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Research Article

Keywords: Rice breeding, G x E Interaction, AMMI analysis, grain yield

Posted Date: October 7th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-10547056/v1

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Additional Declarations: No competing interests reported.

Genotype X Environmental Interaction of Breeding Lines of Rice *(Oryza sativa L.)* for Yield, Yield-components and Quality Traits under Lowland Ecology of Malawi

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Abstract

Rice production is conducted in various agroecological zones and more than half of the global population depends on this crop for food supply. In Malawi, rice is grown in rainfed lowland, rainfed upland and irrigated lowland ecologies. The present study was therefore conducted to evaluate genotypic variation and analyze G × E interactions for yield, yield components, and quality traits in rice, with the aim of identifying stable and superior genotypes under rainfed and irrigated lowland conditions of Malawi. The experiments were conducted at 6 locations during the 2024/2025 rainy season and 2025 irrigated season using a total of 20 rice genotypes, in a Randomized Complete Block Design (RCBD), in three replications per site. The grain yield, yield-components and quality traits data were collected at appropriate rice phenology and analyzed using GenStat 19th Edition Software package. The results showed significant variations among the genotypes in grain yield and related traits. The combined analyses revealed that hybrid rice genotypes consistently outperformed improved lines and landraces under both rainfed and irrigated conditions, achieving mean yields above 7,700 kg ha^{-1}. AMMI and GGE analyses highlighted Domasi as the most stable site, while Mkondezi and Lifuwu were highly discriminatory, useful for detecting specific adaptation. The study underscores the trade-offs between productivity, stability, and grain quality, identifying hybrids lines for high yield potential and suitable for promotion in high-yielding environments. The improved genotypes such as Mtupatupa, Wachangu, Mpheta, KF190029, and IR18A1908 be promoted for adaptability and consumer acceptance, for targeted rice breeding strategies in Malawi.

KEY WORDS: Rice breeding, G x E Interaction, AMMI analysis, grain yield

1.0 Introduction

Rice (*Oryza sativa L.*) is a source of food to more than half of the world's population and its production is done in various agro-climatic zones globally (FAO, 2025; Oladosu et al., 2017). The global population is expected to double by 2050, therefore, an increased rice production of 60 - 110% will be needed to meet the annual food demand. In Malawi, rice is the second most important cereal crop after maize in terms of food security, household income generation and production area, and the fourth most widely produced cereal crop in the sub - Saharan region. Rice in Malawi is cultivated mainly in low-altitude areas along the shores of Lake Malawi, Lake Chirwa, the banks of the Shire River, and is also found in swamps and "dambo" areas in medium -and high-altitude parts of the country. Rice growing areas range in altitude from 50 m to 2500 m above sea level, and are classified into rainfed lowland (80%), irrigated lowland (15%), and rainfed upland (5%) land share (Ahmadi et al., 2020; Abade et al., 2016; Mzengeza, 2010; Ministry of Agriculture, 2024, SES - IRRI, 2013). The availability of information on genotype x environmental interaction leads to successful evaluation of stable rice genotypes, which could eventually be used for general production or further breeding programs (Abdullatif et al., 2012; Al - Samarai and Al - Kazaz, 2015; Yang et al., 2013). One of the complex quantitative traits that is greatly influenced by environmental fluctuations is yield; therefore, selection of superior genotypes based on this trait under multiple environmental conditions and locations is very effective in any breeding program (Wang et al., 2022; Kumar et al., 2020; Sitaresmi et al., 2020). Varietal adaptability to environmental fluctuations plays a pivotal role in stabilizing crop production across locations and years, thereby supporting sustainable agricultural outcomes (Ghazy et al. 2024; Reshma et al., 2024; Lee et al. 2023). Stability is the ability of crops to maintain their yield despite fluctuation of conditions in their growth environments. The

performance of a genotype is a result of the capacity of the genotype (G), environment (E) in which the crop is grown and Interaction (I) of the two. In Malawi, most consumers strongly prefer varieties that are high yielding, good grain quality (aromatic, translucency of the endosperm), intermediate gelatinization temperature, good grain size (long to extra-long, large to slender grains), aromatic grains, as well resilience to biotic and abiotic conditions. The evaluation of introduced genotypes for yield, yield - related and grain quality traits stability in different environments should therefore be an integral part of rice breeding (Mzengeza 2010; Brooks et al. 2010; Agarwal et al., 2008).

An understanding of the causes of genotype x environment interaction can help in identifying traits and environments for better evaluation of rice cultivars (Krishnamurthy et al., 2021; Musila et al., 2017; Li et al., 2020). The evaluation of rice genotypes under rainfed and irrigated conditions may be helpful in identifying rice types with high yield, stability and wide adaptation under rainfall in one season and irrigated in another for doubled production. Furthermore, evaluating different genotypes across different environments or growing seasons helps to identify donor germplasm with adaptive traits for high yields, yield - attributing traits and grain quality in target environments. However, no such comprehensive studies have been conducted to identify donor genotypes with adaptive traits across locations in both rainfed and irrigated conditions in the newly introduced and advanced elite rice genotypes in Malawi. The present study was therefore conducted to evaluate genotypic variation and analyze G × E interactions for yield, yield components, and quality traits in advanced rice, with the goal of identifying stable and superior genotypes under rainfed and irrigated lowland conditions of Malawi. In Malawi, the rice growth conditions are generally described as irrigated (June to November) and rainfed (December – May) with altitudes ranging from 50 to 2500 meters above sea level. The focus was

to identify high yielding and stable rice genotypes across various environments that could be used in further breeding programmes. In the long run, the identified superior genotypes would assist in the replacement of popular rice varieties such as Faya 14 M 68, Kilombero, Nunkire and many others in Malawi which despite their strong grain quality, they are characterized by low yield and photo-period sensitivity.

2.0 Materials and Methods

2.1 Plant Materials

The 20 rice genotypes were sourced from Malawi local cultivars, improved rice varieties and other inbred lines introduced from IRRI and Africa Rice (KAFACI), and the standard check known as Mtupatupa were used in the present study. The other germplasm was obtained from Malawi's Genebank and the general source has been illustrated as DARS/LARS for instance Fayas and are also made available to some farmers (for instance Faya Kachulu) despite that some of them were not officially released at the time of this publication (Table 1). The lines from IRRI were introduced into the Malawi's breeding pipeline through the germplasm exchange program which stood for decades with major rice CGIARs as one way of enhancing the gene pool. The lines that originated from KAFACI were a series of tremendous breeding work where thousands of doubled haploid rice germplasm were developed through anther-culture at Saint Louis, in Senegal. These lines were then shared to each African member country and advanced from the OYT to AYT stages before introduced into this separate study. Generally, the genotypes used in the study comprised the African Glaberrima, Indica from IRRI, Japonica and the Tongil – types from KAFACI.

Table 1: List of plant materials used in the study

ID No	ENTRY NO	Name	Pedigree	Origin	Source
1	G1	Nanyondo	Landrace	Glaberrima	DARS /LARS
2	G2	Faya Kachulu	Landrace	Glaberrima	DARS/LARS
3	G3	Mpheta	IR13N144	Indica	DARS/LARS
4	G4	Makafaci	Sahel 328	Indica	DARS/LARS
5	G5	Wachangu	KF150018	Indica	DARS/LARS
6	G6	Senga	IET 4094	Indica / Glaberrima	DARS/LARS
7	G7	Mtupatupa	TCG S10	Indica	DARS/LARS
8	G8	Hybrid 001	Hybrid 001	Indica /Japonica	Africa Rice
9	G9	Hybrid 002	Hybrid 002	Indica /Japonica	Africa Rice
10	G10	Hybrid 003	Hybrid 003	Indica /Japonica	Africa Rice
11	G11	Hybrid 004	Hybrid 004	Indica /Japonica	Africa Rice
12	G12	KF190023	KF190023	Tongil type	KAFACI
13	G13	KF190242	KF190242	Tongil type	KAFACI
14	G14	KF190202	KF190202	Tongil type	KAFACI
15	G15	KF190232	KF190232	Tongil type	KAFACI
16	G16	KF190028	KF190028	Tongil type	KAFACI
17	G17	KF190029	KF190029	Tongil type	KAFACI
18	G18	IR18A1513	Landrace	Indica	DARS/LARS
19	G19	IR18A1908	IR18A1908	Indica	IRRI
20	G20	KF18007	KF18007	Tongil type	KAFACI

2.2 Experimental Sites

The materials were evaluated for two seasons during the 2024/2025 rainy season and 2025 irrigated season across six experimental sites, namely; Domasi Rice Scheme (Machinga District), Hara Rice Scheme (Karonga District), Kasinthula Agricultural Research Station Experimental Fields (Chikwawa District), Nazolo Rice Scheme (Chikwawa District), Lifuwu Agricultural Research Station Experimental Fields (Salima District), and Limphasa Rice Scheme (Nkhata Bay District). Domasi Rice Scheme is located in the Lake Chirwa basin in southern region of Malawi and irrigation at the site is done by gravitational water. It lies towards the mouth of the Domasi River which empties its water into Lake Chilwa and it comprises latosol soil order which are rich

in clay texture. Kasinthula Experimental Site is situated within Kasinthula Agricultural Research Station, 10 km south of Chikwawa District in the southern region of Malawi. The site lies at 16° 0" S, 34° 5" E in the floor of the Great Rift Valley on 70 masl. It has distinct winter which runs from May to September and summer season from October to April every year. The average annual rainfall for the site is 800 mm and falls between November and May. The soil for the site is generally sandy loam whose average bulk density is 1.7, pH is 7.4, organic matter of 0.03% and 10.5 % (Fandika and Kadyampakeni, 2007). Nazolo Rice Scheme lies at 16° 0" S, 34° 5" E in the floor of the Great Rift Valley on 72 masl. It is located North of Kasinthula Agricultural Research Station, East Bank, off Thabwa - Chapananga main road. Hara Irrigation Scheme is located in Karonga District and has a length of 9 km, built in 1968 - 1969 and water is gravity fed. Lifuwu Agricultural Research Station Experimental Fields geographically lies at an altitude of 500 meters above sea level (masl), forming part of the great expansive seasonally flooded Katete Dambo and is 8.5 km from Parachute Battalion, off Senga Bay Road. It lies at a latitude and longitudinal coordinates of 13.40" S and 34.35" E, respectively. The mean annual temperatures for Lifuwu site ranges between a minimum of 19 degrees Celsius to a maximum of 29 degrees Celsius. Limphasa Irrigation Scheme is located in Chief Kabunduli's area in Nkhata-Bay District. Generally, rice, maize, bananas and cassava are crops grown in this scheme. The descriptions of sites are also illustrated in Table 2. Rainfall across the experimental sites varied considerably, ranging from 729 mm at Lifuwu to 1,200 mm at Domasi. The Shire Valley sites, Kasinthula (1151 mm) and Nazolo (1180 mm), received moderately high but strongly seasonal rainfall, necessitating irrigation to sustain rice beyond the short-wet season. Domasi (1200 mm), recorded the highest and more evenly distributed rainfall, favouring rainfed trials and reducing drought stress. Hara (1186 mm) in the northern lakeshore experienced abundant rainfall moderated by Lake Malawi, supporting vigorous crop growth though with flooding risks in low - lying plots. Mkondezi (1020 mm) also benefited from lakeshore influence, with adequate rainfall but variable distribution that occasionally required supplemental irrigation. Lifuwu (729 mm), the driest site, relied almost entirely on irrigation schemes, as rainfall alone was insufficient for rice cultivation during the season.

Table 2: Description of Experimental Sites

Region	District	Site	Coordinates	Elevation (masl)
South	Chikwawa	Kasinthula	16º08'S; 34º57'E	70
South	Chikwawa	Nanzolo	16º08'S; 34º57'E	72
South	Machinga	Domasi	15º19'S; 35º24'E;	800
Central	Salima	Lifuwu	13 º S, 34 º E	500
North	Nkhata Bay	Limphasa	11º37'S; 34º14'E	508
North	Karonga	Hara	10º29'S; 34º14'E	478

A





B

C





D

Figure 1 (A – D): The 2024 /2025 (rainfed) and 2025 (irrigated) rice trials at 6 locations of the country during heading and maturity stages; where, A is an aerial view of experimental site at Lifuwu for repeated (irrigated) trials, B comprises rainfed trials at Kasinthula, C is maturity stage of trials at Hara Site and D is the rainfed trials at Lifuwu Site

2.3 Experimental Design

The experiments were laid out in a Randomized Complete Block Design (RCBD) of plot size 5 m x 1.2 m (6 m^2), spacing of 20 cm between rows and also 20 cm between hills (stations), in 3 replications, therefore 7 rows and 26 hills, per plot were attained. A space of 40 cm was maintained between plots and 1 m between replications. One seedling of less than 21 days old was transplanted per hill to ensure that accurate data was collected on the target traits. Kayanjamalo and Makafaci were included as improved standard checks in addition to the commonly used Mtupatupa variety. The basal dressing fertilizer was applied at the total rate of 250 kg per ha for the NPK1S6Zn fertilizer and top dressing (N) using Urea at 60 kg per hectare as adopted from the National Rice Development Strategy II paper (Ministry of Agriculture, 2024).

2.4 Data Collection

Data collection was done on target traits, namely; days to attain 50% flowering, number of days to reach physiological maturity, plant height (cm), panicle length (cm), number of productive tillers per plant / hill, number of panicles per plant, number of grains / panicles, 1000 - grain weight (g), Seed Setting Ratio (%), grain size (grain length, grain width) (mm), and grain yield (kg/ha). Pests and disease occurrences were also scored through observations during the two seasons of the study across the sites. The number of productive tillers was recorded at maturity as the count of panicle - bearing tillers per plant. Plant height was measured at the maturity stage in centimeters from five randomly selected hills (plants) using a ruler, taken from the soil surface

to the tip of the main panicles, excluding awns. A random sample of 1,000 well-filled grains per replication was obtained after threshing, counted using an electric grain counter, and weighed with a digital balance. The grain size was measured by randomly selecting five fully matured grains from each genotype and dehulling them (before milling) to determine the sizes using a Vernier caliper. The brown rice length (BRL) and brown rice breadth or width (BRB) were then measured in millimeters and their averages were computed accordingly. Grain yield obtained from net plot area, excluding border rows, and extrapolated in kg/ha at 14% moisture content.

2.5 Data Analysis

Data from each location was exposed to analysis of variance (ANOVA) in RCBD using GenStat 19th Edition Statistical Package Software in order to explore the existing variances among the genotypes for yield, yield related and quality traits. The mean comparison among genotypes means was then estimated by the least significant difference (LSD) test at 5 % level of significance. The AMMI model as earlier used by (Gauch and Zobel, 1996), and later adopted by other researchers (Mengistu et al., 2022), had also been applied in the current study, as follows:

Equation 1: $$Y_{ger} = \mu + \alpha_g + \beta e + \sum n^{\lambda} n_{\gamma gn}{}^{\delta} en + P_{ge} + \varepsilon_g er \qquad (1)$$

Where, Y_{ger} is the observed yield of genotype $_g$ in environment e for replication r; Additive parameters: μ is the grand mean; $\alpha_{g\ is}$ the deviation of genotype $_g$ from the grand mean; and βe is the deviation of environment e; the multiplicative parameters: $^{\lambda}n$ is the singular value for interaction principal component axis (IPCA) n, γ_{gn} is the genotype eigenvector for axis n, and $^{\delta}en$ is the environment eigenvector; P_{ge} PCA residuals (noise portion), and ε_{ger} error term.

Data was then pooled across locations in order to determine the G X E Interactions. Genetic and Genotype x Environment (GGE) biplot stability analysis was adopted using the same GenStat

19th Edition statistical software to evaluate the relative performance of genotypes for target environments based on principal component analysis model that considers main effects and two axes. The GGE mathematical model based on PCA which consists of G and GE as the main sources of variation subjected to singular value decomposition (SVD) as adopted from Yan and Tinker, (2006) was used to visualize the relationship among genotypes and the environments, and the equation is as follows:

Equation 2: $Y_{ge} = \mu + jg + fe + \sum^{\lambda} k^{\alpha} gkYek + \varepsilon_{ge}$ **(2)**

Equation 2: Where: Y_{ge} = Mean grain yield (t ha-1) of the g^{th} genotype in the e^{th} environment; μ is the overall mean; jg is the mean of the g^{th} genotype minus the overall mean, fe is the mean of eth environment minus the overall mean, λk is the square root of the eigenvalue of the principal component analysis (PCA) axis, αgk and λek are the principal component scores for PCAk of the g^{th} genotype and e^{th} environment, respectively, and ε_{ge} is the residual error.

3.0 Results

Analysis of variance (ANOVA)

The combined Analysis of Variance for genotype, environment, and season effects in relation to grain yield is displayed, with pooled results showing highly significant seasonal variation (< 0.001) (Table 3). This underscores the strong influence of season on the performance of the traits. In addition, the genotype × season interaction was significant ($p < 0.05$), suggesting that genotypic responses varied across seasons. In contrast, the main effects of genotype and environment, as well as higher-order interactions (G × E, E × S, G × E × S), were not significant

Table 3: Combined Analysis of Variance (ANOVA) for 20 Rice Genotypes Evaluated Across 6 Locations during the 2 Seasons

Source of Variation	Df	SS	MS	v. r.
Replicate	2	5.854E+05	2.927E+05	1.88
Genotype (G)	19	5.553E+07	2.923E+06	1.24
Environment (E)	5	1.280E+07	2.560E+06	1.09
Season (S)	1	4.886E+06	4.886E+06***	31.31
G x E	95	2.507E+08	2.639E+06	1.12
G x S	19	9.379E+07	4.936E+06*	2.10
E x S	5	1.378E+07	2.755E+06	1.17
G x E x Interaction (GEI) or (G x E x S)	95	2.103E+08	2.213E+06	0.94
Residual (Error)	476	1.120E+09	2.354E+06	
Total	719	1.763E+09		

Note: *, and * stand for statistical significance at P < 0.0001 and P < 0.05 probability levels, respectively.**

The analysis of variance (ANOVA) revealed a significant genotype × environment interaction during the 2024/2025 rainy season, confirming that there was variability in genotypic responses across the six test sites. High-yielding environments such as Hara, Nanzolo, and Kasinthula clearly discriminated superior performers, with Makafaci, Hybrid 003, KF190028, and Wachangu surpassing 7000 kg ha^{-1}. In contrast, the low - yielding site Mkondezi exposed the limitations of traditional landraces, with Nanyondo consistently recording the poorest yields. Notably, Mpheta, Makafaci, and Hybrid 001 demonstrated broad adaptation across environments, while Hybrid 003, KF190023, and KF190028 showed location-specific adaptation, excelling only under favorable conditions.

222

223 **Table 4: Mean Grain Yield (kg ha^{-1}) Performance of 20 Rice Genotypes Across Six Locations**
224 **During the 2024/2025 Rainy Season**

Sr. NO	Genotype	Mean yield (kg ha^{-1})						
		Lifuwu	Mkondezi	Hara	Domasi	Nanzolo	Kasinthula	Mean
1	Nanyondo	3973	4276	4220	4793	4138	4083	4247
2	Faya Kachulu	4217	4047	4860	4597	4667	4686	4512
3	Mpheta	6685	6408	6624	6272	6536	6340	6478
4	Makafaci	7209	7425	7423	7248	7080	6740	7188
5	Wachangu	7017	6709	6837	6745	6603	6921	6805
6	Senga	4019	4248	5907	4787	4095	5390	4741
7	KF18007	5765	6232	7635	6808	5694	5475	6268
8	Hybrid 001	7664	8595	7745	7859	7879	7290	7839
9	Hybrid 002	8172	8704	7427	8101	7690	8374	8078
10	Hybrid 003	7969	8640	8515	8273	8041	7464	8150
11	Hybrid 004	7603	8201	7483	8173	5673	7758	7482
12	KF190023	7527	8269	7620	6107	7637	5854	7169
13	KF190242	7616	5751	8673	7476	7883	6378	7296
14	KF190202	7699	6667	7352	5568	6237	6785	6718
15	KF190232	6384	5472	6120	6279	5615	5105	5829
16	KF190028	6547	4259	7611	5820	5574	6499	6052
17	KF190029	7477	5112	6496	6452	5477	5574	6098
18	IR18A1513	5320	5136	7835	5624	7597	6708	6370
19	IR18A1908	7301	5239	7752	7688	7521	7031	7089
20	Mtupatupa	6191	6037	6112	6155	6443	6392	6222

	Mean	6618	6271	7012	6541	6404	6342	6531
	LSD 0.05	690.4	1109.6	1612.0	689.0	775.0	774.3	
	Prob.	<.001	<.001	<.001	<.001	<.001	<.001	
	CV %	6.3	10.7	13.9	6.4	7.2	7.4	

The results from irrigated season revealed significant differences in grain yield among the tested genotypes at all sites (Prob <0.001), with Nanyondo and Hybrid 002 emerging as the lowest and highest yielders, respectively (Table 5). The improved genotypes such as IR18A1908 and Makafaci also displayed stable performance across sites. The location means varied significantly, with Nanzolo and Kasinthula emerging as the most productive environments.

Table 5: Mean Grain Yield (kg ha-1) Performance of 20 rice Genotypes Across 6 Locations During the 2025 Irrigated Season

Sr. NO	Genotype	Mean yield (kg ha^{-1})						
		Lifuwu	Mkondezi	Hara	Domasi	Nanzolo	Kasinthula	Mean
1	Nanyondo	3620	4349	4133	3678	4190	4170	4023
2	Faya Kachulu	3884	4504	4500	4184	4603	4818	4416
3	Mpheta	6914	6040	6033	6657	6605	6582	6472
4	Makafaci	7042	7325	7200	7059	7034	6816	7079
5	Wachangu	6796	6669	6950	6752	6787	6700	6776
6	Senga	3084	4683	4603	4302	5543	4828	4507
7	KF18007	5663	4893	6585	5494	7219	6502	6059
8	Hybrid 001	7628	8352	6500	7955	7927	8077	7740
9	Hybrid 002	7519	8197	7917	7577	8213	7010	7741
10	Hybrid 003	7315	8120	6624	8167	7453	7251	7488
11	Hybrid 004	7292	7819	7533	7451	7291	7116	7417
12	KF190023	6175	6355	7500	6331	7112	6409	6647
13	KF190242	6815	6667	6000	4264	7049	5999	6132

14	KF190202	4191	6083	6467	4932	5807	6245	5621
15	KF190232	4519	5789	6583	6659	5264	6346	5860
16	KF190028	3433	4851	5804	6569	6404	6685	5624
17	KF190029	5147	6211	5407	5118	5459	6461	5634
18	IR18A1513	6817	7461	6217	5600	6468	6298	6477
19	IR18A1908	7056	7512	6900	7224	7303	6540	7089
20	Mtupatupa	5687	5939	5800	5631	6300	6185	5924
	Mean	5830	6391	6263	6080	6502	6352	6236
	LSD 0.05	869.8	692.9	741.2	631.6	1086.6	911.2	
	Prob.	<.001	<.001	<.001	<.001	<.001	<.001	
	CV %	9.0	6.6	7.2	6.3	10.1	8.7	

The combined analyses for grain yield performance of 20 rice genotypes evaluated under rainfed and irrigated lowland conditions across six locations during the 2024/2025 rainy "wet" season (WS) and 2025 irrigated "dry" season (DS) were revealed (Table 6). The findings showed significant differences (p<0.001) among the tested genotypes at all sites, with mean yields ranging from 4,135 to 7,909 kg ha^{-1}. Hybrid genotypes consistently outperformed improved and conventional varieties. Among the improved entries, Makafaci, IR18A1908 and Wachangu demonstrated competitive performance, approaching hybrid yield levels.

Table 6: Combined Mean Grain Yield (kg ha-1) Performance of 20 Rice Genotypes at 6 Locations During the 2024/2025 Rainfed and 2025 Irrigated Seasons

Sr. NO	Genotype	Mean yield (kg ha^{-1})						
		Lifuwu	Mkondezi	Hara	Domasi	Nanzolo	Kasinthula	Mean
1	Nanyondo	3796	4312	4176	4236	4164	4126	4135
2	Faya Kachulu	4050	4276	4680	4390	4635	4752	4464
3	Mpheta	6800	6224	6328	6464	6570	6461	6475
4	Makafaci	7126	7375	7312	7154	7057	6778	7134
5	Wachangu	6906	6689	6894	6748	6695	6810	6790

6	Senga	3552	4466	5255	4544	4819	5109	4624
7	KF18007	5714	5562	7110	6151	6456	5988.	6164
8	Hybrid 001	7646	8474	7122	7907	7903	7684	7789
9	Hybrid 002	7846	8450	7672	7839	7952	7692	7909
10	Hybrid 003	7642	8380	7570	8220	7747	7358	7820
11	Hybrid 004	7448	8010	7508	7812	6482	7437	7450
12	KF190023	6851	7312	7560	6219	7374	6132	6908
13	KF190242	7216	6209	7336	5870	7466	6188	6714
14	KF190202	5945	6375	6910	5250	6022	6515	6170
15	KF190232	5452	5630	6352	6469	5440	5726	5845
16	KF190028	4990	4555	6708	6194	5989	6592	5838
17	KF190029	6312	5662	5952	5785	5468	6018	5866
18	IR18A1513	6068	6298	7026	5612	7032	6503	6423
19	IR18A1908	7178	6376	7326	7456	7412	6786	7089
20	Mtupatupa	5939	5988	5956	5893	6372	6288	6073
	Mean	6224	6331	6638	6311	6453	6347	6384
	LSD 0.05	1722.0	1513.6	1249.1	1264.6	1117.4	960.4	
	Prob.	<.001	<.001	<.001	<.001	<.001	<.001	
	CV %	13.2	11.4	9.0	9.6	8.3	7.2	

The ANOVA for AMMI Model

The ANOVA results for the AMMI model revealed highly significant genotypic effects ($p < 0.001$), suggesting the presence of substantial genetic variability within the entries (Table 7). The genotype × environment (G×E) interaction was further partitioned into interaction principal component axes (IPCA), and showed that both IPCA 1 ($p < 0.001$) and IPCA 2 ($p = 0.015$) were statistically significant. Generally, the AMMI analysis confirms that genetic diversity is the major cause of performance differences, while environmental heterogeneity has a minimal effect, with significant interactions shaping genotype adaptability and stability.

Table 7: ANOVA table for AMMI model

Source	D.F.	S.S.	M.S.	v.r.	F pr
Genotypes	19	132018215	6948327	33.33	<0.001
Environments	5	2084881	416976	2.00	0.0856
Interactions	95	19805966	208484		
IPCA 1	23	8046158	349833	2.84	<0.001
IPCA 2	21	5472028	260573	2.11	0.0152
Residuals	51	6287780	123290		

The AMMI analysis of yield stability showed substantial variation among rice genotypes in both mean yield and stability indices (Table 8). The hybrid genotypes generally displayed higher mean yields, with Hybrid 002 and Hybrid 003 ranking among the top performers. However, their relatively high ASV values indicate declined stability across environments, suggesting strong yield potential but less consistent performance under different conditions. On the other hand, several improved genotypes such as Mtupatupa, Mpheta and Wachangu demonstrated lower mean yields but superior stability.

Table 8: Yield Stability of 20 Rice Genotypes Across 6 Environments Based on AMMI Scores and ASV

Genotype	Mean Yield (kg / ha)	IPCA1	ASV	Stability Rank
Faya Kachulu	4464	-4.7300	8.02	5
Hybrid 001	7789	19.5410	28.76	18
Hybrid 002	7908	14.0034	20.78	11
Hybrid 003	7820	17.0206	25.34	16
Hybrid 004	7450	17.2893	28.66	17
IR18A1513	6423	-11.3792	21.78	13
IR18A1908	7089	-5.3502	8.27	7
KF18007	6164	-15.9480	23.45	15

KF190023	6908	1.4514	21.80	14
KF190028	5838	-28.1905	45.83	20
KF190029	5866	4.7368	7.32	4
KF190202	6170	-5.5815	12.10	9
KF190232	5845	-0.7835	15.57	10
KF190242	6714	-9.6581	29.06	19
Nanyondo	4135	4.7366	8.07	6
Makafaci	7134	7.8291	11.65	8
Mpheta	6474	4.3126	6.42	3
Mtupatupa	6073	0.8658	1.57	1
Senga	4624	-13.3333	21.52	12
Wachangu	6790	3.1679	4.75	2

Note: AMMI – Additive Main-effect and Multiplicative Interaction, ASV - AMMI Stability Value, IPCA - Interaction principal component analysis.

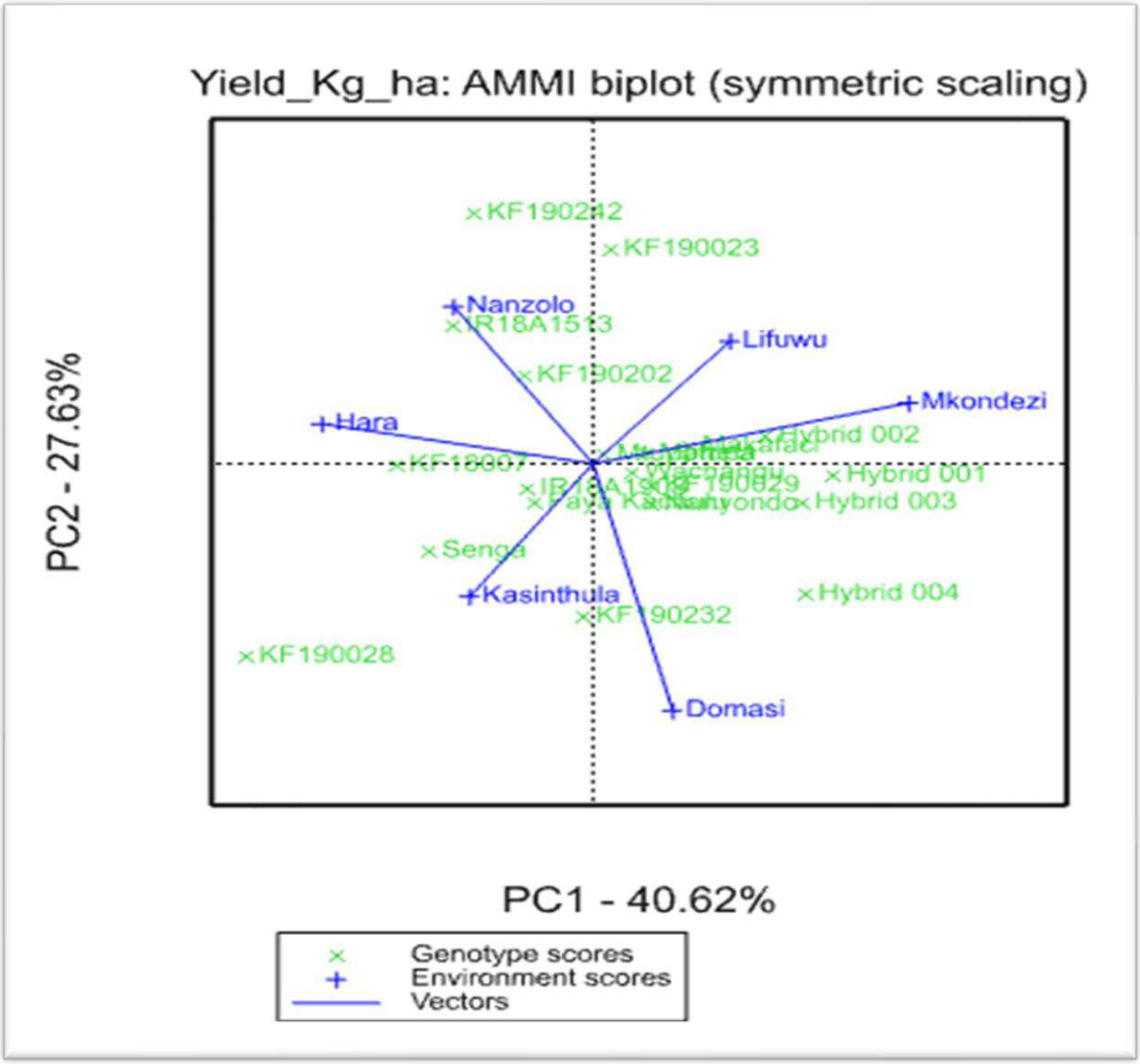
The AMMI analysis showed clear differences among environments in yield and interaction effects (Table 9). Domasi, ranked most stable, had low IPCAe1 scores, indicating minimal genotype × environment interaction and suitability for identifying broadly adapted genotypes. On the other hand, Mkondezi exhibited the highest IPCAe1 score (34.9) and explained the largest variance (23%), making it the most discriminating site for differential responses while the rest of the sites were found to be intermediate.

Table 9: Environment mean yield (kg/ha), stability scores and variance (%)

Environment	Stability Rank	Mean	IPCAe1	Variance Explained (%)
Domasi	1	6311	8.8040	17.4
Hara	2	6638	-29.8834	12.3
Kasinthula	3	6347	-13.5833	10.7
Lifuwu	4	6224	15.1243	21.3
Mkondezi	5	6331	34.8881	23.0
Nanzolo	6	6453	-15.3497	15.3

Note: IPCA = Interaction principal component analysis.

The first two principal components of the AMMI biplot collectively explain 68.25% of the total G × E interaction variance, which is substantial and indicates that the biplot captures most of the interaction structure. The hybrid genotypes such as Hybrid 001, Hybrid 002, Hybrid 003, and Hybrid 004 clustered toward positive PC1 values, indicating strong responsiveness to specific environments but having low stability. The genotypes positioned closer to the origin of the IPCA2 axis exhibited greater yield stability across environments, whereas those with higher IPCA2 scores demonstrated stronger genotype × environment interactions, indicating specific adaptation to particular testing environments. The improved genotypes such as Mtupatupa, Wachangu, and Mpheta were positioned closer to the origin, suggesting greater stability and broad environmental adaptation - ability. Furthermore, KF190028 was far from the origin, consistent with its high ASV (45.83), confirming poor stability and strong environmental - specific responses. The environments such as Mkondezi and Domasi exihibited long vectors, suggesting strong discriminatory ability and high interaction effects. On the other hand, Lifuwu and Nanzolo sites were closer to the origin, indicating that they exerted less differential pressure on genotypes and were more representative of the average conditions (Figures 2, 3, 4).



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287 **Figure 2: AMMI Biplot of Interactive Principal Component Axes (PC 1) and (PC 2) for the**
288 **studied 20 rice genotypes**

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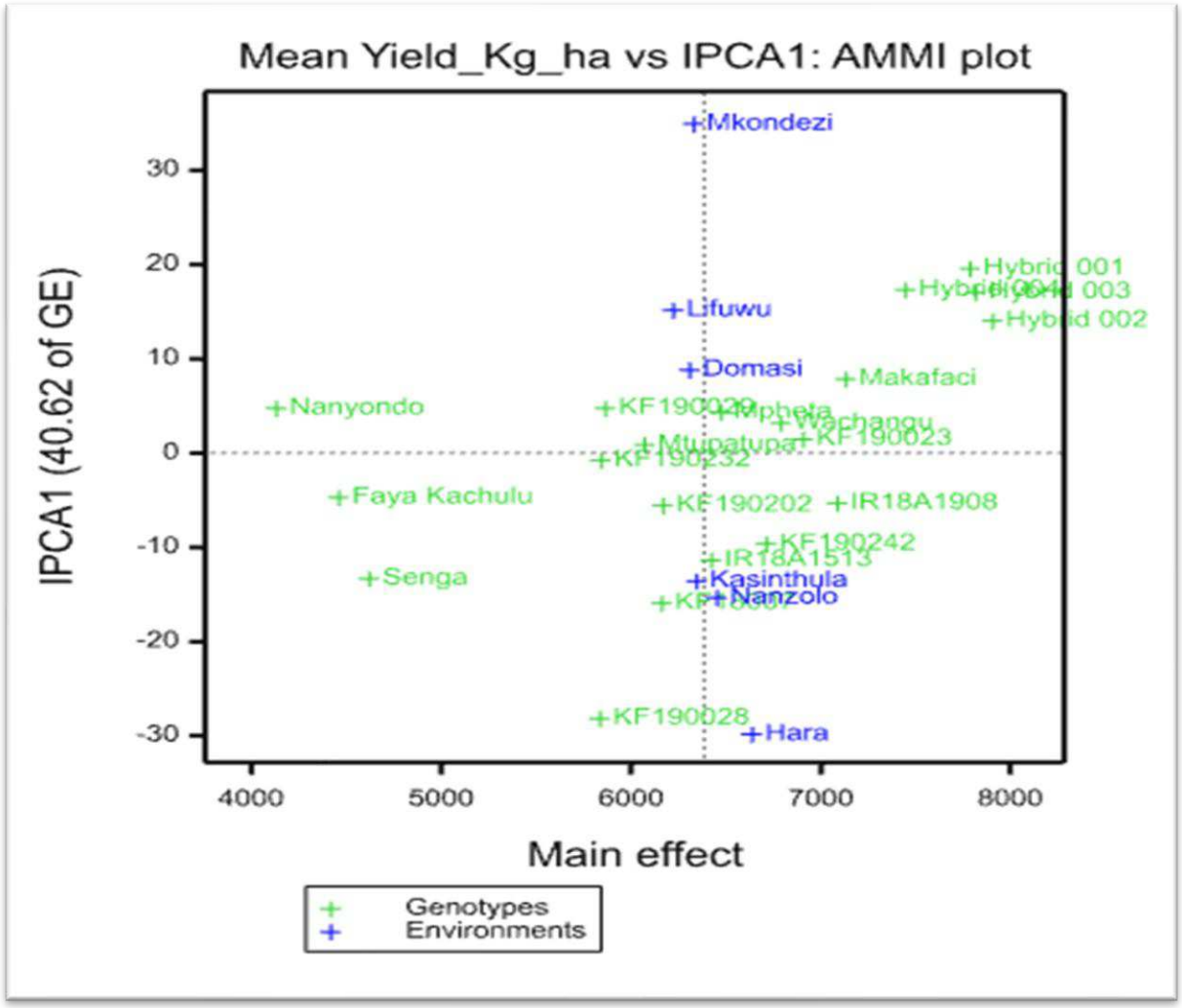


Figure 3: AMMI plot of Interactive Principal Component Axis I (IPCA 1) for the studied 20 rice genotypes

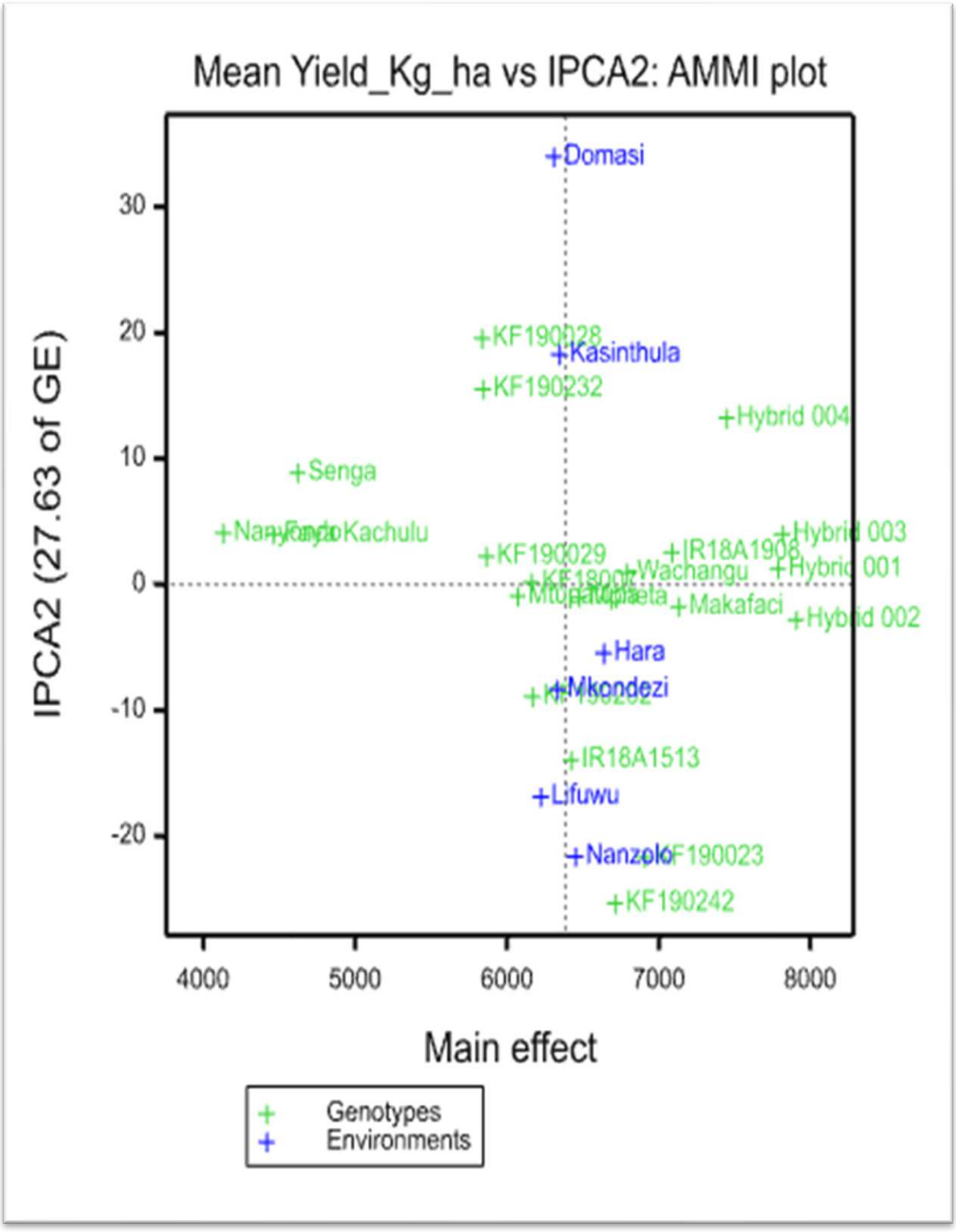


Figure 4: AMMI plot of Interactive Principal Component Axis II (IPCA 2) for the studied 20 rice genotypes

The GGE Biplot Analysis

The GGE biplot is a useful visualization tool for evaluating the performance of rice genotypes in various environments. In the current study, the GGE scatter plot explained a total of 93.03% of variation among 20 rice genotypes across six environments, with PC1 explaining 88.84% and PC2 contributing (4.19%) as displayed in Figure 5. The polygon view of the GGE biplot further displayed Which – Won - Where (W-W-W) arrangement (Figure 5). The polygon has been split into seven sectors using straight lines from the biplot origin to accommodate all the studied genotypes. The six environments have therefore been regrouped into two environments based on mega-environment principle. The first mega – environment comprises Domasi and Mkondezi with hybrid 001 as a winning genotype. The second mega – environment was composed of Lifuwu, Nazolo, Hara and Kasinthula and the winning genotype was hybrid 002. This means the genotypes hybrid 001 and hybrid 002 are more stable and offer high performance levels within their growth environments but poor stability when grown in other environments. On the other hand, genotypes such as Nanyondo and Faya Kachulu showed connected to a polygon vertex line where there is no linkage to any environment, means that these genotypes are providing less yield performance across all environments and are more affected by the environment.

The acute angles and short distances between vectors for Domasi and Mkondezi, Kasinthula and Lifuwu, and Nazolo and Hara, mean that such environments are related, respectively (Figure 6). The long distances and obtuse angles between vectors for Domasi and Hara, as well as Mkondezi and Nazolo indicate that those environments are not related and influence genotypes differently.

Lifuwu and Mkondezi were found to be the representative sites because they were close to the average environment coordinate (AEC) or epicenter (Figure 7). Furthermore, Mkondezi is the most discriminatory sites. Mkondezi is therefore classified as the most ideal because it is both the

most discriminatory site of the tested genotypes and at the same time, representative of the target environments as it is close to the average environment coordinate (AEC). Kasinthula was found to be the most non-representative and non-discriminating environment as evidenced by its shorter vector and longest distance from the AEC (epicenter), seconded by Hara which shared the same descriptions. Other non-representative (longer distance from the average environment) but discriminatory (long vector) environments were Domasi and Nazolo. The GGE Biplot further compared the genotypes with ideal lines located at the center of the ellipse (Figure 7). Genotypes that were located near the epicenter are described as ideal genotypes for stability and high yield as means across seasons and environments. Genotypes such as Hybrid 001, Hybrid 002, Hybrid 003, Hybrid 004, Makafaci Wachangu and IR18A1908 are therefore categorized as ideal. Furthermore, genotypes such as IR18A1513, Mpheta, KF190242 and KF190023 displayed moderate adaptability, performing reasonably well but not ranking among the top performers. On the other hand, genotypes such as Nanyondo, Faya Kachulu, Sengamtali and KF190028 were located far away from the ideal genotypes, indicating that they possess poor stability and reduced yield potential.

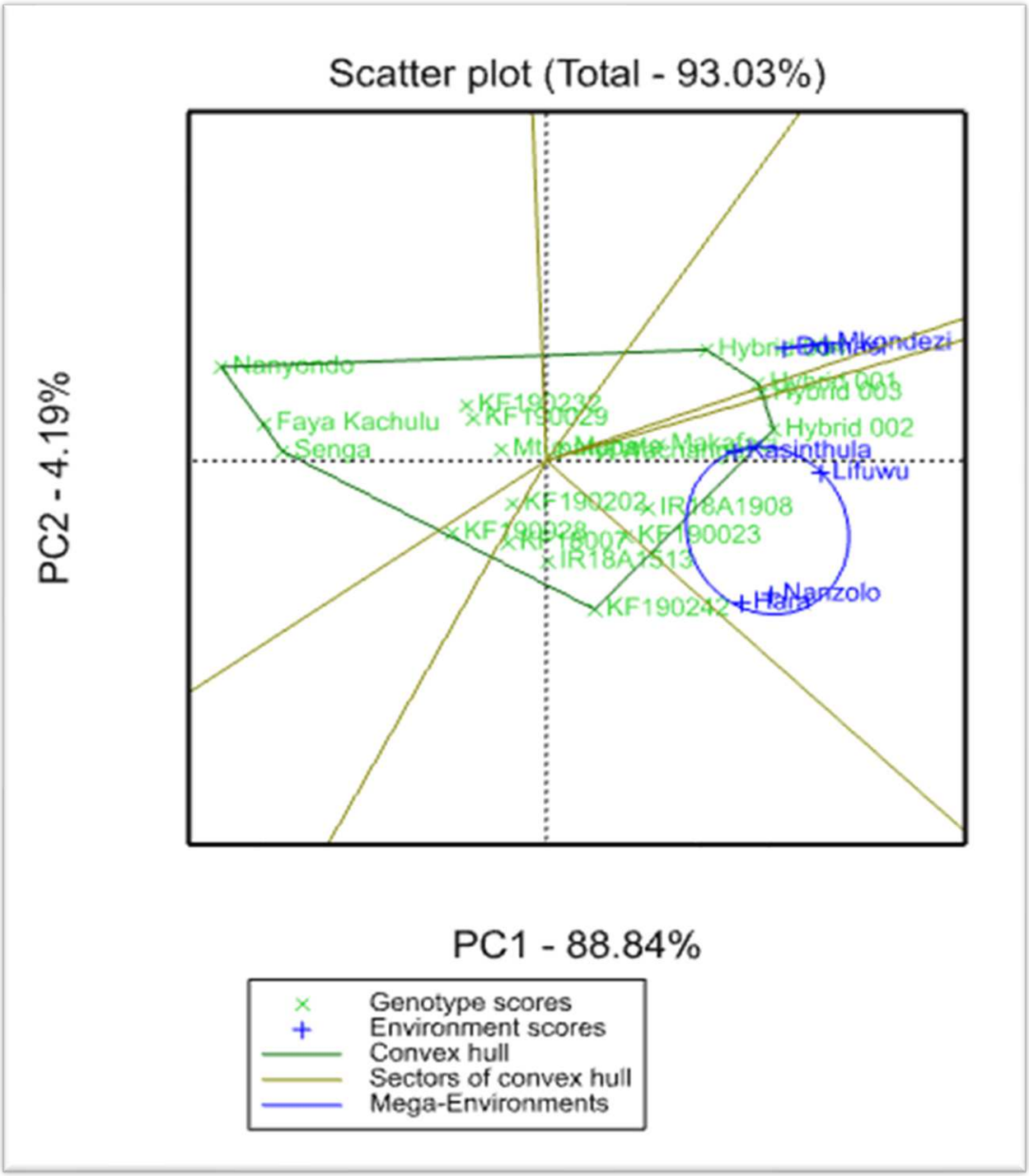


Figure 5: GGE Biplot for Mega-Environment and Which -Won Where of the 20 Rice Genotypes across 6 Locations

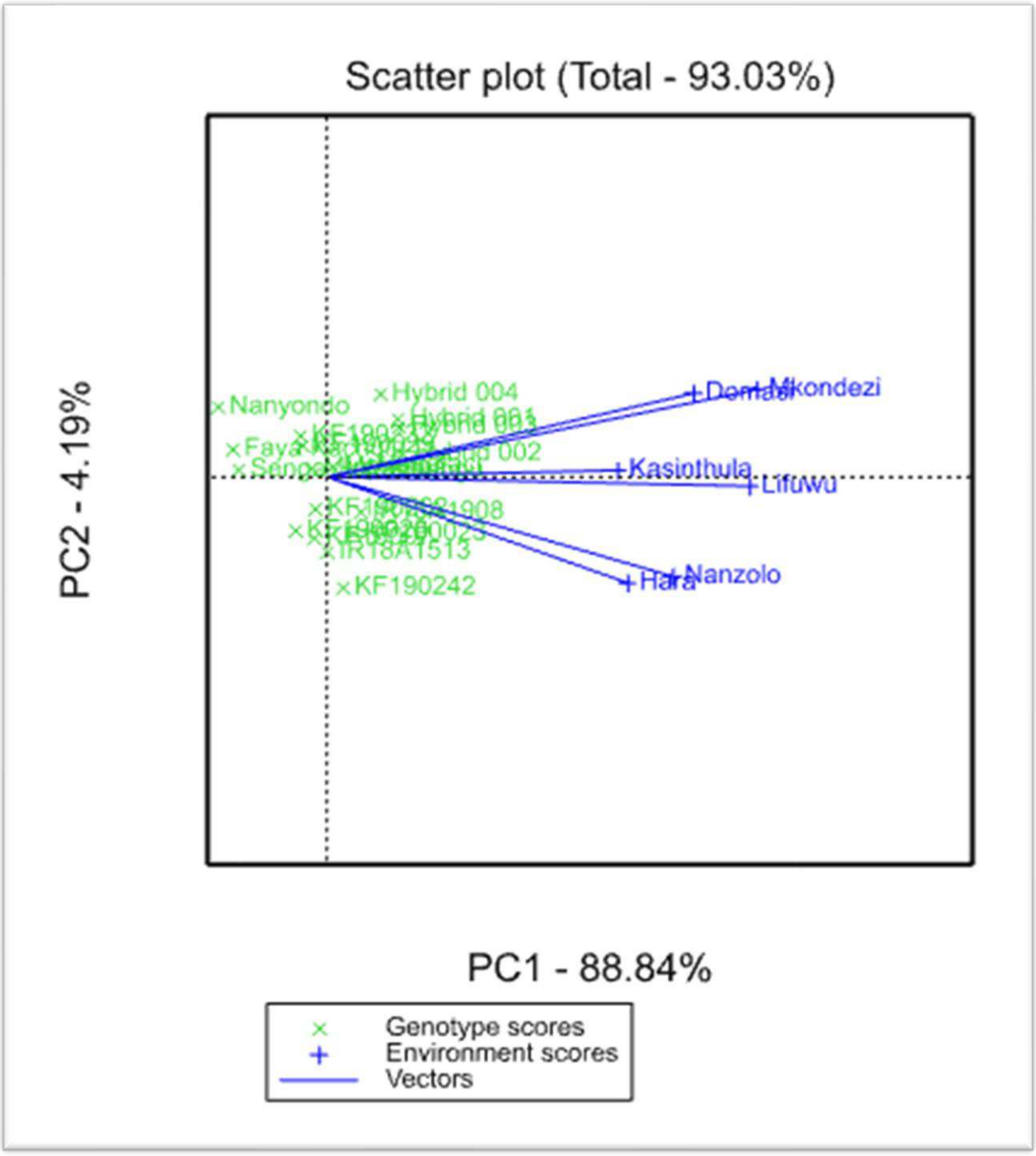


Figure 6: The Relationship Among 6 Experimental Sites for the 20 Rice Genotypes

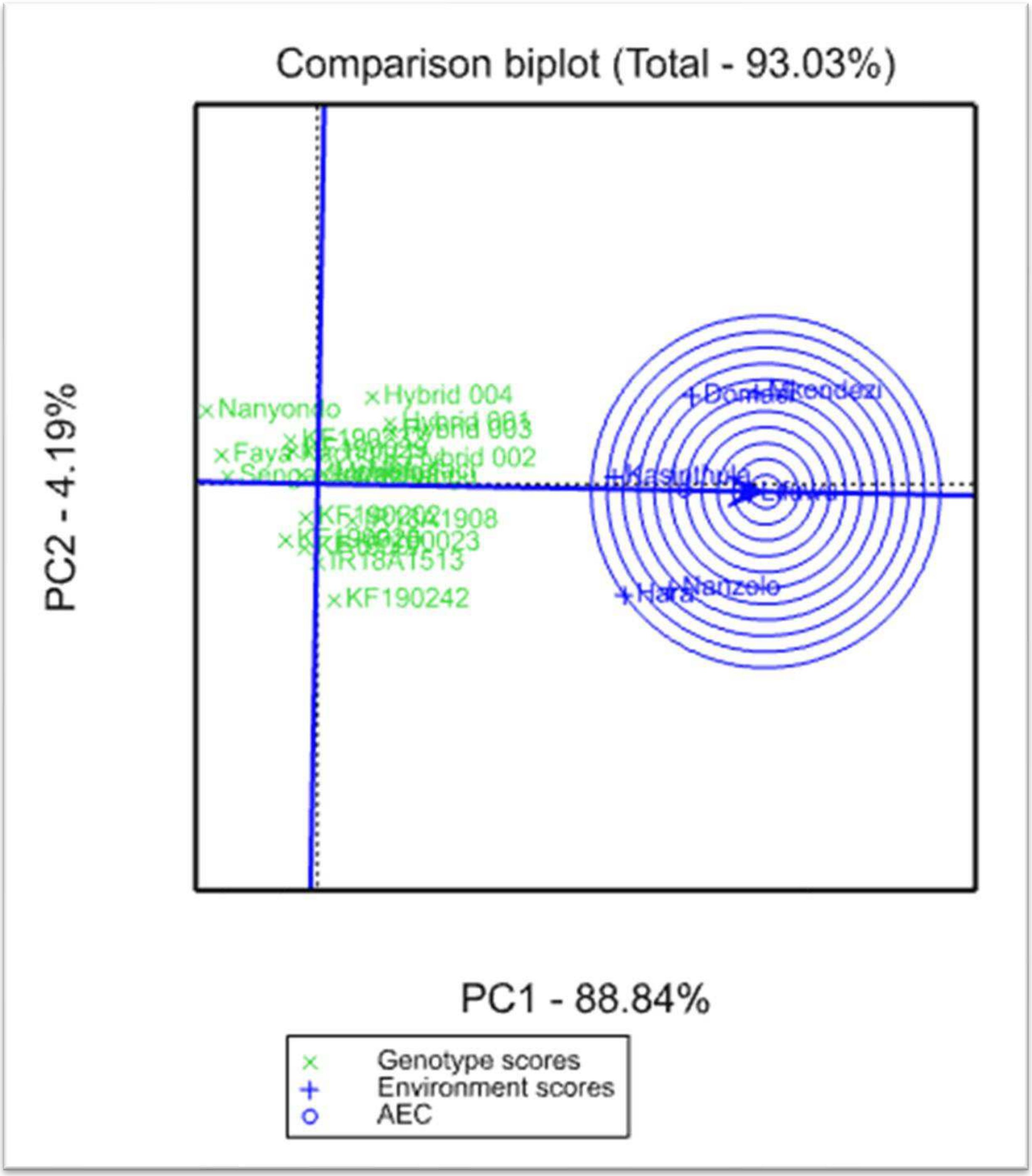


Figure 7: GGE Biplot Showing Representativeness and Discrimination of the 6 Environments for the 20 Rice Genotypes

Yield-attributing and grain quality traits

The fata from two consecutive seasons under 2024/2025 rainfed and 2025 irrigated seasons were pooled and combined means were subjected to the Analysis of Variance (ANOVA) and stability analysis in Genstat (Table 10). The aim was to allow for identification of genotypes with stable performance across varying environments. Traits analyzed include phenology (DTF, DTM), plant architecture (PH, NT, NPP, PL), yield components (Panicles/m², Spikes/panicle, 1000-grain weight, SSR%), and grain quality traits (GL, GW).

Significant differences ($p < 0.001$) were observed for days to 50% flowering, days to maturity and grain length, plant height, number of productive panicles (NPP), and grain width (GW) all compared at ($p < 0.05$). The traits such as number of tillers (NT), panicles per square meter, spikes per panicle, and seed set rate (SSR%) showed no significant variation, indicating stability across genotypes. The variation in days to 50% flowering (DTF) and days to maturity (DTM) among 20 rice genotypes across six environments demonstrated clear differences in phenological behaviour. The mean 1000 - grain weight across 20 rice genotypes showed significant differences in yield potential. The genotypes such as KF190029 and Hybrid 001 recorded the highest grain weights, indicating their superior capacity for grain filling and potential as high - yielding cultivars.

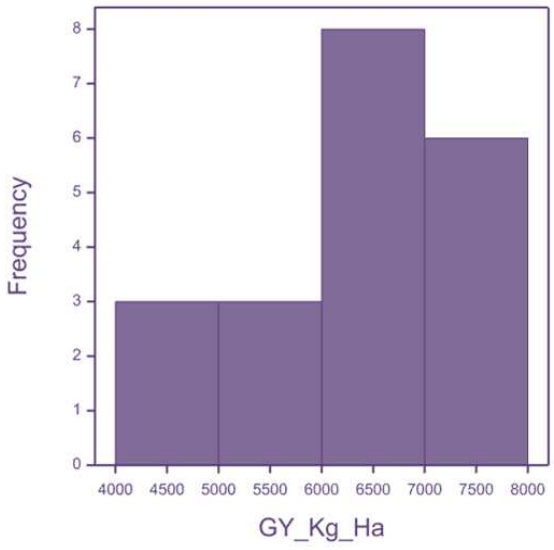
The distribution of grain length and grain width among the genotypes showed considerable variation in grain quality traits. The genotypes such as KF190029 and Mtupatupa combined both long and wide grains, aligning with market-preferred quality attributes and underscoring their suitability for consumer acceptance.

376 **Table 10: Combined Mean Yield-attributing and Grain Quality Traits Performance of 20 Rice Genotypes Across Six (6) Locations During**
377 **the 2024/2025 Rainfed and 2025 Irrigated Seasons**

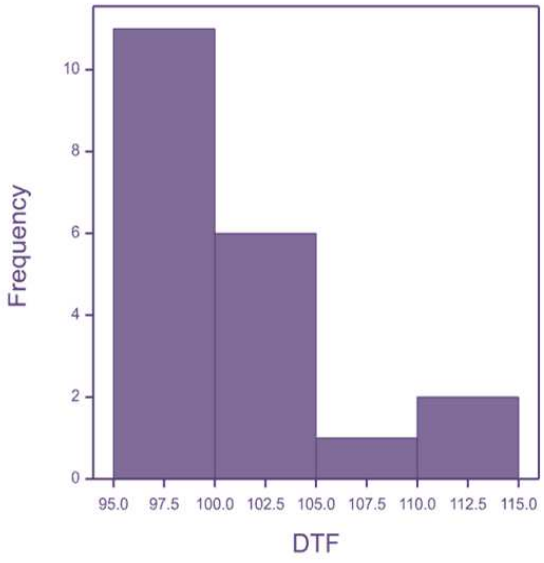
Sr. NO	Genotypes	Traits											
		DTF	DTM	PH (CM)	NT	NPP	PL	Pan _ SqM	Spik/ Pan	1000 gwt	SSR (%)	GL (mm)	GW (mm)
1	Nanyondo	110	117	93	10	10	22.3	168	178	25.8	74	9.5	3.6
2	Faya Kachulu	114	119	89	10	10	21.3	170	183	25.4	73	8.6	3.1
3	Mpheta	101	110	85	9	7	20.7	168	172	25	73	8.8	2.9
4	Makafaci	96	110	86	9	10	21.3	167	176	25.9	73	8.9	3.4
5	Wachangu	98	107	84	7	9	20.9	171	186	25	73	8.8	3.1
6	Senga	100	110	88	10	11	22.2	175	177	26.6	72	9.7	4
7	KF18007	99	105	85	10	10	21.6	164	170	25.5	74	9.4	3.5
8	Hybrid 001	100	110	88	10	10	22.3	172	180	27	73	9.3	3.7
9	Hybrid 002	99	110	87	10	9	22.1	166	178	25.4	70	9.6	3.7
10	Hybrid 003	102	110	89	10	10	22.6	169	178	25.4	74	9.7	3.9
11	Hybrid 004	97	105	87	9	11	22	172	174	26.8	73	9.6	4
12	KF190023	99	109	88	9	11	21.8	159	183	25.9	73	9.5	3.8
13	KF190242	100	110	88	9	9	21.9	161	179	26	74	9.7	4.1
14	KF190202	98	107	86	10	11	22.2	168	180	26.6	74	9.9	4.1
15	KF190232	99	109	88	10	10	22.3	162	181	25.4	75	9.9	4
16	KF190028	101	110	88	11	10	22.5	172	176	26.4	72	10.1	4.1
17	KF190029	101	109	88	9	12	22.5	173	185	27.5	74	10.4	4.4
18	IR18A1513	101	111	86	8	9	21.7	162	171	26.1	73	9.5	3.8
19	IR18A1908	105	113	85	8	9	21.8	167	175	26.1	73	9.5	4
20	Mtupatupa	113	122	87	10	11	22.2	178	190	26.7	72	9.9	4.2
	Mean	102	111	88	9	10	21.9	168	179	26.0	73	9.5	3.8
	LSD 0.05	4.3	3.4	3.94	2.9	2.0	1.21	15.7	17.6	2.03	3.0	0.73	0.68
	Prob.	<.001	<.001	0.022	0.701	0.011	0.148	0.699	0.791	0.549	0.841	0.001	0.003
	CV %	2.6	1.7	2.7	19.1	12.2	3.4	5.6	6.0	4.7	2.5	4.7	10.9

Frequency Distribution of Rice Grain Yield, Yield - attributing and Quality traits

Figure 8 (A - L) is the frequency distribution of the studied 20 rice genotypes across 6 environments for the target traits. Across the six environments, yields ranged between 4000 and 8000 kg/ha, with the majority of observations concentrated in the 6000 – 7000 kg/ha interval. Majority of the genotypes clustered around 6000 – 7000 kg ha^{-1} and a subset approaching 8000 kg ha^{-1}, indicating clear potential for high productivity. Flowering time was relatively uniform (95 – 100 days), with only a few late-flowering outliers, supporting synchronized crop management. Plant height and panicle density exhibited narrow distributions, confirming uniform crop establishment. The number of spikelets per panicle was stable (177), reinforcing yield consistency. Tiller number and panicle length also exhibited limited variability, suggesting reliable stand structure among the genotypes. Quality traits were similarly consistent, with seed setting ratio averaged at 73%, one thousand grain weight centered at 26 g, and grain dimensions (length = 9.5 mm, width = 3.7 mm) showed moderate uniformity with slight skewness. Generally, these distributions reveal that while most agronomic and quality traits are stable across genotypes, yield performance displays exploitable diversity, with a subset of genotypes consistently achieving superior productivity.

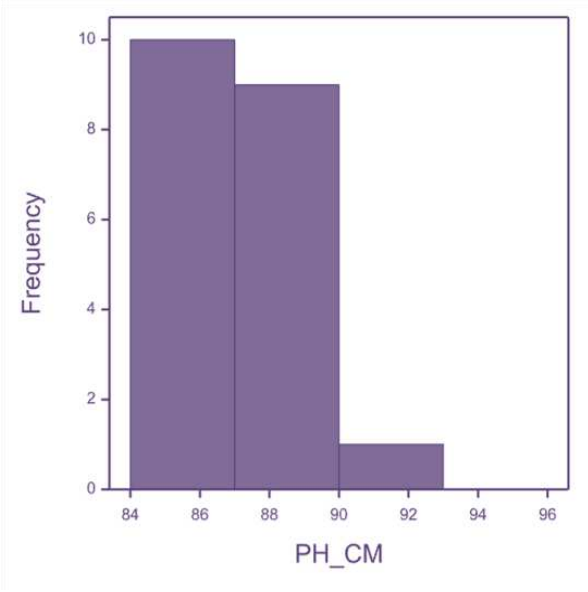


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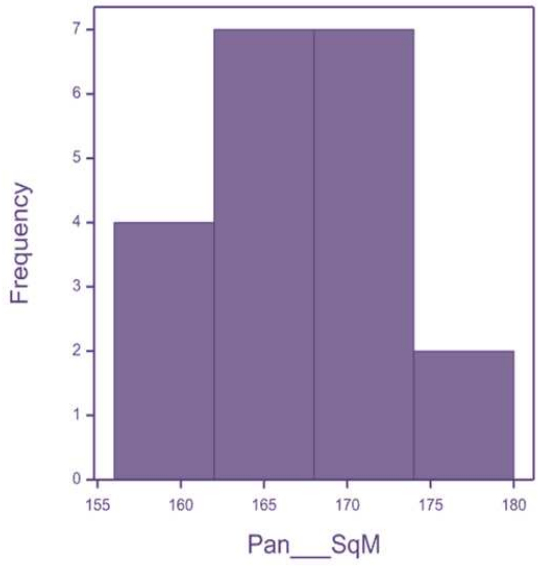


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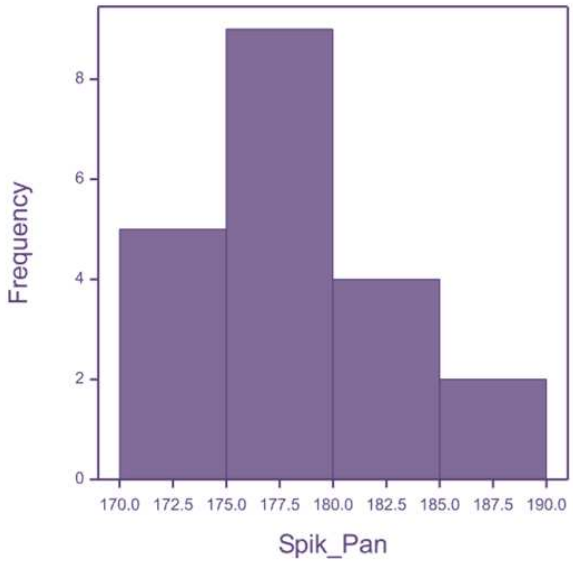
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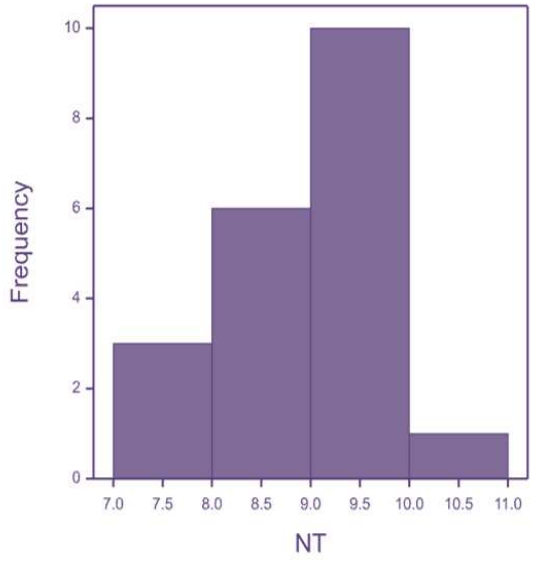
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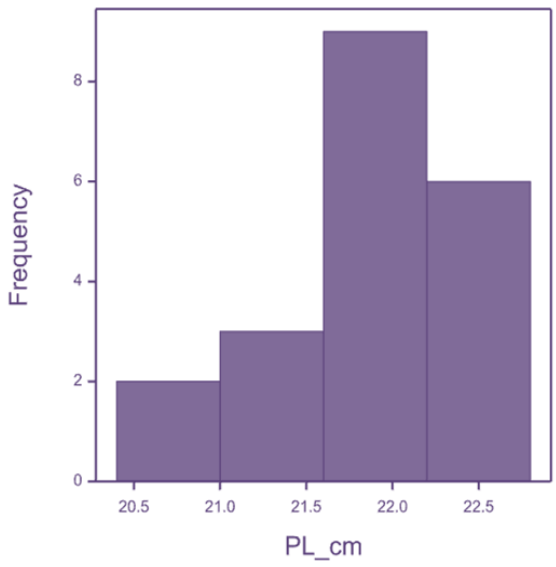

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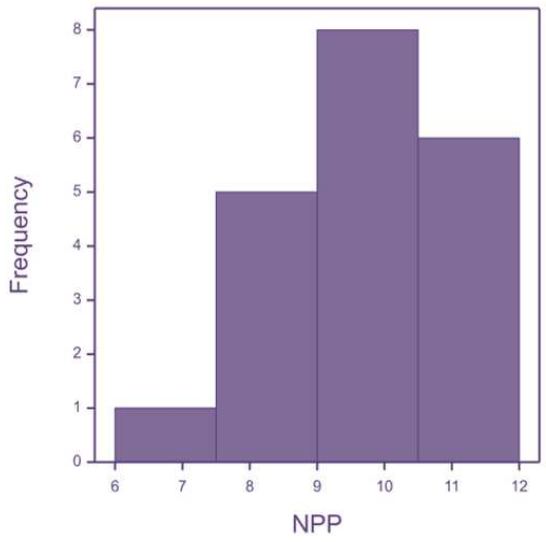

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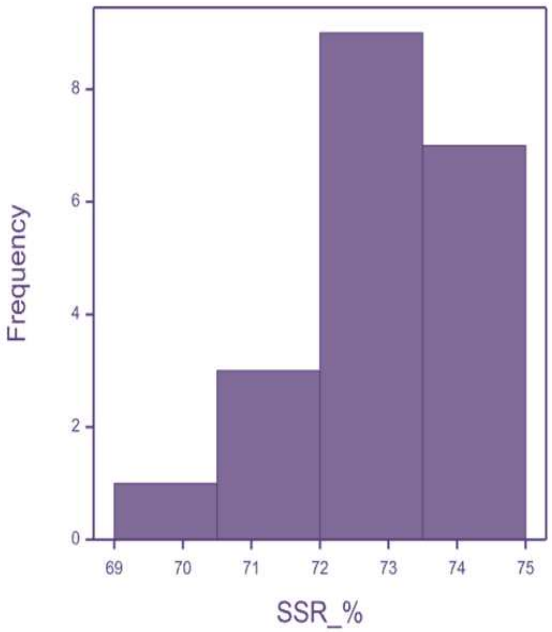

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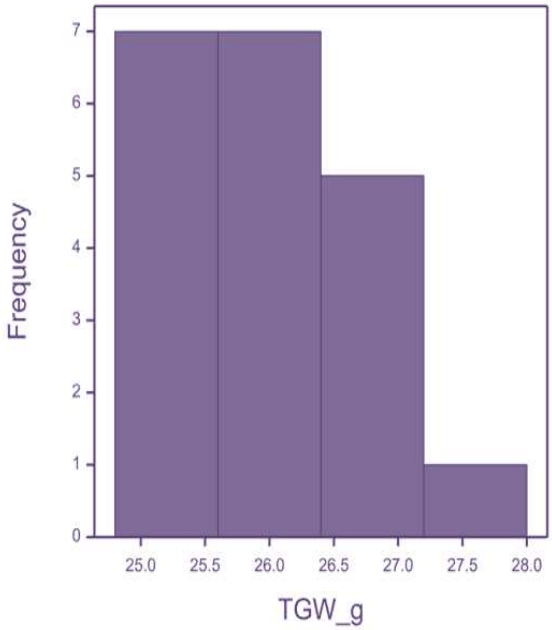
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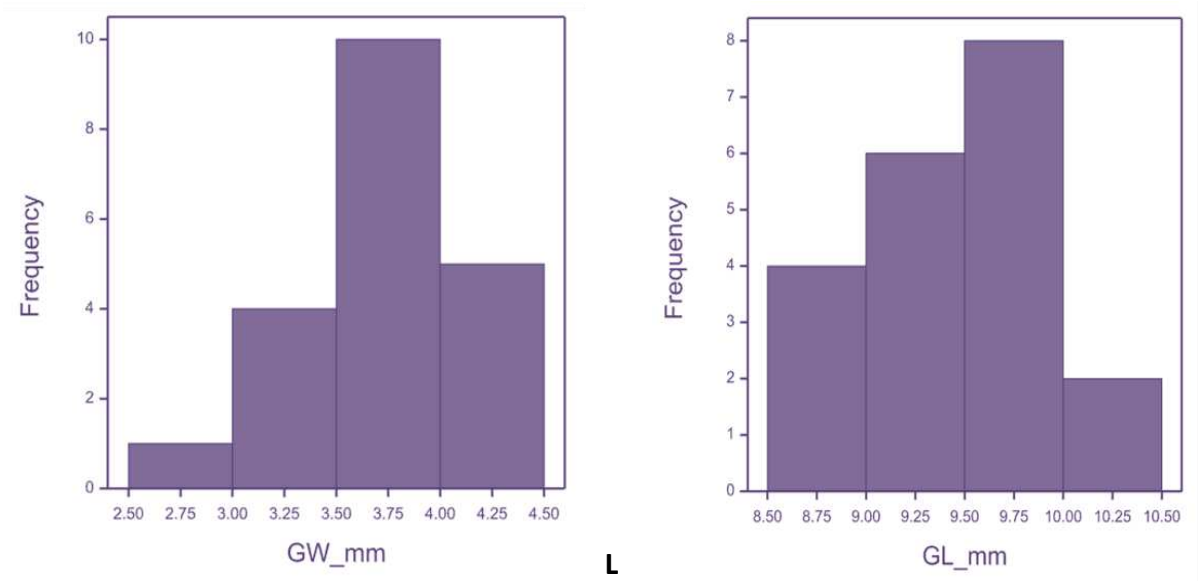
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SSR_%

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Frequency
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26.5
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TGW_g

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Figures 8 (A – L): Frequency Distribution of Rice Grain Yield, Yield - Attributing and Quality Traits of the 20 Rice Genotypes across 6 Environments

Correlations

Correlation analysis revealed clear developmental linkages such that days to flowering and maturity were tightly associated, both positively related to plant height and spikelet number (Table 11). More importantly, grain yield exihibited negative correlations with flowering time, maturity, and plant height, indicating that early-maturing, shorter genotypes are more productive as they escape terminal drought and /or lodging.

Grain size traits were strongly interdependent such that grain length and width correlated closely and were positively linked to panicle length, confirming panicle architecture as a key determinant of grain size. Panicle number and tiller number were positively associated with grain size traits but showed weak or negative associations with yield, suggesting that yield is not directly driven by panicle or tiller counts.

Seed set ratio was largely independent of other traits, although denser panicle stands reduced efficiency, suggesting a trade-off between stand density and reproductive success. Generally, the results underscore that yield performance is more strongly influenced by growth duration and plant stature than by panicle traits, while grain quality traits are closely tied to panicle morphology.

Table 11: Correlation of 12 selected traits for the studied 20 rice genotypes across 6 locations for two seasons

Variable	DTF	DTM	GL	GW	GY	NPP	NT	NP_SqM	PH	PL	Spik_Pan	SSR
DTF	**1.000**	0.930***	-0.100	-0.063	-0.543**	0.044	0.232	0.337	0.450*	0.063	0.373*	-0.062
DTM	0.930***	**1.000**	-0.105	-0.031	-0.445*	0.007	0.207	0.319	0.430*	0.060	0.433*	-0.199
GL	-0.100	-0.105	**1.000**	0.936***	-0.031	0.566**	0.364*	0.120	0.264	0.851***	0.157	0.093
GW	-0.063	-0.031	0.936***	**1.000**	0.046	0.631***	0.257	0.134	0.230	0.834***	0.204	0.081
GY	-0.543**	-0.445*	-0.031	0.046	**1.000**	-0.223	-0.286	-0.191	-0.460*	-0.031	-0.134	-0.204
NPP	0.044	0.007	0.566**	0.631***	-0.223	**1.000**	0.326	0.343	0.346	0.616**	0.444*	0.139
NT	0.232	0.207	0.364*	0.257	-0.286	0.326	**1.000**	0.221	0.540**	0.584**	0.002	-0.094
NP_SqM	0.337	0.319	0.120	0.134	-0.191	0.343	0.221	**1.000**	0.060	0.206	0.360	-0.324
PH	0.450*	0.430*	0.264	0.230	-0.460*	0.346	0.540**	0.060	**1.000**	0.578**	0.203	0.162
PL	0.063	0.060	0.851***	0.834***	-0.031	0.616**	0.584**	0.206	0.578**	**1.000**	0.182	0.063
Spik_Pan	0.373*	0.433*	0.157	0.204	-0.134	0.444*	0.002	0.360	0.203	0.182	**1.000**	-0.021
SSR	-0.062	-0.199	0.093	0.081	-0.204	0.139	-0.094	-0.324	0.162	0.063	-0.021	**1.000**

Note: *, ** and *** = Significant 0.05 (Any $r \geq 0.361$), 0.01(Any $r \geq 0.463$), and 0.001(Any $r \geq 0.623$) levels, respectively.

Agglomerative Hierarchical Clustering

Agglomerative Hierarchical Clustering based on grain yield, yield - related and grain quality traits using the complete-linkage method grouped the 20 rice genotypes into four major clusters (Figure 9, Table 1). Cluster 1 comprised three genotypes (G1, G2, and G6) that grouped at the lowest linkage distances, indicating the highest internal similarity. Cluster 2 contained seven genotypes (G3, G20, G7, G14, G15, G17, and G16), representing the largest and most heterogeneous cluster. Cluster 3 consisted of six genotypes (G4, G5, G19, G12, G13, and G18) and exhibited a well-defined hierarchical structure. Cluster 4 included three genotypes (G10, G9, and G8) that formed a compact group merging with the rest of the dataset only at higher linkage distances. Genotype G11 emerged as the most divergent, joining the clustering structure at the highest linkage level, thereby demonstrating maximal dissimilarity from all other genotypes

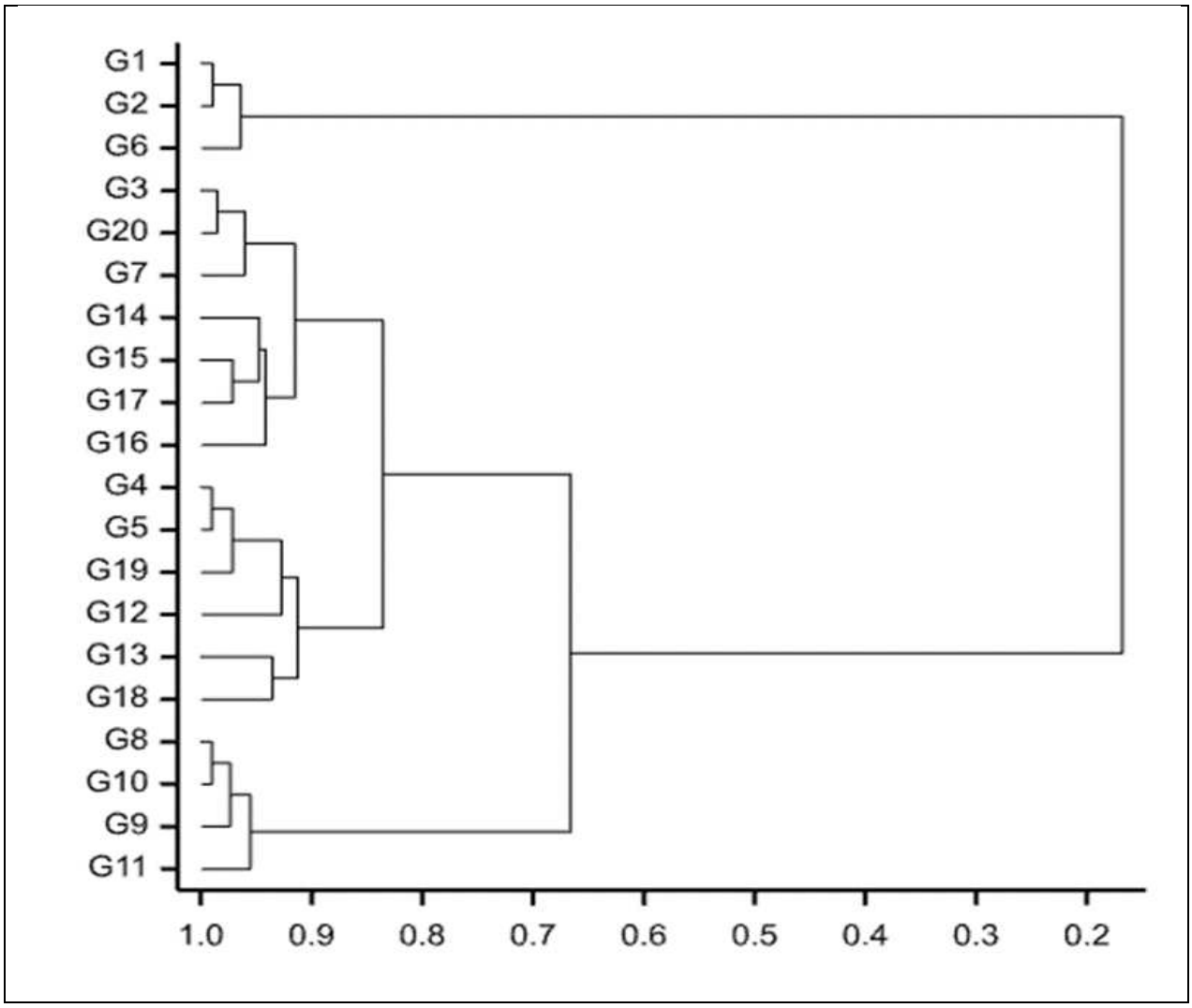


Figure 9: The AHC Pattern of the 20 rice genotypes

4.0 Discussion

The evaluation of 20 rice genotypes across rainfed and irrigated lowland conditions in Malawi revealed substantial genetic variability and complex genotype × environment interactions, underscoring the challenges of breeding for resilience under climatic variability (Tables 3, 4, and 5). The significant genotype × season interaction observed in ANOVA highlights the instability of performance across seasons, reinforcing the need for resilient genotypes and the integration of molecular breeding strategies (Wang et al., 2025; Tanin et al., 2022; Shrestha et al., 2021, Chaity et

435 at., 2026). Furthermore, these results are in agreement with those by Gaballah et al., (2022), who
436 reported significant genotypic variation under irrigated and water-limited conditions in African
437 rice systems, underscoring the relevance of the present findings to regional breeding programs.
438 Hybrids consistently outperformed landraces and improved lines, confirming their superiority for
439 yield potential, while improved entries such as Makafaci and IR18A1908 demonstrated stability
440 approaching hybrid levels, suggesting their value as parental lines.
441 AMMI analysis further clarified the multidimensional nature of G×E interactions and genotypic
442 effects dominated yield differences, with environmental contributions being less pronounced
443 (Table 7). This confirms that genetic diversity is the primary determinant of grain yield
444 performance, consistent with earlier findings by Joshi et al., (2023) and Musila et al. (2017,
445 working in African rice systems), who emphasized the dominance of genotypic effects in yield
446 variation and their fundamental role in regional breeding programs. The trade-off between high
447 yield and stability was evident: hybrids such as Hybrid 002 and Hybrid 003 revealed superior
448 yields but declined stability, whereas improved genotypes such as Mtupatupa and Wachangu
449 displayed moderate yields with greater consistency. Environmental differentiation also emerged,
450 with Domasi serving as a benchmark for general adaptability and the higher amount of rainfall
451 that was received at this site might have contributed to better yield and good adaptation, while
452 Mkondezi and Lifuwu provided discriminatory environments for detecting location specific
453 genotypes. This balance between productivity and adaptability reflects a key antagonistic
454 pleiotropy in rice breeding, echoing previous researchers (Jambhulkar and Pande, 2022; Yusuff
455 et al., 2017; Tariku et al., 2013; Chairi et al., 2020; Barona et al., 2021).
456 The GGE biplot analysis reinforced these insights by explaining over 93% of variation across
457 environments (Table 8, Figure 5, 6, and 7). The “Which-Won-Where” pattern exhibited two
458 mega-environments, with Mkondezi identified as both representative and discriminatory, making

it ideal for selection. Hybrids clustered near the ideal genotype position, confirming their dual advantage of yield and adaptability, while a landrace such as Nanyondo and an improved KF190028 were distant from the epicenter, reflecting poor stability and reduced yield potential. These findings align with earlier reports that emphasized the efficiency of GGE biplots observed in African multi-environment trials when identifying ideal genotypes and environments (Haider et al., 2017; Huang et al., 2021; Rao et al., 2025; Barona et al., 2021). Beyond yield, significant genetic variability was observed in yield-attributing and grain quality traits Figure 8 (A - L)). Phenological diversity, particularly in flowering and maturity duration, emerged as a key determinant of adaptability, with early-maturing genotypes outperforming late-maturing ones in the same conditions likely due to escaping limited terminal water application. Grain weight and grain morphology contributed more to quality and consumer preference by being long and slender than to yield, consistent with reports by previous workers (Rao et al., 2020; Zhou et al., 2024; Chen et al., 2024). Genotypes such as KF190029 combined high grain weight with desirable grain dimensions, making them promising candidates for breeding programs that integrate yield stability with market-preferred traits.

Correlation analysis provided further insights into trait relationships (Table 11, and Figure 9). The strong linkage between flowering and maturity confirmed their developmental interdependence, while their negative correlation with yield emphasized the advantage of earliness under stress-prone agro-ecologies. Plant height and excessive tillering negatively associated with yield, supporting ideotype breeding strategies favouring semi-dwarf, early-maturing genotypes with optimized tiller numbers. Grain size traits, though critical for milling and consumer acceptance, showed weak associations with yield, highlighting the need to balance agronomic efficiency with market demands.

Agglomerative hierarchical clustering grouped the 20 rice genotypes into four clusters, with G11 emerging as the most divergent (Table 1, Figure 9). Cluster 1 showed strong internal similarity, while Cluster 2 revealed as the largest and most heterogeneous, suggesting broad genetic variability. Cluster 3 exhibited a clear hierarchical structure of six genotypes, and Cluster 4 formed a compact group distinct from the rest. These patterns highlight both convergence and divergence in yield-related and grain quality traits, consistent with earlier studies where diverse, compact and heterogeneous clusters in rice were reported (Mohanty et al., 2025; Zhang et al., 2022; Tanaka et al., 2020). The distinctiveness of G11 underscores its potential as a donor genotype for novel allelic combinations, echoing previous reports which emphasized the role of outlier genotypes in broadening the genetic base (Takar et al., 2024; Okamoto et al., 2025).

5.0 Conclusion and Recommendations

The present study was undertaken to evaluate genotypic variation and analyze G × E interactions for yield, yield components, and quality traits in advanced rice, in order to identify stable and superior genotypes under rainfed and irrigated lowland conditions of Malawi. The AMMI analysis demonstrated that genetic diversity is the dominant factor influencing yield performance, while environmental heterogeneity exerts a minor effect. The significant multidimensional G×E interactions highlight the importance of considering both stability and adaptability in genotype selection. This study further demonstrated that seasonal variation was the strongest factor influencing rice grain yield, with significant genotype × season and genotype × environment interactions shaping performance. Hybrid genotypes consistently attained superior yields under both rainfed and irrigated conditions, often exceeding 7,700 kg ha^{-1}, however, their stability across environments was limited. Improved genotypes such as Mtupatupa, Wachangu, and

Mpheta achieved moderate yields but greater stability, making them suitable for variable environments. The yield-attributing and grain quality traits revealed strong genetic diversity, with early-maturing and shorter plants linked to higher productivity, while genotypes such as KF190029, IR18A1908 and Hybrid 001 combined high yield potential with market-preferred grain dimensions. These results highlight the trade-offs between productivity, stability, and grain quality, emphasizing the need for balanced breeding strategies.

Based on these findings, it is recommended that hybrids such as Hybrid 001, Hybrid 002, and Hybrid 003 be promoted in high-yielding environments to maximize rice productivity. Improved genotypes such as Mtupatupa, Wachangu, and Mpheta should be prioritized in breeding programs targeting variable environments to ensure resilience and consistent performance. Genotypes such as KF190029, IR18A1908 and Hybrid 001, which combine high yield potential with desirable grain quality traits, should be advanced for dual-trait improvement to meet both production and consumer demands. The environment-specific selection should be emphasized, with sites such as Mkondezi and Lifuwu exploited for detecting specific adaptability due to their high discrimination, while Domasi should be used as a benchmark for broad adaptation. Overall, rice breeding strategies should integrate hybrids for yield maximization and improved lines for stability and grain quality, thereby developing cultivars suited for both wide adaptation and targeted ecosystems. This integrated approach will accelerate rice improvement programs, enhance food security, and strengthen market competitiveness in Malawi and the region.

6.0 List of Abbreviations

AEC: Average Environment Coordinate

AHC: Agglomerative Hierarchical Clustering

AMMI: Additive Main effects and Multiplicative Interaction

ANOVA: Analysis of Variance

ASV: AMMI Stability Value

CSIR: Council for Scientific and Industrial Research

CV: Coefficient of Variation

DF: Degrees of Freedom

DTFL: Days to Flowering

DTM: Days to Maturity

FAO: Food and Agriculture Organization of the United Nations

G: Genotype

GL: Grain Length

GW: Grain Width

G x E x I: Genotype × Environment Interaction

GY: Grain Yield

IPCA: Interaction Principal Component Axis

IRRI: International Rice Research Institute

KAFACI: Korea - Africa Food & Agriculture Cooperation Initiative

LARS: Lifuwu Agricultural Research Station

LSD: Least Significant Difference

LUANAR: Lilongwe University of Agriculture and Natural Resources

MS: Mean Square

NPP: Number of Productive Panicles

NT: Number of Tillers

PCA: Principal Component Analysis

PH: Plant Height

RCBD: Randomized Complete Block Design

SES: Standard Evaluation System (for rice)

SS: Sum of Squares

SSR%: Seed Setting Rate measured as a percentage

SVD: Singular Value Decomposition

7.0 Declarations:

7.1 Ethics approval and consent to participate

Not applicable. This study involved experimental evaluation of rice genotypes and did not include human participants or animal subjects that would require ethical approval.

7.1 Consent for publication

Not applicable. This study did not involve human participants, personal data, or images requiring consent for publication. Where part of the information from other authors was used, they have been duly cited.

7.3 Availability of data and material

The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request. In addition, all data generated or analyzed during this study are included in this article.

7.4 Competing interests

The authors declare that they have no competing interest

7.5 Funding

The author (s) acknowledge the financial support received from the Africa Center of Excellence in Aquaculture and Fisheries (AQUAFISH: ACE AF - II) of the Lilongwe University of Agriculture

and Natural Resources (LUANAR), Bunda Campus, for the implementation and publication of this work.

8.0 Authors' contributions

EJ: conceptualization, data curation, formal analysis, investigation, methodology, visualization, writing - original draft, writing - review & editing. JB: conceptualization, supervision, validation, visualization, writing - review & editing. RM: conceptualization, supervision, validation, visualization, writing original draft, writing - review & editing. MA: conceptualization, supervision, validation, visualization, writing - original draft, writing - review & editing. KM: conceptualization, supervision, validation, visualization, writing - original draft, writing - review & editing. All authors read and approved the final version of the manuscript.

9.0 Acknowledgment

We are very grateful to the Aqua Fish Center at LUANAR for the financial support when carrying out the field experiments so that this manuscript could be published in a journal. Thanks, are extended to the Department of Crops and Soil Science at LUANAR for allowing authors to undertake this study. Gratitude to fellow scientists and staff from LUANAR and DARS for their tireless support. We are also indebted to the International Rice Research Institute (IRRI), Korea - Africa for Food and Agriculture cooperation Initiative (KAFACI), Africa Rice and the Department of Agricultural Research Services (DARS) through Lifuwu Agricultural Research Station (LARS) for the provision of plant materials used in the current study.

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Figure Legends

Figure 1 (A - D). The 2024/2025 rainfed and 2025 irrigated rice trials conducted across six locations in the country, shown during heading and maturity stages. (A) Aerial view of the experimental site at Lifuwu for repeated irrigated trials; (B) rainfed trials at Kasinthula; (C) maturity stage of trials at Hara site; and (D) rainfed trials at Lifuwu site

Figure 2. AMMI biplot of the first two Interactive Principal Component Axes (PC1 and PC2) showing genotype × environment interactions among the 20 studied rice genotypes.

Figure 3. AMMI biplot illustrating Interactive Principal Component Axis I (IPCA 1) for the 20 rice genotypes under study.

Figure 4. AMMI biplot illustrating Interactive Principal Component Axis II (IPCA 2) for the 20 rice genotypes under study.

Figure 5. GGE biplot showing mega-environment delineation and "which-won-where" patterns of the 20 rice genotypes across six locations.

Figure 6. Relationship among six experimental sites based on the performance of the 20 rice genotypes.

Figure 7. GGE biplot depicting representativeness and discrimination of the six environments for the 20 rice genotypes.

Figure 8 (A–L). Frequency distributions of grain yield, yield-attributing traits, and grain quality parameters for the 20 rice genotypes across six environments.

Figure 9. Agglomerative hierarchical clustering (AHC) dendrogram illustrating the genetic relationship among the 20 rice genotypes.

Table Legends

Table 1. List of rice plant materials used in the study, along with their sources.

Table 2. Description of the experimental sites, including location, and agro-ecological characteristics.

Table 3. Combined analysis of variance (ANOVA) for 20 rice genotypes evaluated across six locations during two growing seasons.

Table 4. Mean grain yield (kg ha^{-1}) performance of 20 rice genotypes across six locations during the 2024/2025 rainfed season.

Table 5. Mean grain yield (kg ha^{-1}) performance of 20 rice genotypes across six locations during the 2025 irrigated season.

Table 6. Combined mean grain yield (kg ha^{-1}) performance of 20 rice genotypes across six locations during the 2024/2025 rainfed and 2025 irrigated seasons.

Table 7. Analysis of variance (ANOVA) results for the AMMI model applied to grain yield data.

Table 8. Yield stability of 20 rice genotypes across six environments, based on AMMI scores and the AMMI Stability Value (ASV).

Table 9. Environment mean yield (kg ha^{-1}), stability scores, and variance (%) across six locations.

Table 10. Combined mean performance of yield - attributing traits and grain quality parameters for 20 rice genotypes evaluated across six locations during the 2024/2025 rainfed season and the 2025 irrigated season.