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Resistance to groundnut rosette disease and yield performance of advanced groundnut lines in northern Mozambique

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Groundnut rosette disease (GRD) is a major constraint to groundnut production in sub-Saharan Africa, causing severe yield losses, particularly under low-input smallholder farming systems with limited access to external inputs. Because resistance to this pathogen is strongly influenced by environmental factors, quantifying genotype-by-environment (G×E) interactions is essential for identifying GRD-resistant varieties and optimal testing locations. This study analyzed the effects of genotype (G), environment (E), and their interaction (G×E) on GRD resistance and grain yield of groundnut in northern Mozambique. Twenty advanced groundnut lines (*Arachis hypogaea* L.) were assessed across 11 environments from 2014 to 2018 using an alpha-lattice design with two replications under low-input conditions. Measured traits included phenology, number of emerged plants, number of plants at harvest, yield components, grain yield, and GRD incidence. General and mixed linear models, stability analysis, AMMI and SREG models, and Pearson correlations were applied. Significant G×E interaction was observed, indicating a strong environmental influence on trait expression. GRD incidence was highest in the NPL_15 environment, where the susceptible cultivar JL-24 reached 56% and SREG analysis identified this site as a suitable hotspot for resistance screening. Genotypes ICGV-SM 7508, ICGV-SM 7510, ICGV-SM 7518, ICGV-SM 7533, ICGV-SM 7558, ICGV-SM 7566, ICGV-SM 8530 and ICG 405 showed resistance. No consistent relationship was observed between GRD incidence and grain yield; however, yield reductions were mainly associated with plant losses during the growing season. Genotypes ICGV-SM 7518 and ICGV-SM 7510 showed broad adaptation, combining high yield and GRD resistance across environments.

KEYWORDS

AMMI1, broad adaptation, GGE, G×E interaction, incidence, selection

1 Introduction

Groundnut Rosette Disease (GRD) is a viral disease affecting groundnut (*Arachis hypogaea* L.) crops in Africa. It is (Nigam et al., 1994; Nigam et al., 2004; Walker et al., 2006; Muitia, 2015; Arias and Libombo, 1994; Muitia, 2011; MADER, 2021; USDA, 2025; Kankam et al., 2020; Zuza Jnr et al., 2017; Muitia, 2011) endemic to the region and can cause yield losses of up to 100% (Arias and Libombo, 1994; Subrahmanyam et al., 1998; Naidu et al., 1999; Zuza Jnr et al., 2017), resulting in estimated annual economic losses of approximately USD 156 million across Sub-Saharan Africa (Kayondo et al., 2014).

Groundnut Rosette Disease (GRD) includes three distinct types: chlorotic rosette, green rosette and mosaic rosette, each with a distinct geographic distribution. Chlorotic rosette is prevalent throughout Africa and is characterized by bright yellow leaves with fine mottling. Green rosette, currently restricted to western Africa, exhibits a mosaic pattern ranging from light to dark green, often accompanied by downward-curved leaf margins (Mugisa et al., 2016; Desmae and Sones, 2017; Mabele, 2020). Mosaic rosette primarily affects younger leaflets, which display conspicuous mosaic symptoms (Subrahmanyam et al., 1998), and has been reported in eastern and southern Africa (Mabele, 2020). Affected plants also exhibit a bushy phenotype accompanied by stunted growth (Awoke et al., 2025).

The disease is caused by a viral complex consisting of Groundnut Rosette Virus (GRV), a satellite RNA, and Groundnut Rosette Assistant Virus (GRAV). The characteristic symptoms of the disease occur only when these three components act together, whereas infection by the individual components, does not result in the expression of rosette disease symptoms (Kayondo et al., 2014).

GRD is transmitted by the aphid *Aphis craccivora* (Kayondo et al., 2014). Climatic factors such as high temperatures, intermittent rainfall and the presence of alternative host species enhance aphid survival and virus inoculum (Mugisa et al., 2016; Waliyar et al., 2007). As a result, disease prevalence and spread are frequently favored under prolonged drought conditions (Muitia, 2011; Mabele, 2020). Management strategies to reduce disease incidence include insecticide application during the early stages of crop development, early planting to allow the crop to escape periods of high aphid pressure and intercropping which acts as a physical or biological barrier that disrupts aphid movement (Engels, 2010; Owusu-Akyaw et al., 2014). However, insecticide use is often not economically viable for smallholder farmers. In addition, because groundnut production is mainly rainfed, the feasibility of early sowing depends on the timing and occurrence of rainfall, while the adoption of intercropping systems is often constrained by management complexities and market dynamics. This highlights the need for farmers to have access to GRD-resistant varieties.

Varietal susceptibility largely determines epidemic intensity, with resistant or partially resistant lines showing reduced systemic infection and lower virus transmission rates (Deom et al., 2000). In Mozambique, Spanish- and Virginia-type materials are predominant and generally well adapted to local agroecological conditions (Muitia, 2011; Conde et al., 2024). Crosses between Spanish and

Virginia genotypes have proven effective in increasing genetic variability and improving the inheritance of key agronomic traits, such as yield and disease resistance (Singh and Oswalt, 1991). Virginia-type germplasm has contributed resistance to foliar diseases (Bhat et al., 2024) and to GRD (Achola et al., 2023).

Disease expression occurs only when the so-called “disease triangle” is fulfilled, which states that the occurrence and severity of a disease depend on the simultaneous interaction of a susceptible host, the presence of the pathogen, and favorable environmental conditions (Subrahmanyam et al., 2002; Naidu et al., 1999; Waliyar et al., 2007; Mugisa et al., 2016).

To overcome the limited variability of GRD-resistant germplasm the Agricultural Research Institute of Mozambique (IAM) conducted multi-environment trials (METs) in northern Mozambique to evaluate Spanish × Virginia breeding lines provided by ICRISAT, previously selected for GRD resistance under controlled conditions. Although the phenotyping of resistant cultivars is contingent upon exposure to high-pressure environments, disease severity is strongly influenced by the surroundings, which limits predictability. Given the marked spatio-temporal variability of environmental conditions, resistance expression is frequently confounded by significant genotype-by-environment (G×E) interactions, which has been reported in different crop species, including ryegrass (Fois et al., 2021), field pea (Das et al., 2019), and faba bean (Tekalign et al., 2017), where resistance to different diseases was strongly influenced by genotype-by-environment (G×E) interactions (Fois et al., 2021). METs are widely used to assess the adaptability and stability of grain yield and other agronomic traits, particularly when G×E interaction accounts for a substantial proportion of phenotypic variation. In this context, AMMI and GGE analyses are commonly applied to understand genotype performance patterns across environments (Forbes et al., 2005; Tekalign et al., 2017; Das et al., 2019).

The Additive Main Effects and Multiplicative Interaction (AMMI) model integrates analysis of variance (ANOVA) for genotype and environment main effects with principal component analysis (PCA) of G×E interaction. By partitioning interaction variance into interaction principal components (IPCA), AMMI improves estimation accuracy of genotype performance and stability across environments (Yan et al., 2000; Gauch, 2006; Yan and Tinker, 2006; Gauch, 2013).

The Genotype plus Genotype × Environment (GGE) biplot focuses on genotype and the G×E interaction as these are the effects most relevant for cultivar evaluation and selection. GGE biplots provide a powerful visual framework to assess genotype performance, identify “which-won-where” patterns, determine mean vs. stability relationships, rank genotypes relative to an ideal, and evaluate the discriminating ability and representativeness of test environments (Yan and Kang, 2002; Yan et al., 2000; Yan and Tinker, 2006; Gauch et al., 2008).

These multivariate methods have been widely applied in crop breeding research, including groundnut, cereals, legumes and root crops, to identify high-yielding, stable and adapted genotypes across diverse environments, demonstrating their utility in breeding decisions (Yan et al., 2000; Gauch, 2006; Gauch et al., 2008). This analysis captures complex G×E patterns and provides clear visual

interpretation of this interaction, which cannot be effectively achieved using other methods such as regression approaches and ecovalence (Yan and Kang, 2002).

Since resistance to this pathogen is strongly influenced by environmental factors, quantifying the magnitude of genotype-by-environment (G×E) interactions is essential for identifying GRD-resistant varieties and optimal testing locations. Consequently, the objective of this study was to analyze the effects of genotype (G), environment (E), and their interaction (G×E) on GRD resistance and grain yield of groundnut in northern Mozambique.

2 Materials and methods

2.1 Experiment site

The experiments were conducted in three Experimental Stations of the Agricultural Research Institute of Mozambique (IIAM) in northern Mozambique: Nampula (15° 09' 00" S, 39° 30' E) and Namapa (13° 43' 41" S, 39° 50' 41" E) in Nampula Province, and Mapupulo (13° 13' S, 39° 03' E) in Cabo Delgado Province (Figure 1). The trials were established with 20 genotypes and implemented across four consecutive growing seasons (2014, 2015, 2016, and 2018). The final season was conducted only in Nampula and Namapa, resulting in a total of 11 environments.

2.2 Treatments and experimental design

Eighteen genotypes derived from crosses between Spanish- and Virginia-types were used, along with one commercial variety from

Mozambique (JL-24) and one local variety (Table 1). JL-24 was included as a susceptible check for GRD (Muitia, 2015). The 18 cross-derived genotypes were provided by ICRISAT Malawi, where they had been selected for GRD resistance under controlled conditions. The 20 genotypes were arranged in an alpha-lattice design with two replications, each divided into four incomplete blocks. Replications were separated by 1 m. Each genotype was planted in a plot consisting of two rows, 5 m in length, with a spacing of 50 cm between rows and 10 cm between plants.

2.3 Experiment management

The experiments were sown between 15 December and 5 January, a period characterized by regular rainfall. Weeding was carried out manually whenever necessary. Earthing-up was performed 60 days after germination, at the onset of peg formation, to facilitate soil penetration. To simulate typical farmer management conditions, the seed used in the experiments was not treated, and no fertilizers, pesticides, or irrigation were applied.

2.4 Measured variables

Days to emergence (DE) and days to flowering (DF) were recorded when 50% of the plants in the plot had reached the respective growth stage. Days to harvest (DH) were recorded when more than 80% of the plants showed signs of maturity, such as leaf yellowing and pod hardening. All these variables were recorded from the day of sowing. The number of emerging plants (IPS) was assessed 15 days after sowing, and the number of plants at harvest (FPS) was also counted. The number of pods per square meter (PN_M2) was determined at harvest. Pods were sun-dried and then

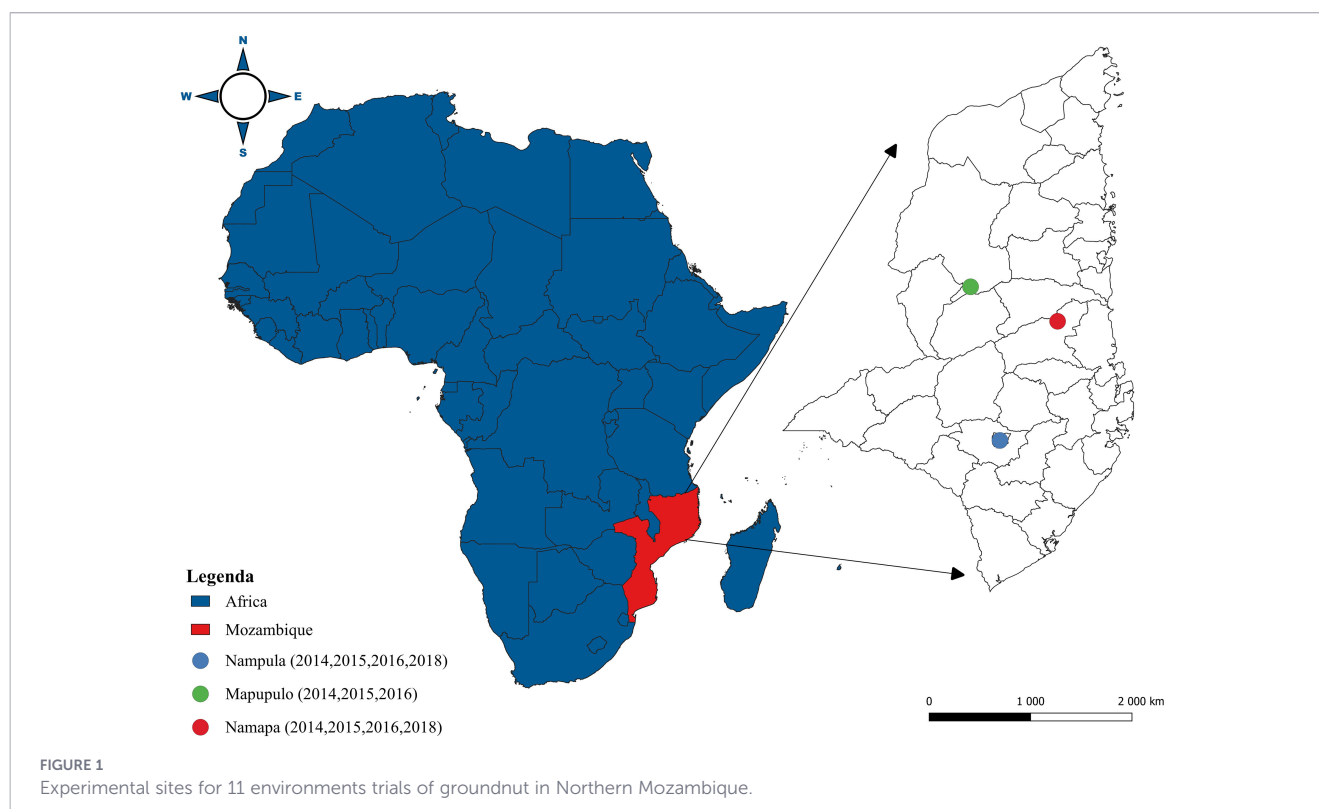


TABLE 1 Genotypes.

Entry	Genotypes	Market type	Source	Entry	Genotypes	Market type	Source
1	ICGV -SM 7505	Advanced line	ICRISAT	11	ICGV -SM 7558	Advanced line	ICRISAT
2	ICGV -SM 7508	Advanced line	ICRISAT	12	ICGV -SM 7566	Advanced line	ICRISAT
3	ICGV -SM 7510	Advanced line	ICRISAT	13	ICGV -SM 8530	Advanced line	ICRISAT
4	ICGV -SM 7518	Advanced line	ICRISAT	14	ICGV -SM 9511	Advanced line	ICRISAT
5	ICGV -SM 7531	Advanced line	ICRISAT	15	ICGV -SM 95741	Advanced line	ICRISAT
6	ICGV -SM 7532	Advanced line	ICRISAT	16	ICGV -SM 96714	Advanced line	ICRISAT
7	ICGV -SM 7533	Advanced line	ICRISAT	17	ICG 405	Advanced line	ICRISAT
8	ICGV -SM 7539	Advanced line	ICRISAT	18	ICG 6057	Advanced line	ICRISAT
9	ICGV -SM 7543	Advanced line	ICRISAT	19	JL-24	Spanish	IIAM
10	ICGV -SM 7544	Advanced line	ICRISAT	20	LOCAL	Spanish	IIAM

weighed to obtain pod yield (PY); they were subsequently shelled, and the grains were weighed to determine grain yield (GY). The grain percentage (Gr) was calculated as the ratio between dry grain weight and total pod weight. The 100-seed weight (SW₁₀₀) was measured from a sample of 100 seeds.

The maturity percentage (Mat) was obtained from a sample of 50 pods randomly selected at harvest. The pods were shelled and classified according to the color of the inner pod wall: white, yellow, orange, brown, and black. White and yellow were considered immature pods, whereas orange, brown, and black were classified as mature. The maturity percentage was calculated as the proportion of orange, brown, and black pods relative to the total number of pods.

The incidence of rosette disease (GRDI) was recorded through direct field observations using disease evaluation descriptors (Kayondo et al., 2014). Each plant was monitored for the presence or absence of rosette symptoms at 90 days after sowing. Disease incidence was calculated as the percentage of symptomatic plants relative to the total number of plants in the plot (Waliyar et al., 2007), as shown in Equation 1.

$$GRD \text{ Incidence } (\%) = \frac{\text{Number of infected plants}}{\text{Total number of plants}} \times 100 \quad (1)$$

To determine disease resistance, we followed the criteria described by Subrahmanyam et al. (2002) and Ntare and Olorunju (2001), which classify groundnut genotypes into three categories based on disease incidence under high infection pressure: highly resistant (0% incidence), moderately resistant (<10%), and susceptible (>10%). High infection pressure refers to environmental conditions that trigger severe and uniform GRD epidemics, serving as a stringent benchmark to effectively differentiate between resistant and susceptible genotypes (Subrahmanyam et al., 2002).

2.5 Statistical analysis

General and mixed linear models were used, considering Genotype (G), Environment (E), and their interaction (G×E) as fixed effects. To address heterogeneity of variances across genotypes and environments, heteroscedastic variance structures were applied. For mean comparisons, the DGC multiple comparison test was used

at the 5% significance level ($\alpha = 0.05$) (Di Rienzo et al., 2008). To explore the G×E interaction, an Additive Main Effects and Multiplicative Interaction model (AMMI1) (Balzarini et al., 2005) was used to identify the most stable genotypes, as described by the following equation (Crossa et al., 1998):

$$Y = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger}$$

Where Y = yield of the i-th genotype g in the j-th environment e and in the r-th replication. The additive parameters are: μ = grand mean. α_g = deviation of genotype g from the grand mean. β_e = deviation of environment e. The multiplicative parameters are: λ_n = singular value for the n-th interaction principal component axis (IPCA). γ_{gn} = eigenvector of genotype g for the n-th axis. δ_{en} = eigenvector of environment e for the n-th axis. ρ_{ge} = sum of the interaction effects not explained by the retained IPCAs (residual GEI). ε_{ger} = residual associated with genotype g in environment e in replication r.

To identify mega-environments (genotypes specifically adapted to particular environments), the model proposed by Yan et al. (2000) was used based on the GGE biplot approach. The biplot was constructed using the first two principal components obtained from principal component analysis (PCA), applying the Site Regression (SREG) model according to the following linear model (Yan et al., 2000):

$$Y_{ij} - \bar{y}_j = (\lambda_1 \xi_{i1} \eta_{j1}) + (\lambda_2 \xi_{i2} \eta_{j2}) + \varepsilon_{ij}$$

Where Y_{ij} is mean yield of genotype i in environment j , $\bar{y}_j$ is mean yield of all genotypes in environment j (environmental marginal mean), $\lambda_1 \xi_{i1} \eta_{j1}$ is the first principal component (PC1), $\lambda_2 \xi_{i2} \eta_{j2}$ is the second principal component (PC2), λ_1 and λ_2 are singular values associated with PC1 and PC2, respectively, ξ_{i1} and ξ_{i2} = eigenvectors for genotype i corresponding to the first and second principal components, respectively, η_{j1} and η_{j2} are eigenvectors for environment j corresponding to the first and second principal components, respectively, and ε_{ij} = residual error associated with genotype i in environment j .

(Yan et al., 2000) Pearson correlations were performed to assess associations among variables. All analyses were performed using InfoStat and InfoGen software packages (Balzarini et al., 2005; Di Rienzo et al., 2020).

3 Results

The percentage contribution to total variance across the eleven environments showed that the environment accounted for a large proportion of the variation for all variables except DE and SW_100. In contrast, Mat was almost entirely influenced by the environment. For the remaining variables, the G×E interaction showed a relative contribution similar to, or several times greater than, that of the genotype (Table 2).

3.1 Groundnut rosette disease incidence

The environmental effect on GRDI accounted for 92.9% of the total variability (Table 2), and incidence across environments ranged from 1 to 21%. The highest incidence was observed in NPL_15, MPP_14, NMP_15 and MPP_15 (Table 3). No association was detected between GRDI and any agronomic variable (Supplementary Data: environment-specific correlation matrix).

Although genotypes had a statistically significant effect on GRDI, they accounted for only 1.1% of the total variability (Table 2). As expected, the highest rosette incidence was observed in the susceptible commercial variety JL-24 (13%), which differed from the other 19 genotypes which showed an average incidence of 5% (Table 4).

The G×E interaction had a greater effect than genotype alone, explaining 6% of the total variability (Table 2). Although JL-24 showed disease incidence in all environments, the highest incidence for this genotype was observed in NPL_15 and NPL_14, with values of 56% and 21%, respectively. However, in NPL_14, low variability among genotypes in disease incidence was observed, whereas in NPL_15, high variability was detected under conditions of high infection pressure, highlighting the strong discriminating ability of this environment (Table 5). According to the criteria described by Subrahmanyam et al. (2002) and Ntare and Olorunju (2001), genotypes evaluated in NPL_15 were classified into three categories: highly resistant, moderately resistant, and susceptible (Table 5). One genotype was highly resistant (ICGV-SM 8530), six were moderately resistant (ICGV-SM 7508, ICGV-SM 7518, ICGV-SM 7533, ICGV-SM 7558, ICGV-SM 7566, and ICGV 405), and thirteen were susceptible (ICGV-SM 7510, ICGV-SM 7505, ICGV-SM 7531,

ICGV-SM 7532, ICGV-SM 7539, ICGV-SM 7543, ICGV-SM 7544, ICGV-SM 9511, ICGV-SM 95741, ICGV-SM 96714, ICGV 6057, JL-24, and the local variety) (Table 5).

NPL_15 allowed the identification of genotypes with different levels of GRD incidence. Its representativeness as a selection site was assessed using a GGE biplot, which identify mega-environments based on genotype performance, explaining 68.4% of the total observed variability. The NPL_15 environment clustered with NPL_14, NPL_16, NPL_18, NMP_14, NMP_16, and MPP_16; all years evaluated in Nampula fell within this mega-environment, confirming NPL_15 as a suitable site for GRD selection. In this mega environment, JL-24 showed the highest susceptibility to the disease, followed by the local variety (Figure 2).

3.2 Grain yield and other agronomic traits

The environmental effect on grain yield accounted for 71.1% of the total variability (Table 2), and grain yield across environments ranged from 248 to 1192 kg ha⁻¹ (Table 3). Positive associations were detected between GY and PN_M2 ($r = 0.89$; $p = 0.0002$), Gr ($r = 0.77$; $p = 0.0057$), PY ($r = 0.69$; $p = 0.0177$), IPS ($r = 0.80$; $p = 0.0032$), and FPS ($r = 0.80$; $p = 0.0032$) (Supplementary Data: environment-specific correlation matrix).

Although genotypes had a statistically significant effect on grain yield, it explained only 3.5% of the total variability (Table 2). Genotype ICGV-SM 9511 showed the highest grain yield (870 kg ha⁻¹), whereas the local variety had the lowest (444 kg ha⁻¹) (Table 4). Grain yield was strongly influenced by FPS ($r = 0.51$; $p = 0.0214$), PY ($r = 0.86$; $p < 0.0001$), and PN_M2 ($r = 0.68$; $p = 0.001$), and no association was observed between yield and GRDI.

The G×E interaction had a greater effect than genotype, accounting for 25.4% of the total variability (Table 2), indicating that yield responses varied among genotypes across environments. This interaction was further explored using AMMI1 analysis, which showed that genotypes ICGV-SM 7518, ICGV-SM 7510, ICGV-SM 7533 and ICGV-SM 95741 were the highest-yielding and most stable, as they were located near zero on PC1. In contrast, the highest-yielding but most unstable genotypes were ICGV-SM 9511 and ICGV-SM 96714. JL-24 and the local variety, although stable, had the lowest yields (Figure 3).

TABLE 2 Percentage of the variances of all evaluated traits.

FV	GRDI	PY	Gr	GY	IPS	FPS	PN_M2 (%)	SW_100	DE	DF	DH	Mat ¹
Environment	92.9	74.2	79.5	71.1	86.5	92.8	74.2	19.3	35.1	79.9	76.2	100
Genotype	1.1	4.8	0.9	3.5	6.4	0.6	4.8	4.2	9.4	4.7	5.7	0
G×E	6.0	20.9	19.6	25.4	7.1	6.6	20.9	76.5	55.4	15.4	15.4	0
Significance												
Environment	***	***	***	***	***	***	***	***	***	***	***	***
Genotype	**	***	**	***	*	*	***	***	***	***	***	Ns
G×E	**	***	***	***	***	***	***	***	***	***	***	Ns

GRDI, Groundnut rosette disease incidence; PY, Pod yield; Gr, Grain percent; GY, Grain Yield; IPS, Initial plants stand; FPS, Final plants stand; PN_M2, pods per square meter; SW_100, 100 seed weight; DE, Days to emergency; DF, Days to flowering; Mat, maturity percentage; ¹ - analysis conducted in a few environments. Ns- not significant; * - Significant ($p < 0.05$); ** - Highly significant ($p < 0.01$) and *** - Very highly significant ($p < 0.001$) according to the DGC test.

TABLE 3 Environments independent of genotype.

Environments	GRDI (%)		PY (Kg ha ⁻¹)		Gr (%)		GY (Kg ha ⁻¹)		IPS (Plants ha ⁻¹)		FPS (Plants ha ⁻¹)		PN_M2 (Pods m ⁻²)		SW100 (g)		DE (days)		DF (days)		DH (days)		Mat ¹ (%)	
MPP_14	12	b	1222	b	97	a	1189	a	127229	c	103976	b	219	a	43	a	9	a	37	b	104	a	--	
MPP_15	7	c	1209	b	99	a	1192	a	128268	c	106253	b	220	a	44	a	9	a	37	b	104	a	97	a
MPP_16	4	d	625	e	40	d	248	d	53260	h	48889	e	112	d	39	b	9	a	37	b	104	a	40	c
NMP_14	1	d	880	d	54	b	473	c	65946	g	52665	e	179	b	39	b	9	a	37	b	104	a	--	
NMP_15	10	b	696	e	97	a	673	b	116340	d	94197	c	168	b	43	a	9	a	37	b	104	a	96	a
NMP_16	2	d	982	c	52	b	513	c	63169	g	56922	e	174	b	34	c	9	a	37	b	104	a	--	
NMP_18	2	d	1092	c	48	c	523	c	70896	f	57507	e	140	c	36	c	9	a	37	b	104	a	95	a
NPL_14	1	d	1942	a	59	a	1140	a	152736	a	139484	a	202	a	39	b	8	b	41	a	96	b	--	
NPL_15	21	a	559	e	97	a	540	c	136767	b	110356	b	175	b	40	b	9	a	37	b	104	a	97	a
NPL_16	1	d	1108	c	48	c	528	c	82438	e	73735	d	165	b	42	a	8	b	41	a	96	b	48	b
NPL_18	2	d	1012	c	46	c	467	c	76296	f	69392	d	158	b	40	b	8	c	41	a	96	b	54	b
Average	6		1030		67		681		97577		83034		174		40		9		38		102		75	
S. Deviations	6		361		23		317		33431		28171		31		3		0		2		4		25	

GRDI, Groundnut Rosette Disease Incidence; PY, Pod yield; Gr, Grain percent; GY, Grain Yield; IPS, Initial plants stand; FPS, Final plants stand; PN_M2, pods per square meter; SW_100, 100 seed weight; DE, Days to emergency; DF, Days to flowering; Mat, maturity percentage; ¹- analysis conducted in a fewer environments. Ns- not significant; *- Significant (p<0, 05); **- Highly significant (p<0.01) and *** – Very highly significant (p<0.001) according to the DGC test. Bold values represent the overall mean (average) and standard deviation (SD) for each trait.

TABLE 4 Yield and other agronomic traits of groundnut according to genotype.

Genotypes	GRDI (%)		PY (Kg ha ⁻¹)		Gr (%)		GY (Kg ha ⁻¹)		IPS (Plants ha ⁻¹)		FPS (Plants ha ⁻¹)		PN_M2 (Pods m ⁻²)		SW_100 (g)		DE (days)		DF (days)		DH (days)		Mat (%)	
ICGV-SM 7505	4	b	990	a	68	a	674	b	99740	a	82554	a	165	b	41	b	9	b	37	a	104	a	78	a
ICGV-SM 7508	5	b	1048	a	62	a	654	b	86846	a	73778	a	163	b	36	c	9	b	37	a	104	a	70	a
ICGV-SM 7510	5	b	1121	a	68	a	763	b	101264	a	85653	a	182	b	39	b	9	b	37	a	104	a	73	a
ICGV-SM 7518	3	b	1240	a	67	a	829	a	97162	a	87945	a	203	a	40	b	9	b	37	a	104	a	77	a
ICGV-SM 7531	6	b	814	b	66	a	539	c	103815	a	85224	a	160	b	39	b	9	b	37	a	104	a	82	a
ICGV-SM 7532	5	b	1008	a	65	a	658	b	100353	a	86747	a	179	b	36	c	9	b	37	a	104	a	80	a
ICGV-SM 7533	2	b	1073	a	68	a	730	b	99851	a	90724	a	170	b	41	b	9	b	37	a	104	a	80	a
ICGV-SM 7539	4	b	1074	a	69	a	745	b	95677	a	81929	a	171	b	40	b	9	b	37	a	104	a	78	a
ICGV-SM 7543	9	b	1036	a	64	a	668	b	92717	a	81540	a	176	b	38	c	9	b	37	a	104	a	72	a
ICGV-SM 7544	8	b	924	b	69	a	636	b	97596	a	83342	a	164	b	38	c	9	b	37	a	104	a	80	a
ICGV-SM 7558	2	b	1024	a	69	a	705	b	100706	a	81247	a	168	b	39	b	9	b	37	a	104	a	74	a
ICGV-SM 7566	5	b	1174	a	65	a	764	b	97133	a	81868	a	184	b	38	c	9	b	37	a	104	a	78	a
ICGV-SM 8530	3	b	1070	a	68	a	725	b	107254	a	91759	a	197	a	44	a	9	b	37	a	104	a	72	a
ICGV-SM 9511	8	b	1189	a	73	a	870	a	109540	a	94657	a	212	a	40	b	9	b	37	a	104	a	75	a
ICGV-SM 95741	8	b	1069	a	68	a	728	b	100577	a	82504	a	193	a	41	b	9	b	37	a	104	a	70	a
ICGV-SM 96714	6	b	1136	a	70	a	794	b	90519	a	77370	a	161	b	40	b	9	b	37	a	104	a	70	a
ICG 405	5	b	901	b	66	a	597	c	94299	a	76578	a	151	b	41	b	9	b	37	a	104	a	73	a
ICG 6057	5	b	803	b	71	a	574	c	88276	a	77296	a	142	b	41	b	9	b	37	a	104	a	80	a
JL-24	13	a	1018	a	51	a	514	c	96047	a	78647	a	181	b	42	b	8	c	35	b	97	b	75	a
LOCAL	9	b	882	b	50	a	444	c	92164	a	79321	a	151	b	40	b	10	a	37	a	104	a	65	b
Average	6		1030		66		681		97577		83034		174		40		9		37		104		75	
S. Deviation	3		116		6		105		5688		5263		18		2		0		0		2		4	

Bold values represent the overall mean (average) and standard deviation (SD) for each trait.

TABLE 5 Groundnut Rosette Disease Incidence in all evaluated environments.

Genotypes	Environments										
	MPP_14	MPP_15	MPP_16	NPL_14	NPL_15	NPL_16	NPL_18	NMP_14	NMP_15	NMP_16	NMP_18
ICGV-SM 7505	24	34	1	0	11	0	6	6	4	1	0
ICGV-SM 7508	8	3	0	0	7	0	0	1	3	0	0
ICGV-SM 7510	7	22	1	0	21	0	0	0	2	0	7
ICGV-SM 7518	10	3	2	0	9	0	1	0	5	0	4
ICGV-SM 7531	8	7	0	3	25	4	2	0	7	5	8
ICGV-SM 7532	8	5	0	0	38	0	1	1	2	0	2
ICGV-SM 7533	2	12	0	0	2	0	0	0	1	0	0
ICGV-SM 7539	1	0	0	1	33	1	0	0	7	5	0
ICGV-SM 7543	12	20	0	0	18	1	3	2	44	1	0
ICGV-SM 7544	21	0	0	0	34	0	0	0	17	6	1
ICGV-SM 7558	4	0	0	0	8	3	0	0	1	0	2
ICGV-SM 7566	20	0	4	1	4	0	7	0	19	0	1
ICGV-SM 8530	14	6	0	1	0	0	0	0	7	0	0
ICGV-SM 9511	25	0	1	0	28	0	4	4	12	13	1
ICGV-SM 95741	14	0	12	1	22	1	0	0	36	0	0
ICGV-SM 96714	16	0	2	0	33	0	0	0	11	0	1
ICG 405	11	6	23	0	2	0	6	0	0	3	0
ICG 6057	16	6	11	0	16	0	0	0	2	0	0
JL-24	5	8	10	21	56	4	13	4	9	8	5
LOCAL	8	0	9	1	51	4	3	0	10	5	4
Average	12	7	4	1	21	1	2	1	10	2	2
S. Deviations	6, 8	8, 9	6, 0	4, 5	15, 9	1, 5	3, 3	1, 7	11, 3	3, 5	2, 4

Bold values represent the overall mean (average) and standard deviation (SD) for each trait.

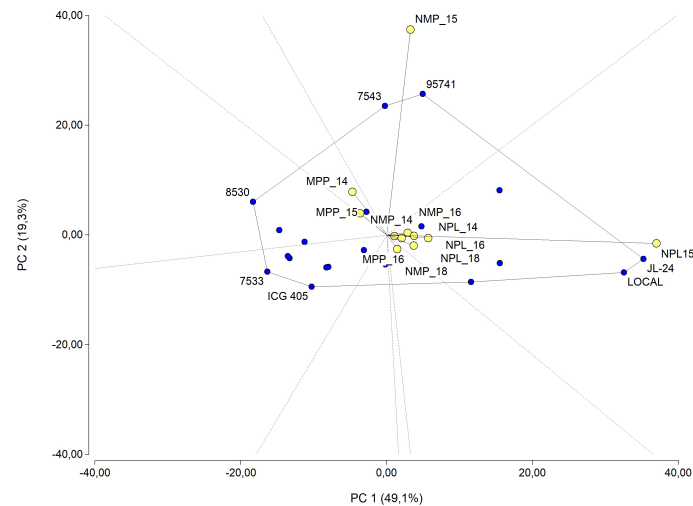


FIGURE 2

GGE Biplot showing genotype x environment interaction for Groundnut Rosette Disease (GRD) incidence in 20 genotypes across 11 environments. Blue points represent the genotypes and yellow points the environments. The polygon view identifies vertex genotypes and illustrates the "which-won-where" pattern used to detect potential mega-environments.

Figure 4 presents the SREG biplot for grain yield. Genotypes located at the vertices of the polygon represent those with the highest grain yield for each mega-environment. Accordingly, a large sector was identified including environments MPP_15, NPL_15, and NMP_16 where genotype ICGV-SM 9511 was the highest-yielding. This was followed by a second sector including environments NMP_14, NMP_15, and NPL_14, where genotype ICGV-SM 96714 was the best performing genotype. Finally, in a third sector, genotype ICGV-SM 7539 showed superior performance and was associated with environments MPP_14, MPP_16, and NPL_18.

Notably, different years within the same location were separated into distinct mega-environments, highlighting the importance of considering yield stability, in addition to mean grain yield, when selecting genotypes, to ensure consistent performance across years.

Variation in grain yield across G x E means was significantly associated with IPS ($r = 0.64$; $p < 0.0001$), FPS ($r = 0.66$; $p < 0.0001$), PN_M2 ($r = 0.63$; $p < 0.0001$), PY ($r = 0.78$; $p < 0.0001$), SW_100 ($r = 0.63$; $p < 0.0001$), and Gr ($r = 0.55$; $p < 0.0001$). IPS and FPS were the most influential, as the remaining traits were strongly correlated with them.

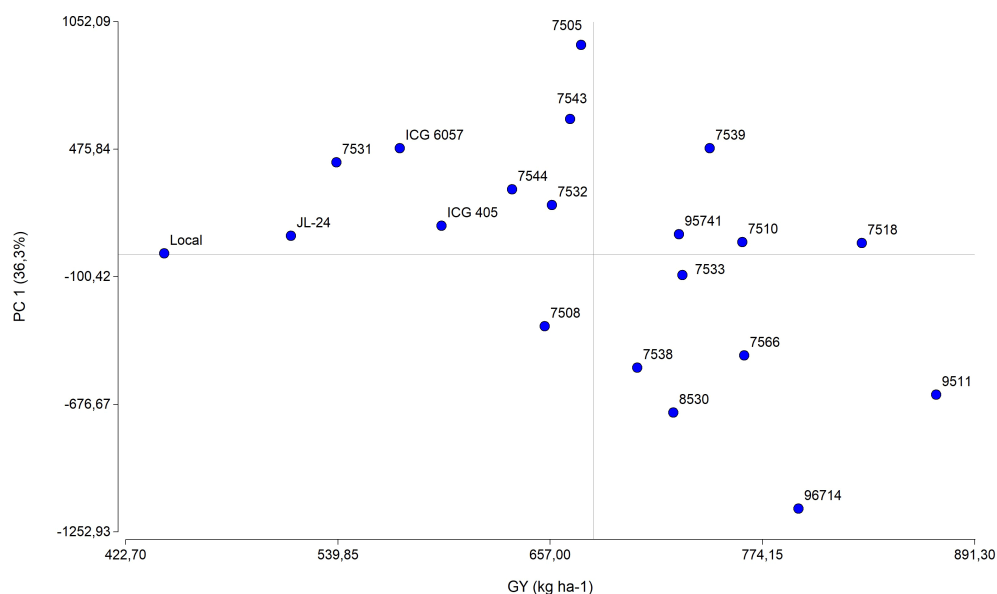


FIGURE 3

AMMI1 biplot showing genotype x environment interaction for grain yield of 20 groundnut genotypes in Northern Mozambique. Blue points represent the genotypes. Genotypes located near the zero line of PC1 are the most stable, and genotypes positioned on the right side of the x-axis have higher yield.

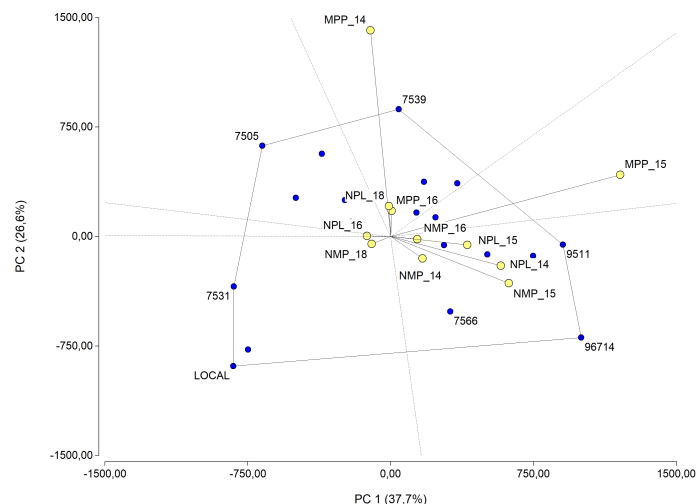


FIGURE 4

GGE biplot illustrating genotype x environment interaction for grain yield of 20 groundnut genotypes evaluated across 11 environments in northern Mozambique. Blue points represent genotypes, and yellow points represent the environments. The polygon view identifies winning genotypes in different sectors and potential mega-environments.

Both IPS and FPS exhibited significant G×E interaction, explaining a proportion of the variance comparable to or greater than that explained by genotype alone (Table 2). FPS was strongly correlated with IPS ($r = 0.96$; $p < 0.0001$).

Differences in IPS were observed among high yielding and stable genotypes. Genotype ICGV-SM 7510 showed a stable and relatively high IPS, whereas genotypes ICGV-SM 7533 and ICGV-SM 95741 exhibited above average IPS values but greater instability than ICGV-SM 7510. In contrast, genotype ICGV-SM 7518 showed stable IPS values close to the mean (Figure 5).

4 Discussions

4.1 Groundnut rosette disease incidence

Since resistance to GRD is strongly influenced by environmental factors, quantifying genotype-by-environment (G×E) interactions is essential for identifying resistant genotypes and optimal testing environments. Accordingly, the agronomic performance and GRD resistance of 20 advanced groundnut lines, selected by ICRISAT under controlled conditions, were evaluated across 11 environments in northern Mozambique.

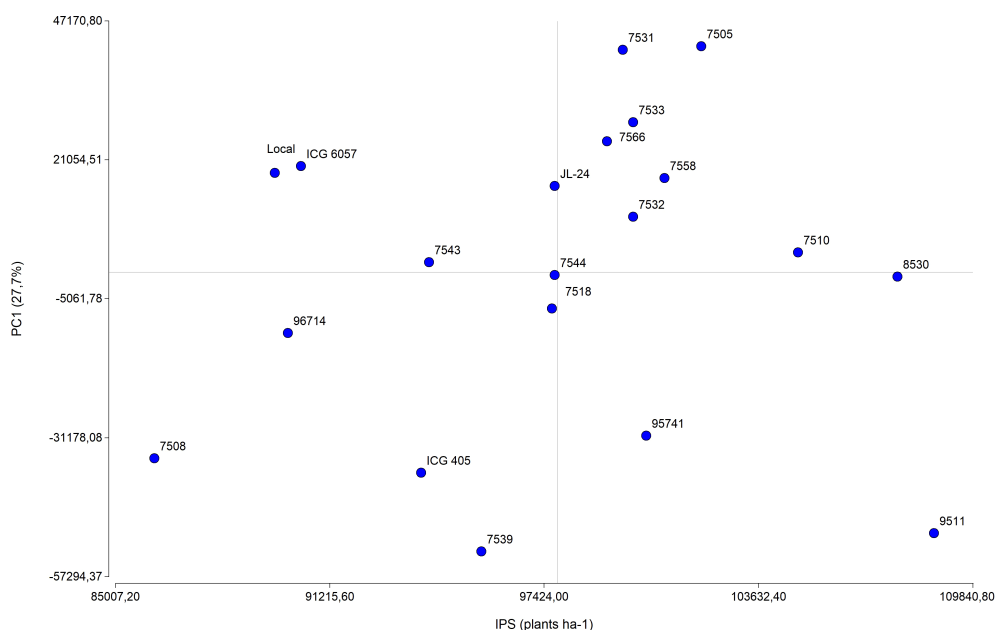


FIGURE 5

AMMI1 biplot for Initial Plant Stand (IPS) in groundnut in Northern Mozambique. Blue points represent genotypes. Genotypes located near the zero line of PC1 are the most stable, and genotypes positioned on the right side of the x-axis have higher IPS.

Not all material selected under controlled conditions exhibited resistance to rosette disease under field conditions. This highlights the importance of multi-environment trials for identifying true disease resistance that is useful for smallholder farmers. Disease incidence among genotypes was largely driven by the environmental effects, which accounted for 92.9% of the total variance (Table 2). Consequently, the G×E interaction was substantial, explaining a proportion of the variance six times greater than that attributed to genotype alone. Similarly, inconsistent genotype performance across environments has been reported in several studies (Das et al., 2019; Yáñez-López, 2012; Pokhrel, 2021; Elad and Pertot, 2014). This variability is largely driven by the unpredictability of environmental conditions, underscoring the importance of identifying representative sites for effective selection for disease resistance.

Crossa (1996); Yan and Kang (2002); (Yáñez-López, 2012; Pokhrel, 2021; Elad and Pertot, 2014) The selection of disease-resistant genotypes requires that the disease be expressed in the evaluation environment (Subrahmanyam et al., 2002; Naidu et al., 1999; Waliyar et al., 2007; Mugisa et al., 2016). To ensure disease presence, the susceptible variety JL-24 was used as a control. Substantial variation in disease incidence was observed among environments (Table 3). The NPL_15 environment exhibited the highest expression, with an average incidence of 21%, while JL-24 reached 56% (Table 5). In this environment, the highest phenotypic variability for GRD resistance was observed, highlighting its high discriminating ability and enabling the identification of promising genotypes for the groundnut breeding program.

Following the classification of GRD resistance proposed by Subrahmanyam et al. (2002) and Ntare and Olorunju (2001), one highly resistant genotype (ICGV-SM 8530) and six moderately resistant genotypes (ICGV-SM 7508, ICGV-SM 7518, ICGV-SM 7533, ICGV-SM 7558, ICGV-SM 7566, and ICG 405) were identified in NPL_15. This classification is based on the disease incidence observed under conditions of high infection pressure and has been widely used in field-based resistance assessment studies (Waliyar et al., 2007; Kankam et al., 2020).

The representativeness of the NPL_15 environment as a selection site was validated using a GGE biplot analysis. This approach allowed the identification of environments with similar discriminatory ability for rosette disease, ensuring that the discrimination criteria are consistent and reliable for the breeding program. Nampula emerged as a suitable site for selection, as all evaluated years (NPL_14, NPL_15, NPL_16, and NPL_18) clustered within the same mega-environment and maintained a consistent ranking of genotypes for resistance to rosette disease, whereas in other locations some years showed no disease occurrence (Figure 2). In addition, the high phenotypic variability observed under these conditions highlights the high discriminating ability of this site, enabling the identification of promising genotypes for groundnut breeding.

In NPL_15, however, GRDI was not correlated with grain yield. Similarly, Kankam et al. (2020) reported no effect on yield for disease incidence levels below 15% (early leaf spot, late leaf spot, and GRD) in their evaluation of mutant groundnut genotypes. These findings indicate that, under certain conditions, disease incidence may not be directly associated with yield performance.

In this study, resistance was evaluated based on disease incidence. Although this variable allows the detection of the disease presence, it does not capture the extent of damage to affected tissues (Shaner and Finney, 1982; Bock et al., 2010).

4.2 Grain yields of genotypes

In northern Mozambique, the average groundnut yield is approximately 300 kg ha⁻¹ (USDA, 2025) whereas in the present study, the average yield reached 681 kg ha⁻¹. The G×E interaction explained 25.4% of the total variability (Table 2), far exceeding the proportion explained by genotype. This interaction was strongly influenced by year, as shown by the GGE analysis, where different years within the same location were grouped into distinct mega-environments (Figure 4). These results indicate that interannual climatic variation had greater impact on yield than differences among locations.

When the year-to-year variation drives the G×E interaction, the selection of broadly adapted genotypes is recommended Yan et al. (2000); Yan and Tinker, 2006; Begna, 2020; Yali (2022); Begna (2020), that is, genotypes that exhibit high and stable yields across years. From the standpoint of yield, its stability, and resistance to rosette disease, the following genotypes stood out: ICGV-SM 7518, ICGV-SM 7510, ICGV-SM 7533, and ICGV-SM 95741 (Figure 3). Although other high-yielding genotypes were identified, some showed unstable performance and susceptibility to groundnut rosette disease, such as the genotype ICGV-SM 9511. Therefore, its suitability for cultivation in Mozambique may be limited, given the high interannual climatic variability, the predominance of low-input smallholder farming systems, and the endemic presence of rosette disease.

Variation in yield was associated mainly with IPS and FPS. On average, IPS and FPS reached 68% and 55% of the expected 200,000 plants ha⁻¹, respectively, with IPS being the primary determinant. The Mozambican groundnut breeding program simulates farmers' conditions; therefore, the reduction in IPS may result from variability in soil moisture, due to either rainfall deficit or excess after sowing (Dias and Silva, 2017), as well as the absence of preventive fungicide or insecticide treatments (Ruark et al., 2010) (Table 3). The reduction in IPS constitutes a key limitation that should be addressed by local agricultural research institutions.

Under these conditions, the genotype ICGV-SM 7510 exhibited a high and stable IPS and grain yield, along with moderate resistance to GRD. In contrast, the disease resistant genotype ICGV-SM 8530 showed high and stable IPS and grain yield within the mega-environment where the disease occurred. These results highlight the importance of selecting genotypes that combine yield stability and disease resistance to ensure reliable performance under variable environmental conditions.

Groundnut genotypes with high and stable yield, along with high to moderate resistance to Groundnut Rosette Disease (GRD), were identified. These genotypes could be particularly useful in low-input agricultural systems where the disease is present and interannual rainfall variability is common, a condition characteristic of many sub-Saharan African countries (Cooper and Messina, 2021); (Tittonell and Giller, 2013). This is especially relevant in

Mozambique, where groundnut production is predominantly carried out under low-input systems, with 97.8% of producers being resource-poor smallholder farmers who rely mainly on local Spanish-type landraces and do not use fertilizers or pesticides (Arias and Libombo, 1994; Muitia, 2011; MADER, 2021). Under these conditions, average yields are approximately 300 kg ha⁻¹ (USDA, 2025), far below the potential yield of 3,000–4,000 kg ha⁻¹ reported under experimental conditions (Kankam et al., 2020), and also below the average yields for sub-Saharan Africa (600–700 kg ha⁻¹) (Zuza Jnr et al., 2017). Therefore, the identified material, due to its resistance and high and stable yield performance, represents a valuable source of parental lines for breeding programs and a promising option to improve productivity under these constraints.

5 Conclusion

The evaluated environments exhibited substantial variation in disease incidence and grain yield, with a strong genotype × environment (G×E) interaction. Regardless of the year, Nampula proved to be a suitable selection site for rosette disease. Among the advanced lines derived from the Spanish × Virginia cross, ICGV-SM 8530 was identified as resistant, while ICGV-SM 7508, ICGV-SM 7510, ICGV-SM 7518, ICGV-SM 7533, ICGV-SM 7558, ICGV-SM 7566, and ICG 405 were classified as moderately resistant. Grain yield also showed a strong G×E interaction primarily driven by year; accordingly, high-yielding and stable advanced lines were identified, with ICGV-SM-7510 and ICGV-SM-7518 exhibiting broad adaptation. Notably, the rosette-resistant genotype ICGV-SM 8530 maintained high and stable yield under environments with the highest disease incidence.

Data availability statement

The original contributions presented in the study are included in the article/Supplementary Material. Further inquiries can be directed to the corresponding author.

Author contributions

CB: Writing – original draft, Writing – review & editing, Formal analysis, Software. PS: Writing – original draft, Writing – review & editing. MO: Writing – original draft, Writing – review & editing. AM: Conceptualization, Investigation, Methodology, Supervision,

Writing – original draft, Writing – review & editing. MC: Conceptualization, Investigation, Methodology, Validation, Writing – original draft, Writing – review & editing.

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Conflict of interest

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Supplementary material

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fagro.2026.1783823/full#supplementary-material>.

References

- Achola, E., Wasswa, P., Fonckea, D., Clevenger, J. P., Bajaj, P., Ozias-Akins, P., et al. (2023). Genome-wide association studies reveal novel loci for resistance to groundnut rosette disease in the African core groundnut collection. *Theor. Appl. Genet.* 136. doi: 10.1007/s00122-023-04259-4
- Arias, F. J., and Libombo, M. (1994). "Groundnut Evaluation in Mozambique: preliminary results for the 1993/1994 season in Maputo Province," in *Sustainable groundnut production in southern and eastern africa*. Eds. B. J. Ndunguru, G. L. Hildebrand and P. Subrahmanyam (International Crops Research Institute for the Semi-Arid Tropics, Mbabane, Swaziland), 41–42.
- Awoke, R. W., Okello, D., Mafurah, J., and Kimurto, P. (2025). Agricultural technologies and practices for groundnut diseases management in Africa: a review. *Discover Agriculture*. 3 (1), 206. doi: 10.1007/s44279-025-00377-3

- Balzarini, M., Bruno, C., and Arroyo, A. (2005). *Análisis de Ensayos Agrícolas Multiambientales. Ejemplos en Info - Gen* (Córdoba, Argentina: Universidad Nacional de Córdoba), 141.
- Begna, T. (2020). The role of genotype by environmental interaction in plant breeding. *Int. J. Agri Biosci.*, 209–215. Available online at: www.ijagbio.com.
- Bhat, R. S., Motagi, B. N., Naidu, G. K., Nadaf, H. L., Giritamannavar, V. A., and Hunje, R. V. (2024). The scientific and economic impact of the foliar disease-resistant peanut variety GPBD 4. *Australas. Plant Pathol.* 53, 285–290. doi: 10.1007/s13313-024-00976-6
- Bock, C. H., Poole, G. H., Parker, P. E., and Gottwald, T. R. (2010). Plant disease severity estimated visually, by digital photography and image analysis, and by hyperspectral imaging. *Crit. Rev. Plant Sci.* 29, 59–107. doi: 10.1080/073526810.03617285
- Conde, S., Rami, J. F., Okello, D. K., Sambou, A., Muitia, A., Oteng-Frimpong, R., et al. (2024). The groundnut improvement network for Africa (GINA) germplasm collection: a unique genetic resource for breeding and gene discovery. *G3: Genes Genomes Genet.* 14. doi: 10.1093/g3journal/jkad244
- Cooper, M., and Messina, C. D. (2021). Can we harness “enviromics” to accelerate crop improvement by integrating breeding and agronomy? *Front. Plant Sci.* 12. doi: 10.3389/fpls.2021.735143
- Crossa, J. (1996). Análisis estadísticos de ensayos multilocales. *Avances En Agronomía* 44, 55–85.
- Crossa, J., Wescott, B., and Gonzales, C. (1998). Análisis de la estabilidad del rendimiento de genotipos de maíz usando el modelo espacial. *Theor. Appl. Genet.*, 863–868.
- Das, A., Parihar, A. K., Saxena, D., Singh, D., Singha, K. D., Kushwaha, K. P. S., et al. (2019). Deciphering genotype-by- environment interaction for targeting test environments and rust resistant genotypes in field pea (*Pisum sativum* L.). *Front. Plant Sci.* 10. doi: 10.3389/FPLS.2019.00825/BIBTEX
- Deom, C. M., Naidu, R. A., Chiyembekeza, A. J., Ntare, B. R., and Subrahmanyam, P. (2000). Sequence diversity within the three agents of groundnut rosette disease. *Phytopathology* 90, 214–219. doi: 10.1094/PHYTO.2000.90.3.214
- Desmae, H., and Sones, K. (2017). *Groundnut cropping guide* (Nairobi: Africa Soil Health Consortium), 44.
- Dias, D. C. F. S., and Silva, L. J. (2017). *Qualidade fisiológica de sementes: fundamentos e aplicações* (Viçosa, Brazil: UFV – Universidade Federal de Viçosa).
- Di Rienzo, J. A., Casanoves, F., Gonzalez, L. A., Tablada, E. M., Díaz, M. P., Robledo, C. W., et al. (2008). Estadística para las Ciencias Agropecuarias. Available online at: <http://agro.uncor.edu/~estad/depeca.zip>.
- Di Rienzo, J. A., Casanoves, F., Balzarini, M. G., Gonzalez, L., Tablada, M., and Robledo, C. W. (2020). *InfoStat versión 2018* (Argentina: Centro de Transferencia InfoStat, FCA, Universidad Nacional de Córdoba).
- Elad, Y., and Pertot, I. (2014). Climate change impacts on plant pathogens and plant diseases. *J. Crop Improv.* 28, 99–139. doi: 10.1080/15427528.2014.865412
- Engels, J. (2010). *Groundnut grower's guide for Mozambique: Production, harvesting and post-harvest handling* (Nampula, Mozambique: Olipa-Odes).
- Fois, M., Malinowska, M., Schubiger, F. X., and Asp, T. (2021). Genomic prediction and genotype-by-environment interaction analysis of crown and stem rust in ryegrasses in European multi-site trials. *Agronomy* 11. doi: 10.3390/agronomy11061119
- Forbes, G. A., Chacón, M. G., Kirk, H. G., Huarte, M. A., Van Damme, M., Distel, S., et al. (2005). Stability of resistance to *Phytophthora infestans* in potato: an international evaluation. *Plant Pathol.* 54, 364–372. doi: 10.1111/j.1365-3059.2005.01187.X
- Gauch, H. G. (2006). Statistical analysis of yield trials by AMMI and GGE. *Crop Sci.* 46, 1488–1500. doi: 10.2135/cropsci2005.07-0193
- Gauch, H. G. (2013). A simple protocol for AMMI analysis of yield trials. *Crop Sci.* 53, 1860–1869. doi: 10.2135/cropsci2013.04.0241
- Gauch, H. G., Piepho, H., and Annicchiarico, P. (2008). Statistical analysis of yield trials by AMMI and GGE: Further considerations. *Crop Sci.* 48, 866–889. doi: 10.2135/cropsci2007.09.0513
- Kankam, F., Kojo, K. Y., and Addai, I. K. (2020). Evaluation of groundnut (*Arachis hypogaea* L.) mutant genotypes for resistance against major diseases of groundnut. *Pakistan J. Phytopathol.* 32, 61–69. doi: 10.33866/phytopathol.032.01.0554
- Kayondo, S. I., Rubaihayo, P. R., Ntare, B. R., Gibson, P. T., Edema, R., Ozimati, A., et al. (2014). Genetics of resistance to groundnut rosette virus disease. *Afr. Crop Sci. J.* 22, 21–29.
- Mabele, A. S. (2020). *Occurrence, distribution and molecular diversity of groundnut rosette virus causing groundnut rosette disease in western Kenya* (Kakamega, Kenya: Masinde Muliro University of Science and Technology).
- MADER (2021). *Inquérito agrícola integrado 2020* (Maputo, Mozambique: Ministério da Agricultura e Desenvolvimento Rural - Moçambique), 84.
- Mugisa, I. O., Karungi, J., Akello, B., Ochwo-Ssemakula, M. K. N., Biruma, M., Okello, D. K., et al. (2016). Determinants of groundnut rosette virus disease occurrence in Uganda. *Sci. Direct -Crop Prot.* 79, 117–123. doi: 10.1016/j.cropro.2015.10.019
- Muitia, A. (2011). *Farmer perceptions and genetic studies of rosette disease in groundnut (Arachis hypogaea L.) in northern Mozambique* (KwaZulu-Natal, South Africa: African Centre for Crop Improvement School of Agricultural, Earth and Environmental Sciences University of KwaZulu-Natal Republic of South Africa).
- Muitia, A. (2015). *Manejo da cultura de amendoim* (Maputo, Mozambique: Instituto de Investigação Agrária de Moçambique (IIAM), 20.
- Naidu, R. A., Bottenberg, H., Subrahmanyam, P., Kimmins, F. M., Robinson, D. J., and Thresh, J. M. (1999). Epidemiology of groundnut rosette virus disease: current status and future research needs. *Ann. Appl. Biol.* 132, 525–548. doi: 10.1111/j.1744-7348.1998.tb05227.x
- Nigam, S. N., Giri, D. Y., and Reddy, A. G. S. (2004). *Groundnut seed production manual* (Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics), 32.
- Nigam, S. N., Upadhyaya, H. D., Dwivedi, S. L., and Reddy, L. J. (1994) (Hyderabad - India: Indian Society of Oilseeds Research), 28–37.
- Ntare, B. R., and Olorunju, P. E. (2001). Variation in yield and resistance to groundnut rosette disease in early- and medium-maturing groundnut genotypes in Nigeria. *Afr. Crop Sci. J.* 9. doi: 10.4314/acsj.v9i2.27617
- Owusu-Akyaw, M., Mochiah, M. B., Gyasi-Boakye, S., and Asafu-Agyei, J. N. (2014). *Integrated practices to manage diseases, nematodes, weeds and arthropod pests of groundnut in Ghana* (Council for Scientific and Industrial Research (CSIR) - Crops Research Institute (CRI), Kumasi, Ghana, West Africa and North Carolina State University (NCSU), USA), 15–116.
- Pokhrel, B. (2021). Effects of environmental factors on crop diseases. *J. Plant Pathol. Microbiol.* 12, 553.
- Ruark, M. D., Sturgul, S. J., and Speth, P. E. (2010). Soilborne disease control through seed treatment: An overview. *Plant Dis. Manage. Rep.* 4.
- Shaner, G., and Finney, R. E. (1982). Resistance in soft red winter wheat to *Mycosphaerella graminicola*. *Phytopathology* 72, 154. doi: 10.1094/Phyto-72-154
- Singh, F., and Oswalt, D. L. (1991). *Genetics and breeding of groundnut* (Patancheru, India: International Crops Research Institute for the Semi-Arid Tropics), 59.
- Subrahmanyam, P., Hildebrand, G. L., Naidu, R. A., Reddy, L. J., and Singh, A. K. (1998). Sources of resistance to groundnut rosette disease in global groundnut germplasm. *Ann. Appl. Biol.* 132, 473–485. doi: 10.1111/j.1744-7348.1998.tb05223.x
- Subrahmanyam, P., Merwe, P. J. A. V., Chiyembekeza, A. J., and Chandra, S. (2002). Integrated management of groundnut rosette disease. *Afr. Crop Sci. J.* 10, 99–110. doi: 10.4314/acsj.v10i1.27560
- Tekalign, A., Sibiyi, J., Derera, J., and Fikre, A. (2017). Analysis of genotype × environment interaction and stability for grain yield and chocolate spot (*Botrytis fabae*) disease resistance in faba bean (*Vicia faba*). *AJCS* 11, 1835–2707. doi: 10.21475/ajcs.17.11.10.pne413
- Tittonell, P., and Giller, K. E. (2013). When yield gaps are poverty traps: The paradigm of ecological intensification in African smallholder agriculture. *Field Crops Res.* 143, 76–90. doi: 10.1016/j.fcr.2012.10.007
- USDA (2025). United States Department of Agriculture -Peanut explorer Mozambique. Available online at: <https://lpad.fas.usda.gov/CropeXplorer/> (Accessed June 6, 2025).
- Waliyar, F., Kumar, P. L., Ntare, B., Monyo, E., Nigam, S., Reddy, A., et al. (2007). *A century of research on groundnut rosette disease and its management* (International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), 40. Available online at: https://oar.icrisat.org/3178/1/354_2007_IB75_Gnut_Rosette_Dis.pdf.
- Walker, T., Pitoro, R., Tomo, A., Siteo, I., Salência, C., Mahanzule, R., et al. (2006). Priority setting for public-sector agricultural research in Mozambique with the national agricultural survey data.
- Yali, W. (2022). Review on effect of genotype x environment interaction and yield stability among sorghum genotypes. *Int. J. Genet. Genomics* 10, 12. doi: 10.11648/j.jigg.20221001.13
- Yan, W., Hunt, L. A., Sheng, Q., and Szlavics, Z. (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Sci.* 40, 597–605. doi: 10.2135/cropsci2000.403597x
- Yan, W., and Kang, M. S. (2002). *GGE biplot analysis: A graphical tool for breeders, geneticists and agronomists* (Boca Raton, FL, USA: CRC Press). doi: 10.1201/9781420040371
- Yan, W., and Tinker, N. A. (2006). Biplot analysis of multi-environment trial data: Principles and applications. *Can. J. Plant Sci.* 86, 623–645. doi: 10.4141/P05-169
- Yáñez-López, R. (2012). The effect of climate change on plant diseases. *Afr. J. Biotechnol.* 11. doi: 10.5897/AJB10.2442
- Zuza Jnr, E., Muitia, A., Amame, M. I., Brandenburg, R. L., and Mondjana, A. M. (2017). Effect of harvesting time on groundnut yield and yield components in Northern Mozambique. *J. Postharvest Technol.* 5, 55–63. Available online at: <http://www.jpht.info>.