Australian Journal of
Crop Science
AJCS

Aust J Crop Sci. 20(01):14-20 (2026) | ISSN:1835-2707
https://doi.org/10.21475/ajcs.26.20.01.p55

# Genotype-by-environment interaction, adaptability and stability analysis of cotton (*Gossypium hirsutum* L. race *latifolium* H.) in northern Mozambique

**Manuel P. Maleia[1], Joaquim João[1], Sudanaily A. M. Salé[1], Celestino M. Domingos[1], Jaime O. Teca[1], Afonso Raimundo[1], Jorge Ussene[1], Banu Irénio[1], Vidigal Kimeles[1], Amisse Chicola[1], Talibo Perar[1], Hélder F. De Sousa[2], Dércia B. Guedes[2], Edson C. Jamal[2], Osman Carimo[2], Dreutse E. Muhala[2], Paulo Tebulo[3], Celso André[4]**

**[1]Instituto de Investigação Agrária de Moçambique, Av. das FPLM, 2698. C.P. 2698, Maputo, Mozambique.**
**[2] Instituto de Algodão e Oleaginosas de Moçambique, Av. Eduardo Mondlane, 2221, Maputo, Mozambique.**
**[3]Universidade Católica de Moçambique, Faculdade de Ciências Agronómicas, Rua do Aeroporto - C.P.22, Cuamba, Mozambique.**
**[4]Sociedade Algodoeira do Niassa, R. Eduardo Mondlane, Cuamba, Mozambique.**

**Corresponding author: mmaleia@gmail.com**
**ORCID ID: 0009-0004-0329-4670**

***Submitted:* *04/05/2025***

***Revised:* *12/09/2025***

***Accepted:* *12/09/2025***

**Abstract:** Cotton, the "white gold", is one of the most important crops in the world. In Mozambique, cotton is a cash and foreign exchange crop and is regularly on the list of agricultural exports. Cotton cultivation in the country is performed mainly by small-scale farmers, who face many challenges, characterized by low yields (< 500 kg. $ha^{-1}$), due to the use of seeds from unimproved varieties that are poorly adapted to local cultivation conditions and the systematic use of recycled and noncertified seeds. Research has introduced new varieties in addition to the genotypes developed in the country. The objective of this study was to evaluate the adaptability and stability of 2 cotton varieties and 2 inbred lines for cottonseed and fiber yield. The trials were conducted under rainfed conditions in three consecutive seasons, 2021, 2022 and 2023, in Namialo, Namapa, Montepuez, and Ribáuè and two seasons, 2001 and 2023, in Cuamba, resulting in a total of 14 environments. The treatments, consisting of 9 cotton varieties/genotypes, were established in an RCBD with 4 replications. Individual and combined ANOVA for seed cotton and fiber yields was carried out, and adaptability and stability were applied via the GGE methodology. There was a significant genotype-by-environment interaction. The PL-164/2 genotype was the most stable, with greater predictability, followed by Flash and MP2020. The MP2020 genotype presented greater fiber maturity, whereas PL-164/2 presented a standard fiber length in relation to the minimum required length. PL-164/2, Flash and MP2020 are recommended for registration and release for production in the country.

**Keywords:** Biplot, cottonseed yield, fiber quality, GGE analysis, inbred lines.
**Abbreviations:** ANOVA: Analysis Of Variance; GGE: Genotype + Genotype x Environment; ICAC: International Cotton Advisory Committee; RCBD: Randomized Complete Block Design; PC1: Principal Component 1; PC2: Principal Component 2.

## Introduction

Cotton (*Gossypium hirsutum* L.), which is also known as "white gold", is one of the most important crops in the world and in the country. The largest producers of this crop, globally, include India, China, Brazil, the United States of America and Pakistan, accounting for approximately 77% of the global production, whereas China and India account for approximately 53% of the global production (ICAC 2022). In Mozambique, although cotton production is not significant at a global level, approximately 0.05% of global production (ICAC, 2022), it is a cash crop and a foreign exchange earner and is regularly on the list of agricultural exports.

Cotton cultivation in the country is practiced mainly by small-scale farmers (approximately 90% of production), who face many challenges, which are normally characterized by low yields (500 kg $ha^{-1}$) compared with the world average yield (1900 kg.$ha^{-1}$) and neighboring countries, such as Malawi, Zimbabwe, and Tanzania (> 500 kg ha-1) (ICAC, 2022). One of the reasons for low productivity has been the use of seeds from unimproved varieties poorly adapted to local growing conditions, combined with the occurrence of pests, especially in varieties with poor hairiness, which makes them more susceptible to attack by sucking pests (Fok, 2000). Furthermore, there has been pressure to import the use of varieties without due evaluation, and varieties in wide use are proving to be degenerate (CA 324, Albar SZ 9314) owing to the use of recycled, noncertified seeds. Four cotton varieties are currently used in Mozambique: CA 324 (released in 1999, 44.7% coverage), Albar SZ 9314 (released in 1999, 54.1% coverage), Chureza (the year of release is unknown, 1.1%) and CIMSAN 2 (released in 2017, 0.2% coverage) (ICAC, 2022).

The evaluation of new varieties also plays an important role in determining their potential productivity compared with those currently in use. Thus, the best varieties can be identified and recommended for cultivation by producers.

The improvement of the evaluated varieties and lines was carried out via conventional methods based on crosses of no genetically modified parental lines followed by genealogical selection and identification of new varieties through "on-station" trials in Zimbabwe and Turkey for the introduced varieties, parental and successive genealogical selection and identification of elite inbred lines at the Cotton Research Center of Namialo.

The objective of this study was to evaluate the genotype-by-environment interaction, adaptability and stability of 2 cotton varieties and 2 inbred lines in terms of cottonseed and fiber yield.

## Results

### *Individual ANOVA of cottonseed yield*

Individual ANOVA revealed significant differences ($p < 0.05$) in seed cotton productivity between the evaluated genotypes in 6 out of 14 total environments (Table 1).

### *Combined ANOVA of cottonseed yield*

The combined ANOVA verified the significant effect of the genotype × environment (G × E) interaction on seed cotton productivity at the 5% probability level (Table 2).

The results also revealed that the effect of the environment (E) was significant at a 1% probability and of high magnitude, suggesting a variation in environmental quality, and the significant interaction (G × A). This also suggests a change in the pattern of the phenotypic response of genotypes to variation in environmental quality (Table 2); therefore, justifying the study of stability and adaptability (Cruz and Carneiro, 2006). These results suggest that the different environments differ from each other. Thus, some genotypes performed better in one environment and poorly in others, which resulted in a change in the performance pattern under environmental variation, as revealed by the GxE interaction (Table 2 and S1 Table).

There were favorable environments, with a yield mean above the overall mean of the 14 environments highlighted for Namapa 2021, Ribáuè 2022 and 2023, and Montepuez 2023, which was the best of all environments and unfavorable environments, with a yield mean below the general average of the environments (all locations in 2021 and 2022, except for Namapa; and Namapa 2023). These groups of environments contrasted. These results illustrate that within the same site, the variation in years changed the potential of each environment. The results revealed that, compared with that of Cuamba, the yield of Albar QM 302 was greater in Montepuez in the 2021 and 2023 seasons but was lower in the 2021 and 2022 seasons. The genotypes MP2020 and PL-164/2 was worse in Namialo and Montepuez in 2023 and were better in Namialo and Cuamba in 2022. The Flash variety was worse in Namialo and Cuamba in 2021 but was evident in Namialo and Cuamba in 2023 (S1Table).

### *Adaptability and stability analysis*

The first two principal components (PC1 and PC2) explained 94.04% (48.89 and 45.15) of the variation in cottonseed yield, indicating good efficiency of the biplot analysis (Figures 2; 3 and 4).

### *Analysis of mega-environments and best genotypes in each environment*

The results show the grouping of genotypes/varieties and visualize the environments where each genotype was superior, enabling the definition of different mega-environments.

Figure 2 shows 4 groups of mega-environments, the 1st containing 1 environment, A3: Montepuez; the 2nd group, A14: Ribaué 23; the 3rd for the A1 environments: Namialo 21; A4: A4: Ribaué 21 and A6: A6: Namialo 22; and the 4th, the largest, with 9 environments, A2: Namapa 21; A5: Cuamba 21; A7: Namapa 22; A8: Montepuez 22; A9: Ribaué 22; A10: Cuamba 22; A11: Namialo 23; A12: Namapa 23; and A13: Montepuez 23. G2: Albar QM 302 and G8: MP2020 had the best performance in environments corresponding to A3: Montepuez 21 and A14: Ribaué 23, respectively. The genotypes G1: Flash and G9: PL-164/2 were closer to environments A1: Namialo 21, A4: Ribaué 21 and A6: Namialo 22, in the sector where G8: MP2020 had the highest performance, showing relative performance in these environments (Figure 2).

### *Genotype/varieties indicate performance and stability*

Figure 3 shows the classification of the genotype mean performance as follows: G7: Albar SZ 9314 > G2: Albar QM 302 > G4: CIMSAN 1 > G5: CIMSAN 2 > G6: CA 324 > general average > G3: Edessa > G1: Flash > G9: PL-164/2. > G8: MP2020.

Among the new varieties and genotypes, G2: Albar QM 302 presented a high mean performance, above the overall mean, and G1: Flash, G9: PL-164/2. and G8: MP2020 presented a mean performance below the overall mean; in this order and in terms of stability, G9: PL-164/2 was more stable, followed by G1: Flash and G8: MP2020, whereas G2: Albar QM 302 was less stable.

Among the genotypes under evaluation, G1:Flash followed by G9: PL-164/2 and G8: MP2020 were interesting because of their relative stability associated with high mear performance, meaning that the relative performance and its respective stability were consistent, even though they were far from ideal genotypes and were more desirable than G2: Albar QM 302 and G3: Edessa were (Figure 4).

## Discussions

The presence of significant GxE interactions, shown in Table 1, can be attributed to predictable factors, such as the management of the crop itself (sowing, thinning, pest control, weeding, and harvesting, among others), unpredictable factors, such as climatic conditions (precipitation, temperature, and relative humidity), solar radiation throughout the crop cycle, among others), and the relative performance of genotypes in relation to environmental variation (location and year). In the presence of significant GxE interactions, stability parameters are estimated to determine the superiority of individual genotypes across a range of environments (Pinki et al., 2018). Similar results were reported by (Maleia et al., 2010; Pinki et al., 2018; Maleia et al., 2019, and Dique et al., 2023).

GGE-Biplot analysis allows visualization of the performance of different genotypes in different environments, average performance and stability of genotypes and identification of the best genotype. Phenotypic variation results from genotypic effects, the environment and the interaction between genotype and the environment (Yan and Kang, 2003). In this methodology, only the main effects of the interaction between genotype and GxE are important and must be considered concomitantly. The main effect of the environment is not relevant in variety selection. This is because, in the selection of varieties and formation of mega-environments, the adaptive capacity of genotypes is

**Table 1.** Summary of individual ANOVAs of seed cotton yield.

| Environment | | | Mean Square | | | | Mean | CV (%) |
|---|---|---|---|---|---|---|---|---|
| # | Location | Season | Block | Genotype | | Error | (kg.ha$^{-1}$) | |
| Env1 | Namialo | 2021 | 151580.41 | 30074.08 | | 105582.04 | 1327.93 | 24.47 |
| Env2 | Namapa | 2021 | 195854.36 | 116898.56 | | 84276.84 | 2460.00 | 11.80 |
| `Env3 | Montepuez | 2021 | 677462.38 | 1394699.60 | ** | 283860.60 | 1831.96 | 29.08 |
| Env4 | Ribáuè | 2021 | 91957.79 | 83274.72 | | 73257.12 | 1563.36 | 17.31 |
| Env5 | Cuamba | 2021 | 66534.66 | 89265.06 | ** | 17837.97 | 1519.95 | 8.79 |
| Env6 | Namialo | 2022 | 470828.86 | 166969.88 | | 110681.90 | 2100.47 | 15.84 |
| Env7 | Namapa | 2022 | 297133.38 | 141730.57 | | 99580.97 | 2139.07 | 14.75 |
| Env8 | Montepuez | 2022 | 28315.79 | 201043.91 | * | 69336.36 | 1782.46 | 14.77 |
| Env9 | Ribáuè | 2022 | 399615.23 | 313079.64 | * | 110326.71 | 2327.94 | 14.27 |
| Env10 | Cuamba | 2022 | 57842.56 | 60636.01 | | 284921.20 | 1879.70 | 28.40 |
| Env11 | Namialo | 2023 | 93955.38 | 319505.78 | * | 286058.36 | 2875.45 | 18.60 |
| Env12 | Namapa | 2023 | 44126.78 | 30494.34 | | 37244.23 | 1285.26 | 15.02 |
| Env13 | Montepuez | 2023 | 190463.44 | 153421.21 | | 123855.91 | 3059.92 | 11.50 |
| Env14 | Ribáuè | 2023 | 292907.66 | 364257.44 | * | 241307.69 | 2628.45 | 18.69 |
| | **DF** | | 3 | 8 | | 24 | - | - |
| | Hartley's Fmax test = 16.036 ** | | | | | | | |

** significant at 1% probability. * significant at 5% probability; **DF**- degrees of freedom.

**Table 2.** Summary of combined ANOVA results for seed yield.

| **Source of variation** | **DF** | **Mean square** | |
|---|---|---|---|
| Block | 3 | 77883.59 | |
| Genotype (G) | 8 | 237146.76 | |
| Environment (E) | 13 | 11252451.45 | ** |
| G x E | 74 $^{(1)}$ | 348995.03 | * |
| Error | 234 $^{(1)}$ | 235970.75 | |
| Total | 503 | | |
| Overall mean | 2055.85 | | |
| CV (%) | 23.63 | | |

$^{(1)}$ Values adjusted by the Cochran method (1954) due to the heterogeneity of the estimates of residual variances (mean square of residuals) from the individual ANOVA. ** significant at 1% probability. * significant at 5% probability. **DF**- degrees of freedom.

**Table 3.** List of evaluated treatments.

| # Treatment | Variety/ Inbred line | Origin | Year of Registration and Release in the country | Note |
|---|---|---|---|---|
| **1** | FLASH | Turkey | N/A | Introduced |
| **2** | ALBAR QM 302 | Zimbabwe | N/A | |
| **3** | EDESSA | Turkey | 2020 | Registered Check Varieties |
| **4** | CIMSAN1 | Mozambique | 2017 | |
| **5** | CIMSAN2 | Mozambique | 2017 | |
| **6** | CA 324 | Mozambique | 1999 | |
| **7** | ALBAR SZ 9314 | Zimbabwe | 1999 | |
| **8** | MP2020 | Mozambique | N/A | Developed by Cotton Research Center |
| **9** | PL-164/2 | Mozambique | N/A | |

more important in relation to agroclimatic conditions (Camargo-Buitrago et al., 2011). This methodology is more efficient than other biplot-based techniques (Yan, 2011).

Visualizing the GGE biplot "Mean versus Stability" is an effective tool for evaluating genotypes in both aspects (Yan et al. 2007; Yan, 2011) and identifying those that may be close to the ideotype; which is, the ideal genotype for a given environment represents the desired objective, as it presents high average performance and high stability in mega-environments.

The "average-environment axis" or AEA is a straight line with a single arrow that passes through the origin of the biplot and the average environment, with the exact point pointed out by the end of this arrow in Figure 3, representing the "average-environment" and defined by the average coordinates of all environments, and after that, it points to a higher average performance among the evaluated genotypes. The line that passes through the origin of the biplot and is perpendicular to the AEA indicates that the greater the distance from the origin is, the greater the performance variability (less stability) in both directions (Yan, 2002; Yan, 2011).

High stability only makes sense when associated with mean performance; the stable genotype is desired only when it presents high average performance (Yan and Tinker, 2006; Yan, 2011). Therefore, an ideotype is represented by the genotypes that are on the center of the concentric circle or close to the AEA axis, in the positive direction and have a vector length equal to the longest vectors of the genotypes on the positive side of the AEA, i.e., the highest performance. Therefore, the genotype located closer to the center of the concentric circles is more desirable than the one that is farther away (Yan, 2011)

The total variation of 94.04% shown by the principal components, AXISs 1 and 2, of the cottonseed yield emphasized the reliability of the biplot analysis. According to Yang et al. (2009), for higher reliability of the GGE biplot analysis, the first two principal components should capture more than 60% of the total variation. Similar results were reported by Maleia et al., 2010; Pinki et al., 2018; Maleia et al., 2019, and Dique et al., 2023.

**Table 4.** Locations and environment descriptions.

| Environment | Season | Location | Agroecological Zone | Geographic coordinates | Rainfall (mm) |
|---|---|---|---|---|---|
| A1 | 2021 | Namialo | R7/R8 | 14°56'51.74"S<br>40°01'10.06"E | 839.50 |
| A2 | 2021 | Namapa | R7 | 13°43'33.26"S<br>39°46'22.50"E | 553.50 |
| A3 | 2021 | Montepuez | R7 | 13°13'00.81"S<br>38°52'12.81"E | 1014.90 |
| A4 | 2021 | Ribáuè | R7 | 14°58'11.45"S<br>38°14'24.70"E | 910.55 |
| A5 | 2021 | Cuamba | R7/10 | 14°46'39.76"S<br>36°31'19.98"E | 917.90 |
| A6 | 2022 | Namialo | R7/R8 | 14°56'42.30"S<br>40°01'12.04"E | 758.50 |
| A7 | 2022 | Namapa | R7 | 13°43'29.29"S<br>39°46'28.43"E | 485.80 |
| A8 | 2022 | Montepuez | R7 | 13°13'00.41"S<br>38°52'09.71"E | 880.30 |
| A9 | 2022 | Ribáuè | R7 | 14°58'11.97"S<br>38°14'25.82"E | 618.60 |
| A10 | 2022 | Cuamba | R7/10 | 14°46'40.97"S<br>36°31'19.99"E | 447.10 |
| A11 | 2023 | Namialo | R7/R8 | 14°56'48.27"S<br>40°01'16.80"E | 665.00 |
| A12 | 2023 | Namapa | R7 | 13°43'31.66"S<br>39°46'24.25"E | 725.30 |
| A13 | 2023 | Montepuez | R7 | 13°12'58.40"S<br>38°52'12.10"E | 798.20 |
| A14 | 2023 | Ribáuè | R7 | 14°58'11.22"S<br>38°14'26.20"E | 723.70 |

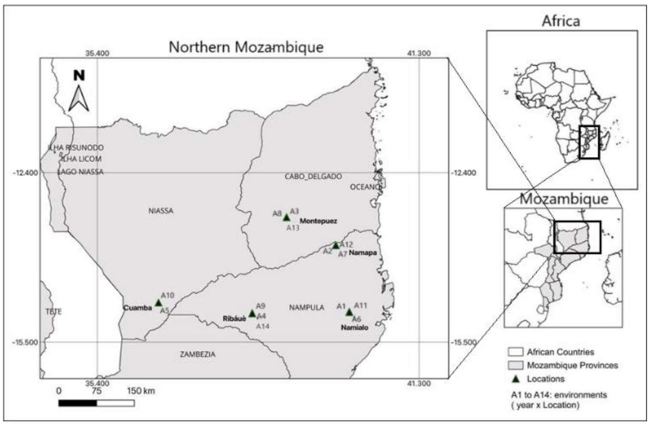

Figure 1. Map of experiment locations, showing the different evaluation environments. **A1:** Namialo 21; **A2:** Namapa 21, **A3:** Montepuez 21; **A4:** Ribaué 21, **A5:** Cuamba 21; **A6:** Namialo 22; **A7:** Namapa 22, **A8:** Montepuez 22; **A9:** Ribaué 22, **A10:** Cuamba 22; **A11:** Namialo 23; **A12:** Namapa 23, **A13:** Montepuez 23; **A14:** Ribaué 23.

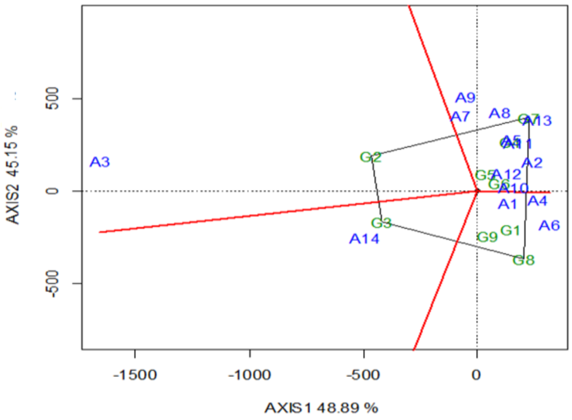

**Figure 2.** GGE biplot graph of seedcotton yield mean of 9 genotypes (G1 to G9) showing which genotypes won at where of the 14 environments (A1 to A14). G1: genotype Flash; G2: genotype Albar QM 302; G3: genotype Edessa; G4: genotype CIMSAN 1; G5: genotype CIMSAN 2; G6: genotype CA 324; G7: genotype Albar SZ 9314; G8: genotype MP2020; G9: genotype PL-164/2. A1: Namialo in the season 2021; A2: Namapa in the season 2021, A3: Montepuez in the season 2021; A4: Ribaué in the season 2021; A5: Cuamba in the season 2021; A6: Namialo in the season 2022; A7: Namapa in the season 2022, A8: Montepuez in the season 2022; A9: Ribaué in the season 2022, A10: Cuamba in the season 2022; A11: Namialo in the season 2023; A12: Namapa in the season 2023, A13: Montepuez in the season 2023; A14: Ribaué in the season 2023.

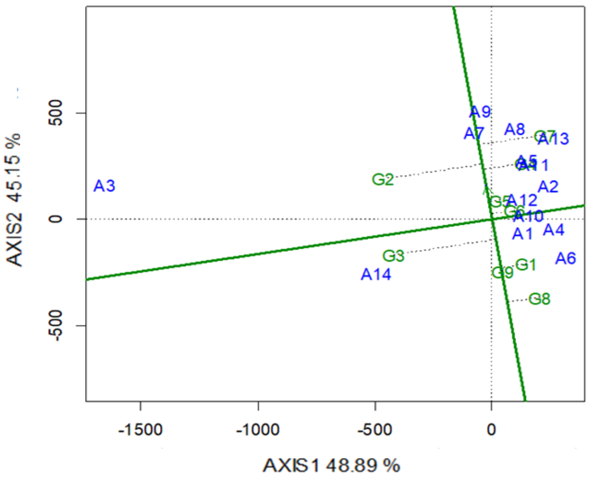

**Figure 3.** GGE biplot graph of seed cotton yield mean of 9 genotypes (G1 to G9) in 14 environments (A1 to A14) versus their stability. G1: genotype Flash; G2: genotype Albar QM 302; G3: genotype Edessa; G4: genotype CIMSAN 1; G5: genotype CIMSAN 2; G6: genotype CA 324; G7: genotype Albar SZ 9314; G8: genotype MP2020; G9: genotype PL-164/2. A1: Namialo in the season 2021; A2: Namapa in the season 2021, A3: Montepuez in the season 2021; A4: Ribaué in the season 2021; A5: Cuamba in the season 2021; A6: Namialo in the season 2022; A7: Namapa in the season 2022, A8: Montepuez in the season 2022; A9: Ribaué in the season 2022, A10: Cuamba in the season 2022; A11: Namialo in the season 2023; A12: Namapa in the season 2023, A13: Montepuez in the season 2023; A14: Ribaué in the season 2023.

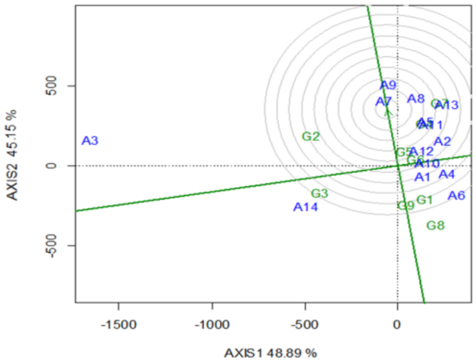

Figure 4. Seed cotton yield classification of the 9 genotypes (G1 to G9) evaluated in 14 environments (A1 to A14) compared to the ideal genotype. G1: genotype Flash; G2: genotype Albar QM 302; G3: genotype Edessa; G4: genotype CIMSAN 1; G5: genotype CIMSAN 2; G6: genotype CA 324; G7: genotype Albar SZ 9314; G8: genotype MP2020; G9: genotype PL-164/2. A1: Namialo in the season 2021; A2: Namapa in the season 2021, A3: Montepuez in the season 2021; A4: Ribaué in the season 2021; A5: Cuamba in the season 2021; A6: Namialo in the season 2022; A7: Namapa in the season 2022, A8: Montepuez in the season 2022; A9: Ribaué in the season 2022, A10: Cuamba in the season 2022; A11: Namialo in the season 2023; A12: Namapa in the season 2023, A13: Montepuez in the season 2023; A14: Ribaué in the season 2023. **A1:** Namialo 21; **A2:** Namapa 21, **A3:** Montepuez 21; **A4:** Ribaué 21, **A5:** Cuamba 21; **A6:** Namialo 22; **A7:** Namapa 22, **A8:** Montepuez 22; **A9:** Ribaué 22, **A10:** Cuamba 22; **A11:** Namialo 23; **A12:** Namapa 23, **A13:** Montepuez 23; **A14:** Ribaué 23. **G1:** Flash; **G2:** Albar QM 302; **G3:** Edessa; **G4:** CIMSAN 1; **G5:** CIMSAN 2; **G6:** CA 324; **G7:** Albar SZ 9314; **G8:** MP2020; **G9:** PL-164/2.

## Materials and methods

### *Plant materials*

The treatments consisted of 9 cotton varieties/genotypes, of which five (5) were considered check varieties registered in Mozambique, CA324, Albar SZ 9314, CIMSAN2, currently in use and others CIMSAN 1 and Edessa, which are still in the dissemination phase. Two (2) introduced (Flash and Albar QM 302) and two (2) advanced inbred lines developed by the Cotton Research Center in Namialo (Table 3).

### *Experimental locations and environments*

The trials were conducted at five locations in different agroecological cotton-growing regions in Mozambique (R7, R8, R10) during three consecutive seasons, 2020/21, 2021/22 and 2022/23, in Namialo, Namapa, Montepuez, Ribaué and Cuamba. Cuamba's trials were set up in only 2 seasons, the last one, 2022/23, having lost the trial due to flooding caused by Cyclone Freddy in March 2023 (Figure 1). Each combination of location and year was considered an environment (Table 4).

### *Environment classification and agroecological zone descriptions*

Northern Mozambique's environment is characterized by a tropical savanna climate (Aw), according to the classification of Köppen. This region experiences a warmer climate with mean temperatures ranging from 25 to 30°C during the warmer months, with an annual average around 26°C. The northern region also receives significant rainfall (400 – 1200 mm) during the warmer months (November to April). It has a fertile, well-drained soil, making it suitable for agriculture.

The R7 agro-ecological region is a vast area encompassing lands with elevations between 200 and 1,000 m inland in Zambézia, Nampula, southern Cabo Delgado, and Niassa Province. The average annual precipitation and potential evapotranspiration range from 100 to 1,400 mm; some areas of this region experience higher temperatures (above 25°C) and others moderately warm (between 20 and 25°C). Soil texture is variable and consistent with the topography. Much of the region has significant potential for cotton production, which has been practiced for several decades. The R8 region, on the other hand, encompasses the coastal region of the provinces of Zambézia, Nampula, and Cabo Delgado. The average annual precipitation ranges from 800 to 1,200 mm, and evapotranspiration ranges from 1,400 to 1,600 mm. Soils are generally sandy, becoming heavy in low-lying areas. Low soil fertility is one of the main limitations in this area. In the R10 region, which includes areas above 1,000 m, the average annual precipitation exceeds 1,200 mm, and average air temperatures range from 15 to 22.5 °C. Soils are generally heavy.

### *Experimental design and crop management*

The treatments/genotypes (Table 5) were arranged in a randomized complete block design with four replications, resulting in a total of 36 experimental plots in each experiment/trial. In all the trials, each experimental unit consisted of 5 rows of plants, 5.0 m long, spaced 0.80 m between rows and 0.15 m between plants within the rows, totaling 33 plants per row. The two lateral rows of each plot, one on each side, were considered lateral borders. Data were collected from the three central lines of each plot, which were considered usable areas and corresponded to 12 m$^2$.

The trials were carried out under rainfed conditions. Cotton was planted from December 30 to January 20 and harvested from May 5 to June 20. Weeds were controlled manually via a hoe whenever deemed necessary. Spraying was carried out once with acetamiprid insecticide (222 g.lt$^{-1}$) for the first control of pests at a dosage of 50 ml.ha$^{-1}$, followed by one application of lambda-cyhalothrin (60 gL$^{-1}$)+acetamipride (40 gL$^{-1}$), one application of lambda-cihalothrin (60 gL$^{-1}$), two applications of lambda-cyhalothrin (48 gL$^{-1}$)+profenofos (600 gL$^{-1}$) and one application of lambda-cyhalothrin (60 gL$^{-1}$`)+acetamipride (60 gL$^{-1}$) every two weeks from the fourth week after the emergence, at a dosage of 250 ml.ha$^{-1}$. Insecticides were applied with a microulva (ULV). The variable evaluated was the seed cotton yield (kg.ha$^{-1}$).

### *Evaluated parameters*

The cottonseed yield (kg.ha$^{-1}$) was estimated via formula (1):

$$Cottonseed\ yield\ (\frac{Kg}{ha}) = \frac{Weight\ of\ cottonseed\ from\ \ each\ plot\ (Kg)x\ 10\ 000\ m2}{12\ m2} \qquad (1)$$

### *Statistical analysis*

Analysis of variance was carried out via the GENES statistical package (Cruz, 2013). Before the analysis of variance (ANOVA), in each environment, experimental errors were subjected to tests of normality and homogeneity of variances that were carried out in SAS software (2008), applying the Shapiro–Wilk tests (Shapiro and Wilk, 1965) and Bartlett test (Bartlett, 1937), respectively, at 5% probability to verify whether they obeyed the basic assumptions of normality and homogeneity of variances (Pimentel Gomes 1987; Banzatto and Kronka, 2006).

### Individual Analysis of Variance (ANOVA)

For each combination of site and season (environment), an individual ANOVA was carried out, in which fixed effects were considered for genotypes and random effects for blocks, via the following statistical model (2):

$$Y_{ij} = \mu + G_i + B_j + \varepsilon_{ij} \qquad (2)$$

where $Y_{ij} =$ is the observed value relative to the i$^{th}$ genotype in the j$^{th}$ block; $\mu =$ is the overall mean; $G_i =$ is the fixed effect of the i$^{th}$ genotype (i = 1, 2..., g); $B_j =$ is the random effect of the j-$^{th}$ block (j = 1,2...,b); and $\varepsilon_{ij} =$ is the experimental error.

### Combined Analysis of Variance (ANOVA)

Before proceeding with the combined ANOVA, the homogeneity of residual variances between environments was assessed via Hartley's Fmax test (Hartley, 1950) at 5% probability to guarantee the feasibility of applying the analysis of combined variance.

After verifying the heterogeneity of the variances, the degrees of freedom of the error and the GxA interaction were adjusted according to Cochran's method (1954). In the combined ANOVA, the variety effect was adopted as fixed, and the environment and block effects were random, based on the statistical model (Cruz et al., 2004) (3):

$$Y_{ijk} = \mu + G_i + A_j + GA_{ij} + B / A_{jk} + \varepsilon_{ijk} \qquad (3)$$

where $Y_{ijk} =$ represents the observed value relative to the ith genotype in the kth block within the jth environment; $\mu =$ represents the overall mean; $G_i =$ represents the fixed effect of the i$^{th}$ genotype (i = 1, 2..., g); $A_j =$ represents the random effect of the j$^{th}$ environment (j = 1, 2..., a); $GA_{ij} =$ represents the interaction effect of the i$^{th}$ genotype with the j$^{th}$ environment; $B / A_{jk} =$ represents the random effect of the k$^{th}$ block within the j$^{th}$ environment (k = 1, 2..., r); and $\varepsilon_{ijk} =$ represents the experimental error.

Means were compared with the Tukey means comparison test via the GENES statistical package (Cruz, 2013).

### *Adaptability and stability analysis*

Once the G x A interaction was significant, the analysis of phenotypic adaptability and stability was carried out via the GGE (Genotype + Genotype Environment Interaction) biplot methodology, explained by the statistical model (4):

$$Y_{ij} = \mu + \alpha_i + \beta_j + \phi_{ij} \qquad (4)$$

where $Y_{ij}$ = the expected performance of the ith genotype in the jth environment; μ = the general average of observations; $\alpha_i$ = the main effect of the ith genotype; $\beta_j$ = the main effect of the j$^{th}$ environment; and $\phi_{ij}$ = the interaction between the ith genotype and the j$^{th}$ environment.

The GGE biplot groups the genotype additive effect together with the multiplicative effect of the GE interaction and submits both of these effects to the principal component analysis. The GGE biplot can aid researchers in better understanding complicated GxE interactions in multienvironment trials. The observation of G+G×E is more effective in the biplot graph in this approach.

The adaptability and stability analyses were carried out via the R statistical package (Wright and Laffort, 2020).

## Conclusions

The combined analysis of variance allowed us to verify a significant effect of the genotype × environment (G × E) interaction only for seed yield;

The genotype PL-164/2 was the most stable, with greater predictability in the face of varying environmental conditions, followed by Flash and MP2020.

## Ethics approval and consent to participate

Not applicable.

## Consent for publication

Not applicable.

## Availability of data and material

The datasets during and/or analysed during the current study available from the corresponding author on reasonable request.

## Competing interests

The authors declare that they have no competing interests.

## Funding

This study was funded by the Mozambique Agricultural Research Institute in collaboration with the Mozambique Institute for Cotton and Oilseeds.

## Authors' contributions

MANUEL, JOAQUIM, SUDANAILY and CELESTINO designed the experiment.
MANUEL analyzed the data.
All authors conducted the experiments, collected the data, contributed for the draft and approved the final manuscript.

## Acknowledgements

The authors would like to sincerely thank Mozambique Agricultural Research Institute and the Mozambique Institute for Cotton and Oilseeds for their financial support. The researchers, technicians, field staff, for their valuable contributions to the entire process of this research.

## References

Banzatto DA, Kronka, SN (2006) Experimentação agrícola. Jaboticabal: FUNEP,237p.

Bartlett MS (1937) Properties of Sufficiency and Statistical Tests. Proceedings of the Royal Society of London. Series A, Mathematical and Physical Sciences, vol. 160, no. 901, pp. 268–82. JSTOR, http://www.jstor.org/stable/96803. Accessed 27 June 2024.

Camargo-Buitrago I. (2011) Identificación de mega-ambientes para potenciar el uso de genótipos superiores de arroz en Panamá. Pesquisa Agropecuária Brasileira, 46:1601-1069.

Cochran WG (1954) The combination of estimates from different experiments. Bioometrics, 10:101 – 129.

Cruz CD, Carneiro PCS (2006) Modelos biométricos aplicados ao melhoramento genético. Viçosa:
UFV, 585p.

Cruz CD, Regazzi AJ, Carneiro PCS (2004) Modelos biométricos aplicados ao melhoramento genético. Viçosa: UFV, 480p.

Cruz CD. GENES (2013) A software package for analysis in experimental statistics and quantitative genetics**.** Acta Scientiarum. Agronomy**,** 35:271-276.

Dias P (2012) Analysis of incentives and disincentives for cotton in Mozambique. Technical notes series. MAFAP, FAO, Rome, 36pp.

Dique JEL, Miguel MA, Pedro C.; et al (2023) GGE biplot analysis of the adaptability and stability of wheat genotypes in Mozambique. Pesquisa Agropecuária Brasileira. 2023, 58, e03549.

Fok M Bilan de la recherche d'accompagnement du Projet Lomaco Montepuez, Mozambique. Centre de Coopération Internationale en recherche Agronomique pour le Développement (CIRAD), Montpellier, France. 2000. 39 pp. Available at: <http://agents.cirad.fr/pjjimg/michel.fok@cirad.fr/Bilan_RD_Montepuez_Moz.pdf>. Acessed in: 20 January 2010.

Hartley, HO (1950) The use of range in analysis of variance. Biometrika, 37:271-280.

ICAC [International Cotton Advisory Committee]. Cotton Data Book. Washington DC, USA. 2022. 949pp.

Instituto de Algodão de Moçambique [IAM] (2015) Relatório sobre o ponto de situação do subsector de algodão. Maputo. 29pp.

Maleia MP, Vidigal-Filho PS, Kvitschal MV, et al (2010) Stability and adaptability of commercial cotton cultivars (Gossypium hirsutum L. race latifolium H.) in Mozambique. Afr J Agric Res. 5:539-550.

Maleia MP, Jamal EC, Savanguane JW, et al (2019) Stability and Adaptability of Cotton (Gossypium Hirsutum L.) Genotypes under Multi Environmental Conditions in Mozambique. J Agron Agri Sci. 2:17.

Pinki SS, Siwach RS, Sangwan SS, et al. Stability Analysis for Seed Cotton Yield and Its Components in Upland Cotton (Gossypium hirsutum L.). Int.J.Curr.Microbiol.App.Sci.2018,07:1630-1638.

Shapiro SS, Wilk MB (1965) An analysis of variance test for normality (complete samples). Biometrika. 52:591–611.

Yan W, Kang, MS G (2003) GE biplot analysis: a graphical tool for breeders, geneticists, and agronomists. Flórida: Boca Raton. 286p.

Yan, W (2010) Optimal use of biplots in analysis of multilocation variety test data. Acta Agronómica Sinica. 36:1805-1819.

Yang RC, Crossa J, Cornelius PL, et al (2009) Biplot analysis of genotype x environment interaction: proceed with caution. Crop Scienc. 49:1564-157.