f. sp. ciceris (Foc)) and dry root rot (Rhizoctonia bataticola) are widespread in chickpea fields, as reported by [26]. The current study highlights that in 2021, the genotypes showed a range of responses, from highly resistant (HR) to resistant (RR) for Fusarium wilt, and from highly resistant (HR) to moderately resistant (MR) for dry root rot. During the 2022 cropping season, the genotypes exhibited diverse reactions, with responses ranging from resistant (RR) to moderately susceptible (MS) for Fusarium wilt and from moderately resistant (MR) to susceptible (SS) for dry root rot (Table IV). These results are consistent with previous research by [27] and [28], which emphasize the significant threat posed by these diseases to chickpea production.

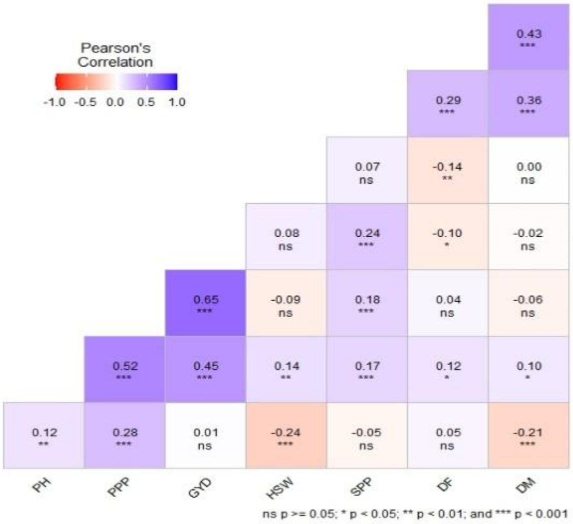
TABLE IV. THE RESPONSE OF GENOTYPES FOR FUSARIUM WILT (FUSARIUM OXYSPORUM F. SP. CICERIS (FOC)), AND DRY ROOT ROT (RHIZOCTONIA BATATICOLA) IN 2021 AND 2022.

Genotype	**Code**	**Year**			
		2021		**2022**	
		Wilt (%)	***DRR (%)***	***Wilt (%)***	***DRR (%)***
DZ-2012-CK-0298	G2	6.0(RR)	8.7(RR)	13.3(MR)	12.7(MR)
DZ-2012-CK-0288	G3	3.6(HR)	3.3(HR)	9.5(RR)	6.0(RR)
24(MONINO)	G4	2.0(HR)	6.0(RR)	10.3(MR)	2.0(HR)
Flip-93-93c	G5	2.3(HR)	13.0(MR)	6.0(RR)	47.7(SS)
Flip-09-76c	G6	4.3(HR)	13.0(MR)	9.3(RR)	20.0(MR)
DZ-2012-CK--0025	G7	4.7(HR)	1.7(HR)	8.7(RR)	13.0(MR)
Flip-09-187c	G8	5.0(HR)	10.0(RR)	10.7(MR)	18.9(MR)
Flip-86-5c	G9	2.0(HR)	9.3(RR)	11.3(MR)	36.7(SS)
Arerti	G10	1.7(HR)	18.0(MR)	18.7(MR)	43.0(SS)
Flip-93-146-c	G11	2.3(HR)	7.3(RR)	5.7(RR)	55.3(SS)
DZ-2012-CK-0291	G12	4.3(HR)	6.7(RR)	8.0(RR)	20(MR)
DZ-2012-CK-0306	G13	1.3(HR)	14.3(RR)	13.0(MR)	32.3(SS)

NOTE: * wilt- Fusarium wilt, DRR-dry root rot, HR - highly resistant, RR-resistance, MR-moderately resistant, MS-moderately susceptible, SS- susceptible

C. *Correlation of Grain Yield and the Yield-Related Traits*

The prison's correlation coefficient indicates the positive and significant correlation between the traits. Among the recorded traits, plant height, pods per plant, and seeds per pod positively respond to grain yield (Fig. 3). Similar results were reported by [23] and [29], in which the number of pods per plant and plant height positively correlated with grain yield. The current findings suggest that the breeder is aiming to enhance overall productivity by prioritizing breeding strategies that increase the number of pods per plant.



Note: *DF-Days to flowering, DM- days to maturity, PH-plant height, PPP-pod per pod, SPP-seed per pod, PB-primary branch, HSW-hundred seed weight, GYD-grain yield

Fig. 3. The prison's correlation coefficient of eight traits for thirteen genotypes in eleven environments

D. *Stability Analysis*

1) Mean Vs Stability, and Which –Won –Where a View of GGE Biplot

The evaluation of stability across multiple environments using the "mean vs. stability" analysis of the genotype plus genotype by environment (GGE) bi-plot is an appropriate approach [30], [31]. A genotype that lies closer to the origin of the AEC plot has a low average yield and low stability, which is less desirable. In contrast, a genotype that is far from the origin but along the x-axis shows a higher average yield, is more stable across environments, and is considered highly productive and stable [32]. The uppermost grain yield was recorded on DZ-2012-CK-0291 (G12), DZ-2012-CK-0306 (G13), Flip-09-187c (G8), and ICCI449XEjerip6-14 (G1), as well as DZ-2012-CK-0298 (G2), while Flip-93-93c (G5) and Flip-93-146-c (G11) exhibited similar to the grand mean (Fig. 4a). In contrast, Acosdubie (G4) and Flip-86-5c (G9) recorded the lowest mean grain yield. The stability indicated by a vertical line signifies high variability across environments, indicated by the blue dots being longer than the others (fig. 4a). In this experiment, DZ-2012-CK-0291 (G12), ICCI449XEjerip6-14 (G1), variety Arerti (G10), Flip-09-76c (G6), and Acosdubie (G4) were the most stable varieties across the environment. On the other hand, DZ-2012-CK-0306 (G13), Flip-09-187c (G8), DZ-2012-CK-0298 (G2), and Flip-93-93c (G5) showed greater variability across the environments. Following the present result, various investigators also found stable chickpea genotypes [33], [34]. Illustrates polygon patterns titled "Which Genotype Won Where/What," emphasizing how different genotypes perform best in specific environments, with a particular emphasis on yield performance [30], [31]. In the current study, genotypes DZ-2012-CK-0291 (G12) demonstrated excellent performance at E3, E8, E9, E10, and E6. Moreover, DZ-2012-CK-0306 (G13) and Flip-09-187c (G8) exhibited superior performance at E1, E2, E7 and E11 (Fig. 4b).

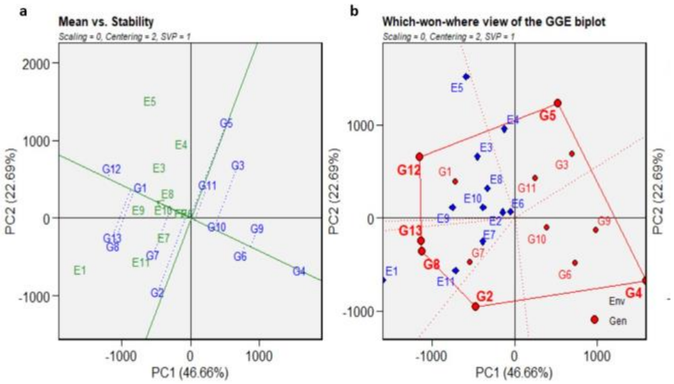


Fig. 4. (a) The GGE biplot's depiction of the "mean vs. stability" pattern. (b) The which–won–where a view of 13 genotypes across 11 environments. The biplot was created based on centering = 2, SVP = 1, and scaling = 0.

2) Ranking Environment and Ranking Genotypes

The genotype ranking biplot, as shown in (Fig. 5a), is used as a valuable tool for identifying superior-performing genotypes in comparison [35]. The biplot shows that the first PCA captured 46.66% of the variability, and the second PCA explained 22.69%, together representing a significant share. Notably, genotypes such as DZ-2012-CK-0291 (G12) and ICCI449XEjerip6-14 (G1) stand out as top candidates due to their proximity to the concentric circle of the plot. The top-performing genotype, located near the concentric circle, exhibits high yield and stability across various environments [36].

Similar to the ideal genotype, the ideal environment is located in the first or near the first concentric circle in the environment-focused biplot, and desirable environments are close to the ideal environments. Environments E9 and E3 were closer to the ideal environment (concentric) than the other tested environments (Fig. 5b), they should be regarded as the most suitable for selecting widely adapted genotypes. E6, E4, E5, E11, and E1 were far from the concentric circle and considered undesirable environments. The ideal environment is representative and has the highest discriminating power [37].

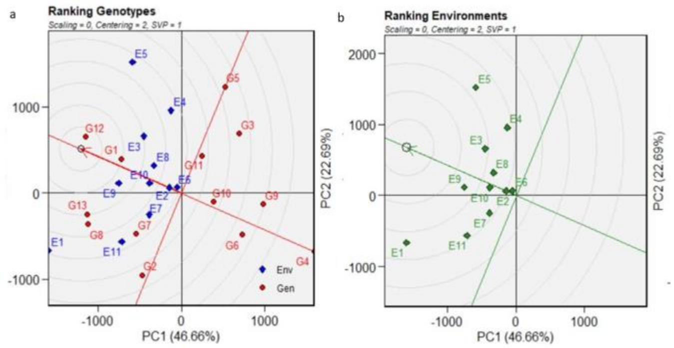


Fig. 5. (a) The ranking genotypes view of 13 genotypes across 11 environments. The biplot was created based on centering = 2, SVP = 1, and scaling = 0. (b) Ranking environment view of 13 genotypes across 11 environments. The biplot was created based on centering = 2, SVP = 1, and scaling = 0.

3) The Multi-Traits Stability Index (MTSI)

For biological experiments, multivariate data are applicable using data from multiple traits to reach better conclusions [38]. The genotypes were categorized into two groups, selected and non-selected, based on the data from the eight measured traits (Fig. 6). As a result, genotypes DZ-2012-CK-0291 (G12) and Flip-93-146-c (G11) were the selected genotypes, which are the most stable genotypes across environments. The current results suggested that the top-performing genotypes could be utilized as parent lines in future hybridization efforts to create chickpea genotypes with improved agronomic performance. Furthermore, the Multi-Trait Stability Index (MTSI) is a stability index used in plant breeding, particularly within the context of the Multi-Trait stability Indexing Value. Based on this, the selected genotypes showed a lower MTSI value, where genotype DZ-2012-CK-0291 (G12) recorded 0.841 and genotype Flip-93-146-c (G11) showed 1.22, and those genotypes were above the cut-off point of the circle in (Fig. 6), and the lowest MTSI value is in (Table V). [39] reported a lower MTSI value, which is consistent with the current study.

TABLE V. . The Value Of The Multi-Triats Stability Index Value (Mtsi) For Thirteen Genotypes Based On Eight Traits Across Eleven Environments.

Genotypes	code	MTSI	Rank
DZ-2012-CK-0291	G12	0.841	1
Flip-93-146-c	G11	1.22	2
Acosdubie	G4	1.4	3
DZ-2012-CK-0298	G2	1.46	4
Flip-86-5c	G9	1.54	5
DZ-2012-CK-0306	G13	1.54	6
Flip-09-187c	G8	1.67	7
ICCI449XEjerip6-14	G1	1.93	8
DZ-2012-CK-0288	G3	2.26	9
DZ-2012-CK--0025	G7	2.36	10
Flip-09-76c	G6	2.43	11
Arerti	G10	3.87	12
Flip-93-93c	G5	4.06	13

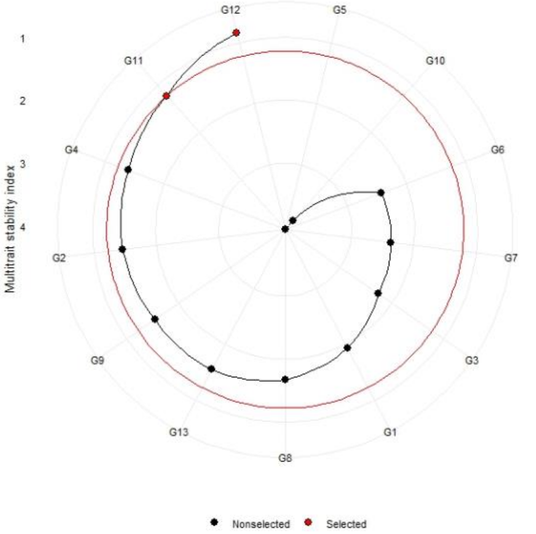


Fig. 6. Genotypes selected by multi-trait stability index applied on the traits of days to flowering (DF), days to maturity (DM), plant height (PH), pod per plant (PPP), seed per pod (SPP), hundred seed weight (HSW), primary branch (PB), and grain yield (GY).

IV. Conclusion And Recommendation

The combined analysis of variance indicated significant differences among the tested genotypes and the genotype-by-environment interaction for most measured parameters, including grain yield and hundred-seed weight. The GGE-biplot analysis for grain yield stability also demonstrated substantial variation among the genotypes in terms of their yield stability across the testing environments. Additionally, the tested genotypes showed considerable variation in their responses to various chickpea diseases and their environmental adaptability over the years. The MTSI analysis across all measured traits and testing environments further confirmed the wide variation among the genotypes. DZ-2012-CK-0291 (G-12), based on their mean grain yield, DZ-2012-CK-0025 (G-7), large seed size, and DZ-2012-CK-0306 (G-13), better reaction for disease and specific adaptability, were selected and recommended for the variety verification trial. The National Variety Release Committee (NVRC) evaluated these genotypes alongside the standard check for grain yield, yield-related traits, disease resistance, and farmer preference. Of these, DZ-2012-CK-0291 (G-12) was officially approved for full release under the local name TANA, intended for major chickpea-producing areas in the Amhara region, which are Takusa, Dembia, Gondar-Zuria, Dabat, and similar regions in Ethiopia

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