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Yield Adaptability and Stability in Chickpea Based on AMMI, Eberhart and Russell's, Lin and Binns's, and WAASB Models

Osmar Artiaga [1], Carlos Roberto Spehar [1], Nathalia Ramos Queiroz [1], Giovani Olegário Silva [2], Fabio Akiyoshi Suinaga [2,*] and Warley Marcos Nascimento [2]

[1] Faculdade de Agronomia e Medicina Veterinária (FAV), Campus Darcy Ribeiro, Universidade de Brasília (UnB), ICC-Sul, Asa Norte, Brasília 70910-900, DF, Brazil; osmar.artiaga@hotmail.com (O.A.); spehar@unb.br (C.R.S.); nrq.queiroz@gmail.com (N.R.Q.)

[2] Embrapa Hortaliças (CNPH), Rodovia BR 060 Km 9—Samambaia Norte, Brasília 70351-970, DF, Brazil; giovani.olegario@embrapa.br (G.O.S.); warley.nascimento@embrapa.br (W.M.N.)

* Correspondence: fabio.suinaga@embrapa.br

Abstract

Chickpeas are a pulse crop that originated in Eurasia and are a source of protein for many people. The objective of this research is to select stable, high-yielding chickpea genotypes using uni- and multivariate methods of adaptability and stability analysis. Fifteen genotypes were tested in the 2020 and 2021 agricultural years. The experimental design was a completely randomized block design with three replications. The collected data were yield (kg/ha) values, and the stability analyses were performed using Eberhart and Russell's, Lin and Binns's modified by Carneiro's, additive main effects and multiplicative interaction (AMMI), and weighted average of absolute scores (WAASB) methods. The average sum of ranks (ASR) was then calculated by ranking genotypes according to their yield and stability indices. The AMMI analysis of variance showed significant effects ($p < 0.05$) for environments, genotypes, and the interaction between genotypes and environments. From AMMI, the first three principal components (PCs) had significant effects, and the cumulative variance on the PC1 and PC2 axes was 86%. FLIP02-23C, FLIP03-109C, and Jamu 96 had the lowest ASR, indicating that these genotypes are the most stable and productive chickpea genotypes. According to AMMI2, genotypes FLIP03-109C, FLIP03-35C, FLIP02-23C, and FLIP06-155C could be adapted to irrigated environments.

Keywords: pulses; *Cicer arietinum* L.; breeding

1. Introduction

The word "pulse" originates from the Latin "puls", which means thick soup or thick slurry [1]. In agronomy, pulses refer to the dry, edible seeds of leguminous plants [2]. Crop pulses include bambara beans, dry beans, faba beans, chickpeas, cowpeas, dry peas, pigeon peas, lentils, lupins, and vetches [3]. Among those crops, chickpea (CP) (*Cicer arietinum* L.) is the most important pulse species [4] and is a good source of proteins and carbohydrates, fiber, essential minerals, and vitamins, which are all properties related to the maintenance of good health [5].

CP is produced worldwide in more than 50 countries, and the five largest producers are India, Australia, Turkey, Ethiopia, and Russia [6]. Regarding their grain characteristics, CPs can be divided into two types: "Desi" and "Kabuli". The "Desi" type has pigmented plants, light purple flowers, and darker seeds, while the "Kabuli" type typically has white flowers and beige seeds [7]. The most significant production is from Desi types, which

are grown in South Asia, East Africa, and Australia, whereas Kabuli types are grown in the Mediterranean Basin, the Near East, and East Asia [8]. Regarding biotic stresses, the principal component of loss production is fungal diseases, highlighting the importance of *Fusarium* wilt and *Ascochyta* blight [9]. On the other hand, the effects of heat, cold, drought, and salinity could be detrimental to yield [10]. In this context, the most effective way to address these concerns is to develop new cultivars of CP [11].

Crops, including CP, are significantly influenced by the environment, and the performance of a cultivar is not solely determined by its genotype. Instead, it is often more influenced by the complex interaction between the genotype and environment (GEI) [12]. To estimate the effects of GEI, elite lines are commonly evaluated in multi-environment trials (METs), which aid in making genotype recommendations. Pour-Aboughadareh et al. [13] define METs as experiments in which a set of genotypes is evaluated across different environments, such as years, locations, planting dates, or combinations of these. Various statistical methods are employed to estimate adaptability and stability. These methods serve the crucial purpose of providing a quantitative understanding of how cultivars respond to different environments, each with its own set of assumptions [13].

Genotype stability is studied using several methods, and these methods have distinct assumptions, such as those of analysis of variance (ANOVA) [14] and simple linear regression [15,16]. However, these methods have some weaknesses [13]. Firstly, ANOVA is based on an additive model, which may not accurately reflect how genotypes and environments interact to influence GEI. The complex nature of these interactions needs a more advanced statistical approach than ANOVA for a better understanding of the phenomena. Secondly, linear regression analysis loses its efficiency when the assumption of linearity is missed. Furthermore, these analyses are highly influenced by the tested genotypes and environments, and attempting to fit the effects of interactions in a single dimension thereby reduces the effectiveness of the response models [17].

Alternative methods to ANOVA and linear regression analyses are additive main effects and multiplicative interaction (AMMI) [18] and the weighted average of absolute scores (WAASB) [19]. In addition, nonparametric methods, like those developed by Annicchiarico [20] and Huehn [21], provide viable options. Another choice is Lin and Binns's method [22], modified by Carneiro [23], where the statistic Pi is partitioned into suitable (Pi+) and unsuitable (Pi−) environments.

The AMMI model uses analysis of variance (ANOVA) for additive or main effects, followed by principal component analysis (PCA) for multiplicative or interactive effects [24]. It makes AMMI a powerful method for analyzing GEI in multi-environment trials (METs), as it estimates the effect of GEI for each genotype and environment [18]. Currently, a new approach defined as WAASB has been introduced, which merges the strengths of AMMI with the mixed model BLUP (best linear unbiased predictor) techniques. In addition to the benefits of utilizing random effects, WAASB accounts for the whole variability, rendering a biplot highly comprehensive [19]. It is important to consider that the selection of the methodology is influenced by the number of available environments, the level of required precision, and the nature of the data [17].

In the last five years, several studies have been conducted concerning GEI in chickpeas. In this sense, Karimizadeh et al. [25] found significant effects of E, G, and GEI on grain yield. Similar findings were observed in [26] for yield and drought tolerance, in [27] for yield and seed size, in [28] for yield and heat tolerance, in [29] for yield, protein concentration, and seed weight, and in [30] for yield components in lineages from interspecific crosses. In addition, the majority of them analyzed GEI using AMMI, genotype-plus-genotype × environment (GGE), and WAASB [25–30].

In this context, this research aims to select stable, high-yielding chickpea genotypes using uni- and multivariate methods of analysis and to study their adaptation to various environmental conditions.

2. Materials and Methods

2.1. General Conditions

The trials were conducted in the fall and winter of two agricultural years: 2020 and 2021. The 2020 essays were conducted at Embrapa Hortaliças, Rodovia BR-060, Km 9, DF, Brazil, on four different planting dates. These planting dates were chosen based on chickpea cultivation and soil moisture from the previous rainfall season. Moreover, the 2021 trials were conducted at Futurama Farm, located on Rodovia BR 251, km 13, Cristalina—GO, Brazil, on three different planting dates. In this case, the planting dates were selected based on the viability of the maize, chickpea, and cotton crop arrangement. The environments were a combination of locations and planting dates, and their main characteristics are shown in Table 1. The experimental areas were prepared by plowing and furrowing, and the fertilization of environments E1 to E3 was 15 kg per hectare of nitrogen, 75 kg per hectare of phosphorus, and 45 kg per hectare of potassium. A top-dressing application of 100 kg per hectare of nitrogen was performed thirty days after sowing. Regarding E4–E7, basal fertilization was 25 kg per hectare of nitrogen, 60 kg per hectare of phosphorus, and 35 kg per hectare of potassium. The same amount of top dressing was applied to these fields. In all environments, weeds were managed with 1920 g of glyphosate (Bayer Crop Science, Belford Roxo, Brazil) + 480 g of metribuzin per hectare (Syngenta, Paulinia, Brazil), followed by 100 g of carfentrazone-ethyl (FMC, Uberaba, Brazil) per hectare for pre-planting desiccation and 1920 g per hectare of S-metolachlor (Syngenta, Paulinia, Brazil) in post-emergence. Cotton bollworm infestation was managed by spraying 600 g per hectare of methamidophos (Arysta, Salto do Pirapora, Brazil), followed by 20 g per hectare of lufenuron (Syngenta, Paulinia, Brazil).

Table 1. Environments (E), planting dates, locations, and water management of the experimental trials.

E	Planting Dates	Location	Coordinates	Altitude (m)	Type of Soil	Management	Accumulated Rainfall (mm)	Water Supply (mm)
E1	20 January 2020						563	0
E2	20 March 2020	Embrapa Hortaliças	S 15° 56.087'; W 048° 08.439'	898	Dystrophic Red Oxisol	Rainfed	320	0
E3	10 April 2020						114	0
E4	10 April 2020						118	0
E5	30 April 2021	Futurama farm	S 16° 16.501'; W 047° 21	1005	Dystrophic Yellow Oxisol	Irrigated	12	213
E6	20 May 2021						0	191
E7	9 June 2021						0	216

Treatments were composed of seven cultivars: Astro, Blanco Sinaloa, Cícero, IAC Marrocos, Joly, Jamu 96, and Nacional 29; six homozygous lines from the International Center for Agricultural Research in the Dry Areas (ICARDA): ILC 1929, FLIP03-109C, FLIP03-35C, FLIP02-23C, FLIP06-155C, and FLIP06-34C; and two homozygous lines from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT): ICCV 10 and BG1392. Genotype details used in this research are shown in Table 2.

Table 2. Details of chickpea genotypes studied in this research.

Genotypes	Origin	Pedigree	Grain Type	Growth Habit	1000 Seeds Weight (g)
Astro	Mexico	Local landrace	Kabuli	Semi-erect	570
Blanco Sinaloa 92	INIFAP/Mexico	Comercial variety	Kabuli	Semi-erect	506
BG 1392	ICRISAT/India	Not Available	Kabuli	Semi-erect	599
Cícero	EMBRAPA/Brazil	Comercial variety	Kabuli	Semi-erect	520

Table 2. *Cont.*

Genotypes	Origin	Pedigree	Grain Type	Growth Habit	1000 Seeds Weight (g)
FLIP03-35C	ICARDA/Lebanon	X98TH18/S96114 x FLI92-148C	Kabuli	Semi-erect	403
FLIP06-155C	ICARDA/Lebanon	X98TH58/(Malik 1 x ILC7795 x FLIP94-92C) x S96233	Kabuli	Semi-erect	430
FLIP06-34C	ICARDA/Lebanon	Not Available	Kabuli	Semi-erect	391
FLIP02-23C	ICARDA/Lebanon	X98TH18/S96114 x FLI92-148C	Kabuli	Erect	359
FLIP03-109C	ICARDA/Lebanon	X00TH51/FLIP98-52C x FLIP 98-47C	Kabuli	Semi-erect	407
IAC Marrocos	ICARDA/Lebanon	Comercial variety	Kabuli	Prostrate	285
ICCV 10	ICRISAT/India	P 1231 x P 1265.	Desi	Semi-erect	273
ILC 1929	Syria	Local landrace	Kabuli	Semi-erect	381
Jamu 96	INIFAP/Mexico	Comercial variety	Kabuli	Erect	440
Joly	Spain	Local landrace	Kabuli	Semi-erect	544
Nacional 29	INIFAT/Cuba	Comercial variety	Kabuli	Prostrate	505

2.2. Experimental Design

The experimental design was completely randomized with three replications. The experimental plots consisted of four lines of each genotype, each 5 m in length. The spacing was 0.10 m between plants and 0.50 m between rows of plants. The sowing density was 40 seeds per square meter. To determine yield, grain from the plots was harvested, cleaned, and weighed. As the results were expressed in g/7.5 m^2, the yield was finally converted to kg/ha.

2.3. Statistical Analysis

The statistical model for Eberhardt and Russell's [15] analysis is as follows:

$$Y_{ij} = \beta_{0i} + \beta_{1i}I_j + \delta_{ij} + \overline{\epsilon_{ij}}$$

where Y_{ij} is observed mean of genotype i in environment j; β_{0i} is general mean of genotype i; β_{1i} is coefficient of regression of genotype i and I_j is environmental index j; δ_{ij} is deviation of the regression of genotype i in environment j; and $\overline{\epsilon_{ij}}$ is mean error associated with the average. In addition, I_j is calculated as follows:

$$I_j = \overline{Y_{.i}} - \overline{Y_{..}} \text{ with } \sum_{j=1}^{n} I_j = 0$$

where n is the number of environments.

In Lin and Binns's [22] procedure the index P_i is calculated as follows:

$$P_i = \sum_{j=1}^{n} \left(X_{ij} - M_j\right)^2 / 2_n$$

where P_i is the superiority index of genotype i; X_{ij} is the number of days to anthesis of genotype i in environment j; M_j is the number of days to anthesis of the genotype with the maximum response among all genotypes in environment j; and n is the number of environments.

In additive main effects and multiplicative interaction (AMMI) [18] method is as follows:

$$Y_{ij} = \mu + \alpha_i + \beta_j + \sum_{k=1}^{n} \lambda_k \gamma_{ik} \delta_{jk} + \rho_{ij} \overline{\epsilon_{ij}}$$

where Y_{ij} = mean response of genotype i (i = 1, 2,..., g genotypes) in environment j (j = 1, 2,..., e environments); μ = general mean of the experiments; α_i = fixed effect of genotype i; n = number of principal axes (principal components) needed to describe the pattern of the interaction between the *i*-eth genotype with the *j*-eth environment;

β_j = fixed effect of environment j; λ_k = k-eth single value of the original interactions matrix (called G X E matrix); γ_{ik} = is the value corresponding to the i-eth genotype in the k-eth single vector column of G X E matrix; δ_{jk} = value corresponding to the j-eth environment in the k-eth single vector (row vector) of G X E matrix; ρ_{ij} = noise associated with the (ga)ij term of classic interaction of i-eth genotype with j-eth environment; and $\overline{\epsilon_{ij}}$ = mean experimental error.

The weighted average of absolute scores (WAASB) [19] method comprises the following:

$$\text{WAASB}_G = \sum_{n=1}^{p} \left| IPCA_{gn} \text{x} EP_n \right| \Big/ \sum_{n-1}^{p} EP_n$$

where WAASB$_G$ is the weighted average of absolute scores of the genotype g, IPCAgn is the score of the genotype g in the nth interaction principal component axis (IPCA), and EPn is the amount of the variance explained by the nth IPCA.

Individual and joint analyses of variance were performed using SAS PROC GLM (version 9.1.3, SAS Institute Inc., Cary, NC, USA) [31] at $p < 0.05$. The individual effects of genotype/environment and environment were analyzed using Scott and Knott's [32] method at $p < 0.05$. Details of the calculation of degrees of freedom for the AMMI analysis of variance are presented in Table S1 (Supplementary Material). Once the genotype-by-environment interaction was significant ($p < 0.05$), stability analyses were performed according to the protocols of AMMI [18], Eberhardt and Russell [15], Lin and Binns [22], and WAASB from the singular value decomposition of the matrix of the best linear unbiased predictor (BLUP) for the genotype x environmental (GxE) effects generated by a linear mixed model [19]. AMMI and WAASB analyses were run with the R 3.5.2 package metan [33] using the statistical program R Core Team. Eberhardt and Russell's and Lin and Binns's analyses were performed in Genes statistical software (version 1990. 2023. 92, Universidade Federal de Viçosa, Viçosa, Brazil) [34].

3. Results

The results of the combined analysis of variance are shown in Table 3. From this analysis, highly significant effects ($p < 0.01$) were observed for environment (E), genotype (G), and the genotype-by-environment interaction (GEI). Moreover, the partitioning of the total square sum (SST) accounted for 86.25% of the effects due to E, G, and GEI. Hence, E corresponded to 24.55%, G to 34.87%, and GEI to 26.93% of SST (Table 3). Yields of genotypes in the studied environments are presented in Table 4. In four of seven environments (E1, E3, E5, and E6), genotypes were divided into three groups, with Astro, Blanco Sinaloa 92, BG 1392, and Cícero showing the lowest yields. The remaining genotypes did not show a clear trend and changed positions in yield performance (Table 4). It is also possible to note the composition of four clusters of environments, with E6 and E7 showing the highest mean yields, whereas E2 and E4 showed the lowest (Table 4). The significance of GEI is evident in the differences between genotypes across environments, ranging from 20.67 kg/ha in environment E2 (ICCV 10) to 1161.33 kg/ha in environment E6 (FLIP03-109C). Regarding Eberhardt and Russell's environmental index, E1, E5, E6, and E7 were considered favorable environments, whereas E2, E3, and E4 were in an unfavorable cluster (Table 4).

Table 3. Additive main effects and multiplicative interaction (AMMI) analysis of variance for chickpea yield during the 2020–2021 agricultural years.

Source of Variation	DF	MS	Cumulative (%)
Replication/Environment	14	44,376.83	1.94
Environment	6	1,312,820.81 **	24.55

Table 3. *Cont.*

Source of Variation	DF	MS	Cumulative (%)
Genotype	14	799,014.10 **	34.87
Genotype × Environment	84	102,845.35 **	26.93
PC_1	19	336,273.35 **	74.00
PC_2	17	64,072.28 **	86.60
PC_3	15	33,679.87 *	92.40
PC_4	13	28,326.65 ns	96.70
PC_5	11	19,339.75 ns	99.10
PC_6	9	8267.19 ns	100.00
Environment (linear)	1	7,876,924.87 **	
Genotype x Environment (linear)	14	373,177.16 **	
Pooled Deviation	75	45,527.05 **	
Error	196	19,178.52	11.72

*, ** Significant at 5 and 1%, respectively. ns: non-significant.

Table 4. Yield (Kg/ha) of 15 chickpea genotypes across seven environments during the 2020–2021 agricultural years.

Genotypes	Yield [1]/Environments						
	E1	E2	E3	E4	E5	E6	E7
Astro	263.33 C	46.00 b	164.00 C	73.67 A	111.67 c	149.33 C	212.00 D
Blanco Sinaloa 92	419.33 C	61.00 b	215.00 C	134.00 A	223.33 c	314.67 C	324.67 D
BG 1392	280.00 C	91.00 b	177.67 C	159.33 A	98.67 c	138.00 C	214.00 D
Cícero	79.33 C	30.12 b	207.67 C	98.00 A	80.67 c	100.00 C	128.00 D
FLIP03-35C	514.67 B	105.67 b	257.67 C	285.67 A	964.67 a	1040.67 A	876.00 B
FLIP06-155C	559.33 B	177.00 a	184.33 C	218.33 A	905.00 a	1045.67 A	1250.00 A
FLIP06-34C	369.33 C	296.00 a	295.67 B	175.67 A	488.00 b	531.67 B	919.33 B
FLIP02-23C	522.67 B	231.00 a	364.00 B	207.33 A	960.67 a	1140.67 A	1075.33 A
FLIP03-109C	811.33 A	219.00 a	479.33 A	254.00 A	889.67 a	1161.33 A	965.33 B
IAC Marrocos	390.00 C	401.33 a	344.33 B	49.33 A	422.67 b	634.67 B	506.00 C
ICCV 10	68.67 C	20.67 b	163.33 C	241.00 A	147.67 c	563.00 B	622.00 C
ILC 1929	767.33 A	146.00 b	206.67 C	105.00 A	270.67 c	371.33 B	337.33 D
Jamu 96	370.67 C	31.33 b	294.00 B	174.00 A	445.00 b	480.67 B	504.00 C
Joly	345.33 C	103.00 b	207.67 C	155.67 A	135.67 c	158.67 C	312.00 D
Nacional 29	264.00 C	43.67 b	323.00 B	221.00 A	196.33 c	180.67 C	203.33 D
Average	401.69 B	132.67 D	258.96 C	170.13 D	422.69 B	534.07 A	563.29 A
Environmental Index [2]	46.90	−222.12	−95.83	−184.65	67.90	179.28	208.50

[1] Means followed by the same lowercase letters did not differ by Scott Knott's test at $p < 0.05$, and the same capital letters indicate no difference at $p < 0.01$. [2] Obtained from Eberhardt and Russell: $I_j = \overline{Y_{.i}} - \overline{Y_{..}}$ with $\sum_{j=1}^{n} I_j = 0$.

As shown in Table 5, FLIP03-109C, FLIP02-23C, and FLIP06-155C exhibited the highest yields. The genotypes were separated into three categories according to regression coefficients (β_{1i}) ($p < 0.05$). Hence, FLIP06-34C, IAC Marrocos, ICCV 10, ILC 1929, and Jamu 96 had $\beta_{1i} = 1$; FLIP03-35C, FLIP06-155C, FLIP02-23C, and FLIP03-109C had $\beta_{1i} > 1$; and Astro, Blanco Sinaloa 92, BG 1392, Cícero, IAC Marrocos, Joly, and Nacional 29 had $\beta_{1i} < 1$. Astro, Blanco Sinaloa 92, BG 1392, Cícero, FLIP03-109C, Jamu 96, Joly, and Nacional 29 did not have significant variance of regression deviation (σ_{di}^2) ($p < 0.05$). Only FLIP03-35C, FLIP06-155C, FLIP02-23C, FLIP03-109C, and Jamu 96 had a coefficient of determination (R^2) superior to 80%. The lowest P_i's were found in FLIP02-23C and FLIP03-109C, and these cultivars did not exhibit the same trend for weighted average of absolute scores (WAASB Index), as the lowest estimates were observed in IAC Marrocos, ICCV 10, and Jamu 96. Finally, genotypes with the lowest average sum of ranks (ASR) were FLIP02-23C, FLIP03-109C, and Jamu 96. The advantage of using the ASR is the integration of yield and several methods of stability analysis in a single number. Thus, it facilitates the interpretation of adaptability and stability indices and the selection of stable genotypes.

Table 5. Stability and adaptability statistics for chickpea yield estimated in seven environments during the 2020–2021 agricultural years.

Genotypes	Yield (Kg per Hectare)	Eberhardt and Russell			Lin and Binns's Modified by Carneiro (Pi's/1,000,000)			WAASB Index	Average Sum of Rank
		β_{1i}	σ_{di}^2	R^2	P_i	P_i+	P_i-		
Astro	145.71 (14)	0.29 **	−2434.75 ns	43.24	572.43 (14)	271.42 (13)	301.02 (13)	5.91 (6)	12.00
Blanco Sinaloa 92	241.71 (10)	0.57 *	−16.81 ns	64.21	475.09 (9)	216.73 (10)	258.36 (10)	4.63 (5)	8.80
BG 1392	165.52 (13)	0.13 **	−1688.72 ns	10.98	557.46 (13)	275.25 (14)	282.20 (12)	7.12 (9)	12.20
Cícero	101.57 (15)	0.07 **	−2557.04 ns	4.09	610.70 (15)	294.13 (15)	316.58 (15)	7.7 (11)	14.20
FLIP03-35C	577.86 (4)	2.05 **	20,715.27 **	84.38	254.8 (3)	38.24 (4)	216.56 (3)	10.25 (13)	5.40
FLIP06-155C	619.95 (3)	2.51**	15,992.02 **	90.75	267.56 (4)	35.75 (3)	231.82 (5)	12.96 (15)	6.00
FLIP06-34C	439.38 (5)	1.21 ns	14,143.29 **	71.23	365.63 (5)	132.13 (5)	233.49 (7)	3.57 (4)	5.20
FLIP02-23C	643.10 (2)	2.25 **	13,721.99 **	89.81	228.23 (2)	29.38 (1)	198.85 (2)	11.05 (14)	4.20
FLIP03-109C	682.86 (1)	2.09 **	1859.02 ns	94.90	174.36 (1)	30.33 (2)	144.03 (1)	9.07 (12)	3.00
IAC Marrocos	392.62 (6)	0.77 ns	11,294.57 *	54.08	369.09 (6)	137.25 (6)	231.84 (6)	1.77 (2)	5.20
ICCV 10	260.90 (9)	1.02 ns	24,756.36 **	54.07	498.76 (11)	187.87 (8)	310.89 (14)	2.87 (3)	9.00
ILC 1929	314.90 (8)	0.68 ns	36,175.64 **	27.76	411.37 (8)	193.48 (9)	217.9 (4)	6.85 (8)	5.40
Jamu 96	328.52 (7)	0.98 ns	−3504.13 ns	92.09	399.16 (7)	155.57 (7)	243.59 (8)	0.78 (1)	4.00
Joly	202.57 (12)	0.27 **	1221.42 ns	25.20	525.66 (12)	259.85 (12)	265.81 (11)	6.52 (7)	11.00
Nacional 29	204.57 (11)	0.11 **	2064.51 ns	4.67	497.57 (10)	252.01 (11)	245.55 (9)	7.62 (10)	10.20

*, ** Significant at 5 and 1%, respectively. ns: non-significant.

Regarding additive main effects and multiplicative interaction (AMMI) analysis of variance, the GEI was split into six principal components (PCs). The first three PCs had significant effects—at least $p < 0.05$—and the remaining PCs were not significant. In this sense, PC1 accounted for 74% of the total variation, PC2 for 12.6%, PC3 for 5.8%, PC4 for 4.3%, PC5 for 2.4%, and finally PC6 for 0.9% (Table 3). In AMMI 1, the abscissa describes the yield means, while the ordinate represents the IPCA1 scores of each chickpea genotype. The graph's origin indicates an average yield and no genotype-by-environment interaction. Coordinates on the right yielded greater results than those on the left. The farther the coordinate is from the abscissa, the less stable it is (Figure 1A). Environment E6 had the greatest influence on yield because it is the farthest from the origin, followed by environments 2 and 4. On the other hand, E1 is the closest environment to the origin, meaning it had little influence on yield. Similarly, genotype Jamu 96 (G3) is the closest to the origin, followed by IAC Marrocos (G2), ICCV 10 (G11), and FLIP06-34C (G15) (Figure 1A). Genotypes FLIP03-109C, FLIP03-35C, FLIP02-23C, and FLIP06-155C showed yields greater than the general mean. On the other hand, the environments with the lowest yield were E2, E3, and E4.

The AMMI2 biplot shows the effects of genotype-by-environment interaction on genotype ranking. In this case, genotypes farther from the origin exhibit greater genotype-by-environment interaction and thus lower stability. From the biplot AMMI 2 (Figure 1B), a great divergence can be observed between environments E4 and E7, and similarly between genotypes FLIP06-155C (G14) and Nacional 29 (G4). Moreover, the coordinates based on environments and genotypes are shown on AMMI2 (Figure 1B). In this sense, cultivars IAC Marrocos and Jamu 96 were close to the origin. Additionally, FLIP03-35C was close to E5, and Cícero, Nacional 29, and BG 1392 were plotted next to E2, E3, and E4 (Figure 1B).

Genotypes and environments were plotted in a weighted average of absolute scores (WAASB) statistics dispersion graph based on their mean yield and stability values. As proposed by Yue et al. [24], the coordinates of environments and genotypes were plotted on a dispersion graph across four regions. Environments E2, E3, and E4 were placed in the first quadrant, and the second quadrant contained enclosed environments E5, E6, and E7, along with genotypes FLIP03-109C, FLIP03-35C, FLIP02-23C, and FLIP06-155C. Following the analysis, Cícero, Nacional 29, Astro, Joly, ILC 1929, FLIP03-109C, ICCV 10, Blanco Sinaloa 92, and BG 1392 belonged to the third quadrant. In the last quadrant, environment E1 and the genotypes FLIP06-34C and IAC Marrocos were identified (Figure 2).

(A)

(B)
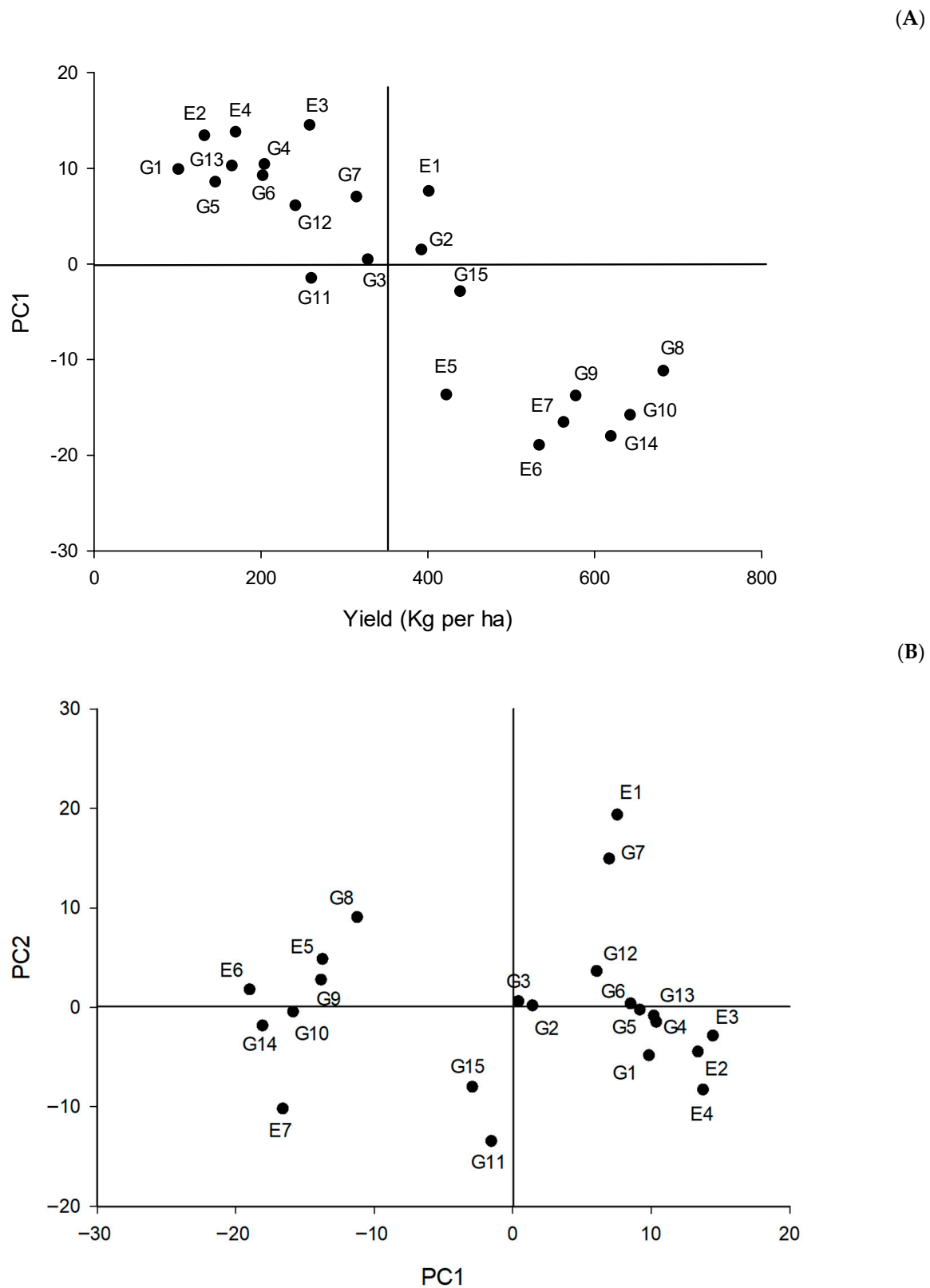
Figure 1. Chickpea yield, and stability analysis based on (**A**) the AMMI1 biplot and (**B**) the environmental stability GGE biplot. The genotypes codes are G1: Cícero, G2: IAC Marrocos, G3: Jamu 96, G4: Nacional 29, G5: Astro, G6: Joly, G7: ILC 1929, G8: FLIP03-109C, G9: FLIP03-35C, G10: FLIP02-23C, G11: ICCV 10, G12: Blanco Sinaloa 92, G13: BG 1392, G14: FLIP06-155C, and G15: FLIP06-34C.
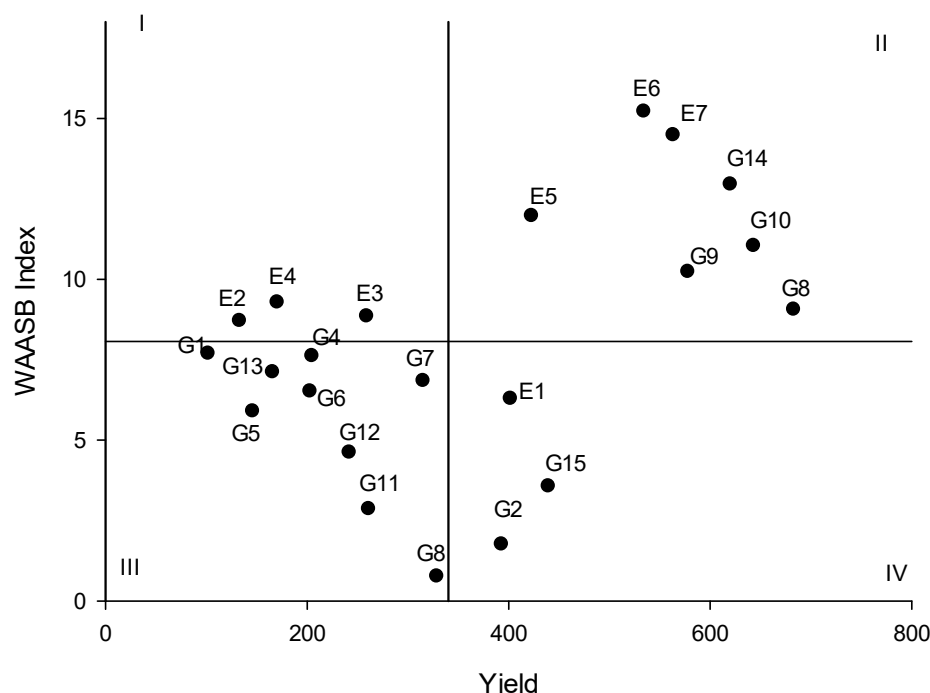
Figure 2. Biplot of chickpea yield vs. weighted average of the absolute scores (WAASB Index). The genotype codes are G1: Cícero, G2: IAC Marrocos, G3: Jamu 96, G4: Nacional 29, G5: Astro, G6: Joly, G7: ILC 1929, G8: FLIP03-109C, G9: FLIP 3-35C, G10: FLIP02-23C, G11: ICCV 10, G12: Blanco Sinaloa 92, G13: BG 1392, G14: FLIP06-155C, and G15: FLIP06-34C.

4. Discussion

As found in the additive main effects and multiplicative interaction (AMMI) analysis of variance, the highly significant effect of genotype-by-environment interaction (GEI) (linear) indicates low similarity among genotypes in the studied environments [35]. The effects of GEI on genotype performance, in the present case estimated by yield, make the selection of broadly adapted genotypes difficult [36]. One of these effects is the reduction in the yield heritability. In addition, significant GEI for complex traits, such as yield, poses a challenge to selection, making it difficult to develop newly adapted chickpea cultivars [8].

Considering that the effects of the linear environment were significant ($p < 0.01$), environmental variations can promote shifts in genotype yields [17]. It is also observed that, when a linear environment is significant, the regression coefficients (obtained from Eberhardt and Russel [15]) among genotypes differ [37]. Furthermore, the yield stability can be influenced by both linear and non-linear effects, as evidenced by the significant pooled deviation. Considering these aspects, analyzing the data using multivariate and nonparametric approaches could enrich the research [38].

Differences among the environmental indexes ($p < 0.05$) were analyzed from −222.12 to +208.50, reflecting an average yield in the environments ranging from 563.29 Kg/ha to 132.67 Kg/ha. In this case, Molina et al. [39,40] and Istanbuli et al. [41] highlighted the importance of water supply to chickpeas, and these authors also observed reductions in yield up to 70%. Hence, a comprehensive study of the influence of water supply on chickpea yield in an experiment with fewer genotypes could be a follow-up to this study. Environments E2 and E7 had the highest and lowest mean yields, respectively, and the difference between them was 430 Kg/ha. This result could be particularly helpful for chickpea growers, especially in cultivation under unfavorable environments. In this case, considering the following aspects—high variation in the trait per se, stability, and adaptability—could help develop high-yield chickpea genotypes and improve yield stability performance [42].

As mentioned by Pour-Aboughadareh et al. [42], considering the GEI effect on the breeding programs increases the efficiency of selection processes and identifies genotypes with high adaptability and stability. Hence, estimates of adaptability and stability are important for selecting superior genotypes. According to Eberhardt and Russell's methodology [19], genotypes are classified using criteria based on regression coefficients, the variance of the regression deviations, and the magnitude of the coefficient of determination. FLIP03-35C, FLIP06-155C, FLIP02-23C, and FLIP03-109C tend to be adapted to favorable environments, as they have $\beta_{1i} > 1$ and yield superior to the general mean. On the other hand, an important observation should be made regarding IAC Marrocos's specific adaptation to unfavorable environments and its performance in terms of yield, despite the low regression coefficient. None of the evaluated genotypes has broad adaptability ($\beta_{1i} = 1$) and predictable responses ($\sigma_{di}^2 = 0$) according to Eberhardt and Russell's recommendations. However, this concept might be redesigned to select genotypes with high expression of the trait under unfavorable environments, which is more efficient than searching for genotypes with $\beta_{1i} = 1$ [43]. These authors also pointed out that these genotypes ($\beta_{1i} = 1$) can perform less under unfavorable environments than those with $\beta_{1i} < 1$, for example. Another option is to associate highly predictable genotypes with high trait performance using an R^2 greater than 80% as the criterion, instead of the original $\sigma_{di}^2 = 0$ [44].

Regarding the additive main effects and multiplicative interaction 1 (AMMI1) biplot, the genotypes Cícero, Jamu 96, Nacional 29, Astro, Joly, ILC 1929, ICCV 10, Blanco Sinaloa 92, and BG 1392 had the lowest yields. This finding can be attributed to the fact that these genotypes are not well adapted to the edaphic conditions of the Brazilian Cerrado region. Considering the AMMI2 model, cultivars IAC Marrocos and Jamu 96, according to Zobel et al. [18], are stable. However, a remark posted by Danakumara [28] should be considered, which suggests that the selection process should consider not only stability aspects but also yield.

Regarding the weighted average of absolute scores (WAASB) analysis, only environments were located in the first quadrant of the biplot, indicating that they have a greater influence on GEI [13]. In the following quadrant (II), genotypes FLIP03-109C, FLIP03-35C, FLIP02-23C, and FLIP06-155C could be considered unstable, although they exhibit high performance in yield [45]. Moreover, environments 5 through 7 are the most suitable for selecting chickpeas based on yield. The third quadrant encompasses the majority of tested genotypes, and these are characterized as low-performance and widely adapted genotypes due to their lower values of WAASB [19]. Also, no environments were placed in the third quadrant. In the last quadrant (IV), the cultivars IAC Marrocos and FLIP06-34C could be considered stable with yields above the general mean, and environment E1 is favorable but with low discrimination power [45]. Moreover, environments E2 to E4 were classified as unsuitable environments based on Eberhardt and Russell, AMMI, and WAASB protocols.

According to Wicaksana et al. [46], one way to overcome genotype selection based on a single statistic is to use the average sum of ranks (ASR), in which lower values indicate greater stability. In the present case, the advantage of using ASR is that it involves yield values and stability, facilitating the selection of high-yielding, stable genotypes. In this sense, FLIP02-23C, FLIP03-109C, and Jamu 96 were the most stable genotypes found in this research. Also, genotypes FLIP03-109C, FLIP03-35C, FLIP02-23C, and FLIP06-155C appear to be better adapted to irrigated environments (E5 to E7), achieving the highest yields in these sites.

5. Conclusions

In this research, the stability of the yield of 15 chickpea genotypes was evaluated in multi-environment trials using additive main effects and multiplicative interaction

(AMMI), Eberhart and Russell's, Lin and Binns's, and weighted average of absolute scores (WAASB) techniques. From the AMMI analysis of variance, it was observed that yield was influenced by genotype, environment, and the interaction between genotype and environment (GEI). Using the average sum of ranks is an interesting approach to combine the results of several methodologies for GEI estimation. Based on this, FLIP02-23C, FLIP03-109C, and Jamu 96 were found to be the most stable genotypes in this research. According to AMMI2, genotypes FLIP03-109C, FLIP03-35C, FLIP02-23C, and FLIP06-155C are adapted to irrigated environments.

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