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Morphological characterization of 18 varieties of local rice in Mozambique

Salvado Kissoky Moses Nduma Mropes[1], Leonel Domingos Moiana[2,3]*, Leonel Abel Alberto[1], Jacinto Manuel Andreque[2], Hermínio Abade[2]

[1]Zambezi University. FEAF. Estrada Nacional N º 1. Vila de Mocuba. Nacogolone-Zambézia. Mozambique
[2]Regional Research Center of leadership for Rice, Instituto de Investigação Agrária de Moçambique, National Rood Number 1, W/N, Namacurra-Zambezia.
[3]Department of Agriculture and Animal Health, School of Agriculture and Life Sciences, University of South Africa, Roodepoort, South Africa

***Corresponding author: leonel.moiana@gmail.com**

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Abstract: The morphological characterization of 18 rice varieties in Mozambique is essential to identify and preserve genetic diversity, selecting high-yielding varieties that are adaptable to our country's ecosystem and can support future breeding programs for sustainable agriculture. For this study, the most produced varieties in our country were chosen, as they are drought tolerant and have a good smell. The study was carried out at the Regional Center for Rice Leadership and Research/IIAM using a randomized block design with three replications. Sixteen descriptors were analyzed, of which six were qualitative characteristics (ligule color, auricle color, leaf color, flag leaf posture, stalk growth habit and leaf pubescence) and ten were quantitative characteristics (flowering days, full flowering days, stalk length, stalk diameter, panicle length, number of tillers, fertile tillers, harvest days, 1000 grain weight). The statistical package RStudio version 4.5.0 was used for data analysis. Regarding productivity, there was a statistical difference between the averages and the Simão variety presented the highest productivity, 2,614.17 kg/ha. Mahalanobis distancing was used because it allows quantifying the degree of dissimilarity between different genotypes based on multiple morphological characters. The Manhattan distance analysis identified genetic diversity among varieties, where the largest distances observed between Humwenhe and Simão (1245.085), Nene and Simão (1215.392) and others. Cluster analysis grouped the varieties into four distinct groups. highlighting potential crosses for breeding programs. These findings provide valuable insights for rice genetic improvement and conservation efforts.

Keywords: Genetic improvement, Morphological Characterization, Genetic Diversity, Rice.

Abbreviations: ANOVA_Analysis of Variance. MS_Mean Squares. GD_Genetic Distance. UPGMA_unweighted pair group method with arithmetic mean.

Introduction

Rice (*Oryza sativa* L.) is one of the most important crops for humanity and provides food for 50% of the world's population (Wambugu et al., 2021). The genus Oryza has 24 species, only two of the 24 existing Oryza species have become agronomically productive: the “Asian rice”, Oryza sativa, and the “African rice”, Oryza glaberrima (Wambugu et al., 2018). The Sativa L species originates from the region located southeast of the Himalayas, although the regions of Madras, in India, and Orissa, in the Philippines, can also be identified as primary and secondary centers of the species (Singh 2021).

Rice in Mozambique is produced by small scale farmers on less than 0.5 ha in many parts of the country but also by large scale farmers in few places in irrigation schemes (Ismael et al., 2021). Local rice varieties play a crucial role in morphological characterization. as they represent a vast genetic diversity adapted to the specific agroecological conditions of each region. These varieties are the result of natural selection and continuous interaction between farmers and the environment over generations (Ronald et al.. 2024).

The study of the morphological characterization of these varieties allows their identification. preservation and potential use in genetic improvement programs. ensuring food security and production sustainability. (Dantas et al., 2024) thus. the choice of certain traditional varieties for morphological characterization studies is justified by their genetic importance. adaptability. potential for improvement and contribution to the sustainability of rice production in Mozambique (Azevedo et al., 2019).

China is the world's largest rice producer. with 148 million tons grown on 30 million hectares. followed by India and Indonesia (STATISTA. 2023). In Africa. Nigeria. Egypt. and Madagascar lead production. with the continent yielding 40 million tons on 16 million hectares. Mozambique contributes with 365 thousand tons on 290 thousand hectares (FAOSTAT, 2022).

Rice is a crucial global crop. feeding nearly half the world's population. including Mozambique. Average consumption is 85 kg/person in asia and 6 kg/person in Europe. making rice a key economic commodity in preventing hunger and malnutrition (FAO 2023). Besides being a staple food. rice also supports employment and is used in various industries. including cosmetics. paper. chemicals. and alcohol production (Stein et al., 2018).

Morphological diversity is the variation in the physical and external characteristics of plants and genetic diversity is the distance between population (Beck et al., 2023) individuals or organisms. according to characteristics ranging from morphological. physiological or biochemical aspects to molecular aspects (Cai et al., 2021). Several quantitative or predictive methods are used to analyze genetic diversity within a plant population. among which the analysis of molecular markers and the analysis of morphological markers stand out (Mathew et al., 2021).

A standard approach applied to study genetic diversity is the comparison of individual genotypes within and between populations using a genetic dissimilarity matrix of all possible pairwise combinations of individuals to characterize the population structure based on the relative affinity of each with all other individuals evaluated (Bhandari et al., 2017). Several measures, including Euclidean, Manhattan, Mahalanobis and Gower coefficients of dissimilarity, are frequently employed in the analysis of dissimilarity of individuals using phenotypic attributes (Cortese et al., 2010).

In Mozambique, there are few studies on the morphoagronomic characterization of local rice varieties using morphological markers, but there are some studies that have evaluated the adaptability and stability of rice varieties introduced from the Philippines, China, Madagascar, Nigeria, among other countries with the aim of increasing the production of this cereal, which in most cases have not been successful include reference for rice in Mozambique.

The identification of divergent genotypes, associated with the morphoagronomic characteristics of the varieties produced in our country, will provide the best combinations to be recommended for rice improvement programs in Mozambique.

In this context, the present study aimed to morpho-agronomically characterize 18 local rice varieties using morphological markers to identify genetic dissimilarity. This research will benefit rice Breeding Program and in the near future the farmer using local varieties with good traits

Results and Discussion

Analysis of Variance

The analysis of variance (ANOVA) showed that there were significant differences at 5% for the quantitative variables regarding flowering period. full flowering period. stem diameter. stem length. panicle length. variety cycle. 1000 seed mass and yield (Table 1). The coefficients of variation have values between 2.57% and 39.44%. these values are within the acceptable standards of precision. Number of tillers. stem diameter. and fertile tillers had a CV value greater than 10%.

Comparison of means test

Flowering period (Fp)

The analysis of the Tukey mean test results (Table 2) revealed significant variability among the 18 rice varieties regarding the onset of flowering. The varieties Nene and Chupa presented the earliest flowering onset, with an average of 67.67 days, whereas Humwenhe exhibited the latest onset, averaging 100.67 days. These findings contrast with the results reported by Remme et al. (2023), who observed flowering onset ranging from 113 to 131 days among rice varieties evaluated in their study.

Comparatively, Ferdous et al. (2023), when studying F4 populations of upland rice, reported a range between 70 and 110 days for flowering onset, indicating that genetic background and environmental factors play critical roles in the expression of this trait.

In a study conducted by Shrestha et al. (2021) on rice genotypes in Nepal, the onset of flowering ranged from 80 to 120 days, with significant genotype × environment interaction effects. These results further highlight the adaptability of early-flowering varieties like Nene and Chupa, while also contextualizing the delayed flowering of Humwenhe within the normal variability range observed in diverse agroecological zones.

Cai et al. (2021) emphasized that early-flowering varieties are often preferred in drought-prone areas, as they complete their reproductive cycles before the onset of severe water deficits. Accordingly, the early-flowering characteristics of Nene and Chupa may provide strategic advantages in regions with limited rainfall or shortened growing seasons.

Additionally, Wambugu et al. (2021), focusing on Oryza glaberrima domestication, reported that early flowering serves as a crucial mechanism for escaping environmental stresses such as drought and unpredictable rainfall. This aligns with the strategic importance of selecting early-flowering genotypes like Nene and Chupa to ensure yield stability under adverse climatic conditions.

Full flowering period (Ffp)

The mean values of the period of full flowering up to 80% indicated significant variations among the varieties analyzed. The lowest means were observed in the Faya, Oziveliwa, and Rosa Nhanguela varieties, with 85.33 days, while the Mbiguidi variety presented the highest mean, with 131.33 days (Table 2). Similar observations were reported by Dikshit et al. (2013), who found a range of 45.0 to 145.0 days to reach 80% flowering in native varieties, with an average of 116.97 days.

Furthermore, Shrestha et al. (2021) reported considerable variation in flowering time among rice genotypes in Nepal, ranging from 75 to 125 days, reinforcing the influence of genetic background and environmental conditions. Ferdous et al. (2023) also noted a flowering time between 80 and 120 days in an F4 upland rice population, highlighting the variability important for selecting early- or late-flowering genotypes in breeding programs. Similarly, Cai et al. (2021) emphasized that the manipulation of flowering period is a key strategy in molecular breeding programs to develop varieties better adapted

Table 1. Summary of ANOVA of quantitative variables of 18 local rice varieties.

		MS				
FV	**GL**	**Fp**	**Ffp**	**nrT**	**Sl**	**Cl**
Varieties	17	0.0000079**	0.0000031**	19.152ns	0.018529**	777.39**
Block	2	0.0000019	0.0000015	33.359	0.043889	275.28
Waste	34	0.0000001	0.0000001	10.426	0.004869	64.71
Total	53					777.39**
Avarage		0.013	0.011	12.53	0.30	69.13
CV%		2.57%	2.91%	23.43%	16.31%	8.82%

Cont…

		MS				
FV	**GL**	**Ct**	**Ft**	**Cycle V**	**m1000**	**Yield**
Varieties	17	14.763**	0.00064073ns	0.0000004**	0.281992**	427385**
Block	2	0.983	0.00079	0.0000017	0.05716	919317
Residuos	34	4.339	0.00041	0.0000001	0.090439	80797
Total	53					
Avarage		20.87	0.034	0.009	6.00	2453.95
CV%		9.62%	39.44%	4.17%	5.42%	14%

**Significant a 0.05; * significant a 0.01; NS Not significant.

Table 2. Comparison table of means of significant quantitative variables obtained by the Tukey test.

	Variables							
Treatments	**Fp**	**Ffp**	**Sl**	**Cl**	**Pl**	**Cycle V**	**m1000**	**Yield Kg/Ha**
Namurava	89.33c	97.33b	0.40a	105.53c	25.47b	127.33b	30.46b	1639.68a
Faya	78.33b	85.33a	0.43a	75.47a	22.27a	118.33a	28.11b	2189.91b
Oziveliwa	78.33b	85.33a	0.33a	60.40a	20.47a	118.33a	27.95b	1802.71a
Rosa Nhanguela	78.33b	85.33a	0.40a	107.80c	19.07a	127.33b	29.70b	2157.97b
Mantega	94.33c	100.33b	0.53b	113.27c	22.60a	127.33b	30.08b	2111.03b
Simão	89.33c	97.33b	0.40a	73.13a	20.93a	127.33b	26.82b	2614.17b
Mamima	94.67c	106.33b	0.47a	91.80b	24.00b	127.33b	30.40b	1884.99a
Muworoma	98.33d	106.33b	0.43a	100.13b	21.13a	134.33b	29.50b	2222.55b
Bebe	98.33d	106.33b	0.37a	89.93b	19.73a	118.33a	30.63b	1653.23a
Nene	67.67a	102.67b	0.40a	85.00a	18.27a	117.67a	32.22b	1465.26a
Chupa	67.67a	102.67b	0.43a	91.67b	21.33a	126.67b	30.00b	1772.26a
Mbiguidi	101.67d	131.33c	0.40a	91.87b	21.27a	133.67b	30.00b	1757.12a
Sinabibi	93.67c	97.67b	0.40a	100.60b	22.00b	126.67b	24.74a	2580.94b
Vitamina	97.67d	101.67b	0.53a	111.47c	25.33b	126.67b	32.21b	2242.51b
ZM-30-57	77.67b	84.67a	0.37a	68.93a	18.47a	117.67a	36.88c	2529.81b
Humwenhe	100.67d	103.67b	0.47a	99.73b	21.40a	126.67b	34.54b	1431.81a
Casambaua	97.67d	104.00b	0.63b	106.67c	25.33b	126.67b	24.71b	1845.57a
ITA-34	77.67b	96.00b	0.30a	69.13a	20.87a	117.67a	35.57b	2453.95a

Averages followed by the same letters do not differ statistically from each other, according to the Tukey test at the 5% probability level.

to specific agroclimatic conditions. In addition, Remme et al. (2023) found flowering variations among 19 rice varieties released by BRRI, with flowering times ranging from 90 to 130 days, demonstrating the relevance of selecting varieties according to flowering duration to improve yield stability and regional adaptation.

These studies confirm the wide genetic diversity existing among rice varieties regarding the flowering period, which is crucial for the planning of crosses and for the development of new cultivars adapted to different environments and cropping systems.

Steam diameter (Sd)

The mean values observed in the Tukey test for stalk diameter indicated significant differences among the varieties. The ITA 34 variety had the smallest diameter, with 0.33 cm (Table 2), considered thin, while the Casambaua variety had the largest mean, with 0.63 cm, considered thick. Similar observations were reported by Bonow et al. (2007), who characterized eight upland rice varieties with diameters ranging from 0.38 to 0.63 cm.

Recent research supports the importance of stalk diameter in rice morphological characterization. Maji and Shaibu (2022) found significant variations in stalk diameter among traditional and improved rice varieties, with values ranging between 0.36 and 0.67 cm, and highlighted its role in lodging tolerance. Akhter et al. (2021), working with rice landraces in Bangladesh, observed that varieties with thicker stalks demonstrated greater adaptability to water stress conditions.

Similarly, Khatun et al. (2022) reported that stalk thickness was strongly correlated with yield performance in salt-tolerant rice genotypes, with thicker stalks helping plants withstand saline environments. Hossain et al. (2021), in a study on agro-morphological traits, emphasized that thicker stalks contribute not only to mechanical strength but also to better panicle support, ultimately affecting grain yield positively.

Culm length (Cl)

The results of the Tukey test at a 5% significance level indicated notable differences in stem length between the studied varieties. The Oziveliwa variety had an average stem length of 60.40 cm, categorized as short, while Casambaua reached 106.67 cm, classified as intermediate. These results reflect a wide morphological variability among the varieties.

In contrast, Rahman et al. (2021), working with advanced rice lines, observed stem lengths ranging from 105 cm to 145 cm, highlighting that longer stems were associated with greater susceptibility to lodging under high-fertility conditions. Similarly, Suh et al. (2022), studying rice genotypes under tropical conditions, reported stem length variation between 95 cm and 140 cm, emphasizing that shorter plants often show better mechanical strength and resistance to lodging.

Moreover, Zhang et al. (2021) found that genetic regulation of stem elongation is closely related to adaptation mechanisms under water-limited conditions, with stem lengths varying from 90 cm to 130 cm in drought-stressed environments. Additionally, Adeyemo et al. (2022), in a morphological diversity study of rice in West Africa, noted that stem length ranged from 70 cm to 140 cm and was strongly associated with panicle exertion and overall plant architecture improvements.

Panicle length (Pl)

According to the analyses performed by the Tukey test (Table 5), the panicle length showed significant differences at 5% significance, ranging from 18.27 cm in the Nene variety to 25.47 cm in the Namurava variety. These results demonstrate important morphological variability among the studied rice varieties.

Similarly, Akinwale et al. (2020), analyzing genetic diversity in rice germplasm collections, found panicle lengths ranging from 19.5 cm to 27.0 cm, reinforcing the importance of this trait in productivity performance. Nguyen et al. (2021), studying traditional and improved rice cultivars in Southeast Asia, observed variations between 20 cm and 28 cm, highlighting that longer panicles are often associated with a greater number of grains per panicle.

Additionally, Habib et al. (2022), investigating agro-morphological traits in Bangladeshi rice genotypes, reported panicle lengths from 17.8 cm to 26.5 cm, noting that genotypes with intermediate panicle lengths often balance yield and plant stability. Mohammed et al. (2022) also characterized genetic diversity among Sudanese rice varieties and found that panicle length ranged from 18.2 cm to 26.8 cm, suggesting that panicle architecture plays a central role in optimizing grain filling and reducing sterility under stress conditions.

Variety cycle (Cycle V)

The test of comparison of means, obtained by the Tukey test at 5% probability, showed that the Muworoma variety had the longest cycle, followed by the Mbiguidi variety, while the Nene, ZM-30.57, and ITA 34 varieties had the shortest cycles. These differences in cycle duration are essential for the adaptation of varieties to specific growing seasons and environments.

According to Santos et al. (2021), the classification of rice varieties into early, intermediate, or late groups is strongly influenced by genetic factors, particularly genes regulating photoperiod sensitivity and phase transitions during development. Environmental factors such as temperature, photoperiod, and soil fertility, as well as cultural practices, also play significant roles in determining cycle duration.

Similarly, Lu et al. (2022) emphasized that early varieties often possess mutations or downregulation in flowering time genes (such as Hd1 and Ehd1), allowing them to complete their life cycles more quickly in shorter growing seasons. Conversely, late varieties retain sensitivity to environmental cues, prolonging vegetative growth.

Moreover, Rahman et al. (2020), working with rice genotypes under varying climatic conditions, demonstrated that early-maturing varieties are crucial for regions prone to drought or floods, as they escape terminal stress events, whereas late-maturing varieties can exploit longer rainy seasons to maximize yield potential.

Lastly, Zhang et al. (2021) found that breeding programs targeting cycle duration improvements have increasingly focused on the balance between early maturity (for adaptability) and maintaining sufficient biomass accumulation to avoid yield penalties, highlighting the importance of genetic selection combined with agronomic management.

Mass of a thousand seeds (m1000)

The average thousand-seed weight values showed significant variations among the studied varieties. The Zm-30-57 variety had the highest weight, with 36.88 g, while the Casambaua variety had the lowest weight, with 24.71 g. Similar results were observed by Remme et al. (2023), where the highest thousand-seed weight was 35.90 g.

Supporting this finding, Kumar et al. (2022) reported that thousand-seed weight is a highly heritable trait influenced by genetic factors and moderately affected by environmental conditions, with recorded weights in different rice genotypes ranging from 22.5 g to 38.2 g.

Additionally, Hossain et al. (2021) emphasized that heavier thousand-seed weights are generally associated with larger grain size and better grain filling efficiency, which are important breeding targets for improving both yield and milling quality.

Similarly, Luo et al. (2020), in their study of rice germplasm collections, found thousand-seed weights varying from 23.1 g to 39.5 g, reinforcing the idea that significant variability exists among different varieties, largely driven by their genetic background.

Finally, Bhattarai et al. (2022) pointed out that thousand-seed weight is not only crucial for yield formation but is also linked to consumer preferences in many regions, where heavier grains are preferred for certain culinary uses.

Table 2. Manhattan dissimilarity (D^2) estimates among the 18 genotypes, based on morphological characters and continuous variables.
1=Namurava; 2=Faya; 3=Oziveliwa; 4=Rosa Nhanguela; 5=Mantega; 6=Simão; 7=Mamima; 8=Muworoma; 9=Bebe; 10=Nene; 11=Chupa; 12=Mbiguidi; 13=Sinabibi; 14=Vitamina; 15=Zm-30-57; 16=Humwenhe; 17=Casambaua; 18=ITA 34.

Genotyps	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2	629.072	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3	259.239	406.629	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4	563.444	84.162	418.777	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5	498.325	166.681	413.412	94.319	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6	1026.797	466.323	863.090	525.619	564.206	-	-	-	-	-	-	-	-	-	-	-	-	-
7	287.065	378.345	171.000	334.649	261.862	776.536	-	-	-	-	-	-	-	-	-	-	-	-
8	625.600	127.160	529.521	132.422	146.809	455.397	368.935	-	-	-	-	-	-	-	-	-	-	-
9	70.809	610.251	236.418	588.755	513.370	1025.308	264.776	607.577	-	-	-	-	-	-	-	-	-	-
10	245.261	780.335	404.568	763.373	721.320	1215.392	480.726	830.459	235.856	-	-	-	-	-	-	-	-	-
11	190.300	482.960	111.191	443.794	397.943	903.415	156.549	511.082	171.559	333.351	-	-	-	-	-	-	-	-
12	199.134	540.606	168.773	502.644	428.083	938.331	175.735	511.198	162.313	385.129	97.618	-	-	-	-	-	-	-
13	969.847	460.573	862.276	470.669	498.186	76.444	725.782	393.113	978.492	**1187.776**	863.131	892.645	-	-	-	-	-	-
14	627.973	147.859	554.488	144.975	150.140	443.792	399.620	56.831	635.916	858.088	532.223	560.889	375.508	-	-	-	-	-
15	982.247	369.001	756.362	436.185	522.550	146.790	736.166	415.573	949.438	**1120.900**	829.081	898.567	143.042	392.410	-	-	-	-
16	244.420	847.696	478.195	795.332	714.479	**1245.085**	489.083	814.086	250.243	102.357	391.002	384.086	1181.735	834.759	**1191.037**	-	-	-
17	235.031	438.177	151.794	372.859	294.228	836.708	76.012	409.069	239.076	459.026	136.049	159.761	760.264	416.300	794.112	442.851	-	-
18	888.208	299.630	688.457	372.414	427.845	201.805	645.461	320.868	861.667	1034.327	739.042	805.862	204.057	300.371	96.839	**1096.998**	704.073	-

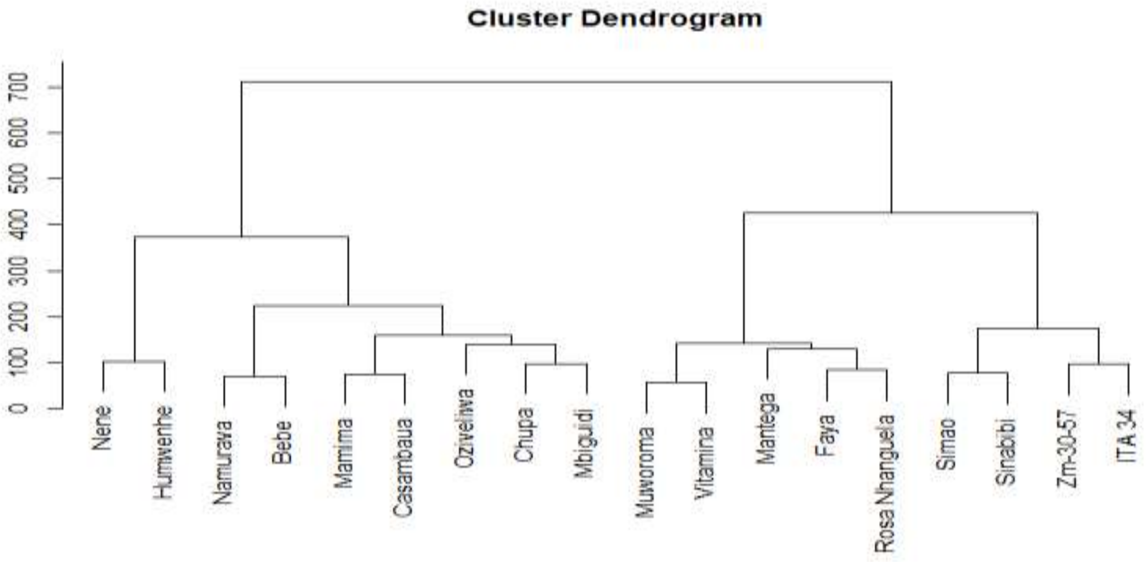

Figure 1. Dendrogram representing the genetic dissimilarity between 18 local rice varieties based on quantitative traits, obtained by the UPGMA method, using the nearest neighbor method.

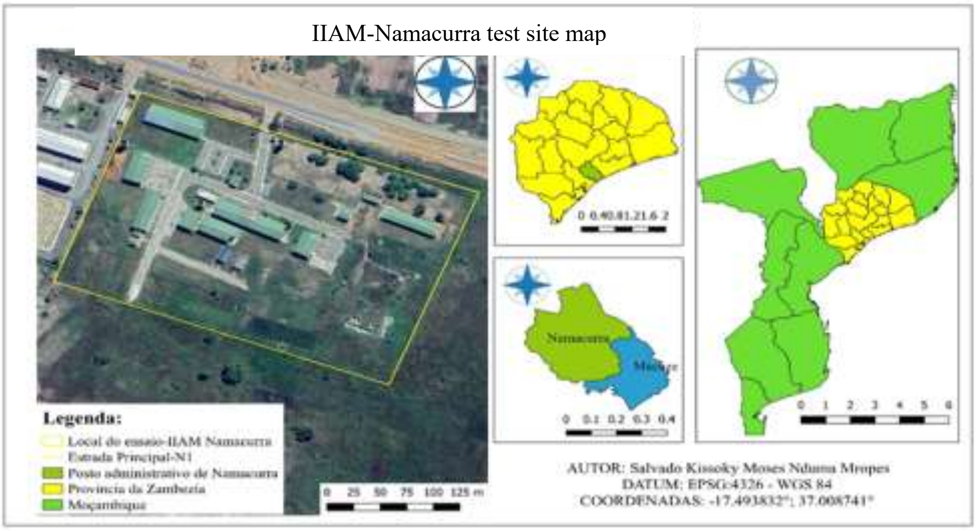

Figure 2. Geographic location of the test site.

Table 4. Description of varieties and origin (Localidades circunvizinhas do distrito de Namacurra).

Varieties	Descriptions	Origin	Burn tolerance	Seed size
Namurava	Local variety	Mutange	Not tolerant	Far away
Faya	Local variety	Batela	Not tolerant	Short
Oziveliwa	Improved variety	IIAM-CliPA	Not tolerant	Far away
Rosa Nhanguela	Local variety	Mutange	Tolerant	Far away
Mantega	Local variety	Batela	Tolerant	Far away
Simão	Improved variety	IIAM-CliPA	Tolerant	Far away
Mamima	Local variety	Mutange	Tolerant	Short
Muworoma	Local variety	Mutange	Tolerant	Far away
Bebe	Local variety	Batela	Tolerant	Far away
Nene	Local variety	Batela	Tolerant	Far away
Chupa	Local variety	Mutange	Tolerant	Short
Mbiguidi	Local variety	Mutange	Tolerant	Short
Sinabibi	Local variety	IIAM-CliPA	Tolerant	Far away
Vitamina	Local variety	IIAM-CliPA	Not tolerant	Far away
ZM-30-57	Improved variety	IIAM-CliPA	Tolerant	Short
Humwenhe	Local variety	Batela	Tolerant	Short
Casambaua	Local variety	IIAM-CliPA	Not tolerant	Far away
ITA-34	Improved variety	IIAM-CliPA	Tolerant	Far away

Yield per hectare (Yield Kg/Ha)

In relation to yield, the Simão variety presented the highest yield of 2614.17 kg/ha (Table 2). According to IIAM (2015), at the time of its release, Simão showed a potential yield of up to 10 tons/ha under flooded conditions, having been specifically bred for such an environment.

Supporting this, Biswas et al. (2022) emphasized that rice varieties adapted to flooded ecosystems generally exhibit higher yields due to physiological traits such as enhanced root porosity and tolerance to submergence stress, facilitating better nutrient uptake and oxygen transport.

Similarly, Ali et al. (2021) found that in flooded conditions, varieties bred specifically for such environments could outperform upland or general-purpose varieties by 30–50% in yield due to genetic adaptations related to tillering capacity and grain filling efficiency.

Moreover, Nguyen et al. (2020) reported that breeding programs focusing on flooded rice ecosystems prioritize traits like lodging resistance, rapid recovery from submergence, and increased harvest index to maintain high yield potential, aligning with the observed performance of Simão.

Finally, Timsina and Jat (2020) highlighted that the management practices (e.g., water control, fertilization timing) combined with genetically improved varieties for flooded conditions could double productivity compared to traditional landraces, emphasizing the role of both genotype and agronomic management in achieving high yields like those recorded for Simão.

Manhattan dissimilarity

Among the varieties analyzed, the largest Manhattan distances observed were 1245.085 between genotypes (Humwenhe and Simão), 1215.392 between varieties (Nene and Simão), 1191.037 (Humwenhe and Zm-30-10), 1187.776 (Sinabibi and Nene), 1120.900 (Zm-30-10 and Nene), and 1096.998 (ITA-34 and Humwenhe), being the crosses to be considered for generating genetic variability in the rice improvement program. The range of values of the observed dissimilarity estimates suggests that there is genetic variability among the set of varieties analyzed.

This observation is consistent with the findings of Ajay et al. (2022), who emphasize that high genetic dissimilarity between rice genotypes—quantified through Manhattan or Mahalanobis distances—can guide the selection of parents for hybridization, maximizing heterosis and recombination potential. Tiwari et al. (2021) also highlighted that multivariate analyses using distance metrics are crucial for exploring genetic diversity in rice breeding, especially in programs aiming to broaden the genetic base of cultivated varieties. Their study confirmed that genotypes grouped in distinct clusters showed greater divergence, which is desirable for parent selection.

Furthermore, Mitra et al. (2020) demonstrated that dissimilarity matrices based on morphological and molecular markers revealed wide variability in rice landraces, and crosses among divergent clusters contributed to transgressive segregation and superior recombinants in subsequent generations. Kandel et al. (2023) reinforced that using dissimilarity metrics helps to identify genetically contrasting parents, allowing the development of high-yielding and stress-resilient cultivars through targeted hybridization.

Cluster analysis

A dendrogram was constructed using the UPGMA clustering method based on the average linkage and Manhattan Euclidean distance among the 18 landraces. Cluster analysis grouped the landraces into four clusters for the quantitative traits.

According to the dendrogram, it was possible to form 4 distinct groups. Group 1 consisted of the varieties Nene and Humwenhe; group 2 consisted of the varieties Namurava, Bebe, Mamima, Casambaua, Oziveliwa, Chupa and Mbiguidi; group 3 contained Muworoma, Vitamina, Mantega, Faya, Roza Nhanguela and group 4 consisted of Simão, Sinabibi, ZM-30-57 and ITA-34.

The UPGMA method combined with the Tocher method allows for better visualization, easy interpretation and efficiency in discriminating genotypes in terms of their genetic distances, according to Nardino et al., (2017).

Materials and methods

Plant materials details

The varieties were collected from different locations in the Namacurra district. These were obtained from some producers in neighboring locations and some varieties belonging to the IIAM CLiPA germplasm (Table 3).

Description of location of study

The experiment was conducted from January 2024 to May 2024, in the experimental area of CLiPA-IIAM (Regional Research Centre of Leadarship for Rice-Instituto de Investigação Agrária de Moçambique) in the district of Namacurra, with the following geographic coordinates: latitude 170 19' 29" S; 370 01' 39" E, The locality belongs to agro-ecological zone 5 (R5) characterized by a tropical rainy savanna climate (Aw), and has a soil of medium texture, deep, poor in organic matter and slightly saline, (MITJANS et al., 2020).

Experimental design

The experimental design was completely randomized blocks, with 18 varieties in 3 replicates. Fourteen local varieties and four improved varieties were used (Table 2), with a distance between rows and plants of 20 cm in 20 cm, respectively. Each plot was allocated in the serpentine system, enabling randomization, where each plot had an area of 0.8 cm X 5 m.

Installation and conduct of experiments

They were transplanted to the experimental field 20 days after the seedlings were established in the nursery. During the vegetative period of the crop, all the activities that the crop requires were carried out. Two different fertilizations were made, the background fertilization that was carried out on the day of the transplantation based on NPK (1.5 kg/repetition) and the top dressing 30 days after the transplantation date based on Urea at 46% Nitrogen (1.80 kg/repetition).

Data collection

The useful area for collecting samples was considered in the two central lines (2m2). 16 descriptors were evaluated,6qualitative and 10 quantitative described by Biodiversity international and IRRI, (2011).

Ligule color (CL): observation made on the penultimate leaf of the plant (first leaf below the flag leaf), between the “booting” and anthesis phases, taking ten plants at random from each plot. Classified as light green, colorless and dark green;

Auricle color (AC): Observation made on the penultimate leaf of the plant (first leaf below the flag leaf), between the “booting” and anthesis phases, taking ten plants at random from each plot. Classified as absent, whitish and yellowish-green auricles;

Leaf color (CF): observation made on the flag leaf, at the beginning of the emergence of panicles, taking ten plants at random from each plot, according to the light green, green and dark green scale;

Flag leaf posture (PFB): Measured near the collar. Connection angle between the flag leaf blade and the main panicle axis. Record the average of five samples. With the following scales: erect, less than 30º; intermediate, between 31º and 60º; horizontal, between 61º and 90º; and descending, greater than 90º;

Stem growth habit (HCC): Average estimated angle of inclination of the base of the main culm in relation to the vertical. Stage: after flowering. Following the scales: Upright (<15°); Semi-erect (intermediate) (~20°); Open (~40°); wide open (>60–80°, culms do not touch the ground);

leaf pubescence (PF): Evaluated both visually and by touch, passing the hand over the surface of the leaf from the tip to the bottom. Stage: advanced vegetative. With the scales: Smooth, Intermediate and pubescent.

Days to floweing (DIF): Date when the first flush of flowers is observed. Refers to the number of days from the actual planting date to the date of onset of flowering;
Days to fullflowering (DFP): Date on which 80% of the plants are in bloom. Refers to the number of days from the actual planting date to the date of full bloom;
Panicle length (PL): distance, in centimeters, from the base of the panicle to the tip of the last spikelet. Stage: 7 days after anthesis or at the stage of complete panicle insertion;
Stem length (SL): Measured from soil level to the base of the panicle. Record the rounded mean of five samples. Stage: cultivated species from flowering to maturity; wild species: 7 days after anthesis. Using the scales: Very short (<50 cm); very short to short (51–70 cm); Short (71–90 cm); short to intermediate (91–105 cm); Intermediate (106–120 cm); intermediate to long (121–140 cm); Long (141–155 cm); Long to very long (156–180 cm); very long (>180 cm);
stem diameter (SC): Measurement of the external diameter of the basal portion of the main stalk using a caliper. Cultivated species: record the average of a sample of three plants during flowering or at the advanced reproductive stage. Using the following scales: Fine (<5 mm); Coarse (≥5 mm);
Number of tillers (NP): Total number of fertile and sterile tillers in five plants Stage: from anthesis to close to maturity. The following rating scale can be used: Low (<10 stems); Intermediate (~15 stalks); Tall (>20 stalks);
Number of fertile tillers (NPF): determined together with the average number of tillers per panicle, considering tillers with grains;
Variety cycle (CV): number of days elapsed from planting to harvesting point (when 80% of the panicles in each plot had two-thirds of the spikelets mature);
Mass of 1000 seeds (MS): evaluated using a thousand seeds collected at random in each plot and subsequently weighed on the scale;
Crop yield (Rend) Ton/ha: The yield (Ton/ha) was obtained using the formula proposed by (Bioversity International et al., 2011).

Massa da área útil---------m^2
X---------------------10000m^2

Statistical analysis of data

The data were decoded in Microsoft® Excel® LTSC MSO (Version 2407 Build 16), processed and analyzed in the statistical package RStudio (version 4.4.1). To verify the normality assumptions of the residuals they were subjected to the Shapiro-Wilk test and the homogeneity of the variables was assessed by the Oneillmathews test at 5% significance, and the comparison of means for quantitative traits was performed by the Tukey test at 5% probability. To obtain the dendrogram, it was obtained by the mean/average grouping method and showed three groups. These analyses were processed using the Rstudio package

Statistical model

$$Y_{ij} = \mu + Ti + Bj + E_{ij}$$

Where:
Y_ij: Observation of treatment i in block j.
μ: Overall Average
Ti: Effect of the i-th treatment
Bj: Effect of the j-th block
E_ij: : Random error associated with observation Y_ij

The mathematical model for obtaining the Manhattan distance obtained by the averages of the descriptors is given by:

$$D(A,B) = \sum_{i=1}^{n} |x_{iA} - x_{iB}|$$

Where:$x_{iA} e x_{iB}$ are the means of the i-th variables of the varieties A and B.

Conclusion

Regarding yield, there were statistical differences between the means and the Simão variety presented the highest yield of 2614.17 kg/ha. The largest Manhattan distances observed were 1245,085 between the varieties (Humwenhe and Simão), 1215,392 between the varieties (Nene and Simão), 1191,037 (Humwenhe and Zm-30-10), 1187,776 (Sinabibi and Nene), 1120,900 (Zm-30-10 and Nene), 1096,998 (ITA-34 and Humwenhe), being the crosses to be considered for generating genetic variability in the Rice improvement program. The dendrogram was obtained by the UPGMA grouping method and showed four groups, Group 1 (Nene and Humwenhe), group 2 (Namurava, Bebe, Mamima, Casambaua, Oziveliwa, Chupa and Mbiguidi), group 3 (Muworoma, Vitamina, Mantega, Faya, Roza Nhanguela) and (Simão, Sinabibi, ZM-30-57 and ITA-34).

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