



Evaluation of Extra-early Maturing Maize Genotypes for Grain Yield and Stability in the Groundnut Basin Agro-ecological Zone of Senegal

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Abstract

Maize is a highly valuable staple food crop in Sub-Saharan Africa regions. Its production is hampered by both biotic and abiotic stress. Early-maturing genetic resources appear as an excellent choice to manage adverse climatic change's effects. This study aimed to find the best extra-early maize genotypes based on genotype by environment interactions in the groundnut agro-ecological zone of Senegal. The trials were conducted in Paoskoto, Ndiédieng, Niore and Keur Sene during the rainy seasons of 2016 and 2017. Six extra-early maize genotypes were evaluated following a randomized complete block design with three replications. Data on grain yield were recorded and analysed using additive main effect and multiplicative interaction and genotype plus genotype by environment biplot methods. Analysis of variance revealed a significant ($P < 0.01$) genotype by environment effect on grain yield. The sum of squares variation was higher (77.2%) explained by the environment effect. The genotype 2008-TZEE-W-STR showed the highest yield performance (3299 kg ha⁻¹) and lowest yield stability index (3). This genotype can be suggested to farmers for its cultivation and a good candidate for early maturing maize breeding program in Senegal.

Keywords: AMMI, G x E, Rainfed, Early-maturation, Yield, Senegal, *Zea mays*.

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Contents

1. Introduction	80
2. Materials and Methods	80
3. Results and Discussion	81
4. Conclusion	83
References	83

Contribution of this paper to the literature

This study contributes to existing literature by finding the best extra-early maize genotypes based on genotype by environment interactions in the groundnut agro-ecological zone of Senegal.

1. Introduction

Maize is one of the most important cereal grown in sub-Sahara African countries, feeding more than 300 millions of people [1]. Its grains are staple food crop and livestock feed [2]. In Senegal, due to the rainfall distribution, maize production is restricted in the southern part of the groundnut basin, Casamance and Senegal oriental agro-ecological zones where annual rainfall may reach more than 800 mm per year. Drought and low nitrogen soil, as well as parasitic weeds, seriously affect cereal production, particularly maize ones [3]. The invasion of the parasitic weed *Striga hermontica* (Del.) Benth coupled with severe drought conditions can cause 50% of yield loss [4]. *Striga alfera* Willd., known as the pink-flowered was also reported destructive for maize production in Senegal Parker [5]. However, Okuyama, et al. [6] reported that the potential of maize yield in Senegal may be increased in the range of 6% on the basis of the current farming practices.

In order to address drought stress issue in maize production in West African savannah zones, development of extra-early-maturing varieties have been implemented by the joint effort of the International Institute of Tropical Agriculture and National Agricultural Research Systems [4]. The basis of early flowering strategy as a drought escape mechanism enables the plant to complete its life cycle before drought stress exacerbation [7]. In addition, sowing date flexibility regarding non-desirable climatic events (for instance short period of rainfall and delay of the rains) is an important advantage of extra-early maturing varieties. Thus, environmental conditions variation can influence maize growth and yield [8]. Variation in phenotypic expression in a target environment for the same genotypes can be related to the genotype, the environment and genotype by environment interaction [9]. Thereby, multi-environment trials constitute a relevant strategy for accurate identification of high-yielding and stable genotype [10]. Yield stability and adaptation spectrum of genotypes over the years, in fluctuating environments, have become an important criteria for plant breeders [11].

Numerous models were proposed to investigate genotype by environment interaction patterns, including Additive Main effect and Multiplicative Interaction (AMMI) and Genotype plus genotype by environment (GGE) biplot. The AMMI model deals with the traditional analysis of variance for additive main effects in combination with principal component analysis [12]; [13]. This model was widely used in the identification of superior genotypes of barley [14] cassava [15] wheat [16] and rice [17]. The GGE biplot method proposed by Yan and Tinker [18] unravels both genotype and genotype by environment interactions based on Gabriel [19] biplot methodology. GGE biplot displays a powerful graphic on genotype stability and performance, genotype by environment interaction and mega-environment identification through “which on where” pattern graph [20]. This two-year study conducted in four locations in the Groundnut Basin agro-ecological of Senegal, aimed to identify high yielding and stable genotypes using both AMMI and GGE biplot methods.

2. Materials and Methods

2.1. Experimental Sites

Experimentation was carried out during the rainy seasons of 2016 and 2017 in four sites (Nioro, Ndiedieng, Paoskoto and Keur Sene) located in the “Groundnut basin” of Senegal. Details of testing environments are given in Table 1.

Table-1. Information on testing environments during rainy seasons 2016 and 2017.

Site	Soil type	Geographical position			Cropping season	Total rainfall (mm)	Temperature (°C)	
		Latitude (N)	Longitude (W)	Altitude (m.a.s.l)			Minimum	Maximum
Nioro	Sandy clay	13°43'48"	15°46'48"	28	2016	663	23.9	31.4
					2017	1103	23.0	31.6
Ndiedieng,	Sandy clay	13°34'12"	16°05'24"	18	2016	377	22.6	31.8
					2017	257	24.5	35.7
Paoskoto	Sandy clay	13°46'48"	15°47'24"	28	2016	1269	22.3	35.2
					2017	1307	23.6	36.0
Keur Sene	Sandy clay	13°50'60"	16°02'24"	25	2016	330	23.3	35.6
					2017	360	24.3	37.9

Source: National Agency of Civil Aviation and Meteorology of Senegal.

2.2. Plant Materials and Test-Environments

Six extra-early maturing maize genotypes Table 2 were evaluated in a randomized complete block design with three replications in each of the environments. Sowing was done with a spacing of 0.75 m between rows and 0.25 m between plants within a row in plots of 6 × 5.25 m² area. Each plot contained 8 rows. A basal 15N-15P-15K fertilizer at a rate of 200 kg ha⁻¹ was applied before sowing. Recommended cultural practices were applied for crop management. At the maturity stage, grains data were recorded and converted to kg ha⁻¹ using the plot size as a factor.

Table-2. Information on extra-early maize genotypes used in this study.

Genotypes code	Pedigree/original name	Origin	Type
G1	2008-TZEE-W-STR	IITA-Ibadan	OPV
G2	2009-TZEE-OR1-STR	IITA-Ibadan	OPV
G3	TZEE-WPop-STRC5	IITA-Ibadan	OPV
G4	TZEE-Y	ISRA-Senegal	OPV
G5	TZEE-W	ISRA-Senegal	OPV

Note: IITA: International Institute of Tropical Agriculture. OPV: Open Pollinated Variety.

ISRA: Institut Sénégalais de Recherches Agricoles.

2.3. AMMI Model

Analysis of variance was performed using AMMI model implemented in statistical software GenStat [21]. Assuming μ is the grand mean of extra early maize genotypes yield, α_g is the genotype deviation of the grand mean, β_e is the environment deviation, λ_n is singular value for interaction principal component (IPC) n and λ_n^2 is the corresponding eigenvalue, γ_{gn} is the eigenvector for genotype g and component n, δ_{en} is the eigenvector for environment e, ρ_e is the residual, $\kappa_{r(e)}$ is the block effect for replication r within environment e and ϵ_{ger} is the error, the yield of genotype g in environment e for replication r (Y_{ger}) is expressed by Gauch [22] model:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_e + \kappa_{r(e)} + \epsilon_{ger}$$

Based on the relative contributions of the IPC 1 and 2 axis scores to genotype by environment interaction effect, the AMMI stability value (ASV) was computed using the following formula described by Danquah, et al. [15]:

$$ASV = \sqrt{\left[\frac{IPC1_{Sum\ of\ squares}}{IPC2_{Sum\ of\ squares}} (IPC1_{score}) \right]^2 + (IPC2_{score})^2}$$

Using based-yield genotypes ranking and ranking based on AMMI stability value, yield stability index was calculated as follows:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_e + \kappa_{r(e)} + \epsilon_{ger}$$

Lower is AMMI stability value and ranking based on yield values, more stable and high yielding is the genotype [23].

2.4. GGE Biplot Analysis

Data recorded on grain yield were arranged in site-maize genotypes two-way table containing mean yields. Biplot graphs were plotted using statistical software GenStat 18 [21] following the GGE biplot model defined by Yan, et al. [24] as follows:

$$y_{ij} = \sum_{n=1}^r \lambda_n \xi_{in} \eta_{jn}$$

where r is the number of principal components required to approximate the original data, λ_n is the singular value of principal components, ξ_{in} and η_{jn} are the ith genotype score and the jth environment score for principal components respectively and y_{ij} the response yield according to ith genotype in jth environment.

3. Results and Discussion

3.1. Performance of the Tested Extra-Early Maize in Different Locations

During the rainy season of 2016, G3 showed the highest yield (3893 kg.ha⁻¹) at Paoskoto, followed by G2 (3846 kg ha⁻¹) at Keur Sene and G5 (3253 kg ha⁻¹) at Paoskoto Table 3.

Table-3. Mean grain yield (kg. ha⁻¹) of maize genotypes in different environments during 2016 and 2017 crop seasons.

Year	Site	G1	G2	G3	G4	G5	Mean	Minimum	Maximum
2016	Nioro	2959	2951	2524	2809	2684	2785	1920	3680
	Ndiédieng	2365	3484	3591	2187	1742	2674	747	4853
	Paoskoto	2951	2258	3893	2382	3253	2948	1173	4053
	Keur Sene	3715	3846	3589	2382	1742	3788	2954	4652
2017	Nioro	3790	3528	3259	2829	4206	3522	1723	4794
	Ndiédieng	3790	2957	3259	2952	2994	2998	2097	4085
	Paoskoto	2400	925	1849	2382	978	1387	587	2667
	Keur Sene	4886	4737	4205	3988	4574	4478	3514	5333

Source: Field data.

Yields ranged from 747 kg ha⁻¹ to 4853 kg ha⁻¹ across environments during 2016 cropping season. In 2017, G1 and G2 showed the highest yields in Keur Sene with 4,886 kg ha⁻¹ and 4737 kg ha⁻¹, respectively.

3.2. Additive Main Effect and Multiplicative Interaction Analysis

The AMMI analysis of variance revealed a significant effect of genotype, environment and genotype by environment on yield variation Table 4.

Table-4. Analysis of variance for AMMI2 model of five extra early maize genotypes in eight environments.

Source of variation	Df	SS	MS	TVE (%)	G × E (%)
Total	119	145733332	1224650	-	-
Treatments	39	112590559	2886937***	-	-
Genotype (G)	4	4941432	1235358**	4.38	-
Environment (E)	7	86901293	12414470***	77.18	-
G × E Interaction	28	20747834	740994**	18.42	
IPC1	10	9279579	927958**	-	44.72
IPC2	8	6508658	813582*	-	31.37
Residual	10	49599596	495960	-	-
Blocks within environments	16	11888665	743042*	-	-
Error	64	21254108	332095	-	-

Note: *significant at 0.05 probability level. **significant at 0.01 probability level. ***significant at 0.001 level of probability. ns: non-significant. df: degree of freedom. SS: sum of square. MS: mean of square. TVE (%): percentage relative to total sum of square. IPC: Interaction Principal Component. G × E (%): percentage of sum of square variation explained by genotype by environment effect.

Environment factor explained the highest (77.2%) part of total variation followed by genotype by environment interaction (18.4%) and genotype (4.4%). The partitioning of the sum of square variances revealed a predominant effect of environment. This suggests that the environment influences range was wider than genotype. As found in several studies [25]; [26] the variability observed in environmental parameters such as rainfall, temperature and soil texture can be related to the strong environmental effect.

IPC1 and IPC2 represent 44.7% and 31.4% of genotype by environment variation, respectively. The IPC 1 effect was highly greater (10 times) than the effect of the genotype and contributed to more than 40% of GE interaction variation. The AMMI IPC1 and IPC2 scores were respectively positive and negative, reflecting location-year crossover pattern in genotype by environment interactions [27].

Table-5. Ranking of the tested genotypes based on ASV and YSI.

Genotype	Mean	Rank (μ)	IPC1	IPC2	ASV	ASV Rank (η)	YSI ($\mu + \eta$)	YSI rank
G1	3299	1	8.93	-12.45	17,81	2	3	1
G2	3086	3	-10.47	27.89	31,63	3	6	2ex
G3	3209	2	-29.12	-19.04	45,68	5	7	4
G4	2704	5	4.13	11.03	12,50	1	6	2ex
G5	3065	4	26.53	-7.42	38,54	4	8	5

Source: Field data.

Based on AMMI stability values (ASV), G4 appeared as the most stable genotype across environments. However, yield stability index (YSI) revealed that G1 was the best genotype followed by G2 and G3 Table 5.

3.3. Genotype Plus Genotype by Environment Biplot Analysis

The genotype by environment patterns were graphically presented in Figure 1 and Figure 2 using GGE biplot model. Principal components 1 and 2 encompass 40.75% and 25.17% of total variation respectively. The Figure 1 represents the average-environment coordination (AEC) view based on yield performance and stability.

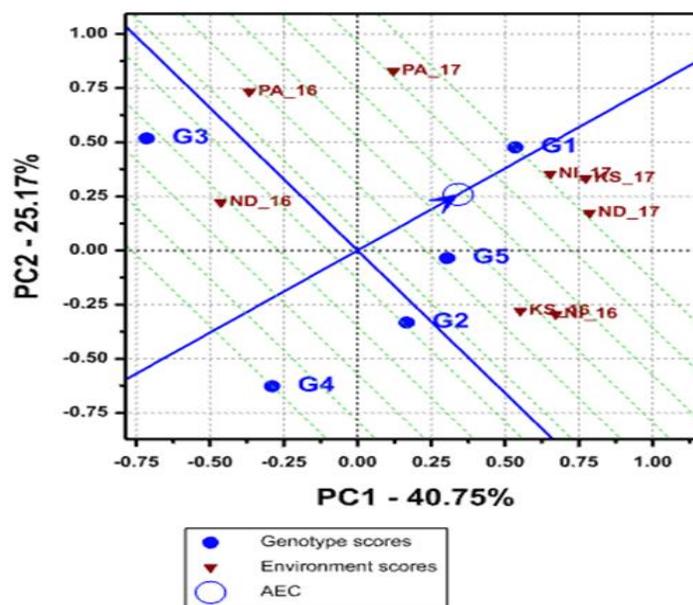


Figure-1. The average-environment coordination view showing mean performance and stability of five extra early genotypes tested in eight environments. The genotypes: G1(2008-TZEE-W-STR), G2(2009-TZEE-OR1-STR), G3 (TZEE-WPop-STRC5), G4(TZEE-Y), G5(TZEE-W). The years: 16 (2016), 17(2017). The locations: KS (Keur Sene), PA (Paoskoto), ND (Ndiediang), NI (Nioro).

Source: Field data.

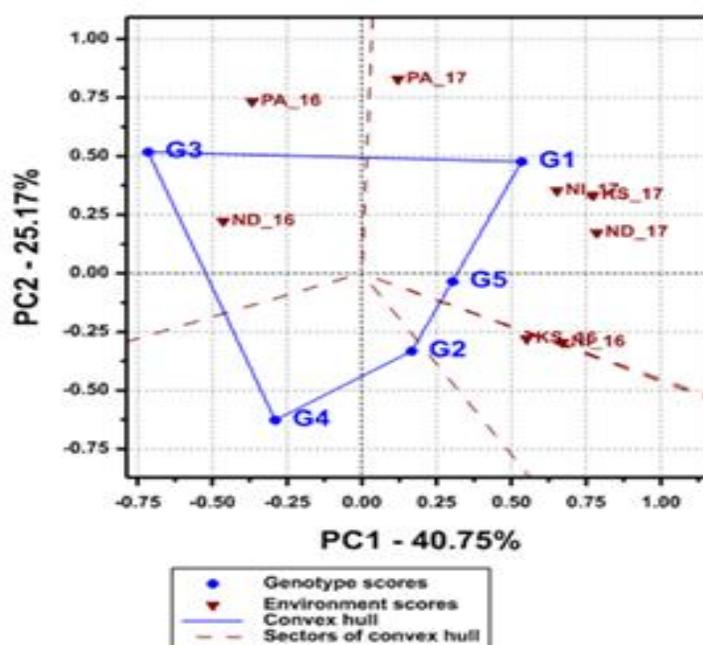


Figure-2. The which-won-where GGE biplot showing five extra early maize genotypes behaviour in eight environments. The genotypes: G1(2008-TZEE-W-STR), G2(2009-TZEE-OR1-STR), G3(TZEE-WPop-STRC5), G4(TZEE-Y), G5(TZEE-W). The years: 16 (2016), 17(2017). The locations: KS (Keur Sene), PA(Paoskoto), ND (Ndiedieng), NI (Nioro).
Source: Field data.

The AEC arrow indicates the highest genotype based on yield performance. The circle represents the ideal genotype, which combines high yield and stability. According to Figure 1, the genotype G1 was the best genotype followed by G5. In contrast, G4 is the most unstable genotype across all environments.

The which-won-where polygon view Figure 2 highlighted the genotype by environment interaction pattern of this study. The genotypes located at the vertex of the polygon showed either best or poor performance in a related environment. The genotypes G1 and G5 had a higher grain yield than average in the environments NI17, KS17, ND17, PA17, KS16 and NI16. G3 was the best genotype in the environments PA16 and ND16. In contrast, G2 and G4 yields were lower than average across the tested environments. The orthogonal lines from the origin of biplot which cut the sides of the polygon allow the comparison between two adjacent genotypes in relationship with their respective environments. Thus, G1 performed better in NI17, KS17, ND17 and PA17, whereas G3 was better in ND16 and PA16. The orthogonal lines in the polygon also revealed the presence of location-year crossover patterns. The environment couples PA16-PA17 and ND16-ND17 were located on opposite sides of orthogonal lines, indicating a location-year effect. GGE biplot polygon view supports this crossover presence, denoting of adaptation of maize genotypes according to a target environment. Various studies [28-30], performed on a wide range of crops, successfully showed the efficacy of AMMI and GGE biplot methods to figure out genotype adaptation patterns.

4. Conclusion

The present study demonstrated a high environment effect in GE variation despite the fact that the environments were located in the same agro-ecological zone. Both AMMI and GGE biplot analysis showed that the genotype 2008-TZEE-W-STR had the highest grain yield and was more stable across environments. It can be recommended for cultivation in the groundnut basin of Senegal and used in maize breeding program as a gene donor regarding yield and stability.

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