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## YIELD STABILITY AND GEI BY MULTIVARIATE AND UNIVARIATE MODELS IN NIGER (*Guizotia abyssinica* L.)

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### ABSTRACT

The present investigation was carried out with forty Niger genotypes at multi-environments for assessment of genotype x environment interaction and identification of high yielding and stable genotypes of Niger crop. Forty Niger genotypes were tested across five multi-environments in a randomized block design with replication thrice during *Kharif*, 2018 and *Kharif*, 2019. Combined analysis of variance and AMMI analysis of pooled data showed that genotype, environment and GEI effect were highly significant ( $p < 0.01$ ) for seed yield. As per AMMI GGE biplots, two different mega-environments (METs) were identified, the first MET consists E1, E3 and E4 which are potential and excellent sites for discrimination of superior genotypes and second MET includes E2 and E5 were stable places. The genotypes, G28, G33, G8, G17, and G3 (seed yield plant<sup>-1</sup>), and G6, G33, G8, G17 and G3 (seed yield plot<sup>-1</sup>) were suitable for favorable environments while G4 and G7 (seed yield plant<sup>-1</sup>), and G27, G20, G1, G37 and G25 (seed yield plot<sup>-1</sup>) were suitable for unfavorable environments. Considering all the stability parameters ( $b_i$ ,  $S^2_{di}$ , IPCA1, ASV and GSI) and AMMI GGE biplots of pooled data, genotypes, G36, G32, G24 and G10 had high mean seed yield and stable across the environments. These superior genotypes about grain yield and GEI impact, and can be recommended for future investigations.

**Keywords:** Niger, Genotype x Environment Interaction, stability, yield, GGE biplot..

### Introduction

The concept of genotype x environment interaction might be mimicked when plants adapting to the new or fluctuating of environment. The other idea of genotype by environment interaction (GEI) could be considered as the pleiotropic effect of particular variants across environments (Malosetti *et al.*, 2013; Juenger, 2013). The term genotype refers to the genetic makeup of an organism while environment refers to biophysical factors that have an effect on the growth and development of crop genotype. Genotype x environment interaction refers to two or more genotype performs differently in different environments (Kim *et al.*, 2014).

Niger crop growers require varieties that are reliable and stable across environments as well as have high yield potential under favorable conditions. However, the response of different genotypes under different environments can be varied. This might be due to the fluctuation of rainfall pattern during cropping season, emerging and re-emerging disease as well as insects and abiotic factors like different soil status, drought and others stresses (Farshadfar *et al.*, 2012). Consequently, a variety which performs well in one environment during one season may not perform in different testing sites. This showed that GEI impede on superior genotypes across environment (Higginson and Reader, 2009). In such situation, it is difficult for breeder to select high yielding stable genotype across tested environments. Thus, plant breeders are

stimulated to test multi-environment trials (METs) and select superior as well as stable genotypes that show high grain yield performance across environments.

Statistical analysis of genotype by environment interaction is important to analysis multi-environment trials, METs. Several biometrical methods reported to analysis a pattern of genotype by environmental interaction (GEI), stability and adaptability. Among these biometrical techniques, Additive Main Effects and Multiplicative Interaction (AMMI) and Genotype and Genotype by Environment Interaction (GGE) Biplot are the most common statistical tools used to analysis of MET data to reveal pattern of GEI (Gauch and Zobel, 1997; Yan *et al.*, 2000). To compute METs, AMMI model analysis the variance (ANOVA) for genotype, environment and their interaction as well as decompose GEI into principal components. It also used to determine stability of genotype across locations using principal component axis. AMMI also an effective tool to detect the GEI patterns graphically. However, interpretation of output from principal components (PCA) is likely difficult for genotype targeting environment. Thus, GGE biplot is suggested and superior to the AMMI to visualize GEI graphically at mega-environments (Yan *et al.*, 2007). Furthermore, GGE biplot analysis is efficient to identify: the best performing genotype in the given tested environment, the discriminating power of environment and it rank the cultivars based on mean yield and stability of cultivars (Yan and Tinker, 2006). Moreover, it helps to assess the relationship between environments and re-planning the targeted environments to test cultivars in plant breeding program (Fan *et al.*, 2007; Dehghani *et al.*, 2009). Therefore, the objective of this study was to evaluate different Niger genotypes at multi-environments, to identify high yielding as well as stable niger genotypes and discriminating environments using GGE-biplot analysis.

## Materials and Methods

The experiments were conducted at five environments which represent a mid-altitude sub-humid agro-ecology of India and their details were given in Table 1. The testing locations were namely; ARS, Phondaghat (E1), ARS, Shirgaon (E2), Dept. of Agril. Botany, Dapoli (E3), RARS, Karjat (E4) and ARS, Plaghar (E5) during *Kharif*, 2018 and *Kharif*, 2019. The experiments laid down in randomized block design with three replications having forty niger genotypes (Table 2). Each genotype was planted with spacing of 30 cm and 10 cm between rows and plant, respectively. All recommended agronomic package practices were applied for healthy crop growth.

The combined analysis of variance was proceeded to look at  $G \times E$  and stability of the genotypes across all environments. The AMMI model, which combines standard analysis of variance with IPC analysis (Zobel *et al.*, 1988), was used to investigate of  $G \times E$  interaction. In AMMI model the contribution of each genotype and each environment to the  $G \times E$  interaction is assessed by use of the biplot graph display in which yield means are plotted against the scores of the IPCA 1 (Zobel *et al.*, 1988).

The regression coefficient ( $b_i$ ) and deviation from regression line ( $S^2_{di}$ ) was estimated as per stability model of Eberhart and Russell (1966). The AMMI stability value (ASV) estimated as per formula given by Purchase *et al.* (2000) and GSI calculated by the formula suggested by Farshadfar *et al.* (2012).

In this study, GGE biplot method was used to investigate Genotype and Genotype  $\times$  Environment interaction analysis was conducted using GGE biplot software to evaluate grain yield stability, identify superior genotypes and to visualize pattern of environments graphically. Thus, GGE biplot analyzed according to Yan *et al.* (2000).

**Table 1 :** Details of the experimental testing environments.

Name of Site	Longitude (East)	Latitude (North)	Rainfall (mm)	Mean sea level	Soil type
ARS, Phondaghat (E1)	73-47°18''	16-22°35''	3500	145.10	Lateritic
ARS, Shirgaon (E2)	73.62°	17.45°	3000	75	Lateritic
Dept. of Agril. Botany, Dapoli (E3)	73°11'8''	17°45'32''	4000	243.84	Lateritic
RARS, Karjat (E4)	73°33''	18°91''	3500	200	Medium black
ARS, Plaghar (E5)	72.76°	16.69°	2500	7	Medium black

## Results and Discussion

Combined analysis of variance and AMMI analysis showed that genotype, environment and GEI effect were highly significant ( $p < 0.01$ ) for seed yield.

The per cent sum of squares explained for genotype (40.04% & 24.31%), environment (10.52% & 3.35%) and GEI (49.01% & 71.57%) for seed yield plant<sup>-1</sup> and seed yield plot<sup>-1</sup>, respectively of the total experimental variations, indicating the importance of genotypic

potential and environment for variations in seed yield (Table 3 & 4). This showed that environments were diverse and affects the seed yield potential of the genotypes. This might be due to fluctuation of rainfall during cropping season, different soil statues and other biotic stress (Farshadfar *et al.*, 2012). This finding also agreed with Fan *et al.* (2007), Mitrovic *et al.* (2012), Bhavsar (2017), Boureima *et al.* (2017), Jay Laxami (2017), Baraki and Gebremariam (2018), Tadele *et al.* (2018), Baraki *et al.* (2019) and Abdelsatar *et al.* (2020). The present study showed that the magnitude of GEI sum of square was triple than genotype mean for seed yield plot<sup>-1</sup>, indicating the difference responses of genotype across environments.

### Stability by Regression model

As per Regression model, genotypes deviated non-significantly from zero, regression coefficient (bi) near to one with higher mean seed yield indicating these genotypes are stable (Eberhart and Russell, 1966). Accordingly, genotypes, G36 ( $S^2di=0.006$ ,  $bi=1.102$  and  $M=3.5g$ ), G32 ( $S^2di=-0.063$ ,  $bi=0.922$  and  $M=3.2g$ ), G24 ( $S^2di=-0.057$ ,  $bi=0.966$  and  $M=3.3g$ ) and G10 ( $S^2di=-0.075$ ,  $bi=-0.947$  and  $M=2.9g$ ) (Table 5) deviated non-significantly from zero, regression coefficient near to one with higher mean seed yield plant<sup>-1</sup>, respectively indicating these genotypes were most stable. Also genotypes deviated non-significantly from zero, regression coefficient (bi) near to one with higher mean seed yield indicating these genotypes are stable (Eberhart and Russell, 1966). Accordingly, genotypes, G36 ( $S^2di=0.10$ ,  $bi=1.840$  and  $M=265g$ ), G32 ( $S^2di=0.59$ ,  $bi=1.557$  and  $M=257g$ ), G24 ( $S^2di=0.01$ ,  $bi=1.032$  and  $M=260g$ ) and G10 ( $S^2di=0.10$ ,  $bi=1.316$  and  $M=257g$ ) (Table 6) deviated non-significantly from zero, regression coefficient near to one with higher mean seed yield plot<sup>-1</sup>, respectively indicating these genotypes were most stable. The similar results were in conformity with findings of Igor *et al.* (2013), Muhammad *et al.* (2013), Patil *et al.* (2014), Bhavsar (2017), Tadale *et al.* (2018), Abdelsatar *et al.* (2020) and Ansarifard *et al.* (2020).

### Stability by AMMI model

As per AMMI model, AMMI stability value (ASV) and Genotype Selection Index (GSI) aids selection of relatively stable high yielding genotypes. Genotypes would have high mean seed yield, IPCA1 score close to zero (positive/negative), small value of ASV and GSI is relatively stable (Farshadfar *et al.*, 2012). Accordingly, Genotype, G36 ( $M=3.5g$ ,  $IPCA1=-0.129$ ,  $ASV=0.16$  and  $GSI=8$ ) had higher mean yield over than average performance (grand

mean) as well as relatively small ASV value and GSI index, respectively, and showed the best stable genotype. Also, G32 ( $M=3.2g$ ,  $IPCA1=-0.296$ ,  $ASV=0.38$  and  $GSI=23$ ), G24 ( $M=3.3$ ,  $IPCA1=-0.075$ ,  $ASV=0.26$  and  $GSI=17$ ) and G10 ( $M=2.9g$ ,  $IPCA1=0.015$ ,  $ASV=0.157$  and  $GSI=11$ ) would have greater mean and small ASV and GSI, and showed relatively stable for seed yield plant<sup>-1</sup> (Table 5). Also, Genotype, G36 ( $M=265g$ ,  $IPCA1=-0.82$ ,  $ASV=1.58$  and  $GSI=15$ ) had higher mean yield over than average performance (grand mean) as well as relatively small ASV value and GSI index, respectively, and showed the best stable genotype. Also, G32 ( $M=257g$ ,  $IPCA1=-0.10$ ,  $ASV=0.19$  and  $GSI=6$ ), G24 ( $M=260g$ ,  $IPCA1=0.40$ ,  $ASV=0.77$  and  $GSI=9$ ) and G10 ( $M=257$ ,  $IPCA1=-0.61$ ,  $ASV=1.18$  and  $GSI=13$ ) would have greater mean and small ASV and GSI, and showed relatively stable for seed yield plot<sup>-1</sup>(Table 6). The similar results were in conformity with findings of Marisol *et al.* (2016), Seyed *et al.* (2016), Ali and Abdollah (2017), Boureima *et al.* (2017), Jay Laxami (2017), Baraki and Gebremariam (2018), Tadale *et al.* (2018), Baraki *et al.* (2019) and Abdelsatar *et al.* (2020).

Considering both models, G36, G32, G24 and G10 deviated non-significantly from zero, regression coefficient near to one, IPCA1 score close to zero, smaller ASV value, less GSI index with high mean seed yield. This suggesting that these genotypes were most stable over the environments (Table 4 and 5). The similar results were in conformity with findings of Abate *et al.* (2015), Mekonnen *et al.* (2015), Marisol *et al.* (2016), Seyed *et al.* (2016), Ali and Abdollah (2017), Bhavsar (2017), Boureima *et al.* (2017), Jay Laxami (2017), Baraki and Gebremariam (2018), Tadale *et al.* (2018), Baraki *et al.* (2019) and Abdelsatar *et al.* (2020).

### AMMI GGE Biplots

AMMI biplot is to visualize the stability and adaptability of genotypes across tested environments (Gauch and Zobel, 1997; Gauch, 2006). Moreover, the model also useful on grouping similar performance genotypes and / or environments and also provide some information about GEI in order to identify the genotypes adapted to specific environment. Accordingly, genotypes, G36, G24, G32, G40 (Fig. 1.1) were exhibited high yield and stable with high additive main effect for seed yield plant<sup>-1</sup> while genotypes, G28, G37, G18, G22, G4, G8, G11 and G17 had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. Genotypes, G28, G37, G18, G22 and G11 were suited for favorable whereas

G4 and G8 were suited for unfavorable environments. Similarly, environments E1, E2 and E4 showed little interaction and environments E3 and E5 were exert maximum interaction.

Similarly, genotypes, G36, G24, G10, G4, G32 and G2 (Fig. 2.1) were exhibited high seed yield and stable with high additive main effect for seed yield plot<sup>-1</sup> while genotypes, G6, G33, G8, G17, G3, G27, G20, G37, G1 and G25 had IPCA1 score (positive or negative) which were indicating the maximum interaction between genotype and environment. Genotypes, G6, G33, G8, G3 and G17 were suited for favorable and genotypes, G27, G20, G37, G1 and G25 were suited for unfavorable environments. Similarly, environments E1, E2 and E4 showed little interaction and environments E3 and E5 were exert maximum interaction. The similar results were in harmony with findings of Abeya *et al.* (2014), Patil *et al.* (2014), Abate *et al.* (2015), Mekonnen *et al.* (2015), Marisol *et al.* (2016), Seyed *et al.* (2016), Ali and Abdollah (2017), Bhavsar (2017), Boureima *et al.* (2017), Jay Laxami (2017), Baraki and Gebremariam (2018), Tadele *et al.* (2018), Baraki *et al.* (2019) and Abdelsatar *et al.* (2020).

The GGE biplot graphically shows GEI of METs and visual genotype to which environment and mega-environments identification (Yan *et al.*, 2000). From the polygon view of the GGE biplot, the vertex genotype showed the one that give the highest seed yield for each environment in which genotypes lie. Accordingly (Fig. 1.2), G38 was the classiest at E1 and E2, G28 and G18 were excellent at E5, G5 and G8 were the best at E4 and G32 was the winning genotype in E3 for seed yield plant<sup>-1</sup> suggesting that these genotype won to which environment lie. No any environment felt in genotypes G25, G11 and G18 located on the vertices of the polygon performed either the best or the poorest in one or more environments. Discriminating environments were ranked from top to bottom as E4>E1>E3>E2>E5. Environments, E1, E4 and E3 were found as ideal environments for discrimination of superior genotypes.

For seed yield plot<sup>-1</sup>(Fig. 2.2), G14 was the winning genotype at E5, G8 was classiest at E2, G17 and G23 were the pre-eminent in E4, G25 and G1 were the excellent at E1 and G6 was best in E3. No any environment felt in genotypes G20, G27 and G8 located on the vertices of the polygon performed either the best or the poorest in one or more environments. Discriminating environments were ranked from top to bottom as E4>E3>E1>E2>E5. Environments, E4, E3 and E1 were observed to be as ideal environments for discrimination of superior genotypes. The similar

results were also reported by Patil *et al.* (2014), Abate *et al.* (2015), Mekonnen *et al.* (2015), Marisol *et al.* (2016), Seyed *et al.* (2016), Ali and Abdollah (2017), Bhavsar (2017), Boureima *et al.* (2017), Jay Laxami (2017), Baraki and Gebremariam (2018), Tadele *et al.* (2018), Baraki *et al.* (2019) and Abdelsatar *et al.* (2020).

### Discriminating ability of tested environments

GGE biplot also view the discriminating and representativeness ability of environments to identify an environment that efficiently discernment the superior genotype in the tested environments. A long/away environmental vector/spoke from origin showed a high capacity to discriminate genotype (Yan and Tinker, 2006). The discrimination ability of the environments can be obtained by the location of environmental spokes away from origin of GGE biplot. Among tested environments, E1, E3 and E4 were the most discriminating environments that provided adequate information on the performance of the genotypes. Further explanation, these environments were powerful for genotype evaluation and interesting sites to identify superior genotypes. On other hand, E2 and E5 environments falls close to the bi-plot origin and the least discriminating environment (Fig. 1.2 and Fig. 2.2) and it provided little information about the performance difference of genotypes. However, these environments were best for deciding the most stable genotypes under study. The similar results were also reported by Patil *et al.* (2014), Abate *et al.* (2015), Mekonnen *et al.* (2015), Marisol *et al.* (2016), Seyed *et al.* (2016), Ali and Abdollah (2017), Bhavsar (2017), Boureima *et al.* (2017), Jay Laxami (2017), Baraki and Gebremariam (2018), Tadele *et al.* (2018), Baraki *et al.* (2019) and Abdelsatar *et al.* (2020).

Therefore, evaluation of multi-environment experiments for distinguishing the effects of the genotype and the environment, and then assess the G x E interaction in a reduced dimensional space with minimum error AMMI stability model is the best and more efficient than joint regression model.

### Conclusion

It is concluded that, the mean sum of squares for genotype, environment, genotype x environment interaction (GEI) and their Interaction Principal Component Analyses (IPCA) were highly significant for all the traits. This showed that environments were diverse and affects the performance potential of genotypes. As per AMMI GGE biplots, two different mega-environments (METs) were identified, the first MET consists E1, E3 and E4 which are potential and excellent sites for discrimination of superior genotypes

and second MET includes E2 and E5 were stable places. The genotypes, G28, G33, G8, G17, and G3 (seed yield plant<sup>-1</sup>), and G6, G33, G8, G17 and G3 (seed yield plot<sup>-1</sup>) were suitable for favorable environments while G4 and G7 (seed yield plant<sup>-1</sup>), and G27, G20, G1, G37 and G25 (seed yield plot<sup>-1</sup>) were suitable for unfavorable environments. Considering all

the stability parameters (Regression model and AMMI model) and AMMI GGE biplots, genotypes, G36, G32, G24 and G10 had high mean seed yield and stable across tested environments. These superior genotypes about grain yield and GEI impact, and can be recommended for future investigations.

**Table 2 :** List of genotypes/varieties and their sources

Sr. No.	Genotype code	Name of Genotypes	Source	Sr. No.	Genotype code	Name of Genotypes	Source
1.	G1	GP-54	ZARS, Igatpuri	21.	G21	NMLT-12	ZARS, Igatpuri
2.	G2	GP-57	ZARS, Igatpuri	22.	G22	NMLT-13	ZARS, Igatpuri
3.	G3	IGPN 14-2	ZARS, Igatpuri	23.	G23	NMLT-14	ZARS, Igatpuri
4.	G4	IGPN 14-6	ZARS, Igatpuri	24.	G24	NMLT-15	ZARS, Igatpuri
5.	G5	IGPN 14-9	ZARS, Igatpuri	25.	G25	NGR -1	ARS, Shirgaon
6.	G6	IGPN 15-1	ZARS, Igatpuri	26.	G26	NGR -3	ARS, Shirgaon
7.	G7	IGPN 15-3	ZARS, Igatpuri	27.	G27	NGR -4	ARS, Shirgaon
8.	G8	IGPN 15-4	ZARS, Igatpuri	28.	G28	NGR -5	ARS, Shirgaon
9.	G9	IGPN 15-5	ZARS, Igatpuri	29.	G29	NGR -6	ARS, Shirgaon
10.	G10	NMLT-1	ZARS, Igatpuri	30.	G30	NGR -18	ARS, Shirgaon
11.	G11	NMLT-2	ZARS, Igatpuri	31.	G31	NGR -22	ARS, Shirgaon
12.	G12	NMLT-3	ZARS, Igatpuri	32.	G32	NGR -24	ARS, Shirgaon
13.	G13	NMLT-4	ZARS, Igatpuri	33.	G33	Devadi Local 2	Devadi, Solapur
14.	G14	NMLT-5	ZARS, Igatpuri	34.	G34	Devadi Local 3	Devadi, Solapur
15.	G15	NMLT-6	ZARS, Igatpuri	35.	G35	Devadi Local 4	Devadi, Solapur
16.	G16	NMLT-7	ZARS, Igatpuri	36.	G36	Devadi Local 5	Devadi, Solapur
17.	G17	NMLT-8	ZARS, Igatpuri	37.	G37	Modnimb Local 2	Modnimb, Solapur
18.	G18	NMLT-9	ZARS, Igatpuri	38.	G38	Sahyadri	ZARS, Igatpuri
19.	G19	NMLT-10	ZARS, Igatpuri	39.	G39	Phule Karala	ZARS, Igatpuri
20.	G20	NMLT-11	ZARS, Igatpuri	40.	G40	Phule Vaitrna	ZARS, Igatpuri

**Table 3:** Combined ANOVA for seed yield plant<sup>-1</sup> and seed yield plot<sup>-1</sup> of 40 niger genotypes tested at five environments.

Characters	Seed yield plant <sup>-1</sup> (g)					Seed yield plot <sup>-1</sup> (g)				
	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	7.46	0.19*	3.26	40.04	39	22224.69	569.86**	1.35	24.31
Replication (R)	2	0.08	0.04	1.91		2	710.06	355.03	1.79	
Environment (E)	4	1.96	0.49**	8.38	10.52	4	3063.10	765.77**	1.82	3.35
G x E	156	9.13	0.05	0.25	49.01	156	65441.41	419.49**	0.80	71.57
Residual	36	0.17	0.004	0.43		36	250.88	6.96	0.08	
Pooled Error	390	90.92	0.23			390	203262.91	521.18		

**Table 4:** ANOVA for AMMI model of pooled data for seed yield plant<sup>-1</sup> and seed yield plot<sup>-1</sup> of 40 niger genotypes tested at five environments.

Characters	Seed yield plant <sup>-1</sup> (g)					Seed yield plot <sup>-1</sup> (g)				
	DF	SS	MS	F	SS% Explained	DF	SS	MS	F	SS% Explained
Genotype (G)	39	9.86	0.252**	12.70	24.71	39	55760.13	1429.74**	16.60	53.91
Environment (E)	4	26.95	0.737**	338.52	67.53	4	34234.06	8558.51**	99.37	33.10
Genotype x Environment	156	3.10	0.019*	-	7.77	156	13435.23	86.12**	-	12.99
IPCA1	42	1.25	0.029**	2.61	3.13	42	8400.21	200.00**	2.32	8.12
IPCA2	40	1.01	0.025**	2.22	2.53	40	4353.53	108.83**	1.26	4.21
IPCA3	38	0.66	0.017*	1.53	1.65	38	430.60	11.33**	0.13	0.42
Residual	36	0.17	0.004	0.43		36	250.88	6.96	0.08	
Pooled Residual	74	0.84	0.011	-		156	13435.23	86.12	-	
Total	199	39.91	0.200	10.07		199	103429.42	519.34	6.03	

**Table 5:** Stability parameters of 40 niger genotypes for seed yield plant<sup>-1</sup> (g)

Sr. No.	Genotype code	Seed yield plant <sup>-1</sup> (g)								
		Mean	RYi	bi	S <sup>2</sup> di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	2.8	5	1.384	-0.046	0.004	0.095	0.10	4	9
2.	G 2	2.9	4	0.706	-0.035	-0.870	-0.084	1.08	24	28
3.	G 3	2.7	6	0.970	-0.054	-0.180	0.024	0.22	12	18
4.	G 4	2.9	4	0.114	-0.006	-0.297	0.077	0.37	19	23
5.	G 5	2.7	6	-0.261	-0.058	-0.151	0.370	0.41	22	28
6.	G 6	2.8	5	-0.789	0.049	0.113	-0.161	0.21	11	16
7.	G 7	2.5	8	-1.143	-0.072*	-0.101	0.122	0.17	8	16
8.	G 8	2.7	6	-0.803	-0.061*	-0.212	0.232	0.35	18	24
9.	G 9	2.6	7	-1.533	-0.078*	-0.076	0.227	0.25	14	21
10.	G 10	2.9	4	-0.947	-0.075	0.015	0.157	0.16	7	11
11.	G 11	2.8	5	-0.011	-0.051	0.201	-0.164	0.30	16	21
12.	G 12	2.6	7	0.813	-0.076*	-0.057	-0.123	0.14	5	12
13.	G 13	2.7	6	1.080	-0.031	0.122	-0.037	0.16	7	13
14.	G 14	2.7	6	0.405	-0.005	0.060	0.066	0.10	4	10
15.	G 15	2.7	6	0.427	-0.061	-0.015	-0.025	0.03	1	7
16.	G 16	2.7	6	4.064**	0.059*	-0.140	-0.080	0.19	10	16
17.	G 17	2.7	6	3.795**	-0.034	0.179	-0.137	0.26	15	21
18.	G 18	2.7	6	2.096**	0.029	0.320	-0.083	0.40	21	27
19.	G 19	2.6	7	2.874**	-0.037	-0.164	0.068	0.21	11	18
20.	G 20	2.5	8	1.962	-0.047*	-0.081	0.216	0.17	8	16
21.	G 21	2.8	5	0.452	-0.052*	-0.052	-0.132	0.08	3	8
22.	G 22	2.7	6	0.492	-0.015	0.287	0.049	0.41	22	28
23.	G 23	2.8	5	0.295	-0.045	-0.007	-0.216	0.10	4	9
24.	G 24	3.3	2	0.966	-0.057	-0.075	-0.101	0.26	15	17
25.	G 25	2.7	6	-1.150*	-0.064*	0.102	-0.242	0.23	13	19
26.	G 26	2.9	4	1.236	0.015	-0.008	-0.188	0.05	2	6
27.	G 27	2.7	6	3.185**	-0.029	0.047	0.054	0.30	16	22
28.	G 28	2.5	8	1.819	-0.041	0.433	0.296	0.55	23	31
29.	G 29	2.7	6	-0.680*	-0.057	0.155	-0.147	0.23	13	19
30.	G 30	2.7	6	1.389	-0.064*	0.136	0.130	0.26	15	21
31.	G 31	2.7	6	0.637	-0.037	-0.103	0.195	0.19	10	16
32.	G 32	3.2	3	0.922	-0.063	-0.296	-0.140	0.38	20	23
33.	G 33	2.8	5	0.884	-0.042	-0.021	-0.114	0.18	9	14
34.	G 34	2.7	6	1.464	-0.024	0.182	0.175	0.25	14	20
35.	G 35	2.9	4	0.736	-0.055	-0.143	0.115	0.32	17	21
36.	G 36	3.5	1	1.102	0.006	-0.129	-0.272	0.16	7	8
37.	G 37	2.7	6	1.376	0.000	0.311	0.033	0.41	22	28
38.	G 38	3.3	2	0.814	0.056	-0.171	-0.144	0.22	12	14
39.	G 39	2.9	4	2.968**	0.013	0.017	0.062	0.18	9	13
40.	G 40	3.3	2	1.362	-0.042	-0.122	-0.175	0.15	6	8

\*Significant at 5% level of significance

\*\*Significant at 1% level of significance

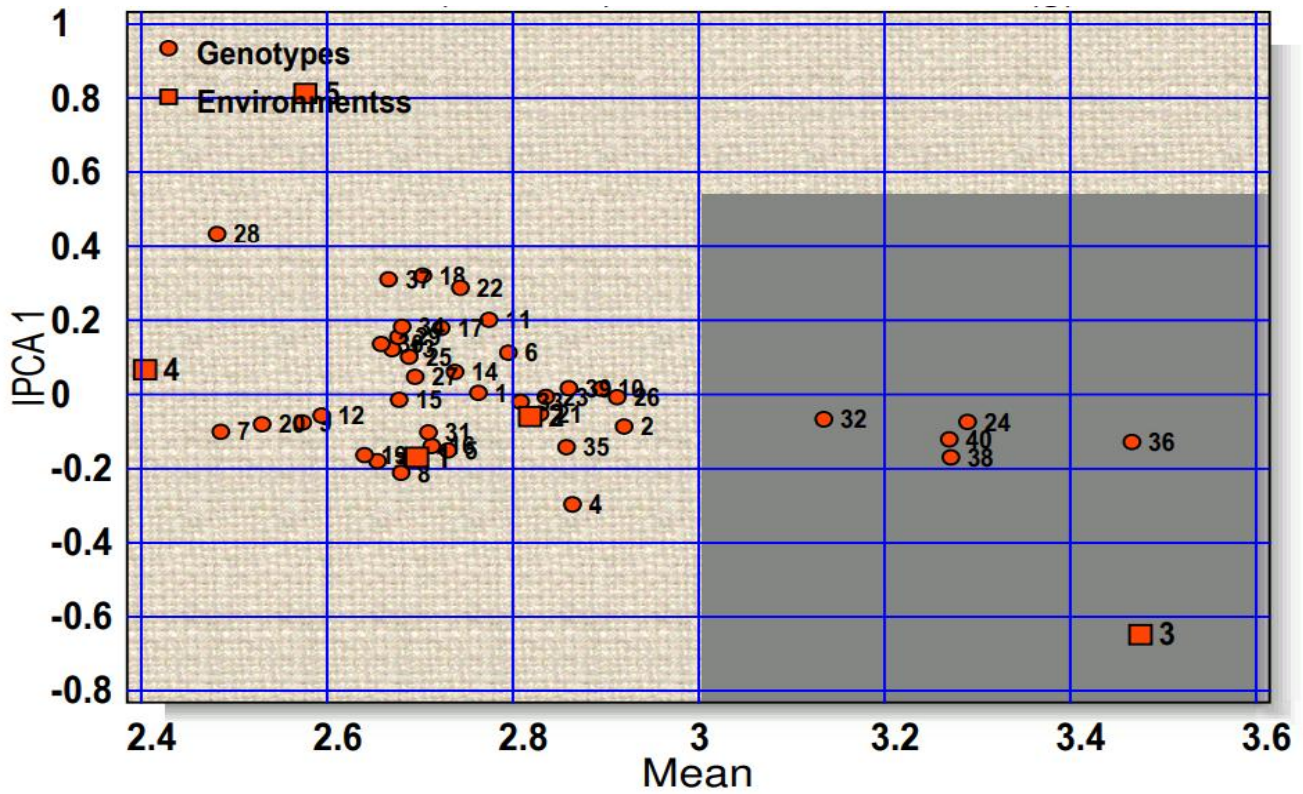


Fig. 1.1 : AMMI1 biplot showing mean performance and adaptability of 40 niger genotypes for seed yield plant<sup>-1</sup> (g) across five tested environments.

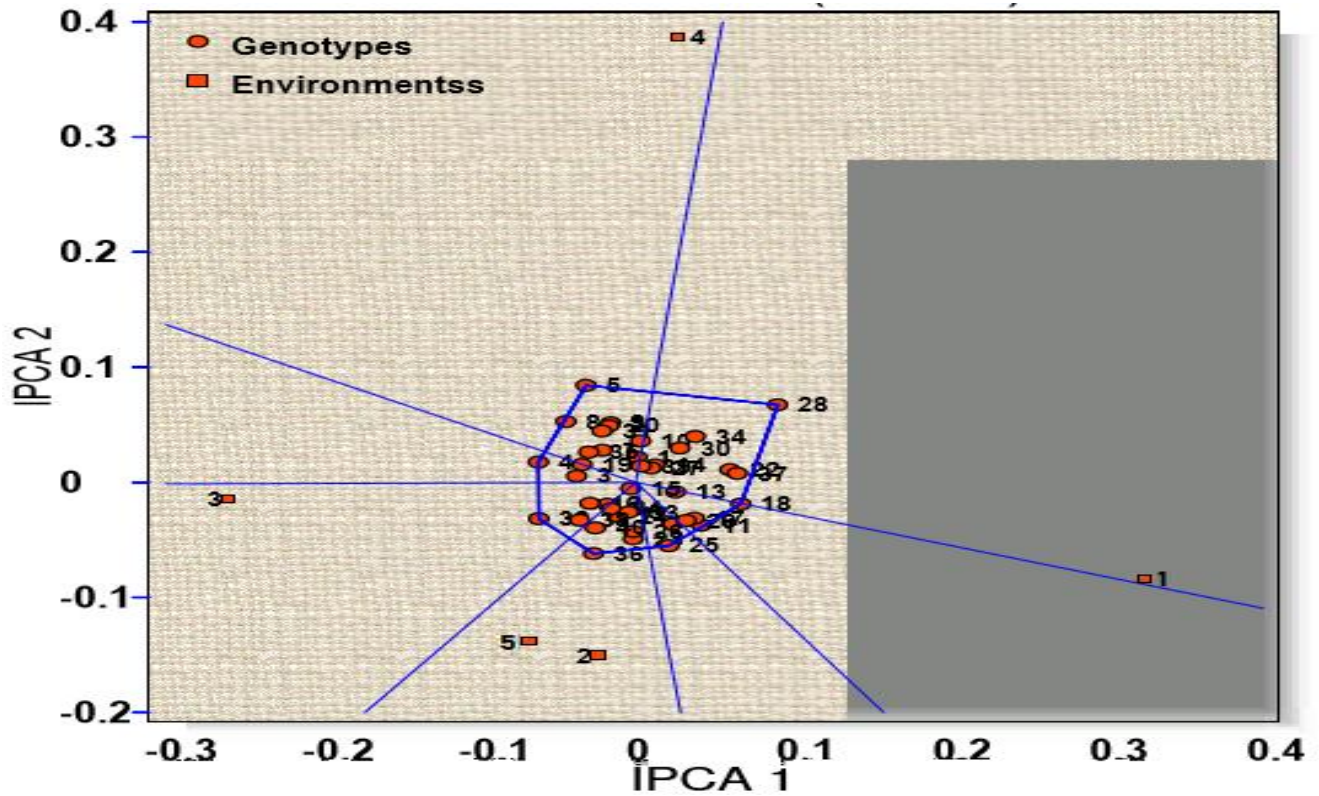


Fig. 1.2 : Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 niger genotypes in five environments.

**Table 6:** Estimation of stability parameters of 40 niger genotypes for seed yield plot<sup>-1</sup> (g)

Sr. No.	Genotype code	Seed yield plot <sup>-1</sup> (g)								
		Mean	RYi	Bi	S <sup>2</sup> di	IPCA1	IPCA2	ASV	RASVi	GSI
1.	G 1	229	7	3.361**	1.04	-2.20	-0.008	4.24	27	34
2.	G 2	246	5	0.291	0.04	-0.70	0.005	1.35	11	16
3.	G 3	214	15	0.642	11.00*	2.20	-0.003	4.24	27	42
4.	G 4	253	4	1.522	0.05	-0.20	-0.004	0.39	4	8
5.	G 5	209	19	2.399*	0.70	0.20	0.005	0.39	4	23
6.	G 6	203	23	4.282**	3.05**	3.90	0.009	7.52	31	54
7.	G 7	222	9	2.711**	4.07**	1.50	-0.014	2.89	23	32
8.	G 8	214	14	0.897	1.00	2.60	-0.017	5.02	29	43
9.	G 9	221	10	4.041**	16.80**	-0.41	0.012	0.79	8	18
10.	G 10	257	3	1.316	0.10	-0.61	-0.011	1.18	10	13
11.	G 11	216	13	-0.771*	0.30	0.81	0.008	1.56	13	26
12.	G 12	222	9	-0.127	1.01	1.11	-0.002	2.14	18	27
13.	G 13	217	12	-0.101	0.90	1.92	-0.004	3.70	25	37
14.	G 14	221	10	0.766	0.17	-0.81	-0.015	1.56	13	23
15.	G 15	221	10	2.173*	14.39**	-0.22	-0.003	0.42	6	16
16.	G 16	206	21	2.133*	0.03	-1.00	0.018	1.93	17	38
17.	G 17	201	24	5.271**	23.67**	2.20	0.025	4.24	27	51
18.	G 18	207	20	2.381*	1.09	0.01	0.007	0.02	1	21
19.	G 19	210	18	5.746**	18.02**	-0.71	-0.002	1.37	12	30
20.	G 20	208	20	4.478**	5.09**	-2.45	0.013	4.73	28	48
21.	G 21	210	19	1.810	0.76	-1.40	0.001	2.70	20	39
22.	G 22	211	18	-0.420	0.24	-0.61	0.008	1.18	10	28
23.	G 23	200	25	-0.760	-1.40*	-0.81	0.023	1.56	13	38
24.	G 24	260	2	1.032	0.01	0.40	-0.010	0.77	7	9
25.	G 25	232	6	0.400	0.99	-2.10	-0.009	4.05	26	32
26.	G 26	221	10	-0.490	1.00	-1.42	0.018	2.74	22	32
27.	G 27	214	14	0.323	0.67	-2.61	-0.006	5.03	30	44
28.	G 28	205	22	0.742	1.15	0.43	0.014	0.83	9	31
29.	G 29	218	11	-0.916*	0.40	-1.20	0.006	2.31	19	30
30.	G 30	212	17	0.289	0.09	1.70	0.002	3.28	24	41
31.	G 31	209	19	4.758**	7.50**	-0.21	0.004	0.41	5	24
32.	G 32	257	3	1.557	0.59	-0.10	-0.013	0.19	3	6
33.	G 33	207	20	0.276	0.80	2.60	0.004	5.02	29	49
34.	G 34	213	16	2.698*	1.02	0.90	-0.008	1.74	15	31
35.	G 35	221	10	0.633	10.99*	1.41	0.006	2.72	21	31
36.	G 36	265	1	1.840	0.10	-0.82	-0.009	1.58	14	15
37.	G 37	217	12	-4.660**	5.60**	-2.20	-0.005	4.24	27	39
38.	G 38	222	9	-3.610**	1.01	-0.05	-0.140	0.17	2	11
39.	G 39	218	12	-3.950**	1.05	-0.91	-0.004	1.76	16	28
40.	G 40	224	8	-5.620**	27.70**	-0.41	-0.019	0.79	8	16

\*Significant at 5% level of significance

\*\*Significant at 1% level of significance



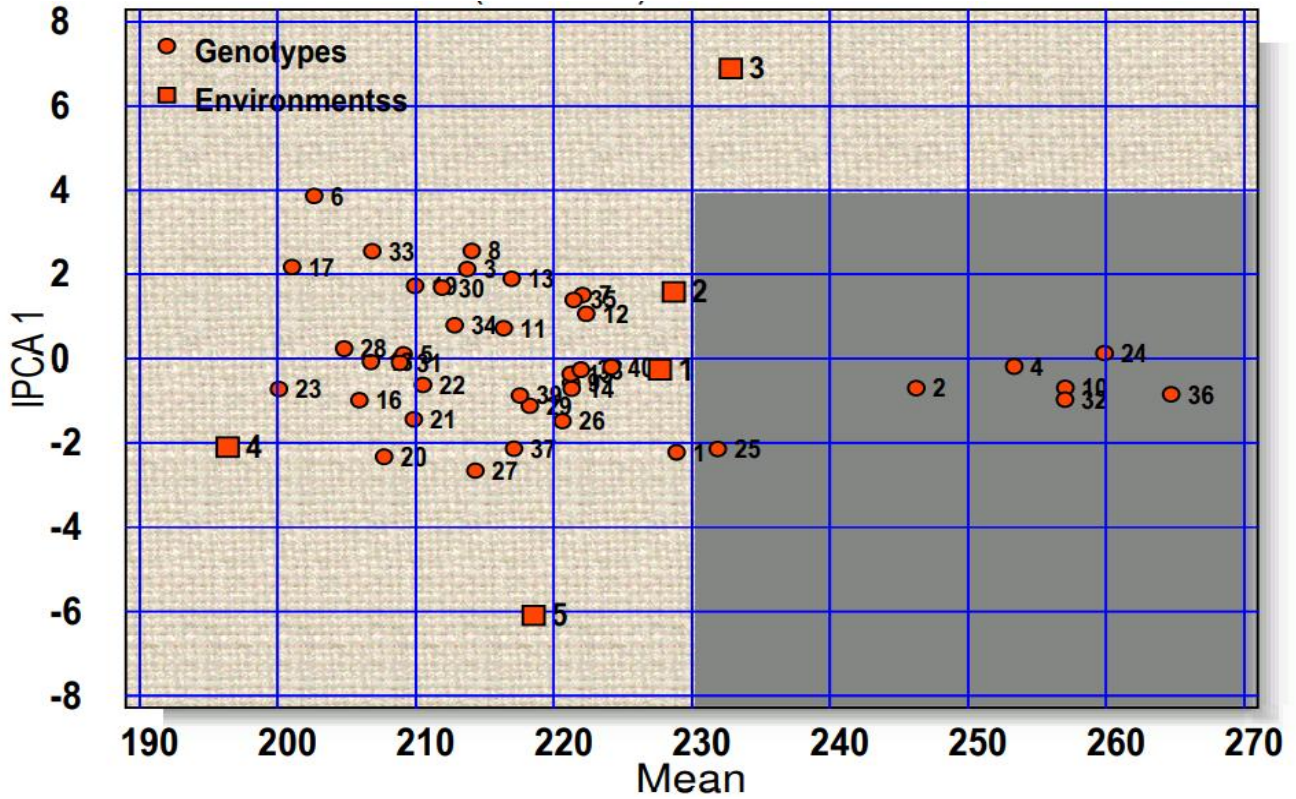


Fig. 2.1 : AMMI1 biplot showing mean performance and adaptability of 40 niger genotypes for seed yield plot<sup>-1</sup> (g) across five tested environments.

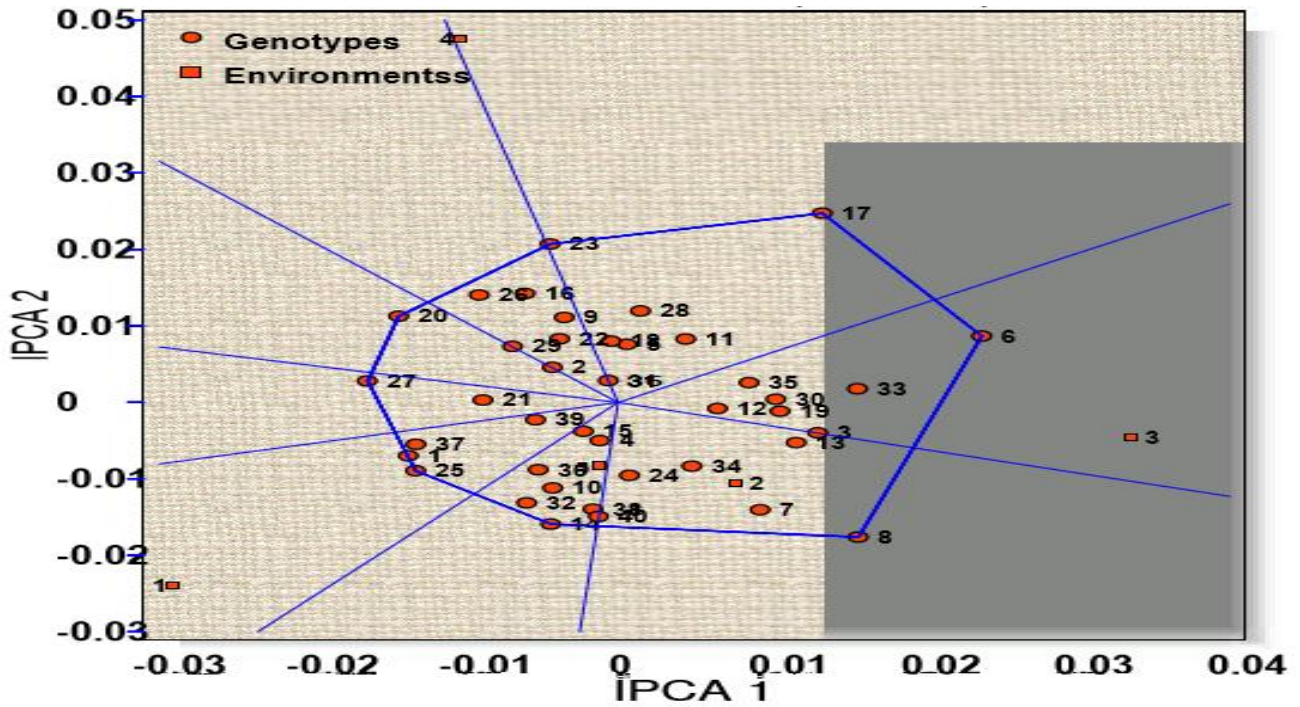


Fig. 2.2 : Polygon view of the GGE biplot (AMMI2) based on genotype x environment interaction of 40 niger genotypes in five environments.

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