

Genotype x Environment Interaction and Yield Stability Analysis of Some Chickpea (*Cicer arietinum* L.) Genotypes across Different Environments in Sudan

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Abstract

Genotype by environment (GE) interaction is considered to be among the major factors limiting the efficiency of breeding programs. Five chickpea genotypes were evaluated to study their adaptability and stability in eight environments of Sudan. The experiments were carried out in randomized complete block design (RCBD) with four replications in four locations in over two years (2017/2018 and 2018/2019). Stability was estimated using additive main effects and multiplicative interaction (AMMI) model. A Combined analysis of variance showed significant effects of genotypes, locations, years and their interactions on seed yield. Mean seed yield ranged between 1.88 and 1.45 t ha⁻¹ for the genotypes FLIP 08-59 C and FLIP 09-187 C, respectively. The genotype FLIP 08-59 C gave the highest average seed yield and out-yielded the two checks, Shiekh Mohamed and Burgeig by 9.5% and 10.1%, respectively. The newly introduced (FLIP 08-59 C) showed non-significant differences in earliness as compared to the other two standard checks resistant to fusarium wilt disease and with good seed weight. The statistical analysis showed that genotype (G), environment (E) and their interaction (GEI) had highly significant ($P \leq 0.001$) effect on seed yield. It also revealed that environmental differences accounted for 90.2% of the total variation. The results of data analysis displayed that the percentages of seed yield by environment, genotype and genotype environment interaction were 90.2%, 3.6% and 6.3%, respectively. The IPCA 1 and IPCA 2 axes (Principal Components) were highly significant ($P \leq 0.001$). The model for seed chickpea yield stability (the Additive Main Effect and Multiplicative Interaction (AMMI) model) showed that the G1 (FLIP 08-59 C) was adapted, high yielding and considered as stable genotype for Gezira, River Nile and Northern States of Sudan. In addition, this genotype is early

flowering with non-significant differences in earliness as compared to the two checks and with good seed weight. Therefore, the above mentioned genotype FLIP 08-59 C could be recommended as commercially stable and high yielding cultivar and/or incorporated as breeding stocks in any future breeding programs aiming to produce high yielding genotypes of chickpea.

Introduction

The chickpea or chick pea (*Cicer arietinum*) is an annual legume, belongs to family Fabaceae, subfamily Faboideae and genus: *Cicer*^[1]. The plant is a self-pollinating diploid ($2n=2x=16$) with a 738 Mbp genome^[2]. At present, the Chickpea has 44 species, of which 35 are perennial, and nine are annual. Chickpea has two market classes—*kabuli* and *desi*—based on seed morphology. The plant grows to 20–50 cm (8–20 in) high and has small, feathery leaves on either side of the stem^[3].

Chickpea (*Cicer arietinum* L.) crop is the second most important edible legume plant grown worldwide. It is rich, with high nutrition elements,, particularly the carbohydrates (27.42 g.), fat (2.59 g.) which includes saturated fat (0.27 g.), non-saturated fat (0.58 g.) and Polyunsaturated, fat (1.16 g.), Protein (8.86 g.), Vitamin [VA 0%,Thiamine (V B1. 10%), (VB2. 5 %) , (VB6. 11%), (VB9. 34 %), (VB12. 0%) (VC.2%), (VE2%),(Vk4%)]. and Minerals like (Calcium 5%), (Iron 22%), (Magnesium14%), (Manganese 49%) (Phosphorus 24%), (Potassium 6%), (Sodium 0%, and (Zinc 16%)^[4]. Therefore, Chickpea has an important role in meeting the protein needs of people in under-developing countries, where people need protein for an adequate and balanced nutrition. However protein and vitamin rich foods should have the priority in human diet^[5]. The crop ranks the third among pulses and accounts for 12% of the world pulses production^[6].

The major contribution (almost 86.73 %) of the world production of chickpea is from Asia, with only 5 % coming from Africa. It is reported that the world area under chickpea cultivation is 13.2 million hectares, with a total production of 11.6 million tons^[7]. The main chickpea producing countries are India, accounting for 67.68 % (7.5 million hectares), and 66.91 % (6.54 million ton) of production followed by Pakistan with 9.75 % (1.08 million hectares and 0.741 million ton. Other chickpea producing countries are Iran, Turkey, Myanmar, Australia, Ethiopia, Canada, Mexico, Syria, USA, Spain, Tanzania and Eritrea^[8].

In Sudan chickpea is traditionally grown as a winter crop in the northern part, however, its production has expanded recently to the central clay plain of central Sudan. The growing season is restricted to a short period of time by the high temperatures prevailing at the beginning and at the end of the season. Chickpea yield in Sudan varies from 0.83 to 2.8 t/ha, depending on weather conditions genotype and cultural practices^[9]. In Sudan it is an important cash crop which faces strong competition from other winter legume crops, mainly faba bean in its traditional area of production in northern Sudan. In recent years, chickpea area has increased steadily in central Sudan, especially in Gezira scheme and New Half in Eastern Sudan^[9].

Environmental factors, such as soil moisture, sowing time, fertility, temperature and day length have great influences during the various stages of plant growth^[10]. Nevertheless, the interaction analysis of G×E is important to identify the superior varieties and their adaptation to and stability in diverse agro-ecological zones^[11]. However, G×E interaction is defined as a variable phenotypic expression of genotypes in response to environmental changes^[12]. This can be performed by the evaluation of genotypes in different environments.

The differences in genotype stability and adaptability to environment can be qualitatively assessed using

the biplot graphical representation that scatters the genotypes according to their principal component values ^[13,14]. To explore the effect of genotype and genotype × environment interaction on grain yield, GGE Bi-plot method is used. Both, AMMI and GGE biplot have frequently been used for explaining GE interaction and to determine high yielding and widely adapted cultivars. These two statistical analyses (AMMI and GGE) have broader relevance for agricultural researchers because they pertain to any two-way data matrices, and such data emerge from many kinds of experiments ^[15].

Obviously, low yield is a major problem in the area of Chickpea production. It is caused attributed to several complexes and interacting factors. Therefore, the main objectives of this study are (i) To evaluate the performance of some introduced chickpea genotypes for seed yield and yield related traits under difference environmental conditions in Sudan. (ii) To identify early flowering and fusarium wilt disease resistant genotypes. (iii) To determine the effects of G×E interaction on yield among some chickpea genotypes in order to identify the stable and high yielding genotypes through multiplication yield trials.

Materials and Methods

The research was conducted the 2017/18 and 2018/19 in four locations under irrigation system. Three studies were conducted in northern region of Sudan. One study was conducted at Shendi Research Station Farm (latitude 16° 41' – 16° 45' N, longitude 33° 25' - 33° 29'E) in the River Nile State. The second was conducted at Hudeiba Research Station Farm (latitude 17° 33' -17° 37'N, longitude 33° 56' - 33° 59'E) with an average annual rainfall of 74 mm/ann., while the third study was carried out at Merowe locality, in Research Station Farm, (Latitude: 18° 27' - 18° 31' N, Longitude: 31° 49' -31° 53' E, Elevation of 258 meters above the sea level). The three Research Station Farms are located in a desert climatic zone, which is characterized by dry and hot climate. In this region, during the winter, temperatures are warm at the day and cool at night, where the temperature can reach to 0°C. The rest of the year, from May to September is very hot, and the temperature could reach to 40 °C, and sometimes could reach up to 50/52°C. Moreover, the wind can raise sandstorms at any time of the year [Sudan Metrology 2022][^{16]} 12. The soil in this region is mostly sand, which is poor due to low nutrient elements and organic matter. except the soil along the river Nile which is mostly loamy clay. The fourth study location was Wad Medani, Gezira State, Gezira Research Station Farm (GRSF) which is located in the central clay plain of Sudan at latitude of 14° 24' N, 14° 36' N, longitude of 33° 29' - 33° 35' E and elevation of 407 meters above the sea level. Where the soil is heavy cracking clay, alkaline (clay 58%, pH 8.3, organic matter 0.02, nitrogen 0.25, phosphorus 0.06 and potash 3.0%). However, the four locations represent different agro-ecological regions for growing chickpea in Sudan.

Three chickpea genotypes were obtained from the advanced materials of the national chickpea breeding program in the Agricultural Research Corporation (ARC)-Sudan. Moreover, two released chickpea cultivars (Shiekh Mohamed and Burgeig) were used in this study as checks (Table 1).

Across all growing seasons and locations, the land was well prepared using disc plowing, disc-harrowing, leveling and ridging. The experiments were arranged in a Randomized Complete Block Design (RCBD) with four replicates in all locations. Each genotype was planted in a separate plot composed of five ridges; each of 5 m in length, with plant-to-plant and row-to-row distance of 10 and 60 cm, respectively. Sowing was done in the second week of November during the two winter seasons. Frequent irrigation was carried out at 14-16 days intervals to avoid water stress. The experimental plots were treated with a starter dose of nitrogen in the form of urea at the rate of 43kg N/ha before the fourth irrigation. Two hand weeding was done. Seed yield was assessed from a net area of 8.28 m² (3 rows x

4.6 m length x 0.6 m).

During the two seasons, data pertaining the Days to 50% flowering [were registered as days from sowing to the date of flowering, when about 50% of the plants bear at least one flower]. Hundred-seed weight (g.) [calculated by 100 seed samples which were randomly selected from each plot], seeds weight [seed weighed using a sensitive balance. The latter parameter was recorded after harvesting, threshing and winnowing (in g or kg)]. The seed yield [was weighed using electronic balance on net plot basis and later converted into t/ha. for each genotype].

The five chickpea genotypes were screened for resistance to Fusarium wilt disease in an infested plot at Gezira Research Station Farm during the winter season of 2018/2019, the evaluated for Fusarium wilt disease was done at three stages during the crop cycle (seedling, flowering and pod setting stages). Where disease incidence (%)=(number of wilted plants/ total number of plants) x 100 was determined, and the level of resistance and susceptibility of each tested genotype was determined by using rating scale, with some modifications, where R = 0-20% wilted plants, MR = 21-40% wilted plant, S=41-80% wilted plants and HS = \geq 80% wilted plants. Furthermore, the wilted plants were checked for vascular discoloration symptoms and re-isolation to confirm the disease was Fusarium wilt caused by fungus *Fusarium oxysporum* f. sp. *Ciceris* [16,17].

The collected data were statistically analyzed using the GenStat 12th edition [18]. The analysis of variance (ANOVA) for measuring all the studied characters was carried out according to the procedure described by [19].

To determine the performance, stability and genotypic superiority across environments or at specific environment, additive main effect and multiplicative interaction (AMMI) model was used [20]. AMMI stability value (ASV) was calculated for each genotype according to the relative contribution of IPCA1 and IPCA2 to the interaction sum square (SS) following the method proposed by [21]. According to ASV, a genotype with lower ASV score is regarded as more stable. To combine both mean seed yield and stability index in a single criterion, the genotype selection index (GSI) was calculated for each genotype based on the rank of mean seed yield of genotypes across environments and rank of AMMI stability value as proposed by. Similar to ASV, genotype with lower GSI value is regarded as more adapted. Also the GGE biplot model [19] was followed to test the seed yield stability performance for the three tested chickpea genotypes plus the two checks [22].

Results and Discussions

The results of data analysis for yield and yield related traits in different locations are presented in the tables 2, 3,4,5,6,7,8,9 and 10 and figures 1 and 2.

Table 1. Accession no., pedigree and origin of the five chickpea genotypes used in this study.

No.	Accession no.	Genetic background (pedigree)	Origin
1	FLIP 08-59 C	X02TH3/FLIP 98-28C X FLIP-97-102C	ICARDA
2	FLIP 09-182 C	X06TH53/FLIP03-128C X FLIP01-25C	ICARDA
3	FLIP 09-187 C	X06TH53/FLIP03-128C X FLIP01-25C	ICARDA
4	Shiekh Mohamed (check)	X99TH62/(FLIP932CxFLIP 94-115C)	Released commercial cultivar
5	Burgeig (check)	ICCC32/(K4/Chafa)	Released commercial cultivar

Considering table 2, presents the analysis of mean seed yield of the genotypes across the eight environments showing significant effects of genotype, location, year and their interactions on seed yield. The highly significant differences among the tested genotypes indicated that those genotypes which have phenotypic variation and genetic diversity showed effectiveness of selection for the development of new

Table 2. Seed yield (t ha⁻¹) of the five chickpea genotypes tested across eight environments (2018/2019)..

Genotypes	2017/18					2018/19				
	MER	GEZ	SH	HU	Mean	MER	GEZ	SH	HU	Mean
FLIP 08-59 C	1.93	2.34	1.41	0.70	1.60	3.39	2.20	1.65	1.40	2.16
FLIP 09-182 C	2.04	2.31	0.71	0.44	1.38	2.56	1.87	1.34	0.93	1.67
FLIP 09-187 C	2.14	1.96	0.82	0.48	1.35	2.79	1.59	1.03	0.78	1.55
Shiekh Mohamed	2.45	2.02	0.89	0.71	1.52	3.41	1.79	1.06	1.25	1.88
Burgeig	2.09	1.67	1.51	0.40	1.41	3.41	1.90	1.21	1.32	1.96
Mean	2.13	2.06	1.07	0.55	1.45	3.11	1.87	1.26	1.14	1.84
S.E ± Years (Y)	0.036***									
S.E ± Locations (L)	0.051***									
S.E ± Genotypes (G)	0.042**									
S.E ± (YxLxG) Interaction	0.071***									
C.V (%)	14.4									

MER = Merowe, GEZ = Gezira, SH = Shendi and HU = Hudeiba

and * = Significant at 0.01 and 0.001 levels of probability, respectively.

genetic cultivars possessing improved traits. For the average seed yield across the eight environments, the genotype FLIP 08-59 C showed the highest average seed yield and out-yielded the checks, Shiekh Mohamed and Burgeig genotypes in the 6th- and 5th- environments, respectively. More-specifically, it out-yielded the check Shiekh Mohamed, in six environments by an average of 20.4% and the second check Burgeig in five environments by an average of 17.4%.

Average seed yield of the five chickpea genotypes across the eight environments varied from 1.45 to 1.88 ton/ha. This indicates the wide variability for yield potential among the chickpea genotypes. The three locations, Merowe, Gezira and Shendi, gave the highest seed yield of 2.62, 1.96 and 1.16 ton/ha, respectively. On the other hand, the Hudeiba site recorded the lowest seed yield (0.84 ton/ha). Across all sites, the highest mean seed yield was recorded by the genotype FLIP 08-59, C (1.88 ton/ha) followed by the check Shiekh Mohamed (1.70 ton/ha).

The genotype FLIP 08-59 C produced the higher seed yield compared to the check Burgeig at Medani and Hudeiba sites. The same genotype gave significantly higher seed yield than the check Shiekh Mohamed at Shendi site. At Merowe site, the genotype FLIP 08 -59 C produced a comparable seed yield to the check Burgeig.

At Gezira site, the genotype FLIP 08-59 C produced the highest seed yield and exceeded the two checks, Burgeig and Shiekh Mohamed by 21.1% and 15.8%, respectively. Whereas at Shendi site, the genotype FLIP 08-59 C recorded the highest yield and out-yielded the two checks, Shiekh Mohamed and Burgeig by 35.9% and 11.1%, respectively. At Hudeiba site, also the genotype FLIP 08-59 produced the higher seed yield and exceeded the two checks Burgeig and Shiekh Mohamed by 18.0% and 6.6%, respectively.

The genotype FLIP 09-182 C at Gezira site gave better seed yield and out – yield the two checks Shiekh Mohamed and Burgeig by 8.6% and 14.3%, respectively.

The above table 3 reflects the combined analysis of variance showing high significant differences ($P \leq 0.001$) among the years, location, genotypes, genotype x year, genotype x location, and genotype x year x

Table 3. Seed yield (t ha⁻¹) of the five chickpea genotypes evaluated across four locations (2018/2019).

Source of variation	DF	Sum of Squares (SS)	Mean of Squares (MS)
Year (Season)	1	6.20	6.20***
Location	3	77.45	25.82***
Year x Location	3	7.69	2.56***
Residual	24	2.45	0.10
Genotypes	4	3.60	0.90***
Year x Genotypes	4	0.82	0.21**
Location x Genotype	12	3.13	0.26***
Year x Location x Genotypes	12	2.38	0.20***
Residual	96	5.43	0.06
Total	159	109.15	

and * Significant at 0.01 and 0.001 levels of probability, respectively.

Table 4. Days to 50% flowering of five chickpea genotypes evaluated across eight environments (2018/2019).

Genotypes	2017/18					2018/19				
	MER	GEZ	SH	HU	Mean	MER	GEZ	SH	HU	Mean
FLIP 08-59 C	47	42	30	48	42	45	39	50	47	45
FLIP 09-182 C	57	48	31	55	48	52	44	52	46	48
FLIP 09-187 C	48	41	31	48	42	43	44	52	48	47
Shiekh Mohamed	40	41	31	46	39	36	37	50	45	42
Burgeig	46	46	31	47	42	40	40	51	46	44
Mean	48	43	31	49	43	43	41	51	46	45
S.E ± Year (Y)	0.27***									
S.E ± Locations (L)	0.382***									
S.E ± Genotypes (G)	0.408***									
S.E ± (YxLxG) Interaction	1.165**									
C.V (%)	5.2									

MER = Merowe, GEZ = Gezira, SH = Shendi and HU = Hudeiba.

and * = Significant at 0.01 and 0.001 levels of probability, respectively.

location interaction for all studied characters including seed yield Table 4, presents the mean days to 50% flowering of genotypes across eight environments displaying the effect of location and interaction between the genotypes. Year and location were found to be highly significant. However, across all sites, there were highly significant differences among genotypes in days to 50% flowering with over all mean of days to 50% flowering, ranging between 39 and 48 days in season 2017/18, whereas ranging between 48 and 42 days in 2018/19. The genotype FLIP 08-59 C was the earliest to reach 50% flowering but with

Table 5. 100-seed weight (g) of five chickpea genotypes evaluated across eight environments (2018/2019).

Genotypes	2017/18					2018/19				
	MER	GEZ	SH	HU	Mean	MER	GEZ	SH	HU	Mean
FLIP 08-59 C	22	18	18	19	19	22	22	27	22	23
FLIP 09-182 C	34	31	31	28	31	34	39	30	34	34
FLIP 09-187 C	29	29	27	28	28	30	31	28	27	29
Shiekh Mohamed	25	25	21	24	24	23	24	23	22	23
Burgeig	18	19	19	18	19	21	22	25	20	22
Mean	26	24	23	24	24	26	28	27	25	26
S.E ± Year (Y)	0.3***									
S.E ± Locations (L)	0.5*									
S.E ± Genotypes (G)	0.5***									
S.E ± (YxL) Interaction)	0.7 ^{n.s}									
C.V (%)	12.1									

MER = Merowe, GEZ = Gezira, SH = Shendi and HU = Hudeiba

*and *** = Significant at 0.05 and 0.001 levels of probability, respectively.

n.s=not significant at 0.05 level of probability.

non-significant differences as compared to the two checks. Table 5, shows the mean 100-seed weight (g) of genotypes across the eight environments. Over all sites, there were highly significant differences among genotypes in 100-seed weight ($P \leq 0.001$). The overall mean of 100-seed weight (g) ranged between 19 and 31g, in season 2017/18, whereas, in season 2018/19 the genotype FLIP 09-182 C recorded the heaviest 100-seeds weight (34 g), while the check Burgeig produced the lowest value of 22 g.

Regarding the evaluation of Fusarium wilt disease (*Fusarium oxysporum* f.sp. *ciceris*), the results summarized in table 6 presenting the five chickpea genotypes under disease conditions at Gezira Research Station Farm during the winter of 2018/2019 showed varied resistance to Fusarium wilt at seedling stage and the percent of the infection ranged between 17.2 to 26.5% which is ranked under the resistance level (Resistance to Moderately resistance) of the used scale for the disease. The highest disease incidence was recorded by variety Burgeig (26.5%) followed by genotype FLIP 09-187 C (25.4%) and variety Shiekh Mohamed (23.0%). The lowest disease incidence (17.2%) was scored by the genotype FLIP 08-59 C.

The study showed significant differences among the genotypes on fusarium wilt incidence at flowering and podding stages which ranged from 11.3 to 22.2% and 24.4 to 39.8%, From the above results, the

genotype FLIP 08–59 C was found to be the most resistant to Fusarium wilt disease among all the tested genotypes.

Regarding the Yield Stability, analysis of variance the study showed high significant differences among

Table 6. Fusarium wilt incidence (%) at seedling, flowering and pod setting stages at Gezira Research Station Farm during the winter season (2018/2019).

Genotypes	Seedling stage	Flowering stage	Pod setting stage	Level of resistance
FLIP 08-59 C	(8.8) 17.24 ^a	(5.5) 11.3 ^b	(15.25) 24.4 ^b	R
FLIP 09-182 C	(13.8) 21.34 ^a	(18.0) 22.2 ^a	(41.75) 39.8 ^b	MR
FLIP 09-187 C	(19.2) 25.4 ^a	(10.0) 18.1 ^{ab}	(35.5) 36.3 ^{ab}	MR
Shiekh Mohamed	(15.5) 23.0 ^a	(12.5) 20.5 ^{ab}	(35) 36.1 ^{ab}	MR
Burgeig	(20.5) 26.5 ^a	(9.0) 17.1 ^{ab}	(34.25) 35.6 ^{ab}	MR
Mean	22.7	17.8	34.4	
S.E ±	3.24 ^{n.s}	3.52*	4.80*	
C.V (%)	28.6	39.5	28.1	

* = Significant at 0.05 level of probability and ns = not significant at 0.05 level of probability.

The actual data between parenthesis.

R = Resistance and MR = Moderately resistance.

Table 7. Analysis of variance for stability for seed yield (t ha⁻¹) of five chickpea genotypes in the eight environments (2018/2019).

Source of variation	DF	Sum of Squares (SS)	Mean of Squares (MS)
Environment (E)	7	91.37	13.05***
Environment (Linear)	1	91.37	91.37***
Deviations	6	0	0
Residual	24	2.462	0.103
Genotypes (G)	4	3.5937	0.8984***
EG interaction	28	6.3420	0.2265***
EG interaction (Linear)	4	0.3541	0.0885 ^{n.s}
Pooled Deviations	24	5.9879	0.2495***
Pooled error	96	5.4365	0.0566
Total	159	109.20	

Probability of greater chi-square for testing homogeneity error variances= 0.0336

Error variances are heterogeneous at 0.05 probability.

*** = Significant at 0.001 level of probability.

n.s: not significant at 0.05 level of probability.

the tested genotypes (G) for seed yield, environments (E) and their interactions (GEI) (Table 7). The highly significant differences observed among environments indicated that these genotypes were evaluated under diverse seasons and locations. The mean square of G x E interaction also showed high significant differences for most of the traits indicating the effect of the environment and genotype interaction. The mean square of G x E (linear) interaction was not significant.

Stability models were followed to carry out the seed yield stability performance for the three tested chickpea genotypes against the two checks. These were the Additive Main Effect and Multiplicative Interaction GGE biplot model [23] and (AMMI) model [24].

Table 8. ANOVA of additive main effects and multiplicative interaction (AMMI) analysis for seed yield (t/ ha) of five chickpea genotypes evaluated across eight environments (2018/2019).

Source	DF	Sum of Squares (SS)	Mean of Squares (MS)	Percent explained
Total	159	109.15	0.686	
Treatments	39	101.26	2.596***	
Genotypes	4	3.6	0.900***	3.6
Environments	7	91.34	13.048***	90.20
Block	24	2.45	0.102*	
Interactions	28	6.33	0.226***	6.3
IPCA 1	10	3.72	0.372***	58.8
IPCA 2	8	2.1	0.262***	33.2
Residuals	10	0.51	0.051 ^{n.s}	
Error	96	5.43	0.057	

*and *** = Significant at 0.05 and 0.001 levels of probability, respectively.

n.s= not significant at 0.05 level of probability.

Table 8, reflects the Analysis of variance (ANOVA) of AMMI showing the chickpea seed yield was high significantly ($P \leq 0.001$) affected by environment (E), genotype (G) and their interaction (GEI). Over all sites, the effect of the environment was significantly, and it was about 90.2% of the total sum of the square, indicating that the environments were diverse. On the other hand, the genotypic effect was explained by significant, but small portion of 3.6% and the (G x E) by (6.3%). The large environmental contribution effect indicated that the maximum variation for the genotypes performance was due to the environmental differences. The significance of the interaction component was 6.3% of the total sum of the square, indicating that the best genotype in one environment is not necessarily the best in another. Therefore, when recommending promising genotypes to an environment we need to take into consider their adaptability and stability.

For the GGE biplot analysis, the GGE refers to the genotype main effect (G) and the genotype x environment interaction (GE) which are the most important sources of variation for a genotype evaluation in multi environmental trials [25]. The presence of genotype x environment interaction (GEI) was clearly demonstrated by the AMMI model. When the interaction was partitioned among the first interactions principal component axis (IPCA), they were found to be significant in the assessment. The first principal component (IPCA1) accounted for (58.8%) of the variation caused by interaction, and the second principal component (IPCA2) accounted for (33.2%) of this variation. These are in agreement with the finding

Table 9. Estimates of stability parameters for yield (t/ha) of five chickpea genotypes tested across eight environments (2018/2019).

Genotypes	Mean	Rank (RSY)*	IPCA		ASV		GSI
			IPCA1	IPCA2	Value	Rank (RASV)	
FLIP 08-59 C (G1)	1.88	1	0.22802	0.41499	0.58	2	6
FLIP 09-182 C (G2)	1.53	4	-0.46955	0.37169	0.91	4	5
FLIP 09-187 C (G3)	1.45	5	-0.57229	-0.24218	1.04	5	7
Shiekh Mohamed (G4)	1.70	2	0.16414	-0.02052	0.29	1	4
Burgeig (G5)	1.69	3	0.38015	0.01243	0.67	3	8

Rank (RSY)*=rank in seed yield, IPCA 1 and IPCA 2=interaction principal component axis 1 and 2, ASV =AMMI stability value, RASV = rank of AMMI stability value, GSI = genotype selection index.

of one of the researchers [26]. who recommended that the most accurate model for AMMI can be predicted using the first principal components (IPCA).

Table 9 shows the estimates of stability parameters for yield (t/ha) of five chickpea genotypes in eight environments. AMMI stability values (ASV) revealed variations in yield stability among the 5 chickpea genotypes. This result agrees with the results obtained by one of the studies [27]. However stability of a variety is defined as one with ASV value close to zero. Consequently, the G1 (FLIP 08-59C) with ASV value of 0.58 is the most stable after the G4 (Shiekh Mohamed) with ASV value of 0.29. While other genotypes, FLIP 09-182 C, FLIP 09-187 C and check Burgeig are the least stable.

Genotype Selection Index (GSI) measure is essential for quantifying and ranking genotypes according to their yield stability. The one with high seed yield and least (GSI) is considered as the most stable [28].

Table 10. The best four genotypes in each environment for seed yield according to AMMI selections.

No.	Environments	Estimated yield (t/ha)	Score	Best four genotypes			
				1 st	2 nd	3 rd	4 th
1	Medani 2017	2.061	0.5916	G2	G1	G4	G3
2	Shendi 2018	1.258	0.204	G1	G2	G5	G4
3	Hudeiba 2017	0.546	0.1735	G4	G1	G2	G5
4	Merowe 2017	2.129	0.1352	G4	G3	G1	G5
5	Medani 2018	1.873	0.0764	G1	G5	G2	G4
6	Hudeiba 2018	1.135	-0.2124	G1	G5	G4	G3
7	Shendi 2017	1.069	-0.4351	G1	G5	G4	G2
8	Merowe 2018	3.114	-0.5333	G5	G4	G1	G3

Table 10.presents the best four genotypes in each environment for seed yield. These are the G1, (FLIP 08-59C), and G4 (Shiekh Mohamed), respectively

Based on the GSI, the most desirable genotypes for selection of both stability and high seed yielding were the genotypes G4 (Shiekh Mohamed), G1 (FLIP 08-59C) and G2 (FLIP 09-182 C), respectively.

For GGE biplot analysis model, the GGE analysis showed 58.81% and 33.16 % of total variation in the data matrix of GGE respectively, and thus they are accounted for 91.97 % of GGE together (Figure 1).

According to GGE analysis, the genotypes with PC1 scores is close to zero expressed general adaptation, whereas the larger scores are for more specific adaptation to particular environments [29]. Figures1 and 2 showed AMMI and GGE biplots of seed yield of 5 chickpea genotypes across eight environments. The G1 (FLIP 08-59C) was the most stable and best genotypes across the different environments in Sudan.

Conclusion and Recommendations

The main effects of genotype and environment as well as the $G \times E$ were highly significant and the environment caused the most variations in seed yield.

FLIP 08-59 C is found to be an early flowering genotype compared to the two checks. It lso showed good 100 -seed weight and resistant to Fusarium wilt disease, which is considered among the major biotic stresses to the production of chickpea in Sudan.

FLIP 08-59 C produced higher seed yield than all other genotypes overall the environments and performed better at most of the places. It exceeded the two standard checks, Shiekh Mohamed and Burgeig by 9.5% and 10.1%, respectively.

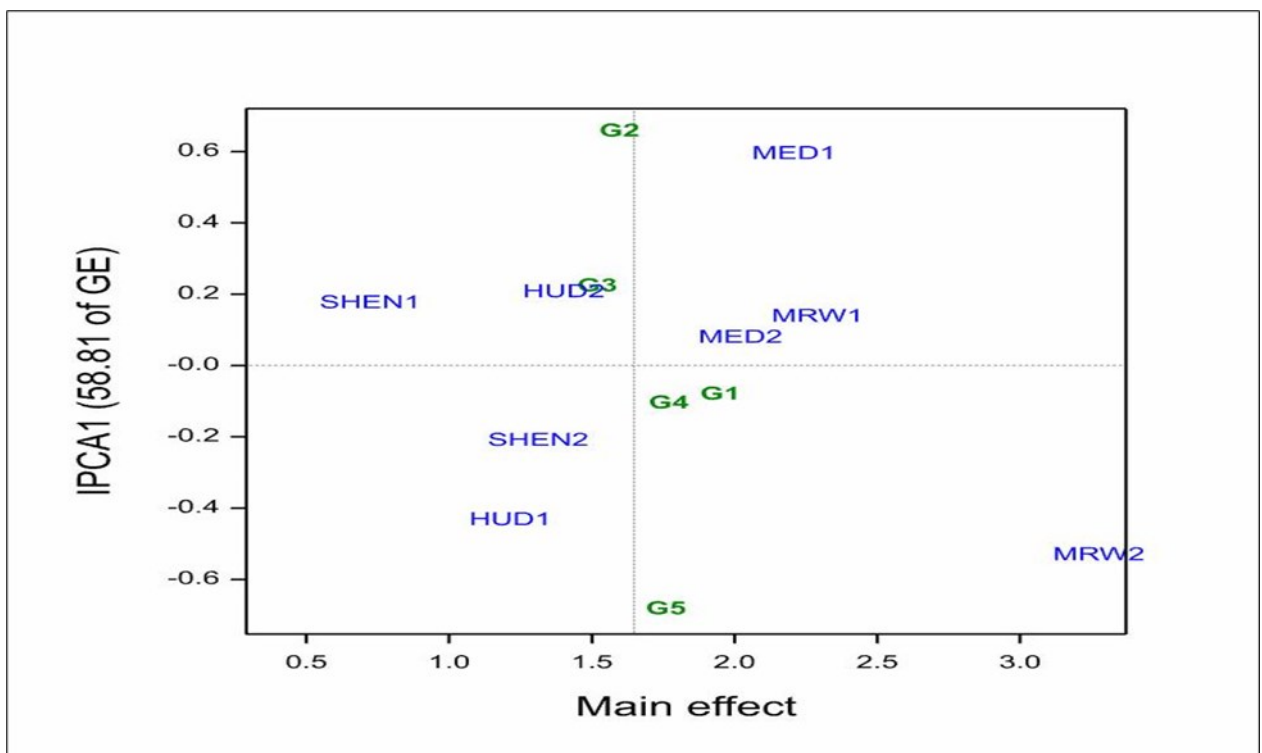


Figure 1. AMMI 1 biplot of first interaction principal component axis (IPCA1) for mean seed yield t/ha.

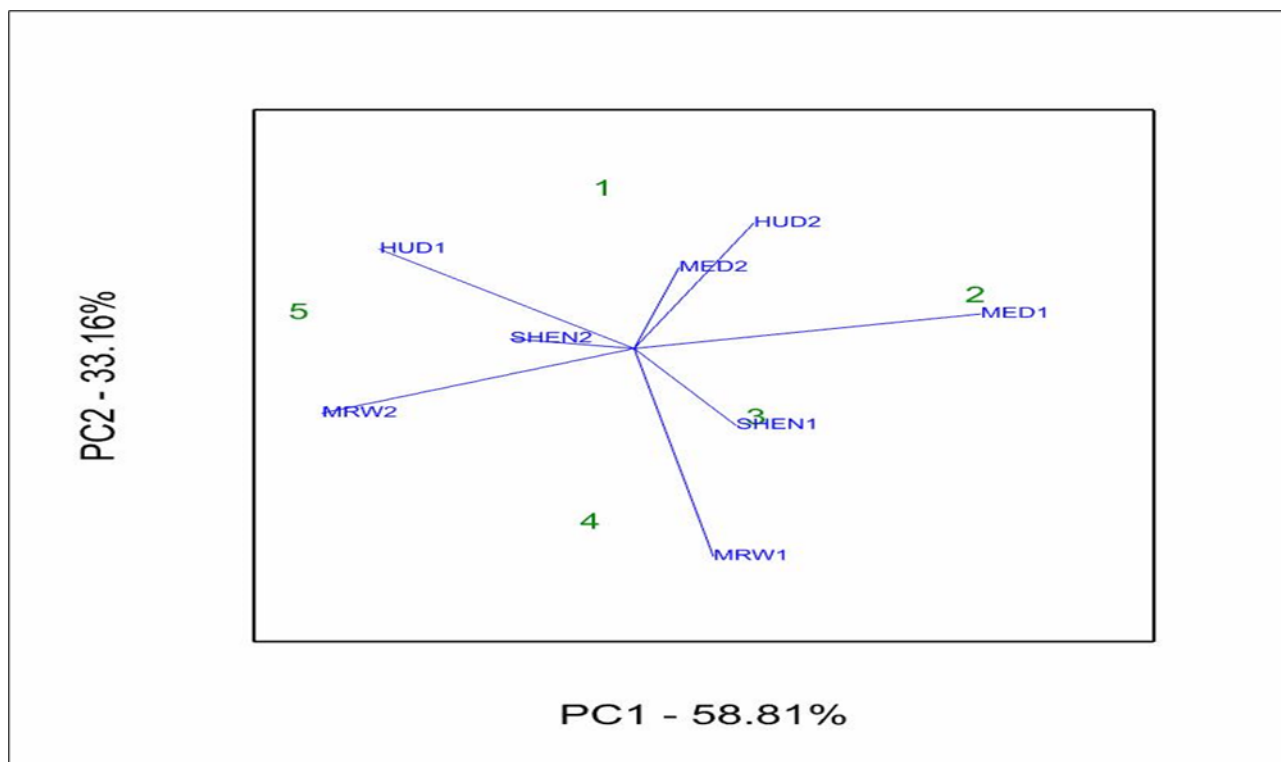


Figure 2. AMMI 2 biplot of the first interaction principal component axis (IPCA1) versus the second interaction principal component axis (IPCA2) for seed yield t/ha.

FLIP 08-59 C was found to be comparatively stable as its performance was hardly affected by the G x E interaction and thus would perform well across a wide range of environments. This genotype also was found to be more adapted across the different tested environments. Therefore, the genotype FLIP 08-59 C is recommended for release as a cultivar to be grown at Gezira, River Nile and Northern states of Sudan. Also may be used in future in the breeding program for the development of high yielding and stable genotypes.

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