AMMI and GGE Analyses of Soyabean (*Glycine max* L. Merrill) Genotypes Infected and Uninfected with *Cucumber mosaic virus*

ABSTRACT

Soyabean is an important source of protein for millions of people in developing countries. However, infection by *Cucumber mosaic virus* (CMV) causes devastating losses. Cultivation of resistant varieties has been identified as the best management strategy. The objective of this study was to identify soyabean genotypes with high stability for growth and seed weight under CMV and disease-free conditions. Eight soyabean genotypes were evaluated as CMV-infected and uninfected, using completely randomised design replicated five times and set up in the screenhouse at the School of Agriculture and Agricultural Technology, Federal University of Minna, (lat.9º40ˊ N;long 6º30ˊ E at an altitude of 220 m.a,s,l) Nigeria in 2018. Soyabean seedlings were infected with the virus by sap transmission at 10 days after sowing. Additive Main Effects and Multiplicative Interaction (AMMI) analysis revealed that environments' effects (infected and uninfected) were significant (p<0.05) and accounted for 100 % Genotype × Environment (G×E) interaction for growth and seed weight. Disease-free soyabean plants produced significantly higher growth and seed weight than the CMV-infected plants. The AMMI and Genotype main effects (G) plus Genotype x Environment (GGE) analyses showed that TGX 1993-4FN was the genotype with the greatest stability for leaf diameter, leaf length, number of leaves per plant, number of days to flowering and seed weight. In the meantime, the soyabean genotype TGX 1993-4FN can be exploited for breeding purposes and strategies that will prevent CMV infection in soyabean fields should be adopted by farmers.

***Keywords*:** AMMI biplot; CMV; GGE biplot; Seed weight; Soyabean; Stability

1. INTRODUCTION

Food is an important basic need for human survival and in developing countries, ensuring food sufficiency has been a mirage for several decades. Inadequate intake of protein-rich food sources further worsens food crisis in the West African subregion. Soyabean (*Glycine max* L. Merrill), as an

annual crop is one of the major sources of high quality and inexpensive protein for human consumption. According to FAO [1], the global soyabean output in 2017 was approximately 352.6 million tonnes, with about 3.1 million tonnes from Africa. Nigeria with about 0.7 million tons, accounted for 23.3 % of the total for Africa. Being a leguminous crop, soyabean plays an important role in biological nitrogen fixation (BNF) into the soil. The ability of soyabean to increase soil nitrogen is aided by the activity of symbiotic bacteria [2]. Studies have shown that soyabean represents 77 % of the total nitrogen fixed by crop legumes by fixing 16.4TgN per annum. This is a major benefit in African farming systems, where there is a serious problem of soil infertility and application of inorganic fertilizer is constrained by high cost and scarcity of supply. Soyabean can be processed into soya milk, soya meat, bread and oil [3]. Soyabean seeds are also used in formulation of livestock, fish and poultry feeds while its haulms are a good source of fodder in the livestock industry.

The crop is well adapted to tropical, subtropical and temperate climates. However, its production is threatened by bacterial, fungal and virus diseases. The economically important viruses infecting soyabean include *Cucumber mosaic virus* (CMV), *Cowpea aphid-borne mosaic virus* (CABMV), *Soybean mosaic virus* (SMV), and *Bean yellow mosaic virus* (BYMV).

Cucumber mosaic virus is a member of the genus *Cucumovirus* in the family *Bromoviridae* [4]. It has a wide host range and causes significant losses in several crops. The virus is transmitted by aphids, infected seeds and through sap inoculation. *Cucumber mosaic virus*, a single stranded RNA (ssRNA) virus, contains about 30 nm icosahedral particles with a tripartite genome encapsidated in three distinctive particles. There are numerous strains of CMV worldwide with variety of symptoms [5]. Visible symptoms in vulnerable plants include leaf chlorosis, mosaic, vein necrosis and stunting. The virus can be controlled through application of insecticides to curtail its aphid vectors. Other measures include the use of healthy soyabean seeds but the most ecologically sound and sustainable approach is the cultivation of resistant soyabean varieties.

Genotype × environment (G×E) interaction can be computed using Additive Main Effects and Multiplicative Interaction (AMMI) model. On the other hand, Genotype main effects (G) plus Genotype x Environment (GGE) interaction biplots are a modification of the AMMI model [6]. The AMMI analysis is a two-stage process: Analysis of Variance (ANOVA) and Principal Components Analysis of the ANOVA adjusted means. In the PCA, G×E interaction is partitioned into IPCA (I for interaction) with the first component accounting for the greatest variation. The efficiency of AMMI and GGE is enhanced by the graphical representation of the output expressed as biplots. A biplot gives a better understanding of the genotypes with specific or broad adaptability and environments which elicit strong (or weak) interactive forces. Although interpretation of AMMI biplot is similar to the GGE biplot, the latter provides information on total genetic variation by approximating the joint effects of the genotypes and G×E interaction. Identification of soyabean genotypes with stable growth and seed weight under CMV endemic and disease-free conditions will be useful for breeding CMV resistant soyabean varieties. Therefore, this study was conducted to identify soyabean genotypes with high stability for growth and seed weight under CMV and disease-free conditions for use in hybridization studies to develop high yielding and CMV resistant soyabean varieties.

2. MATERIALS AND METHODS

2.1 Study Location

The study was conducted at the Teaching and Research Farm, School of Agriculture and Agricultural Technology, Federal University of Technology, Minna, Nigeria (9^{o} 40′ N and 6^{o}30′ E; 220 masl). The site is located in the Southern Guinea Savanna with a mean annual rainfall of 1200 mm. The rainy season normally spans between April and October. The major crops cultivated in Minna include soyabean, cowpea, groundnut, rice, maize, sorghum, millet and rice. Soyabean may be grown as a sole crop or intercropped with maize or sorghum.

2.2 Treatments and Experimental Layout

Treatments consisted of eight soyabean genotypes viz: TGX 1448-2A, TGx 1951-3F, TGx 1987-10F, TGX 1993-4FN, TGX 1994,TGX 2017-6E, TGX 2023-1E and TGX 2025-6E obtained from the Genetic Resources Unit of the National Cereals Research Institute (NCRI), Badeggi, Niger State, Nigeria. The soyabean genotypes were selected from those designated for screening against biotic and abiotic stresses in the country. The experiment was conducted under screenhouse conditions using completely randomised design with five replications.

2.3 Sowing and Seedling Inoculation

Plastic pots with 30cm diameter and 23cm deep were filled with heat sterilized loamy soil. Soyabean seeds were sown on 23rd August, 2018. An isolate of CMV-infected soyabean leaves obtained from the stock in the Department of Crop Production, Federal University of Technology, Minna was used for inoculation. Virus inoculum was prepared by grinding (1g/mL) the CMV-infected soyabean leaves in inoculation buffer containing 0.1M sodium phosphate dibasic, 0.1M potassium phosphate monobasic, 0.01M ethylendiamine tetraacetic acid and 0.001M L-cysteine per litre of distilled water, adjusted to pH 7.2. One μL of β- mercapto ethanol was then added. At 10 days after sowing (DAS), the upper leaf surface of the soyabean seedlings was dusted with carborundum powder (600-mesh) and the virus extract was rubbed on the dusted leaf surface. Distilled water was applied on the inoculated plants and they were observed for symptom development, growth and seed weights. Uninoculated plants of each soyabean genotype were evaluated in a separate screenhouse to serve as control.

2.4 Data Collection and Analysis

Both the CMV-infected and uninoculated plants were observed for height, leaf diameter, leaf length, number of leaves per plant, number of days to flowering and seed weight per plant. Data were subjected to analysis of variance (ANOVA) at 5 % probability level. Determination of genotype

stability was based on AMMI and GGE analyses, using Breeding Management software [7]. In the analyses, infected and uninfected plants were designated as two different environments - diseased and disease-free-. From AMMI biplot, the closest genotype to the axis origin was considered to be the most stable. As for GGE biplot, genotype with the shortest vector projection relative to the biplot origin was rated as the most stable. Wreck's ecovalence method was used for stability coefficients determination. Genotype with the lowest stability coefficient was considered as the most stable.

3. RESULTS

3.1 Growth and seed weight variability

The plants infected with CMV exhibited leaf chlorosis, mosaic and reduced vigour, whereas uninfected plants were apparently healthy. Apart from number of days to flowering and seed weight, genotypic effects were not significant ($p>0.05$) in all the evaluated parameters. On the other hand, the effects of environments, that is, infected and uninfected were significant ($p<0.05$) Table 1). Combined mean heights for infected and uninfected varied from 27.7 cm for genotype TGX 2025-6E to 33.2 cm for genotype TGX 1448-2A. However, the grand mean height of infected plants of 26.3 cm was significantly ($p<0.05$) lower than the grand mean of uninfected plants of 33.1 cm. Considering the infected plants alone, plant height varied between 22.7 cm for genotype TGX 1993-4FN and 30.7 cm for genotype TGX 1448-2A. The mean heights of genotypes TGX 1448-2A of 30.7 cm, TGX 1951-3F of 28.0 cm, TGX 1987-10F of 26.7 cm and TGX 1994 of 28.7 cm were higher than the grand mean of 26.3 cm. In contrast, the heights of uninfected plants ranged between 29.7 cm for TGX 1987-10F and 36.7 cm for TGX 1951-3F (Table 2). As observed in TGX 1951-3F with 36.7 cm tall plants, the genotypes TGX 1448-2A with 35.7 cm, TGX 1993-4FN with 33.7 cm and TGX 1994 with 34.7 cm had higher mean heights than the grand mean of 33.1 cm (Table 2).

The infected plants produced narrow and deformed leaves contrary to the broad and normal shaped leaves from uninfected plants. Combined leaf diameter means varied between 2.5 cm for genotype

TGX 1993-4FN and 4.0 cm for genotype TGX 2017-6E (Table 2). The grand mean of leaf diameter of 3.0 cm from infected plants was significantly (p<0.05) lower than that of healthy plants with 3.6 cm. From the infected plants, the lowest leaf diameter was observed in genotype TGX 1993-4FN with 2.3 cm, whereas genotype TGX 2025-6E recorded the highest leaf diameter of 3.7cm. Moreover, the infected plants of genotypes TGX 1987-10F with 3.3 cm, TGX 2023-1E with 3.3 cm and TGX 2025-6E with 3.7 cm recorded higher leaf diameter than the grand mean with 3.0 cm for the group. Conversely, the leaf diameter of uninfected plants varied between 2.7 cm for TGX 1993-4FN and 5.0 cm for TGX 2017-6E. In addition to genotype TGX 2017-6E with 5.0 cm tall plants, the uninfected plants of genotypes TGX 1987-10F with 3.7 cm, TGX 2023-1E with 4.0 cm and TGX 2025-6E with 3.7 cm tall plants recorded higher leaf diameter than the grand mean of 3.6 cm (Table 2).

Infection of the soyabean plants with CMV resulted in reduced leaf length. Combined means of leaf length ranged from 5.5cm in genotype TGX 1987-10F to 7.2cm in genotype TGX 2025-6E (Table 2). The grand mean of leaf length from infected plants of 5.8 cm was significantly (p<0.05) lower than that of healthy plants of 6.7 cm length. As for the infected plants, the lowest leaf length was observed in genotype TGX 1987-10F with 5 cm, whereas the highest length came from TGX 2025-6E with 6.7 cm. Genotypes TGX 2025-6E, TGX 1994 and TGX 2017-6E recorded the same length of 6.0 cm while genotype TGX 2023-1E produced higher leaf length of 6.3 cm than the grand mean of 5.8 cm.

The leaf length of uninfected plants varied between 6.0cm in genotypes TGX 1951-3F, TGX 1987-10F and TGX 2017-6E and 7.7cm im genotype TGX 2025-6E. Besides genotype TGX 2025-6E, uninfected plants of genottpes TGX 1993-4FN with 7.0 cm, TGX 1994 with 7.3 cm and TGX 2023-1E also with7.3 cm recorded higher leaf lengths than the grand mean of 6.7 cm for the group.

Cucumber mosaic virus infection lowered leaf production (Table 3). Combined number of leaves varied from 38 to 47 per plant in TGX 1987-10F and TGX 1951-3F, respectively. The grand mean

number of leaves per plant from infected plants of 40 leaves was significantly (p<0.05) lower than that of uninfected plants with 45 leaves. Considering the infected plants alone, genotype TGX 1987-10F produced the lowest number of leaves per plant of 36 leaves. In contrast, genotypes TGX 1994, TGX 2017-6E and TGX 2025-6E produced the highest number of leaves per plant of 42 leaves. These three genotypes were the only ones with higher number of leaves than the grand mean of 40 leaves for the group (Table 2). With respect to uninfected plants, a range of 40 in genotype TGX 1987-10F to 53 leaves in genotype TGX 1951-3F was observed per plant. The genotypes which produced higher number of leaves than the grand mean of 45 leaves were TGX 1951-3F with 53 leaves, TGX 2017-6E with 46 leaves and TGX 2025-6E with 47 leaves.

Generally, flowering of uninfected plants was earlier than those infected with CMV (Table 3). Combined data revealed that time of flowering varied between 35 days in genotype TGX 1951-3F and 39 days in genotypes TGX 2017-6E and TGX 2025-6E after inoculation. The grand mean time of flowering in uninfected plants of 36 DAS was significantly (p<0.05) lower than that of infected plants of 38 DAS.

Taking the infected plants alone, time of flowering was observed between 36 days in genotype TGX1951-3F and 40 days in genotype TGX 2017-6E after inoculation. With the exception of genotypes TGX 1987-10F, TGX 1994 and TGX 2025-6E which flowered in 39 days and TGX 2017-6E which flowered in 40 days respectively, all other genotypes recorded lower days to flowering than the grand mean of 38 days for the group.

As for uninfected plants, flowering was earliest at 35 days in genotypes TGX 1951-3F, TGX 1993-4FN and TGX 2023-1E. These three genotypes recorded lower time of flowering than the grand mean of 36

days for the group. Next were genotypes TGX 1448-2A, TGX 1993-4FN and TGX 2023-1E which flowered at 36 DAS. On the other hand, genotypes TGX 2017-6E and TGX 2025-6E flowered at 37 and 39 DAS respectively.

Combined seed weights varied between 1.3 g per plant.in genotype TGX 1448-2A and 35.g per plant. in genotype TGX 1993-4FN (Table 3). The grand mean of seed weight from uninfected plants of.3 g per plant was significantly (p<0.05) higher than that of infected plants of 1.3 g per plant. From the infected plants, genotypes TGX 1993-4FN and TGX 2025-6E with 3.2 and 2.3 g per plant, respectively were the only genotypes whose seed weights were higher than the grand mean of 1.3 g per plant. As for uninfected plants, the lowest seed weight was observed in genotype TGX 1994 with 1.8 g per plant, whereas genotype TGX 1993-4FN with an average of 3.7 g per plant was the highest. Besides genotype TGX 1993-4FN, the seed weights of TGX 2017-6E of 2.4 g and genotype TGX 2025-6E of 2.9 g were also higher than the grand mean for the group of 2.3 g.

3.2 Growth and seed weight stability

None of the genotypes exhibited consistent stability for the entire parameters. Generally, the first axis (IPCA) accounted for 100 % variation in all the parameters (Table 4). Additionally, the two environments (infected and uninfected) were far away from the axis origin. For plant height, AMMI analysis showed that genotype TGX 2025-6E was the closest to biplot origin, followed by genotypes TGX 1994 and TGX 2017-6E, whereas the remaining genotypes were far away (Fig. 1a). From GGE biplot, uninfected plants or disease free environment elicited longer vector along the axis. The genotype TGX 2025-6E exhibited the shortest vector projection to the biplot origin, followed by TGX 1994 and TGX 2017-6E (Fig. 1b). Wreck's stability analysis indicated that genotype TGX 2025-6E had the lowest stability coefficient of 0.147, followed by TGX 1994 and TGX 2017-6E which gave stability coefficient of 0.313 and 0.383, respectively (Table 5). With respect to leaf diameter, genotype TGX

1448-2A was the closest to the AMMI biplot origin, followed by TGX 2023-1E (Fig. 2a). In GGE analysis, diseased environment or infected plants, gave longer vector projection relative to the biplot origin. In all, genotype TGX 1448-2A exhibited the shortest vector projection, followed by TGX 2023-1E (Fig. 2b). Moreover, both genotypes had the lowest stability coefficient of 0.008. Next to them were genotypes TGX 1987-10F, TGX 1993-4FN and TGX 1994 with uniform stability coefficient of 0.022 (Table 5).

For the leaf length, 50 % of the evaluated genotypes made up of genotypes TGX 1448-2A, TGX 1951-3F, TGX 1987-10F and TGX 1993-4FN were the closest to AMMI biplot origin (Fig. 3a). GGE analysis revealed that uninfected plants or disease free environment produced longer vector projection along the axis. Genotypes TGX 1448-2A, TGX 1951-3F, TGX 1987-10F and TGX 1993-4FN exhibited relatively shorter vector projections compared to the remaining genotypes (Fig. 3b), with an equal stability coefficient of 0.001 (Table 5).

With respect to leaf production, the location of genotype TGX 1993-4FN was exactly on the AMMI biplot origin, whereas genotype TGX 2025-6E was the closest to it (Fig. 4a). From GGE biplot, CMV infection or diseased environment encouraged longer vector projection relative to the axis origin. Genotypes TGX 1993-4FN and TGX 2025-6E exhibited relatively shorter vector projections to the biplot origin (Fig. 4b). These two genotypes TGX 1993-4FN and TGX 2025-6E gave stability coefficient of 0.003 and 0.170 respectively (Table 5).

Regarding to number of days to flowering, AMMI analysis showed that genotype TGX 2023-1E was the nearest to the biplot origin. Also close to the biplot origin were genotypes TGX 1951-3F and TGX 1993-4FN (Fig. 5a). In GGE analysis, genotypes TGX 2023-1E, TGX 1951-3F and TGX 1993-4FN exhibited relatively shorter vector projections to the biplot origin. Infected plants or diseased environment exhibited longer vector projection along the axis. (Fig.5b). Wreck's analysis revealed that

TGX 2023-1E had the lowest stability coefficient of 0.022, whereas genotypes TGX 2023-1E, TGX 1951-3F and TGX 1993-4FN gave a uniform stability coefficient of 0.105 (Table 5).

As for seed weight per plant, AMMI analysis indicated that genotypes TGX 1951-3F and TGX 1993-4FN were closest to the axis origin (Fig. 5a). Additionally, GGE biplot showed that CMV infection or diseased environment caused longer vector projection relative to the axis origin (Fig. 5b). The soyabean genotype TGX 1951-3F exhibited relatively shorter vector projections relative to the biplot origin, followed by genotype TGX 1993-4FN. Similarly, genotype TGX 1951-3F gave the lowest stability coefficient of 0.001, which was closely followed by genotype TGX 1993-4FN with 0.002. Other genotypes with relatively low stability coefficients were TGX 2017-6E and TGX 2023-1E with 0.003 and TGX 1994 with 0.004 (Table 5).

4. DISCUSSION

Cucumber mosaic virus is a threat to several crops of economic importance around the globe. The observation that there were no significant effects of genotypes in AMMI analysis was an indication of genetic similarities among the evaluated soyabean genotypes. However, the significant effects of environments underscored the need for adequate measures to prevent infection and adoption of resistant varieties by farmers. Plant height, leaf diameter, leaf length, number of leaves per plant, number of days to flowering are yield components because of their direct relationship with seed production. All these yield contributing factors were affected by CMV, indicating the pathogenicity of the virus on the vulnerable soyabean genotypes. The fact that all the genotypes inoculated elicited disease symptoms indicated absence of immunity. This corroborates the findings of Adamu [8] who obtained similar result from soyabean lines that were inoculated with CMV.

Immune varieties are desirable as a preventive measure against plant pathogenic viruses but are not usually available. This is a condition that necessitates adoption of tolerant cultivars. Therefore, the

soyabean genotypes studied here can be described as being tolerant to CMV. The infected genotypes did not attain maximum potentials particularly seed weight owing to impairment of the growth structures. This agrees with the findings of Anuradha [9] who reported that various biochemical and physiological processes were compromised in *Bunchy top virus*-banana host-pathosystem. Viruses are obligate parasites that utilise their host resources including ribosome and mitochondron for self-replication and establishment. The deleterious impacts of CMV infection as observed in this study arose from its systemic movement within the cells and tissues of the host plants. Studies have shown that systemic movement of a virulent virus is facilitated by intercellular translocation of virus particles within a host plant. This is a phenomenon that triggers host – virus interaction and the outcome is defined by their compatibility [10].

It was observed that the two environments, infected and uninfected genotypes were far away from the axis origin, indicating that they elicited strong interactive forces. This arose from the differences in genotypes' performance with respect to the parameters studied. Apart from plant height, the observation that diseased environment elicited longer vector projection along the axis revealed that it was the main factor responsible for G×E interaction. Moreover, the observed differences in stability of genotypes were the consequences of their genetic variability. The genotypes that were close to the axis origin can be described as being stable across diseased and disease-free environments. Similarly, genotypes with short vector projections on the biplots exhibited high stability. In addition, the genotypes with low stability coefficients can be described as being stable for the investigated characters. This means that they maintained a uniform performance under diseased and disease-free conditions. However, genotype TGX 1993-4FNwhich was consistently the closest to the AMMI biplot origin, with the shortest vector projection on the GGE biplot, and with the lowest stability coefficients can be described as the genotype with the greatest stability.

Most genotypes were not stable for the entire growth and yield traits probably because the genes controlling these traits are quantitatively inherited, indicating that they are under the influence of several genes. Although polygenic or quantitative traits are desirable in plant disease management, the genes involved may not interact synergistically. Although genotype TGX 1951-3F recorded the lowest stability coefficient for seed weight, it was low-yielding. This will affect its acceptability to the famers. The same explanation holds for genotypes TGX 2017-6E, TGX 2023-1E and TGX 1994 which exhibited relatively low stability coefficients but were low in seed weight and cannot be given to farmers for planting. The soyabean genotype TGX 1993-4FN with the highest seed weight per plant, combined with the highest stability for most of the quantitative traits evaluated including seed weight can be described as the most promising and which can be exploited in hybridization studies for the development of high yielding CMV resistant soyabean varieties for farmers. Nevertheless, the observation that not all the genotypes were stable for growth and seed weight shows that there is room for improvement [11].

5. CONCLUSION AND RECOMMENDATIONS

This study revealed the pathogenicity of CMV on the evaluated soyabean genotypes. Disease-free soyabean plants produced significantly higher growth and seed weight than the CMV-infected plants. The AMMI analysis revealed that environments' effects represented by infected and uninfected genotypes were significant ($p<0.05$) and accounted for 100 % Genotype × Environment (G×E) interaction for growth and seed weight. The AMMI and GGE analyses showed that genotype TGX 1993-4FN was the genotype with the greatest stability for leaf diameter, leaf length, number of leaves per plant, number of days to flowering and seed weight. Therefore, the soyabean genotype TGX 1993-4FN can be exploited for breeding purposes. Pending the arrival of such resistant varieties from soyabean breeders, strategies that will prevent CMV infection in soyabean fields should be adopted by farmers.

293 Table 1: Mean squares of the growth and seed weights from soyabean genotypes infected and
294 uninfected with *Cucumber mosaic virus*

		Mean square		
Source of variation	DF	Plant height	Leaf diameter	Leaf length
Genotypes	7	31.4	1.4	2.1
Environments	1	553.5*	3.5*	11.0*
Sensitivities	7	8.9	0.6	0.4
Residual	32	44.3	0.6	0.9
Total	47	48.0	0.8	1.2
Source of variation	DF	Leaves per plant	Days to flowering	Seed weight per plant
Genotypes	7	41.3	9.4	3.4*
Environments	1	374.1*	38.5	8.1*
Sensitivities	7	16.7	1.6	0.1
Residual	32	22.8	2.3	0.3
Total	47	32.1	4.0	0.9

Table 2: Plant height, leaf diameter and leaf length from soyabean genotypes infected and uninfected with *Cucumber mosaic virus*

	Plant height (cm)			Leaf diameter (cm)			Leaf length (cm)		
Genotype	Infected	Uninfected	Combined	Infected	Uninfected	Combined	Infected	Uninfected	Combined
TGX 1448-2A	30.7	35.7	33.2	2.7	3.3	3.0	5.3	6.3	5.8
TGx 1951-3F	28.0	36.7	32.3	3.0	3.0	3.0	5.3	6.0	5.7
TGx 1987-10F	26.7	29.7	28.2	3.3	3.7	3.5	5.0	6.0	5.5
TGX 1993-4FN	22.7	33.7	28.2	2.3	2.7	2.5	5.3	7.0	6.2
TGX 1994	28.7	34.7	31.7	3.0	3.3	3.2	6.0	7.3	6.7
TGX 2017-6E	24.7	32.3	28.5	3.0	5.0	4.0	6.0	6.0	6.0
TGX 2023-1E	25.0	30.7	27.8	3.3	4.0	3.7	6.3	7.3	6.8
TGX 2025-6E	24.0	31.3	27.7	3.7	3.7	3.7	6.7	7.7	7.2
Grand mean	26.3	33.1*		3.0	3.6*		5.8	6.7*	

*Significant at $p \leq 0.05$

Table 3: Number of leaves per plant, days to fruiting and seed weight per plant in soyabean genotypes infected and uninfected with *Cucumber mosaic virus*

	Number of leaves per plant			Days to flowering			Seed weight per plant (g)		
Genotypes	Infected	Uninfected	Combined	Infected	Uninfected	Combined	Infected	Uninfected	Combined
TGX 1448-2A	38	43	41	37	36	36	0.7	1.9	1.3
TGx 1951-3F	40	53	47	36	35	35	1.2	2.0	1.6
TGx 1987-10F	36	40	38	39	36	38	0.9	1.9	1.4
TGX 1993-4FN	39	45	42	37	35	36	3.2	3.7	3.5
TGX 1994	42	43	43	39	36	38	1.1	1.8	1.5
TGX 2017-6E	42	46	44	40	37	39	1.5	2.4	2.0
TGX 2023-1E	38	44	41	37	35	36	1.0	1.9	1.5
TGX 2025-6E	42	47	45	39	39	39	2.3	2.9	2.6
Grand mean	40	45*		38*	36		1.5	2.3*	

*Significant at $p \leq 0.05$

Table 4: Additive main effects and multiplicative interaction (AMMI) of the soyabean genotypes infected and uninfected with *Cucumber mosaic virus*

		Sum of square		
Source of variation	DF	Plant height	Leaf diameter	Leaf length
Genotypes	7	73.2	3.3	5.0
Environments	1	184.5	1.2	3.7
Interactions	7	20.9	1.4	0.8
IPCA 1	7	20.9	1.4	0.8
Residuals	0	0.0	0.0	0.0

Source of variation	DF	Leaves per plant	Days to flowering	Seed weight per plant
Genotypes	7	96.3	21.9	8.0
Environments	1	124.7	12.8	2.7
Interactions	7	39.0	3.8	0.2
IPCA 1	7	39.0	3.8	0.2
Residuals	0	0.0	0.0	0.0

Table 5: Stability coefficients of the growth and yield attributes in soyabean genotypes infected and uninfected with *Cucumber mosaic virus*

Genotype	Stability coefficient					
	Plant height	Leaf diameter	Leaf length	Number of leaves	Days to flowering	Seed weight
TGX 1448-2A	1.605	0.008	0.001	0.420	0.633	0.099
TGx 1951-3F	1.758	0.147	0.001	27.503	0.105	0.001
TGx 1987-10F	7.188	0.022	0.001	0.781	0.383	0.011
TGX 1993-4FN	8.855	0.022	0.001	0.003	0.105	0.002
TGX 1994	0.313	0.022	0.043	9.031	0.730	0.004
TGX 2017-6E	0.383	1.063	0.070	0.781	0.730	0003
TGX 2023-1E	0.633	0.008	0.251	0.281	0.022	0.003
TGX 2025-6E	0.147	0.147	0.459	0.170	1.063	0.041

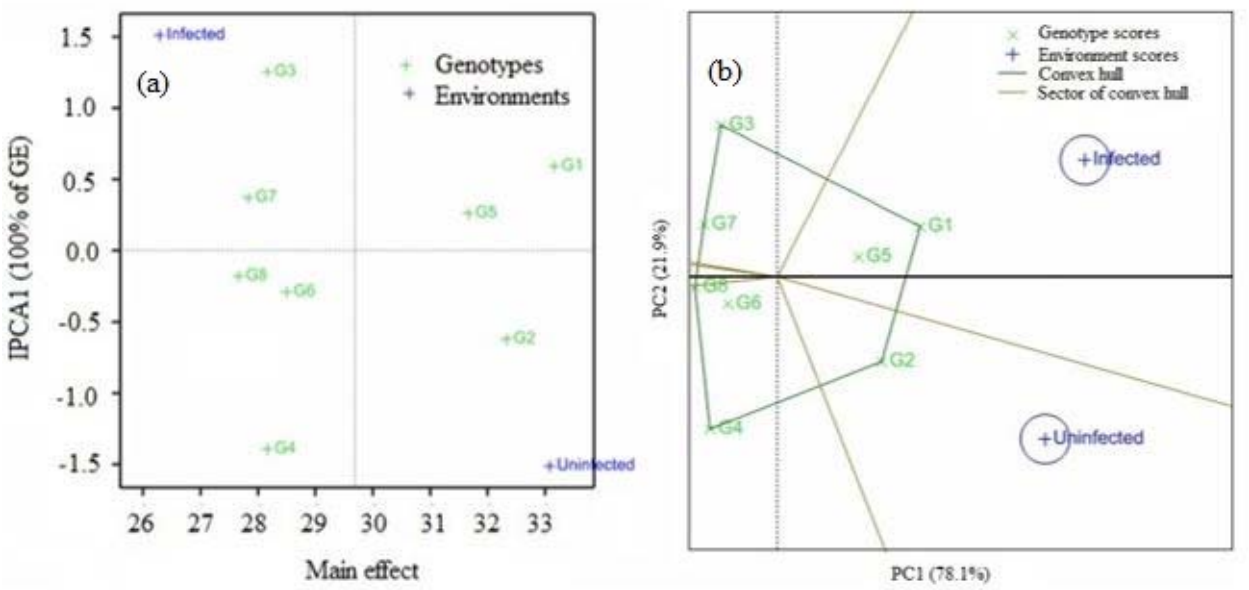

Fig. 1: AMMI plot of genotype and environment means against the first IPCA scores (a) and GGE biplot (b) of the plant height in soyabean genotypes infected and uninfected with *Cucumber mosaic virus*

Note: G1=TGX 1448-2A; G2=TGX 1951-3F; G3=TGx 1987-10F; G4=TGX 1993-4FN; G5=TGX 1994; G6=TGX 2017-6E; G7=TGX 2023-1E; G8=TGX 2025-6E

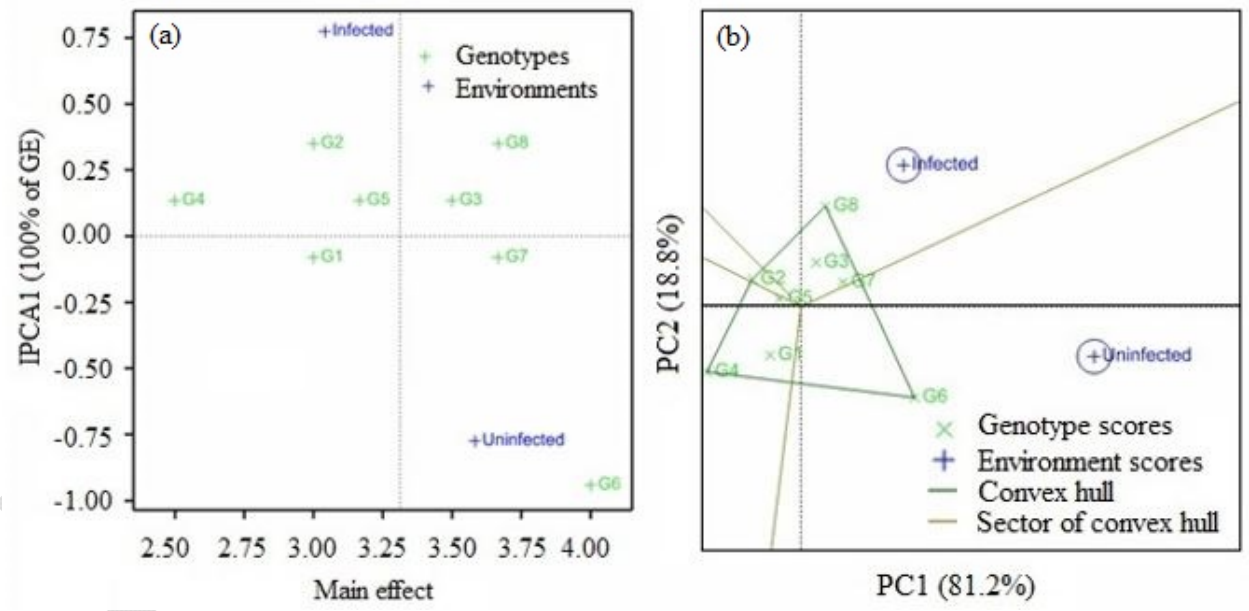

Fig. 2: AMMI plot of genotype and environment means against the first IPCA scores (a) and GGE biplot (b) of the leaf diameter in soyabean genotypes infected and uninfected with *Cucumber mosaic virus*

Note: G1=TGX 1448-2A; G2=TGx 1951-3F; G3=TGx 1987-10F; G4=TGX 1993-4FN; G5=TGX 1994; G6=TGX 2017-6E; G7=TGX 2023-1E; G8=TGX 2025-6E

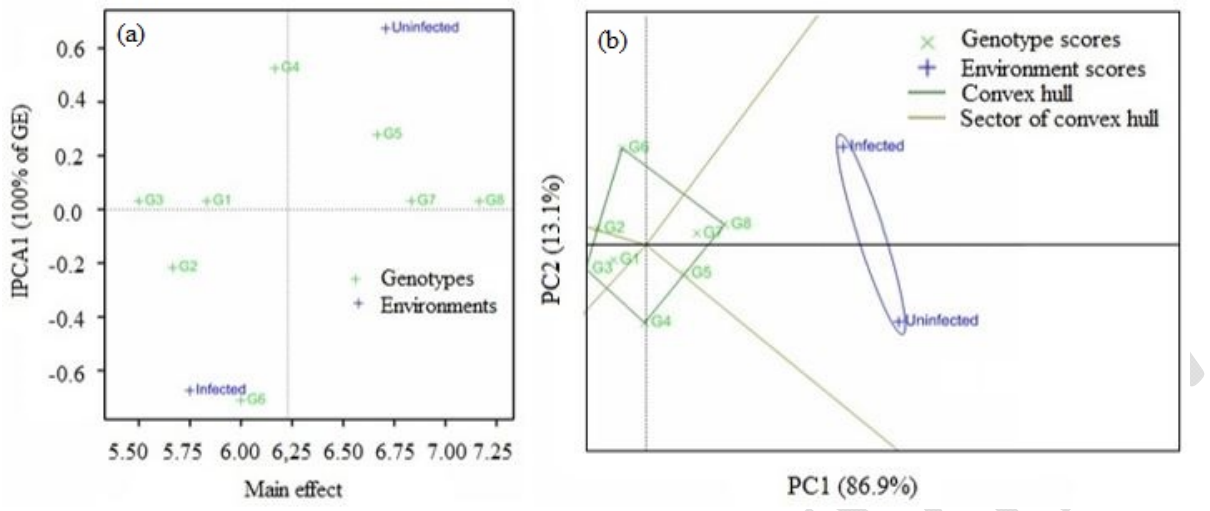

Fig. 3: AMMI plot of genotype and environment means against the first IPCA scores (a) and GGE biplot (b) of the leaf length in soyabean genotypes infected and uninfected with *Cucumber mosaic virus*

Note: G1=TGX 1448-2A; G2=TGx 1951-3F; G3=TGx 1987-10F; G4=TGX 1993-4FN; G5=TGX 1994; G6=TGX 2017-6E; G7=TGX 2023-1E; G8=TGX 2025-6E

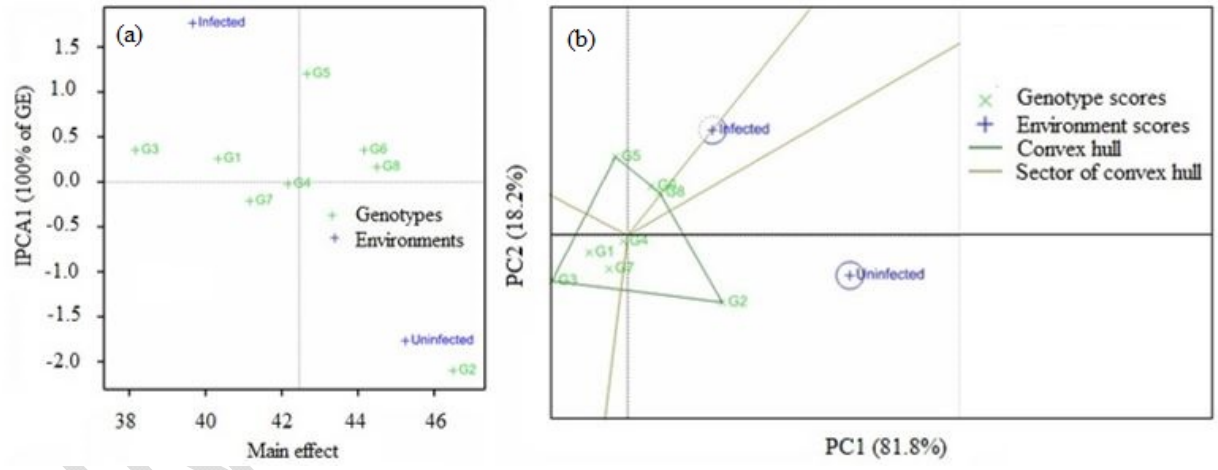

Fig. 4: AMMI plot of genotype and environment means against the first IPCA scores (a) and GGE biplot (b) of the number of leaves per plant in soyabean genotypes infected and uninfected with *Cucumber mosaic virus*

Note: G1=TGX 1448-2A; G2=TGx 1951-3F; G3=TGx 1987-10F; G4=TGX 1993-4FN; G5=TGX 1994; G6=TGX 2017-6E; G7=TGX 2023-1E; G8=TGX 2025-6E

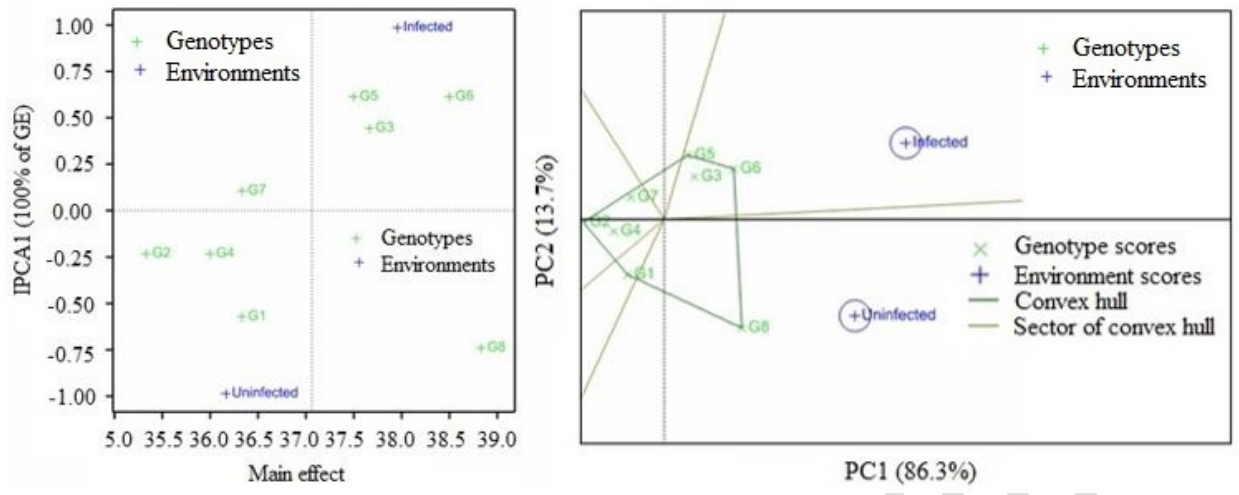

Fig. 5: AMMI plot of genotype and environment means against the first IPCA scores (a) and GGE biplot (b) of the number of days to flowering in soyabean genotypes infected and uninfected with *Cucumber mosaic virus*

Note: G1=TGX 1448-2A; G2=TGx 1951-3F; G3=TGx 1987-10F; G4=TGX 1993-4FN; G5=TGX 1994; G6=TGX 2017-6E; G7=TGX 2023-1E; G8=TGX 2025-6E

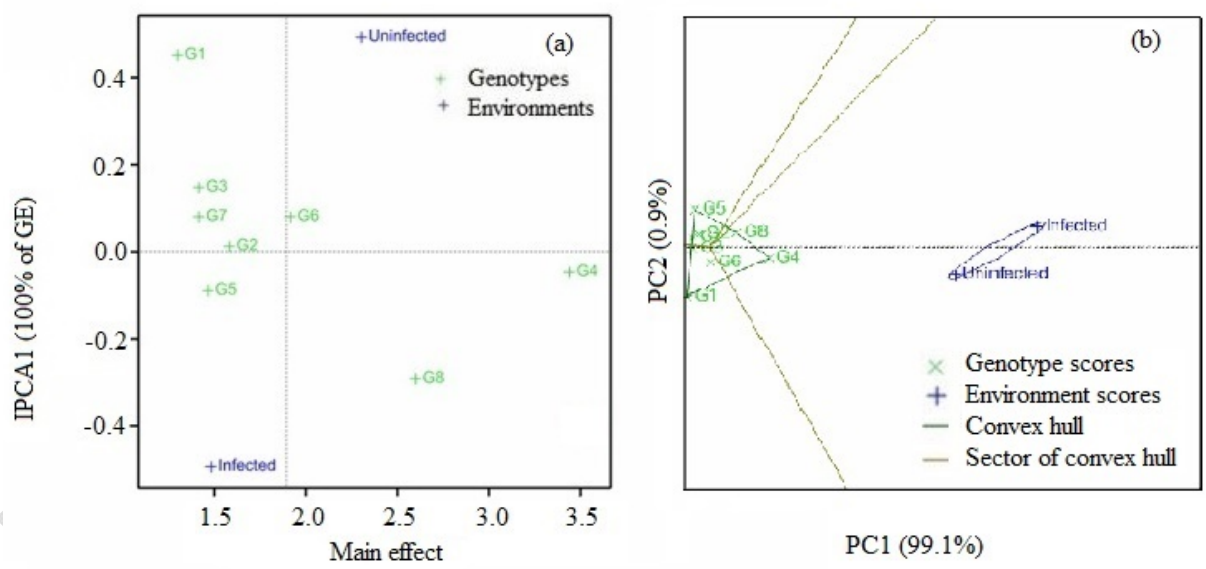

Fig. 6: AMMI plot of genotype and environment means against the first IPCA scores (a) and GGE biplot (b) of the seed weightin soyabean genotypes infected and uninfected with *Cucumber mosaic virus*

Note: G1=TGX 1448-2A; G2=TGx 1951-3F; G3=TGx 1987-10F; G4=TGX 1993-4FN; G5=TGX 1994; G6=TGX 2017-6E; G7=TGX 2023-1E; G8=TGX 2025-6E

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