

Research Article

Variability Studies in Landraces and Improved Rice (*Oryza sativa* L.) Germplasm for Yield and Quality Traits

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Abstract

Rice (*Oryza sativa* L.) is one of the most important staple foods crops whose demand is increasing mainly due to population growth and urbanization. It is ranked first in most Asian countries and second to maize in Malawi. The aim of the current study was to determine variability in local landraces and elite rice germplasm using agro-morphological traits in order to identify and document superior germplasm for conservation and use in further breeding programmes. The experiment was conducted at Lifuwu Agricultural Research Station - Experimental Fields during the 2024/2025 rainy season in Alpha Latic Design (ALD), with three replications and each plot comprised a dimension of 5 m x 0.4 m, length and width, respectively. The number of days to reach physiological maturity ranged from 119 days (G102, G154) to 158 days (G2), while milling recovery was from 57% to 75%. and top- ten highest yielding entries (G17, G127, G14, G130, G175, G171, G132, G119, G16, and G19) produced grain yields ranging from 7396 to 8121 kg/ha, highlighting their potential candidature for breeding and genetic improvement programs. The Agglomerative Hierarchical Clustering (AHC) performed using GenStat 19th Edition produced six main clusters such that cluster 1 comprised 66 germplasm and cluster 6 had 8 germplasm, suggesting germplasm variability, ideal for broad spectrum breeding and least populated lines; respectively. This study has a huge contribution to rice improvement goals in identifying and documenting diverse superior germplasm which could be directly adopted by rice growers after advancement or used in further breeding programs.

Keywords

Rice Germplasm, Variability, Correlation, Agro-morphological Traits, Breeding Programme

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1. Introduction

Rice (*Oryza sativa* L.) is one of the most important staple food crops for more than half of the world's population. It is native to Asia, where 90% of the total global production, approximately 800 million metric tons of paddy rice, is grown annually [13]. The crop exhibits extensive morphological and genetic diversity, and its market demand in sub-Saharan Africa is increasing at about 6% per annum due to shifts in dietary habits, economic growth, and population increase [18, 33].

In Malawi, rice is cultivated across three ecologies: rainfed lowland (80%), irrigated lowland (15%), and rainfed upland (5%) [1, 37]. The cultivars grown are derived from diverse sources, including local landraces and improved germplasm introduced from international breeding programs. The landraces and old cultivars serve as vital reservoirs of useful genes, offering abiotic stress tolerance, biotic resistance, and desirable grain quality traits that can enrich improved cultivars [10, 26, 28]. Knowledge of genetic relationships between local and improved germplasm is therefore essential for guiding parental selection and designing effective breeding strategies. The variability studies are critical for characterizing germplasm into hierarchical classes, particularly when considering heritable traits [7, 29]. In Malawi, rice development faces constraints such as poor grain quality, seed recycling, limited mechanization, and low yields. The major challenge for breeders is the limited information on variability among native landraces and introduced elite germplasm. The availability of elite rice germplasm with high yield and superior grain quality traits from institutions such as International Rice Research Institute (IRRI), the Korea-Africa Food and Agriculture Cooperation Initiative (KAFACI) and Africa Rice has expanded the genetic pool suitable for improvement. The crossing or hybridization of high-yielding germplasm with quality-rich local landraces offers opportunities to exploit heterosis and develop cultivars that combine productivity with consumer-preferred traits such as aroma and grain texture [6, 36].

While local germplasm alone may narrow genetic divergence, incorporating improved germplasm adapted to Malawian conditions can broaden diversity and enhance breeding outcomes. The development of rice populations with farmer-preferred traits such as aroma, milling recovery, grain dimensions, and amylose content is fundamental for adoption and market competitiveness [22]. Consolidating variability information on the existing germplasm and selection are therefore essential for effective incorporation into breeding programs [11, 34]. Agro-morphological traits, alongside grain quality parameters, have long served as markers for characterization to establish distinctness among rice germplasm [4, 30].

This study was therefore aimed at determining variability in local landraces and elite rice germplasm using both agro-morphological and grain quality traits, in order to identify superior germplasm for conservation and use in further breeding programs. This study provides information on variability among

different germplasm of *Oryza sativa*, aiding selection, conservation, and use of diverse germplasm in rice breeding programme in Malawi.

2. Materials and Methods

2.1. Plant Materials

The study utilized 200 rice germplasm (G) comprising Malawi's landrace collections, improved varieties, and advanced breeding lines sourced from the IRRI, Africa Rice, and KAFACI (Appendix). The traditional, locally adapted rice varieties such as Faya 14 M 69 and Kilombero released for the past five decades and had been cultivated by smallholder farmers in Malawi, were used in the current study as standard checks.

2.2. Experimental Site

The experiment was conducted at Lifuwu Agricultural Research Station, Salima District, during the 2024/2025 rainy season as part of a characterization study. The site, located at 500 meters above sea level (masl) within the Katete dambo (13.40 °S, 34.35 °E), received 698 mm of rainfall (56.7% of the annual average), and was supplemented by irrigation from Lake Malawi. The mean temperatures ranged from 16 - 28 °C with relative humidity of 65 - 82%, and the soils are vertisols (45% clay), low in nitrogen and phosphorus, with a pH of 7 - 8.

2.3. Experimental Design

The experiment was carried out using an Alpha Lattice Design (ALD) with three replications, each plot measured 5 m × 0.4 m, with plant spacing of 20 cm × 20 cm, 1 m between replicates, and 40 cm between plots (2, 14, 20). The seedlings (<21 days old) were transplanted singly per hill using a pre-marked guiding rope. Fertilizer was applied at 180 kg/ha, comprising 120 kg/ha NPK6S1.0Zn (23: 10: 5+6S+1.0Zn) at transplanting and 60 kg/ha urea by broadcasting, 45 days later. Weeding was performed twice manually, supplementary irrigation applied when soil cracks appeared, and routine roguing ensured true-to-type germplasm.

2.4. Data Collection

Data were collected from five randomly selected plants per germplasm or per plot, as well as from the net-plot area, to capture variation among the 200 rice germplasm. The observations covered sixteen agro-morphological and grain quality traits following internationally standardized protocols. The quantitative traits included Days to 50% Flowering (DTF) from sowing until half of the plants flowered and Days to 85%

Maturity (DTM), until 85% of grains reached physiological maturity, Plant Height (PH) measured in centimeters from soil surface to the tip of the main panicle excluding awns, Flag Leaf Length (FLL) and Flag Leaf Width (FLW) recorded in centimeters at pre-flowering stage, effective tillers or Number of Panicles per Plant (NPP), Panicle Length (PL) (cm), Number of Panicles per Square Meter (NP_SqM), Spikelets per Panicle (SPP), Seed Setting Ratio (SSR) recorded in percentage (%), 1000 - seed weight (g) determined from well-filled grains, and Grain Yield (GY) per hectare (kg) obtained from net plots excluding border rows and standardized at 14% moisture content. Grain quality traits such as brown rice size

was determined by Brown Rice Length (BRL) (mm), Brown Rice Breadth (BRB) (mm), and Brown Rice Shape (BRS) (length-to-width ratio) using a Vernier caliper, with grains classified into standard categories of length and shape. The rice grains were therefore classified by length into extra-long (>7.5 mm), long (6.6 - 7.5 mm), medium (5.51 - 6.6 mm), and short (≤ 5.51 mm), and by shape into slender (>3), medium (2.1- 3), bold (1.1 - 2), and round (<1.1), [15, 19]. Milling Recovery (MR) was evaluated by dehulling and milling 200 g of paddy, with recovery (%) calculated as the ratio of total milled rice weight to paddy weight as depicted in equation (1).

Equation (1)

$$\text{Milling Recovery \%} = \text{Total Milled Weight of Rice Sample} \times 100 \quad (1)$$

Weight of Paddy Sample

The degree of milling is calculated using the formula displayed in equation (2)

Equation (2)

$$\text{Degree of Milling \%} = \text{Total Weight of Milled Rice Sample} \times 100 \quad (2)$$

Weight of Brown Rice Sample

All measurements followed internationally recognized protocols, ensuring reproducibility and comparability across germplasm [3, 12, 14, 19, 24, 37, 42].

2.5. Data Analysis

Simple statistical parameters such as mean and variance were determined for all the quantitative traits using GenStat statistical software package, 19th Edition. The data was then statistically analyzed according to the technique of analysis of variance (ANOVA) for the alpha lattice design developed by [31] and later adopted by [1] and [2]. The arrangement of genotypes in the ALD into groups gave the possibility for the data analysis as a randomized complete block experiment, and the following ALD linear model was adopted, equation (3)

Equation (3)

$$Y_{ijk} = \mu + t_i + r_j + b_{jk} + e_{ijk} \quad (3)$$

where; Y_{ijk} denotes the value of the observed trait for i -th treatment received in the k -th block within j -th replicate (superblock), t_i is the fixed effect of the i -th treatment ($i = 1, 2, \dots, t$); r_j is the effect of the j -th replicate (superblock) ($j = 1, 2, \dots, r$); b_{jk} is the effect of the k -th incomplete block within the j -th replicate ($k = 1, 2, \dots, s$) and e_{ijk} is an experimental error associated with the observation of the i -th treatment in the k -th incomplete block within the j -th complete replicate.

3. Results

3.1. Quantitative Traits

Rice germplasm were evaluated for agronomical traits

namely number of days to 50% flowering, number of days to reach physiological maturity, flag leaf length, flag leaf width, plant height, number of panicles per plant, number of panicles per square meter, number of spikelets per panicle, seed setting rate and grain yield from.

3.1.1. Number of Days to Flowering at 50% and Days to Maturity

There was not statistically significant variation among the studied rice germplasm as evidenced by F-probability (0.241) at the 5% critical level for the number of days to 50% flowering. A total of 200 rice genotypes (G1–G200) evaluated for had this trait ranging from 100 days (G70, G109, G197) to 133 days (G73), with a mean of 112 days. The early flowering genotypes (≤ 105 days) were G70, G109, G197, G78, G102, G168, G26, G3, G25, G100, G121, G140, G146, G117, G77, G147, G154, G167. On the other hand, the medium and late flowering genotypes (≥ 120 days) were G5, G24, G37, G60, G73, G139, G189), (Appendix).

Among the 200 rice genotypes evaluated for number of days to reach physiological maturity (DTM), the observed DTM ranged from 119 days (G102, G154) to 158 days (G2), with a population mean of 134 days (Appendix). There were no significant differences (F-probability of 0.269) among the studied genotypes. Medium maturing genotypes (111 – 130 days) comprised G102, G154, G129, G167, G109, G112, G194, G3, G36, G51, G70, and G144, and the late maturing genotypes (> 130 days) were G5, G24, G37, G17, G189, G195, G196.

3.1.2. Seed Setting Rate (%)

The seed setting rate (SSR) among the 200 rice germplasm ranged from 74 - 98% (mean 85%), reflecting generally high reproductive success. Low SSR was observed in genotypes

such as G76, G124, and G156 ($\leq 77\%$), while high SSR was recorded in G24, G43, G103, and G101 ($\geq 95\%$), identifying them as promising candidates for breeding programs targeting reproductive efficiency (Appendix).

3.1.3. Plant Height (cm)

Plant height among the studied 200 rice germplasm ranged from 73.9 cm to 134.5 cm, with a grand mean of 97.0 cm (Appendix). The least significant difference (LSD) was 14.3 cm and a highly significant difference ($p < 0.001$) was exhibited among the germplasm and greater heights were attained in germplasm such as G10 (134 cm) and G1 (129 cm).

3.1.4. Panicle Length (cm)

There were significant differences ($p < 0.001$) for panicle length among the studied 200 rice germplasm. The panicle length (PL) among the germplasm ranged from 9.0 cm to 28.8 cm, with a grand mean of 14.0 cm. Notably, entries G66 (28.8 cm), G2 (28.4 cm), and G47 (28.2 cm) exhibited the longest panicles, indicating potential for yield improvement (Appendix).

3.1.5. Flag Leaf Length (mm)

There was significant variation for flag leaf length (FLL) (cm) among the studied 200 rice germplasm as evidenced by the probability value ($F_p < 0.026$), Appendix. The minimum flag leaf length was obtained in G45 (20.5 cm) and the maximum was revealed in G181 (49.4 cm). Germplasm such as G16 (38.5 cm), G49 (37.7 cm), and G172 (36.9 cm), exhibited longer flag leaves, vital for prioritization in future selection processes to optimize canopy architecture.

3.1.6. Flag Leaf Width (mm)

Flag leaf width varied significantly among the 200 rice germplasm ($F_{pr} = 0.019$), ranging from 0.8 - 1.6 cm with a mean of 1.15 cm (Appendix). The germplasm such as G1, G96, and G188 exhibited the widest leaves (≥ 1.5 cm), positioning them as promising candidates for breeding programs aimed at enhancing photosynthetic capacity and yield potential.

3.1.7. Number of Panicles Per Plant (NPP)

The number of panicles per plant, reflecting tillering ability and productive tillers, varied significantly among the 200 rice germplasm ($F_{pr} < 0.001$). The values ranged from 9 to 23, with a mean of 14, indicating moderate variability, and distribution analysis revealed 61 germplasm below the mean, 82 near the mean (14 - 17), and 57 high-performing germplasm (≥ 18). The germplasm such as G40 exhibited the highest NPP (29), while G187 and G192 had the lowest (7). Genotypes such as G40, G199, G152, G140, and G151, with statistically distinct high number of panicles per plant (NPP), represent valuable candidates for yield improvement (Appendix).

3.1.8. Number of Panicles Per Square Meter

A total of 200 genotypes (G1–G200) were evaluated for the number of panicles per square meter (NP_SqM). The values ranged from 153 (G89) to 284 (G120), with a mean of 203. The Least Significant Difference (LSD) at the given probability level was 68.81, indicating the minimum difference required between genotypes to be considered statistically significant. The standard error (SE) was 34.9, and the coefficient of variation (CV%) was 21.1, suggesting moderate variability across genotypes. The F-probability (F_{pr}) of 0.603 implies that the differences among genotypes were not statistically significant at conventional thresholds (Appendix).

3.1.9. Number of Spikelets Per Panicle

The number of spikelets per panicle (SPP) varied widely among the 200 genotypes, from 74 (G162) to 347 (G33), and the mean was 148. The least significant difference (LSD) at the given probability level ($F_{pr} = 0.096$) was 103.3, suggesting that only genotypes differing by more than this value can be regarded statistically distinct. Germplasm such as G33 (347), G85 (269), G140 (257), G164 (250), and G198 (239) exhibited exceptionally high number of spikelets per panicle, whereas germplasm such as G162 (74), G142 (81), G18 (86), and G173 (88) revealed markedly low number of spikelets per panicle (Appendix).

3.1.10. Grain Yield (kg/ha)

The grain yield of 200 rice germplasm varied substantially, ranging from 1669 kg/ha (G101) to 8121 kg/ha (G17), (Appendix). The mean grain yield was approximately 5432 kg/ha, with a standard deviation of 1374 kg/ha, reflecting high variability among the genotypes. The top-performing entries included: G17 (8121 kg/ha), G18 (7396 kg/ha), G125 (7374 kg/ha), G130 (7783 kg/ha), G127 (7861 kg/ha). Conversely, the lowest-yielding entries were G101 (1669 kg/ha), G122 (1789 kg/ha), G40 (1832 kg/ha), G187 (1815 kg/ha), G39 (1946 kg/ha).

3.2. Grain Quality Traits

3.2.1. Brown Rice Length (BRL) (mm)

The brown rice grain length (BRL) showed significant variation among the evaluated 200 rice germplasm with the range 5.9 mm (G139) to 9.4 mm (G84), and a mean value of 8.1 mm. The analysis of variance revealed a highly significant difference ($F_{pr} = 0.005$), indicating substantial genetic diversity for this trait (Appendix).

3.2.2. Brown Rice Breadth (Width) (mm)

The brown rice breadth (BRB) among the 200-germplasm exhibited moderate variability, with values ranging from 2.1 mm to 2.8 mm, (Appendix). The F-probability (F_{pr}) was 0.056, indicating lack of statistically significant variation in

BRB among the genotypes. The overall mean BRB was 2.5 mm and widest grains (2.8 mm) were observed in entries G45 and G67 while the narrowest grains (2.1 mm) were recorded in G182. A majority of germplasm clustered around the mean, suggesting a relatively uniform distribution with a few outliers.

3.2.3. Brown Rice Shape (BRS)

The evaluation of 200 rice germplasm revealed a range of Brown Rice Shape (BRS) as displayed in Appendix, with values from 2.4 to 4.0 and an overall mean of 3.2, indicating moderate variation for this trait across the population. The F-probability (Fpr.) value of 0.079 suggests that the observed differences in BRS among the germplasm are statistically insignificant.

3.2.4. 1000 Grain Weight

The evaluation of 1000-grain weight across 200 rice germplasm revealed substantial variation with weight ranging from 22.4 - 35.3 g and a mean of 28.0 g, although differences were statistically non-significant (Fpr = 0.574) as exhibited in

Appendix. There was not any germplasm which fell into very low (<15 g) or low (15–20 g) categories. Twenty-six rice germplasm had medium weights (21–25 g), 122 were high (26–30 g), and 52 germplasm were very high (>30 g). There were a number of germplasm such as G25, G160, G12, and G24, that exceeded 34 g threshold, highlighting a broad genetic base and identifying promising candidates for yield improvement through breeding.

3.2.5. Milling Recovery

The milling recovery among 200 rice germplasm ranged from 57 - 75% (mean 65.7%), indicating moderate variability, however, no statically significant differences were recorded (Fpr = 0.427). Superior milling quality was observed in G95 (85%) and G173 (75%), while low recovery in G16, G126, G127, G151, and G152 (57%) likely reflects poor grain integrity or higher breakage rates (Appendix). These results highlight genotypes with potential for grain quality improvement and those requiring further evaluation for milling efficiency.

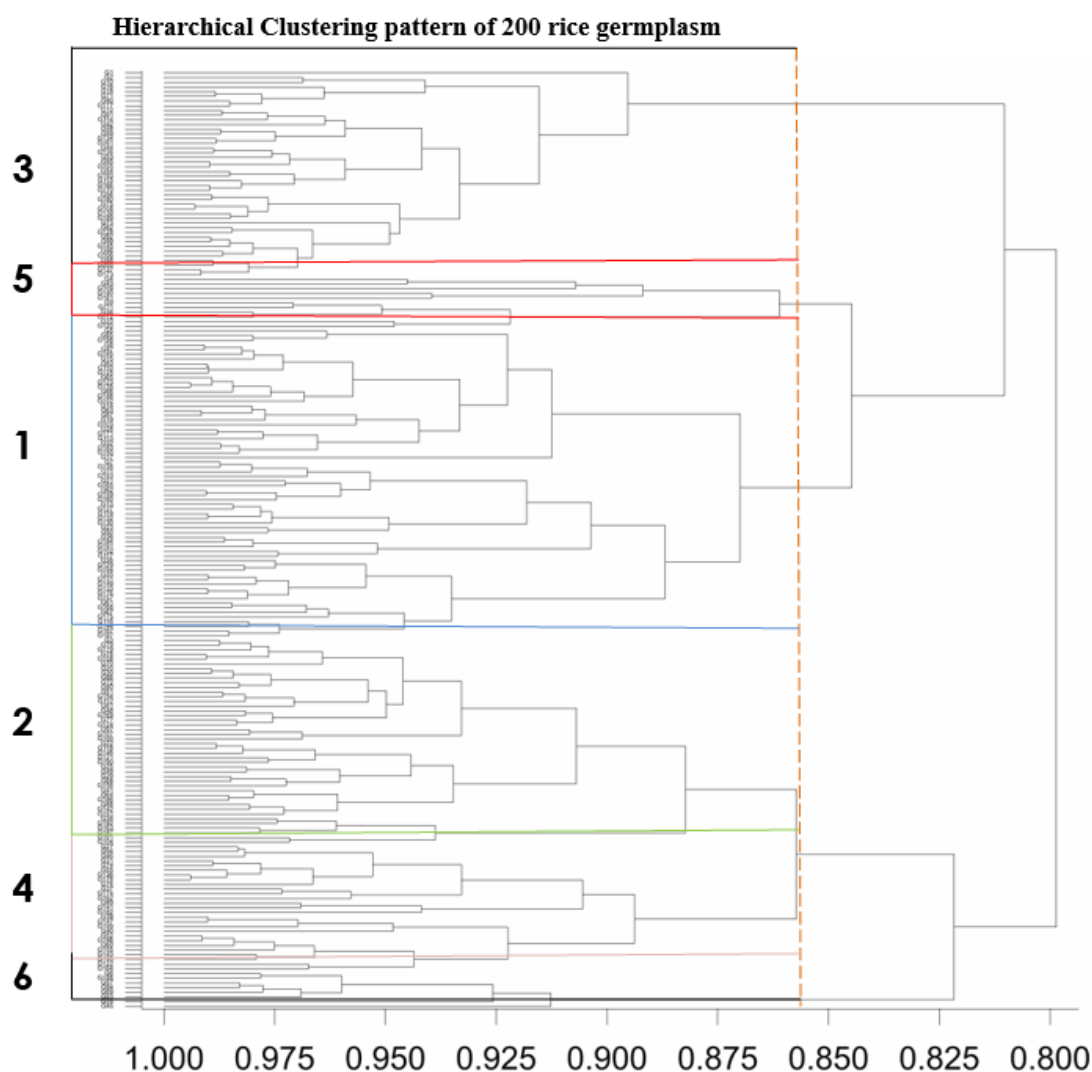


Figure 1. Agglomerative Hierarchical Clustering pattern of 200 rice germplasm.

4. Agglomerative Hierarchical Clustering

Agglomerative Hierarchical Clustering based on 16 quantitative traits stratified the 200 rice genotypes into six distinct groups (Figure 1). Cluster I (66 entries) showed moderate values across traits, representing a genetically diverse but balanced pool. Cluster II (45 entries) was characterized by higher panicle numbers and grain yield, making it suitable for yield-focused breeding. Cluster III (44 entries) comprised early-flowering genotypes with compact grains, valuable for short-duration systems. Cluster IV (26 entries) included taller plants with longer panicles, typical of traditional or landrace types. Clusters V (11 entries) and VI (8 entries) contained germplasm with rare or extreme traits, such as distinctive grain shapes or unusually high yield, representing elite lines with specialized breeding potential.

4.1. Correlations

The Pearson correlation (r) analysis revealed several statistically significant and non-significant relationships among the evaluated traits of the 200 rice germplasm (Table 1). Days to 50% flowering (DTF_50%) showed a strong positive correlation with days to maturity (DTM) ($r = 0.719$, $p < 0.01$), indicating synchronized phenological development across the

genotypes. Brown rice length (BRL) was significantly correlated with brown rice breadth (BRB) ($r = 0.389$, $p < 0.05$), suggesting that grain size components are structurally linked. In addition, panicle length (PL) displayed a significant positive association with number of panicles per plant (NPP) ($r = 0.417$, $p < 0.05$), implying that longer panicles may contribute to increased panicle production.

On the other hand, grain yield (GY) did not exhibit statistically significant correlations with any measured trait, however, moderate positive correlations were observed with plant height (PH), panicle length (PL), and brown rice breadth (BRB). One thousand grain weight (1000-gwt) showed moderate but non-significant correlations with brown rice length (BRL) and brown rice shape (BRB), indicating potential but inconclusive relationships with grain morphology. There was significant negative correlation (-0.392^*) between the brown rice shape (BRS) and number of panicles per plant (NPP), suggesting a trade-off where the plants put more energy in producing panicles rather than the grain shape. Weak negative correlations were revealed among traits such as flag leaf width (FLW), number of panicles per square meter (NP-SqM), and seed setting rate (SSR), however, they were not statistically significant. Generally, these findings highlight key interdependencies among phenological and structural traits, providing potential targets for indirect selection in rice improvement programs.

Table 1. Correlation of 16 selected traits of the studied 200 rice germplasm.

	1000_gwt	DTF_50%	DTM	FLL	FLW	BRL	BRB	BRS	GY	MR	NPP	NP_SqM	PH	PL	SPP	SSR
%1000_gwt	1	0.032	0.103	-0.032	-0.033	0.324	0.266	0.012	0.022	0.147	0.089	-0.029	0.072	0.079	0.121	0.162
DTF_50%	0.032	1	0.719**	-0.038	0.096	-0.043	-0.086	0.005	0.045	-0.101	-0.024	-0.128	0.073	0.021	-0.021	-0.056
DTM	0.103	0.719**	1	0.099	0.089	-0.010	-0.064	0.015	-0.023	-0.026	-0.058	-0.125	0.047	0.046	-0.091	-0.010
FLL	-0.032	-0.038	0.099	1	0.063	-0.019	-0.036	0.052	0.061	0.091	0.115	0.114	0.139	0.307	0.045	0.033
FLW	-0.033	0.096	0.089	0.063	1	0.000	0.073	0.167	-0.094	-0.094	-0.082	0.085	0.159	-0.000	-0.082	-0.075
BRL	0.324	-0.043	-0.010	-0.019	0.000	1	0.389*	-0.088	0.045	-0.055	0.007	0.036	-0.030	-0.044	-0.060	0.092
BRB	0.266	-0.086	-0.064	-0.036	0.073	0.389*	1	0.042	0.117	-0.033	-0.008	0.103	-0.064	-0.086	0.152	0.173
BRS	0.012	0.005	0.015	0.052	0.167	-0.088	0.042	1	0.038	0.051	-0.392*	0.053	0.036	-0.027	0.034	0.046
GY	0.022	0.045	-0.023	0.061	-0.094	0.045	0.117	0.038	1	-0.016	-0.120	0.105	0.152	0.132	0.034	0.040
MR	0.147	-0.101	-0.026	0.091	-0.094	-0.055	-0.033	0.051	-0.016	1	0.157	-0.064	0.002	0.038	0.082	0.099
NPP	0.089	-0.024	-0.058	0.115	-0.082	0.007	-0.008	-0.392*	-0.120	0.157	1	-0.166	0.039	0.417*	0.038	0.058
NP_SqM	-0.029	-0.128	-0.125	0.114	0.085	0.036	0.103	0.053	0.105	-0.064	-0.166	1	0.001	-0.116	0.051	-0.017
PH	0.072	0.073	0.047	0.139	0.159	-0.030	-0.064	0.036	0.152	0.002	0.039	0.001	1	0.238	0.071	-0.092

	1000_gwt	DTF_50%	DTM	FLL	FLW	BRL	BRB	BRS	GY	MR	NPP	NP_SqM	PH	PL	SPP	SSR
PL	0.079	0.021	0.046	0.307	-0.000	-0.044	-0.086	-0.027	0.132	0.038	0.417*	-0.116	0.238	1	-0.009	-0.063
SPP	0.121	-0.021	-0.091	0.045	-0.082	-0.060	0.152	0.034	0.034	0.082	0.038	0.051	0.071	-0.009	1	0.143
SSR	0.162	-0.056	-0.010	0.033	-0.075	0.092	0.173	0.046	0.040	0.099	0.058	-0.017	-0.092	-0.063	0.143	1

Note: *, Significant at 5% level; where correlation ($r \geq 0.361$), **, significant at 1% level; where ($r \geq 0.463$)

4.2. Principal Components Analysis

Principal Component Analysis was carried on 16 rice traits across the 200 rice germplasm; however, seven components were extracted, with the first principal component (PC1) accounting for 99.89% of the total variance (Table 2; Figure 2). The remaining components contributed negligibly ($< 0.1\%$).

Grain yield (GY) is the dominant trait in PC1, exhibiting a perfect loading of 1.0000 while spikelets per panicle (SPP) strongly influenced PC2 with a loading of 0.9985.

The number of panicles per square meter (NP_SqM), plant height (PH), seed setting ratio (SSR), flag leaf length (FLL), and milling recovery (MR) contributed to PC3, PC4, PC6, and PC7, respectively, with loadings of -0.9975, 0.7929, 0.9606, and explicit influence.

Table 2. Eigen Value (Latent roots), differences and latent vectors of the first 7 principal components in 16 morphological quantitative & grain quality traits.

Traits	Vector 1	Vector 2	Vector 3	Vector 4	Vector 5	Vector 6	Vector 7
%1000_gwt	0.0001	0.0079	0.0047	0.0336	0.0178	0.1381	0.0589
BRB	0.0001	0.0003	-0.0004	-0.0016	0.0005	0.0032	-0.0017
BRL	-0.0001	-0.0003	0.0013	-0.0082	0.0009	0.0044	-0.0045
BRS	-0.0002	-0.0006	0.0011	-0.0008	0.0003	-0.0029	-0.0002
DTF 50%	0.0002	-0.0035	0.0295	0.3396	0.5116	-0.0729	-0.2092
DTM	-0.0002	-0.0174	0.0309	0.4859	0.6173	0.0862	0.1796
FLL	0.0001	0.0041	-0.0151	0.0821	-0.0162	0.1306	0.6324
FLW	-0.0001	-0.0003	-0.0006	0.0047	-0.0001	-0.0011	-0.0017
NPP	-0.0003	0.0030	0.0208	0.0021	-0.0566	0.0983	0.3491
NPSM	0.0017	0.0461	-0.9975	0.0290	0.0297	0.0083	0.0017
PH	0.0008	0.0125	0.0071	0.7929	-0.5894	0.0888	-0.1114
PL	0.0001	-0.0007	0.0087	0.0451	-0.0291	0.0122	0.1603
MR	-0.0001	0.0072	0.0101	-0.0219	-0.0396	0.1713	0.5519
SPP	0.0009	0.9985	0.0464	-0.0001	0.0181	-0.0187	0.0004
SSR	0.0001	0.0171	0.0064	-0.0994	0.0534	0.9606	-0.2439
GY	1.0000	-0.0010	0.0017	-0.0006	0.0004	-0.0002	0.0002
Eigen Value	449871183	319978	118290	11996	9325	4525	2894
Variation Accounted for (%)	99.89	0.07	0.03	0.01	0	0	0
Cumulative (%)	99.89	99.96	99.99	100	100	100	100

4.3. Biplot

The biplot revealed that grain yield (GY) dominated the first principal component, explaining nearly all variation (99.89%) whereas the second principal component displayed 0.07% with all remaining components contributing negligibly. The biplot based on the first two principal components (PC1 and PC2), therefore together explain 99.97% of the total variation, revealing distinct trait contributions. Grain yield (GY)

showed a dominant positive loading on PC1 (1.0000), establishing it as the principal source of overall variation, while spikelets per panicle (SPP) loads strongly on PC2 (0.9985), representing a secondary, orthogonal axis of variation independent of grain yield. Most other traits exhibited minimal influence on these components, clustering near the origin, which suggests limited contribution to the major patterns captured by PC1 and PC2 (Table 2, Figure 2).

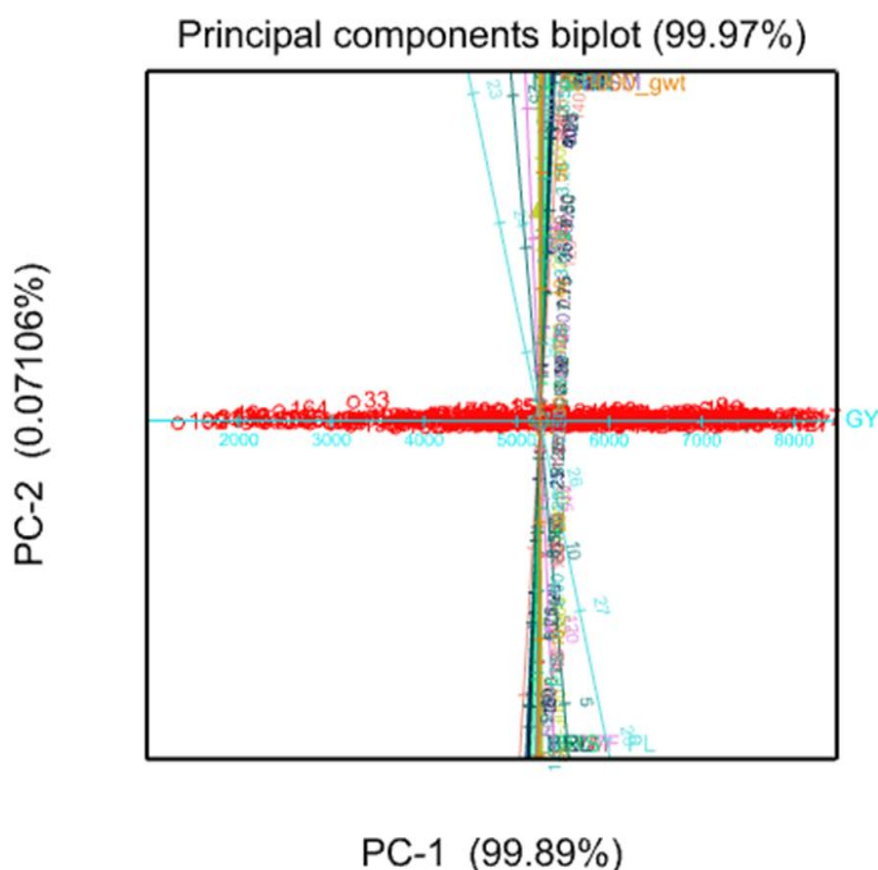


Figure 2. Biplot of the first 2 principal components (PC).

5. Discussion

5.1. Quantitative Traits

The variation in days to 50% flowering among 200 rice genotypes (100 - 133 days) indicates substantial genetic diversity, offering opportunities for selection based on flowering behaviour (Appendix). The early-flowering genotypes are advantageous in short-season or drought-prone environments, while late-flowering types are suitable for longer growing periods and biomass accumulation. These findings corroborate reports of fellow researchers where variation flowering had been reported among rice germplasm [25]. The number of days to maturity (DTM) ranged from 119 to 147, with a mean of 134,

reflecting a moderately late-maturing population. The early-maturing genotypes are valuable for drought escape and short-season adaptation. Similar variability under stress conditions has been reported by previous researchers, reinforcing the present findings [18, 40].

Furthermore, seed setting rate (SSR) averaged 85% (74 - 98%), indicating robust reproductive success among the germplasm. The germplasm such as G24, G43, G103, and G101 revealed superior SSR ($\geq 95\%$), while germplasm exhibited a declined performance ($\leq 77\%$). Despite observable variation ($CV = 9.8\%$), differences were statistically non-significant ($F_{pr} = 0.134$), suggesting uniform reproductive efficiency, and these findings agreed strongly with previous reported on rice under abiotic stress reported by [42].

There were variations for plant height (PH) among the studied germplasm, especially among dwarf types such as G162

(74 cm) and taller germplasm aligning, with previous reports [32]. This diversity supports breeding for lodging resistance, biomass accumulation, weed suppression, and genetic regulation through transcription factors [17]. The panicle length (PL) exhibited significant variation, with 56% of germplasm bearing long panicles (25-30 cm) and 44% short to medium (<25 cm). There was no germplasm that exceeded 30 cm and superior panicle lengths were revealed in G66, G2, and G47 highlights potential for yield improvement, and that is in agreement with earlier studies [35]. The flag leaf traits showed marked diversity, and longer leaves revealed in G181, G172, G49) would enhance canopy architecture and photosynthetic efficiency, while shorter leaves as capture in G45, G101, may confer drought resilience. These findings align with reports in rice [30, 21] and wheat QTL studies [41].

Significant variation among the 200 rice genotypes for panicle number per plant indicate substantial genetic diversity (Appendix). These findings align with [2, 20, 33], who reported rice genomic regions associated with panicle number and its strong correlation with grain yield. Furthermore, [10, 11] also identified high-performing lines with superior panicle numbers under various screening conditions, corroborating strongly with the current results. Collectively, this diversity provides breeders with a broad germplasm base for improving panicle number and enhancing yield potential. Although number of panicles per square meter (NP_SqM) differences were statistically non-significant, the high-performing genotypes such as G120, G20, G34 exceeded thresholds, suggesting breeding potential. Similar correlations with yield in rice were reported by [41]. The wide range in number of spikelets per panicle (SPP) reflects the genetic diversity among the tested germplasm. High-performing genotypes such as G33 and G85 may possess favorable alleles for panicle development and could be considered for breeding programs aimed at yield improvement. However, the relatively high LSD (103.3) and moderate Fpr (0.096) suggest that only extreme differences are statistically reliable under the current experimental conditions. Genetic diversity for number of spikelets per plant had also been reported by earlier researchers [9] and corroborated with the present findings.

The evaluation of 200 rice germplasm for grain yield revealed substantial variability in this trait, underscoring the presence of rich genetic diversity within the population (Appendix). The genotypes such as G17, G127, and G130 consistently recorded superior grain yields, indicating their potential as donor parents in varietal improvement. Results of the current study on high yield and variability are in line with those reported by previous researchers [35, 38, 39].

5.2. Grain Quality Traits

There were significant variations for brown rice length (BRL) among 200 germplasm (5.9 - 9.4 mm; with mean of 8.1 mm, (Fpr = 0.005), confirming substantial genetic diversity and that is in consistent with reports by [27]. Brown rice

breadth (BRB) showed moderate variability (2.1 - 2.8 mm and a mean of 2.5 mm), although differences were statistically non-significant (Fpr = 0.056). The brown rice shape (BRS) ranged from 2.4 to 4.0, however, variation was statistically insignificant (Fpr = 0.079), and that is in agreement with earlier reports by [27] on grain quality diversity. The milling recovery (MR) exhibited moderate variability (CV = 9.1%), with genotypes such as G95 and G173 revealing superior performance, mainly due to favourable grain structure. However, the high probability value (Fpr values) suggest only extreme differences were statistically reliable, and that low-performing germplasm may be prone to breakage or chalkiness, reducing market value.

The thousand grain weight (TGW) displayed broad variation (22.4 - 35.3 g) and a mean of 28.0 g, although statistical differences were non-significant (Fpr = 0.574). Genotypes were classified into medium (21–25 g, 26 entries), high (26–30 g, for the 122 germplasm), and very high (>30 g, for the 52 germplasm). Several germplasm such as G25, G160, G12, G24) exceeded 34 g, representing promising candidates for yield improvement through hybridization in Malawi. These findings are consistent with those by fellow researchers who reported grain weight variability as a yield determinant and 1000 grain weight germplasm for increased productivity [27, 35, 42].

5.3. Agglomerative Hierarchical Clustering

The Agglomerative Hierarchical Clustering of 16 morphological and grain quality traits (GenStat 19th Edition, Euclidean distance, Complete Linkage) categorized 200 rice germplasm into six distinct clusters. Cluster I (66 germplasm) composed of the largest group, while Cluster II (45 accessions) was distinguished by higher panicle numbers and grain yield, indicating its potential for yield-targeted breeding. Moreover, Cluster III (44 germplasm) comprised early-flowering, compact-grain genotypes suitable for short-duration cropping systems. Cluster IV (26 germplasm) included taller plants with longer panicles, reflecting landrace morphotypes. Clusters V (11 germplasm) and VI (8 germplasm) contained rare or extreme trait expressions, including exceptionally high yield. These diversity patterns align with earlier reports [35, 40], which similarly identified yield-related traits as important for cluster differentiation in rice germplasm.

5.4. Correlation

The correlation analysis revealed strong interrelationships among agronomic traits (Table 1), such that days to 50% flowering (DTF) was highly correlated with days to maturity ($r = 0.719$, $p < 0.01$), confirming synchronized phenology. Furthermore, brown rice length (BRL) correlated positively with brown rice breadth (BRB) ($r = 0.389$, $p < 0.05$), indicating coordinated grain shape traits, and that is in tandem with earlier reports by [5, 16]. The panicle length (PL) correlated with panicle number per plant ($r = 0.417$, $p < 0.05$), suggesting

longer panicles enhance rice productivity, as earlier reported by [8]. The grain yield (GY) exhibited no significant correlations, despite moderate associations with plant height, panicle length, and grain breadth; suggesting complex trait interactions, echoing the multifactorial nature of yield determination reported by [16].

5.5. Principal Component Analysis

Principal Component Analysis (PCA) of 16 agronomic traits across 200 rice germplasm displayed seven principal components, with PC1 alone accounting for 99.89% of the total variance, suggesting strong multicollinearity and effective representation of the dataset by PC1 (Table 2, Figure 2). Grain yield (GY) was the most influential trait (loading = 1.0000), underscoring its fundamental role in explaining variation, while SPP, NPSM, PH, SSR, FLL, and MR dominated subsequent small components. These findings corroborate earlier reports [23, 24, 41] that grain yield and related morphological traits are primary drivers of variation in rice germplasm.

6. Conclusions and Recommendations

In order to meet the increasing need of rice improvement, variability information among the local landraces and elite germplasm is very fundamental for identification and documentation of superior germplasm to be used in conservation and/or further breeding programmes. This study revealed substantial variability among 200 rice germplasm across 16 agro-morphological and grain quality traits, underscoring their value for conservation and breeding. Physiological maturity ranged from 119 days (G102, G154) to 158 days (G2), while milling recovery varied between 57-75%. Furthermore, grain yield showed wide divergence, with the top ten germplasm (G17, G127, G14, G130, G175, G171, G132, G119, G16, G19) producing 7396 - 8121 kg/ha, highlighting their potential as elite candidates for improvement. The Agglomerative Hierarchical Clustering grouped the germplasm into six clusters, reflecting broad genetic diversity suitable for targeted breeding. It is therefore recommended that G17, G127 and G132 should be used in varietal improvement owing to their high yielding potential for food security. Breeders should cross semi-dwarf donors (G23, G24) with elite high-yielding genotypes (G17, G18, G125, G127, G130) to exploit F1 heterosis and develop progeny with optimal stature (80 - 90 cm), lodging resistance, and superior yield (>7300 kg/ha). Additionally, quality traits such as extra-long grains observed in G84 (9.4 mm) should be introgressed to meet consumer preferences in Malawi.

Abbreviations

LUANAR Lilongwe University of Agriculture and Natural Resources

DARS	Department of Agricultural Research Services
IRRI	International Rice Research Institute
CSIR	Council for Scientific and Industrial Research
KAFACI	Korea-Africa Food and Agriculture Cooperation Initiative
ACE	Africa Center of Excellence
ALD	Alpha Lattice Design
BRL	Brown Rice Length
BRB	Brown Rice Breadth
BRS	Brown Rice Shape
GY	Grain Yield Per Hectare
RL	Range Lower Value
RH	Range Higher Value
DTF 50%	Days to 50% Flowering
DTM	Days to Maturity
FLL	Flag Leaf Length
FLW	Flag Leaf Width
NPP	Number of Panicles Per Plant
NP_SqM	Number of Panicles Per Square Meter
PH	Plant Height
PL	Panicle Length
MR	Milling Recovery
SPP	Spikelets Per Panicle
SSR	Seed Setting Ratio (%)
G	Germplasm
CV (%)	Coefficient of Variation
LSD	Least Significant Difference
AHC	Agglomerative Hierarchical Clustering
r	Correlation
PCA	Principal Component Analysis
TGW	Thousand Grain Weight

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from the corresponding author, (E. J.), upon reasonable request.

Data Availability Statement

The data that support the findings of this study are available

Conflicts of Interest

The authors declare that there is no conflict of interest.

Appendix

Table 3. Mean Values of 16 Quantitative and Grain Quality Traits for the Studied 200 Rice Germplasm

GERMP LASM ID	SOURCE	GERMPASM NAME	DTF 50%	DT M	PH (cm)	NPP	PL (cm)	FLL (cm)	FLW (cm)	NP_ SqM	SSR (%)	SPP	GY (kg/ha)	1000 gwt	BRL (cm)	BRB (cm)	BRS	MR (%)
G1	MALAW I	Kilombero	108	141	129	11	26.8	26.2	1.6	171	80	152	4375	30.7	8.6	2.5	3.5	67
G2	MA- LAWI	Faya 14 M	123	158	125	14	28.4	36.2	1.4	197	84	141	4638	24.7	7	2.4	3.1	63
G3	KAFACI	KF190232	101	123	95	13	25.9	26.8	1.2	186	81	130	5787	27.5	8.2	2.5	3.3	64
G4	MA- LAWI	Makafaci	108	125	100	17	25.2	27.1	0.8	179	90	159	7043	31	8.1	2.7	3	69
G5	MA- LAWI	Wachangu	111	118	89	12	22.5	24.0	1.1	178	86	205	6739	27.7	8.1	2.6	3.3	67
G6	MA- LAWI	Senga	113	140	105	13	24.2	29.0	1.3	186	84	140	4633	34.1	9	2.6	3.5	66
G7	MA- LAWI	Mtupatupa	110	131	101	20	27.6	25.5	1.2	177	86	217	5224	33	8.4	2.7	3.1	69
G8	MA- LAWI	Mpheta	112	133	102	16	26.4	30.0	1.0	180	82	216	6661	25	8	2.4	3.3	61
G9	Africa Rice	Hybrid 001	107	136	97	12	27.4	30.2	1.3	250	87	287	7044	29.9	7.4	2.6	2.9	69
G10	KAFACI	KF190029	116	143	134	11	27.7	34.2	1.2	216	79	152	7066	29	7	2.4	2.9	70
G11	KAFACI	KF190023	108	134	99	12	26.0	25.3	1.1	190	83	206	6519	34.7	8.4	2.7	3.1	65
G12	KAFACI	KF190202	110	140	107	14	23.8	31.2	1.3	211	85	161	6955	31.4	7.3	2.5	2.9	66
G13	KAFACI	KF190242	116	139	98	13	24.4	24.4	1.0	167	82	172	7393	31.1	8.5	2.4	3.5	66
G14	Africa Rice	Hybrid 004	116	138	91	15	24.4	29.5	1.0	236	88	182	7813	29.5	8.1	2.6	3.1	70
G15	Africa Rice	Hybrid 002	112	133	104	16	26.0	25.7	1.0	219	90	202	7065	24.4	8	2.4	3.3	70
G16	MA- LAWI	KF190028	113	134	98	10	27.4	38.5	1.1	227	84	140	7512	27.1	8.3	2.4	3.4	57
G17	Africa Rice	Hybrid 003	114	146	100	16	25.2	26.2	1.0	188	93	167	8121	25.6	8.3	2.7	3	72
G18	KAFACI	15046	111	132	102	12	26.3	28.1	1.2	229	79	86	5556	27.4	7.6	2.3	3.3	62
G19	IRRI	IR18A1908	112	134	93	15	26.1	22.6	1.2	263	85	140	7396	26.8	8.1	2.5	3.3	69

GERMP LASM ID	SOURCE	GERMPASM NAME	DTF 50%	DT M	PH (cm)	NPP	PL (cm)	FLL (cm)	FLW (cm)	NP_ SqM	SSR (%)	SPP	GY (kg/ha)	1000 gwt	BRL (cm)	BRB (cm)	BRS	MR (%)
G20	MA-LAWI	NERICA -19 L	106	128	95	10	24.1	29.8	1.3	271	83	160	5481	28.2	8.2	2.6	3.1	62
G21	MA-LAWI	Kachambo	112	132	97	19	27.2	28.8	1.2	166	82	144	3017	31.1	7.8	2.7	2.9	64
G22	KAFACI	SR 35285 – HB3469 – 4	113	133	93	11	23.6	25.1	1.1	200	85	199	6442	25.3	8	2.4	3.3	66
G23	MA-LAWI	Sengamfupi	107	134	99	14	25.2	26.5	0.9	218	83	119	5400	34.7	9.1	2.6	3.6	65
G24	KAFACI	SR35300 – HB3467 – 5	120	145	89	12	26.2	27.2	1.2	222	98	150	6223	35.3	8.2	2.7	3	63
G25	KAFACI	SR35300 – HB3467 – 10	104	131	92	11	24.2	29.6	0.9	183	85	153	2527	26.3	8.5	2.7	3.6	70
G26	KAFACI	SR34071(#5- 16)-5-1-2/NE- RICA 8	101	127	102	16	27.7	28.2	1.1	178	87	164	7000	33	8.9	2.4	3.3	65
G27	MA-LAWI	Tambala	114	136	91	14	25.3	31.5	1.1	220	88	113	4711	25.7	8.2	2.6	3.5	69
G28	KAFACI	15022	118	134	94	16	24.1	25.8	1.0	197	85	159	7206	27.6	8.4	2.3	3.3	67
G29	KAFACI	15023	117	138	94	10	24.4	28.4	1.1	161	84	92	5385	27.1	8.7	2.7	3.9	66
G30	KAFACI	15024	111	128	95	11	24.0	25.6	1.3	262	81	148	5072	28.4	8	2.4	3.3	65
G31	KAFACI	15025	104	134	100	14	26.6	25.5	1.0	190	79	92	5927	29.1	8	2.5	3.2	68
G32	KAFACI	15026	115	135	89	17	24.9	26.7	0.9	205	85	119	5460	25.3	8.1	2.5	3.2	66
G33	KAFACI	15053	107	128	98	14	26.5	28.2	1.0	266	85	347	3236	30.6	8.6	2.6	3.3	64
G34	KAFACI	15020	118	140	106	17	26.2	35.1	1.0	270	90	219	5507	28.6	8.2	2.5	3.4	62
G35	MA-LAWI	Kidney	109	132	89	17	24.9	32.5	1.2	206	86	123	4293	30	8.7	2.5	3.4	68
G36	KAFACI	15002	108	125	88	11	25.4	29.3	0.9	187	85	143	3734	28.1	8.5	2.5	3.4	60
G37	KAFACI	15015	120	147	97	9	27.2	25.9	1.0	182	86	151	3853	27.6	8.3	2.4	3.5	66
G38	MA-LAWI	Nanyondo	111	134	81	9	21.4	26.8	0.9	199	86	137	3663	27	7.1	2.4	3	68
G39	MA-LAWI	Mwenelondo	106	127	103	22	27.8	25.0	1.2	196	88	170	1946	28.2	8.2	2.5	3.3	68
G40	MA-LAWI	Sengamtali	117	131	113	29	25.4	28.6	1.0	179	84	198	1832	31.7	8.3	2.5	3.3	66
G41	MA-LAWI	Mangochi	113	143	95	13	26.1	25.6	1.1	181	83	189	3916	24.1	8.7	2.6	3.3	67
G42	KAFACI	15012	110	134	96	15	25.3	26.8	1.4	233	79	189	3875	28.9	7.5	2.4	3.1	64
G43	KAFACI	Mi- lyang295/SR3 2037-1-139	104	133	99	15	26.0	26.9	1.1	190	97	157	3291	32.5	8.2	2.4	3.4	74
G44	KAFACI	Mi- lyang296/SR3 2037-1-114	118	142	106	12	26.1	30.4	1.1	206	79	165	5642	28.2	8.5	2.5	3.4	64

GERMP LASM ID	SOURCE	GERMPASM NAME	DTF 50%	DT M	PH (cm)	NPP	PL (cm)	FLL (cm)	FLW (cm)	NP_ SqM	SSR (%)	SPP	GY (kg/ha)	1000 gwt	BRL (cm)	BRB (cm)	BRS	MR (%)
G45	KAFACI	Mi- lyang288/SR3 2037-1-147	115	141	90	9	21.3	20.5	1.0	185	85	148	3094	34.6	9.1	2.8	3.3	68
G46	Africa Rice	Nerica8_AC- 23	109	128	96	16	25.0	29.5	1.0	233	84	113	2987	27.2	8.5	2.4	3.5	64
G47	KAFACI	KF190153	114	134	101	17	28.2	30.8	1.1	195	84	175	6545	26.7	8.1	2.4	3.5	63
G48	KAFACI	KF18007	109	129	95	10	23.1	25.7	1.2	214	78	160	4959	30.9	8.2	2.7	3.1	67
G49	KAFACI	Mi- lyang288/SR3 2037-1-147	107	127	94	12	24.8	37.7	1.0	186	82	120	4704	26.4	8.4	2.5	3.3	69
G50	KAFACI	KF190159	115	143	94	16	25.5	27.0	0.9	250	81	148	6467	34	8.6	2.7	3.2	65
G51	KAFACI	SR35266-2- 12-5-1-1	110	125	94	15	24.4	26.2	1.1	223	81	109	4834	30.2	8.5	2.5	3.5	69
G52	KAFACI	SR35266-2- 20-3-1-1	117	144	100	19	26.4	25.3	1.2	184	85	144	3744	30.9	8.2	2.5	3.3	66
G53	KAFACI	SR23364-128- 1758-1-HV-1- 1-1	112	133	116	12	27.8	25.8	1.2	210	81	123	4356	30.1	8.8	2.5	3.5	61
G54	KAFACI	SR34598-HB- 16-HV-1-1	119	135	100	18	26.3	31.0	1.1	197	82	159	4183	30.6	8.2	2.4	3.4	70
G55	KAFACI	SR35276-2-4- 3-1-1	112	137	103	13	27.2	32.1	1.0	207	78	121	6239	31.6	7.6	2.4	3.2	69
G56	KAFACI	SR35276-2-4- 3-3-1	117	144	105	14	27.4	28.1	1.1	191	81	134	7185	27.5	8.2	2.4	3.4	63
G57	KAFACI	SR35276-2-4- 3-3-1	117	143	98	11	24.6	29.2	1.4	202	88	135	7899	33.4	8.8	2.6	3.4	63
G58	KAFACI	SR35266-2-5- 2-1-1	116	142	96	10	23.9	26.1	1.2	213	84	129	4748	27.4	8.2	2.6	3.2	62
G59	KAFACI	SR35266-2- 11-4-1-1	117	137	107	9	23.3	24.1	1.1	216	83	170	5915	27.9	8.1	2.5	3.2	66
G60	KAFACI	SR35266-2- 18-3-1-1	120	143	95	19	27.4	30.8	1.3	179	81	127	2283	28.5	7.9	2.5	3.2	69
G61	KAFACI	SR34590- HB3433-1-3- 1-1	107	127	97	12	27.7	27.1	1.1	187	94	148	6445	28.5	8.9	2.7	3.3	62
G62	KAFACI	SR34609- HB3483-29-1- 1	118	140	88	18	25.9	28.1	1.1	186	83	131	6174	32.7	8.6	2.6	3.3	66
G63	KAFACI	SR34598-HB- 7-HV-1-1	109	135	102	11	25.8	30.6	1.0	227	85	115	6695	28.1	7.1	2.5	2.8	67
G64	KAFACI	SR33705- HB3381-1-1-1	116	142	101	13	25.4	25.5	1.1	186	80	105	4581	24.9	8.5	2.6	3.2	59
G65	KAFACI	SR34590- HB3433-1-3- 1-1	109	136	93	15	26.9	25.7	1.1	206	83	167	5067	27.3	8.1	2.5	3.2	66
G66	KAFACI	SR35266-2-	115	133	91	17	28.8	27.2	1.0	179	85	133	5224	26.6	8	2.5	3.3	67

GERMP LASM ID	SOURCE	GERMPASM NAME	DTF 50%	DT M	PH (cm)	NPP	PL (cm)	FLL (cm)	FLW (cm)	NP_ SqM	SSR (%)	SPP	GY (kg/ha)	1000 gwt	BRL (cm)	BRB (cm)	BRS	MR (%)
		11-4-1-1																
G67	KAFACI	SR35266-2- 11-4-1-1	112	126	94	21	25.9	25.9	1.3	199	83	120	7005	27.5	8.7	2.8	3.2	66
G68	KAFACI	SR35266-2- 11-4-1-1	111	139	91	15	24.4	26.3	1.1	186	84	91	4386	27.4	8.5	2.4	3.5	60
G69	KAFACI	SR35266-2- 12-5-1-1	122	147	96	10	23.3	25.3	1.3	228	88	89	6875	29.7	8.9	2.6	3.5	66
G70	KAFACI	SR35266-2- 11-1-1-1	100	125	103	10	23.5	30.9	1.4	196	80	115	4632	26.4	8	2.6	3.1	64
G71	KAFACI	SR35266-2- 11-1-1-1	113	133	101	11	27.2	26.4	1.1	201	75	118	6485	26.4	7.9	2.3	3.4	66
G72	KAFACI	SR33705- HB3381-1-1-1	111	132	96	9	24.7	26.6	1.4	229	85	201	5201	27.3	8.1	2.5	3.2	61
G73	KAFACI	SR35276-2-4- 3-3-1	133	133	107	13	24.8	24.2	1.3	225	84	153	4941	26.5	8.2	2.5	3.4	65
G74	KAFACI	SR34590- HB3433-1-1- 1-1	113	130	98	16	27.1	30.5	1.0	181	82	101	5999	28.6	8.1	2.5	3.2	71
G75	KAFACI	SR35266-2- 12-2-1-1	118	139	92	12	26.2	28.0	1.2	189	86	148	5885	26.9	7	2.6	2.7	66
G76	KAFACI	SR34598-HB- 16-HV-1-1	109	132	100	17	26.8	21.8	1.0	236	74	91	4254	29.6	7	2.6	2.7	68
G77	KAFACI	SR35266-2- 20-3-1-1	105	132	101	15	24.9	24.2	1.2	244	79	124	5621	30.3	8.7	2.5	3.5	64
G78	KAFACI	SR35266-2- 20-3-1-1	103	127	97	13	25.0	28.6	1.4	189	84	155	5963	27	8.5	2.5	3.3	67
G79	KAFACI	SR35266-2- 20-3-1-1	106	127	101	12	25.5	26.7	1.3	198	83	177	7269	28	8.2	2.6	3.2	62
G80	KAFACI	SR35266-2- 12-1-1-1	115	134	99	11	25.5	27.8	1.3	242	81	195	5760	29.4	8.7	2.6	3.3	67
G81	KAFACI	SR35266-2- 12-1-1-1	106	126	117	12	24.8	23.6	1.2	242	85	113	7291	27.7	7.5	2.4	3.1	70
G82	KAFACI	SR35266-2- 12-1-1-1	115	142	107	12	25.5	33.9	1.4	231	83	97	6469	27	7.9	2.6	3.1	65
G83	KAFACI	SR34598-HB- 6-HV-1-1	113	131	106	14	25.0	26.4	1.1	189	87	158	7293	27	8.1	2.5	3.3	62
G84	KAFACI	SR35266-2-5- 2-1-1	114	142	88	12	25.5	26.1	1.3	233	87	105	7212	32.6	9.4	2.7	3.5	63
G85	KAFACI	SR35266-2-5- 2-1-1	117	137	99	12	23.6	25.9	1.4	176	84	269	4836	25.6	7.9	2.4	3.3	67
G86	KAFACI	SR35266-2- 17-1-1-1	110	126	92	10	26.0	23.6	1.3	258	85	138	6218	29.6	8.3	2.6	3.3	67
G87	KAFACI	SR35266-2- 17-1-1-1	111	135	99	12	24.6	26.2	1.0	216	87	158	5989	26.6	8	2.5	3.2	70
G88	KAFACI	SR35266-2-	112	133	99	13	24.7	33.8	1.3	189	86	132	4857	24.7	7.8	2.5	3.2	65

GERMP LASM ID	SOURCE	GERMPASM NAME	DTF 50%	DT M	PH (cm)	NPP	PL (cm)	FLL (cm)	FLW (cm)	NP_ SqM	SSR (%)	SPP	GY (kg/ha)	1000 gwt	BRL (cm)	BRB (cm)	BRS	MR (%)
		18-3-1-1																
G89	KAFACI	SR35276-2-4-3-1-1	116	141	98	15	25.4	26.5	1.4	153	86	101	4292	25.9	7.1	2.3	3.1	70
G90	KAFACI	SR23364-128-1758-1-HV-1-1-1	113	135	101	12	25.5	26.0	1.2	217	87	153	5035	27.3	6.9	2.4	2.9	61
G91	KAFACI	SR34590-HB3433-1-3-1-1	108	136	98	15	24.7	30.2	1.2	177	86	154	6114	30.6	7.8	2.4	3.3	67
G92	KAFACI	SR35266-2-18-3-1-1	118	140	92	15	24.8	28.6	1.3	201	83	156	5811	28.1	8.3	2.6	3.2	65
G93	KAFACI	SR35266-2-11-4-1-1	115	136	94	9	24.7	28.9	1.4	196	88	157	6510	27.2	8.9	2.7	3.4	63
G94	KAFACI	SR35266-2-11-4-1-1	111	135	99	17	25.7	24.8	1.2	229	84	125	2975	26.9	8.2	2.3	3.6	70
G95	KAFACI	SR35266-2-12-5-1-1	113	141	106	18	26.1	25.3	1.3	174	82	111	3636	28.1	8.8	2.6	3.3	63
G96	KAFACI	SR35266-2-20-3-1-1	116	134	92	14	25.5	29.7	1.5	213	87	151	5310	27.7	7.4	2.6	2.9	62
G97	KAFACI	SR23364-128-1758-1-HV-1-1-1	108	133	100	14	23.6	24.8	1.3	269	82	109	4828	26.2	7.1	2.6	2.7	61
G98	KAFACI	SR34598-HB-16-HV-1-1	112	139	99	15	25.8	29.2	1.4	203	80	90	5509	28.5	8.3	2.5	3.3	60
G99	KAFACI	SR35276-2-4-3-1-1	119	140	99	14	25.8	32.9	1.3	199	80	129	4329	25.6	8.3	2.6	3.2	66
G100	KAFACI	SR35276-2-4-3-3-1	104	131	88	13	26.0	28.8	1.3	254	82	124	5290	23.1	8.1	2.6	3.2	66
G101	KAFACI	SR34590/SR34071(#5-16)-5-1	109	132	83	17	22.1	22.2	1.4	178	95	136	1669	29.4	8.4	2.6	3.3	65
G102	KAFACI	SR34071(#5-16)-5-1-2/super	102	119	86	13	23.0	24.0	0.9	193	83	141	6026	29.3	8.9	2.7	3.4	64
G103	KAFACI	SR34071(#5-16)-5-1-2/super	117	139	80	18	24.9	27.1	1.2	220	97	108	5317	28	8.2	2.5	3.3	66
G104	KAFACI	SR34071(#5-16)-5-1-2/super	107	133	96	13	21.3	22.7	1.3	198	85	184	3967	27.2	8.7	2.5	3.6	65
G105	KAFACI	SR34071(#5-16)-5-1-2/super	118	139	95	15	26.6	27.9	1.4	179	82	121	4246	29.3	8.6	2.6	3.4	59
G106	KAFACI	SR34590/SR34071(#5-16)-5-1	114	135	89	15	25.0	33.4	1.4	225	85	128	3924	27.6	8.4	2.4	3.5	65
G107	KAFACI	SR34590/SR3	108	126	91	15	22.4	21.6	1.4	245	86	91	4566	26.4	8.2	2.6	3.2	62

GERMP LASM ID	SOURCE	GERMPASM NAME	DTF 50%	DT M	PH (cm)	NPP	PL (cm)	FLL (cm)	FLW (cm)	NP_ SqM	SSR (%)	SPP	GY (kg/ha)	1000 gwt	BRL (cm)	BRB (cm)	BRS	MR (%)
		4071(#5-16)- 5-1																
G108	KAFACI	SR34071(#5- 16)-5-1-2/su- per	118	137	97	13	25.8	29.7	1.1	206	80	142	6470	28.4	7.9	2.6	3	67
G109	KAFACI	SR34590/SR3 4071(#5-16)- 5-1	100	121	91	19	26.7	26.9	1.1	189	87	165	4296	28.2	7.9	2.5	3.2	85
G110	IRRI	IR17A1958	117	130	94	14	25.4	22.5	1.2	177	84	132	7113	26	7.3	2.5	2.9	66
G111	KAFACI	SR35266-3-2- 4-1-1	115	141	103	14	25.6	25.2	1.3	223	86	223	7006	32.8	8.6	2.7	3.2	67
G112	KAFACI	SR35300-1- HV-1-1-1	108	121	97	14	23.6	26.6	1.3	244	81	134	6263	26.4	8.7	2.5	3.5	69
G113	KAFACI	SR35250-2-4- 2-3-1	113	140	94	16	23.3	24.5	0.9	198	86	108	6384	28	7.8	2.4	3.2	62
G114	KAFACI	15053	114	135	108	9	25.6	24.5	1.3	183	90	204	5950	30	7	2.5	2.8	68
G115	KAFACI	TY 34-1	112	138	106	18	27.5	27.1	1.3	203	83	192	5930	31.5	7.5	2.5	3	67
G116	KAFACI	SR35266-2-7- 1-1-1	103	127	85	13	27.2	28.0	1.0	243	85	144	6132	26.9	8.1	2.5	3.2	64
G117	KAFACI	15065	105	127	89	12	22.5	27.3	0.9	237	89	171	5490	30.6	8.3	2.6	3.1	67
G118	KAFACI	SR34042F3- 22-1-1-1-3-1	112	136	97	12	23.0	27.6	1.1	188	86	142	4746	24.9	8.2	2.5	3.3	65
G119	IRRI	IR18A1513	115	137	104	13	27.0	26.6	1.0	179	79	150	7492	30.3	8.4	2.6	3.2	61
G120	KAFACI	HR32080- HB3567-4	110	130	97	11	23.7	31.0	1.1	284	90	158	3272	33.8	8.6	2.5	3.5	63
G121	KAFACI	15002	105	133	93	13	26.0	23.9	1.1	182	85	178	4410	24.3	7.4	2.5	3	62
G122	KAFACI	HR32083- HB3568-151	113	137	99	13	24.7	25.4	1.1	241	87	162	1789	30.7	7.1	2.7	2.7	64
G123	KAFACI	HR32086- HB3569-37	114	138	92	18	26.7	27.2	1.1	182	84	122	5651	28.7	8.3	2.5	3.4	67
G124	KAFACI	SR35311- HB3497-4	111	135	94	13	23.2	25.0	1.1	218	77	122	6499	28.7	8.2	2.5	3.3	67
G125	IRRI	IR18A1706	110	131	97	12	26.2	24.4	1.0	186	84	135	7374	26.2	7.8	2.5	3.2	67
G126	KAFACI	SR35329- HB3509-106	118	139	103	17	26.8	25.9	1.1	212	84	157	4458	29.4	8.7	2.5	3.5	63
G127	IRRI	IR18A1882	115	139	102	16	25.8	25.8	1.0	186	81	100	7861	32.2	8.1	2.5	3.3	70
G128	KAFACI	SR35311- HB3497-87	114	141	92	16	25.9	34.4	1.3	232	83	149	6857	27.2	6.9	2.6	2.7	64
G129	KAFACI	SR35311- HB3497-88	103	120	106	12	24.9	28.0	1.1	176	88	151	6411	31.9	8.9	2.6	3.4	68
G130	KAFACI	SR35328- HB3508-34	112	132	103	13	26.8	25.9	1.0	188	90	132	7783	34.1	8.7	2.4	3.7	66
G131	KAFACI	SR35329- HB3509-26	109	131	98	16	26.2	28.6	1.1	201	89	119	4922	31	8.5	2.4	3.7	67

GERMP LASM ID	SOURCE	GERMPASM NAME	DTF 50%	DT M	PH (cm)	NPP	PL (cm)	FLL (cm)	FLW (cm)	NP_ SqM	SSR (%)	SPP	GY (kg/ha)	1000 gwt	BRL (cm)	BRB (cm)	BRS	MR (%)
G132	IRRI	IR18A1906	113	133	103	12	25.7	29.6	1.1	196	85	174	7526	31.6	8.7	2.6	3.3	63
G133	KAFACI	SR35266-3-2-4-1-1	110	134	90	15	26.2	25.7	1.1	195	81	118	5355	29.3	8.2	2.5	3.5	66
G134	KAFACI	SR35300-1-HV-1-1-1	119	139	100	13	25.0	24.3	1.1	181	86	153	4134	30.2	8.2	2.5	3.2	64
G135	IRRI	IR17A2077	110	138	103	16	27.1	29.3	1.1	181	82	120	5720	28.7	7.4	2.4	3.3	67
G136	KAFACI	SR32037-1-110/SR34590	109	134	97	17	27.7	29.0	1.2	198	82	106	5244	31.4	8.5	2.5	3	68
G137	IRRI	IR18A1722	112	137	100	15	26.5	28.3	1.3	222	83	103	5774	30.3	8	2.4	3.3	68
G138	IRRI	IR18A1536	110	132	101	16	26.2	28.4	1.4	191	88	211	5875	33.5	8.3	2.6	3.1	67
G139	IRRI	IR17A1141	124	143	102	14	27.2	31.1	1.3	198	87	159	6811	26.1	5.9	2.5	2.4	66
G140	IRRI	IR17A2104	105	128	98	24	27.7	36.2	1.0	181	88	257	6916	32.4	8.1	2.4	3.4	69
G141	KAFACI	SR32037-1-110/SR34590	116	141	108	17	27.8	30.6	1.2	183	96	92	4148	29.2	8	2.4	3.3	68
G142	IRRI	IR18A1894	110	135	93	14	26.8	31.4	1.2	193	81	81	6113	23	7.3	2.5	2.8	69
G143	KAFACI	SR35311-HB3497-87	118	143	90	15	26.6	25.1	1.3	231	86	117	2079	32	8.3	2.5	3.3	66
G144	KAFACI	SR35311-HB3497-88	111	126	93	14	26.5	28.3	1.1	218	82	127	4876	26.6	7.8	2.6	3	57
G145	KAFACI	SR35328-HB3508-34	117	137	89	13	26.4	30.2	1.3	216	86	201	4276	26.5	8.2	2.5	3.3	69
G146	IRRI	IR18A1032	105	128	97	13	21.9	26.4	1.1	207	85	158	5449	24.5	7.3	2.5	3	72
G147	KAFACI	SR34590/Nun keunheugchal	104	129	100	21	27.2	30.4	1.3	185	85	132	2729	28.9	8.4	2.6	3.3	69
G148	IRRI	IR17A2863	114	141	95	16	27.1	22.7	1.1	177	79	92	7149	28	7.7	2.4	3.3	65
G149	KAFACI	SR34590/Nun keunheugchal	103	129	85	17	27.0	25.5	1.1	200	83	130	4354	28.4	8.2	2.6	3.1	64
G150	IRRI	IR18A1891	112	137	102	15	24.8	25.5	0.8	225	83	172	5353	28.6	7.1	2.6	2.7	66
G151	IRRI	IR17A1210	112	133	93	20	26.2	30.4	1.3	186	78	148	3532	22.4	8.2	2.5	3.3	61
G152	IRRI	IR17A1779	117	139	94	23	26.5	27.8	1.1	181	79	154	6711	25.6	8.7	2.5	3.5	63
G153	IRRI	IR17A1739	109	130	95	19	26.1	30.9	1.1	190	85	277	4808	30.7	8.2	2.7	3.1	73
G154	IRRI	IR17A1695	104	119	96	15	25.2	26.5	1.1	234	78	153	5424	28.3	8.2	2.4	3.4	70
G155	IRRI	IR17A1222	109	142	88	19	26.1	33.1	1.0	198	88	136	2390	28	8.1	2.5	3.2	67
G156	IRRI	IR17A2570	115	132	90	13	25.0	23.7	0.9	182	77	177	5046	27.2	8.6	2.3	3.8	68
G157	IRRI	IR17A2469	112	129	101	17	25.6	23.1	1.1	181	90	115	5183	28.7	8.3	2.6	3.3	59
G158	IRRI	IR17A1583	111	132	95	12	25.9	28.9	1.4	189	85	173	5760	29.2	8.4	2.5	3.3	67
G159	IRRI	IR16A3667	115	137	95	15	26.7	29.1	1.0	182	85	124	5846	35.2	8.4	2.6	3.2	69
G160	IRRI	IR17A1425	113	139	82	14	26.9	24.0	1.1	176	85	202	4188	33	8.3	2.4	3.4	65
G161	IRRI	IR20X1008	112	140	100	15	22.7	25.4	1.2	189	84	125	3737	30.8	8.2	2.5	3.4	64
G162	IRRI	IR22MD1306	110	138	74	16	28.5	25.5	1.0	183	79	74	3691	25.9	8.5	2.4	3.5	70

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G163	IRRI	IR22MD1371	116	143	85	11	21.6	23.4	1.3	176	81	138	3560	30.5	8.1	2.4	3.4	66
G164	IRRI	IR22MD1409	116	136	105	14	24.1	21.0	1.0	193	85	250	2433	28.5	8.3	2.5	3.4	67
G165	IRRI	IR22MD1567	117	133	96	19	28.6	26.9	1.0	182	83	188	4400	29.4	8.7	2.6	3.3	65
G166	IRRI	IR22MD1702	114	135	102	15	28.7	27.8	1.2	190	89	134	5603	32.9	8.4	2.5	3.4	68
G167	IRRI	IR22MD1890	104	120	102	16	27.2	25.9	1.1	215	87	159	6237	26.4	7.7	2.5	3	60
G168	IRRI	IR22MD1985	101	127	96	14	27.1	29.4	1.3	208	93	134	5967	25.9	8.6	2.6	3.3	63
G169	IRRI	IR22MD2076	108	132	102	16	22.8	25.7	1.2	220	86	128	5745	32.8	8.4	2.6	3.3	73
G170	IRRI	IR22MD2103	114	134	90	15	28.1	27.1	1.3	186	86	121	6958	30.3	8.3	2.5	3.3	68
G171	IRRI	IR22MD2110	116	135	104	13	22.7	21.6	0.9	190	86	115	7589	27.8	8.6	2.5	3.5	67
G172	IRRI	IR22MD2227	112	142	95	15	25.4	36.9	1.0	226	90	230	4190	30.8	8.1	2.6	3.1	64
G173	IRRI	IR22MD2256	114	139	102	13	25.6	31.7	1.3	205	86	88	4827	28.8	8	2.5	3.2	67
G174	IRRI	IR22MD2386	116	142	101	16	28.4	26.6	1.1	180	80	106	3775	31	8.8	2.3	3.8	63
G175	IRRI	IR22MD2407	106	133	96	18	26.5	30.0	1.0	246	86	164	7734	27.4	8.4	2.6	3.3	65
G176	IRRI	IR22MD2567	111	134	98	16	26.1	29.3	1.0	195	86	150	6174	28.8	8.8	2.5	3.6	60
G177	IRRI	IR22MD2638	116	135	96	11	25.1	28.3	1.2	234	82	124	6711	24	7.4	2.4	3.1	63
G178	IRRI	IR22MD2664	114	132	104	16	27.4	29.3	1.2	200	83	111	4871	31.7	8.2	2.4	3.4	65
G179	IRRI	IR22MD2715	108	127	102	12	25.7	28.6	1.1	199	83	194	5823	24.9	8.6	2.6	3.3	69
G180	IRRI	IR22MD2726	120	142	93	13	26.2	27.2	1.2	203	80	158	7185	29.2	8.6	2.4	3.6	63
G181	IRRI	IR22MD2768	108	138	93	15	26.1	49.4	1.0	215	86	173	5348	31	8.6	2.5	3.4	75
G182	IRRI	IR22MD3015	116	136	88	14	25.0	23.7	1.0	182	86	146	5043	30.7	7.2	2.1	3.4	66
G183	IRRI	IR22MD3020	110	131	96	11	24.9	26.8	0.8	222	84	159	5855	25.4	8	2.5	3.2	65
G184	IRRI	IR22MD3080	109	129	85	10	24.6	25.8	1.1	176	84	147	3554	29.5	8	2.5	3.2	64
G185	IRRI	IR22MD3320	108	130	88	18	26.8	25.1	1.0	200	85	166	6742	27.3	6.5	2.3	2.8	65
G186	IRRI	IR22MD3413	113	137	93	9	24.6	26.0	1.0	193	81	118	2766	23.9	8.3	2.6	3.2	62
G187	IRRI	IR22MD3433	112	137	88	7	23.9	24.6	1.3	177	84	148	1815	28.9	7	2.3	3	65
G188	IRRI	IR22MD3630	115	140	88	10	22.5	25.9	1.5	218	82	148	3968	33.4	8.8	2.7	3.2	67
G189	IRRI	IR22MD3638	122	146	104	17	25.2	25.3	1.2	194	80	156	6500	28.3	8	2.5	3.2	66
G190	IRRI	IR22MD3893	110	131	96	15	22.3	24.5	1.1	183	88	168	3361	23.2	7.8	2.4	3.2	57
G191	IRRI	IRRI 154	110	129	89	12	22.9	22.9	1.0	165	86	161	3283	30.8	8.5	2.4	3.5	57
G192	IRRI	IRRI 174	112	140	95	7	20.8	26.7	1.1	206	85	119	1341	25.1	8.3	2.5	3.3	70
G193	IRRI	IR16A3891	115	131	98	17	25.1	25.5	1.3	179	83	173	4969	28.9	7.4	2.4	3	69
G194	IRRI	IR16A4085	108	123	97	15	25.2	25.3	1.1	189	83	204	5050	31.2	8.4	2.7	3.2	66
G195	IRRI	IR16A3838	117	145	97	14	27.4	26.4	1.1	192	79	150	2277	32	7.3	2.6	2.8	72
G196	IRRI	IRRI 123	117	145	104	17	25.9	30.1	1.2	188	84	93	3207	29	8.5	2.5	3.4	65
G197	IRRI	IRRI 168	100	120	102	17	25.7	25.8	1.2	229	88	124	4427	26.3	7.4	2.5	2.9	61
G198	IRRI	IRRI 156	119	140	95	15	24.7	25.8	1.1	193	82	239	5764	27.6	7.9	2.4	3.3	64
G199	IRRI	IR16A4261	113	135	104	23	27.6	30.2	1.3	222	83	135	2225	27.5	8.8	2.3	4	70

GERMP LASM ID	SOURCE	GERMPASM NAME	DTF 50%	DT M	PH (cm)	NPP	PL (cm)	FLL (cm)	FLW (cm)	NP_ SqM	SSR (%)	SPP	GY (kg/ha)	1000 gwt	BRL (cm)	BRB (cm)	BRS	MR (%)
G200	IRRI	IRRI 104	113	134	96	18	26.6	28.3	1.4	185	83	115	4789	28	8.2	2.6	3.2	65
Range _lower value			100	121	73	9	21	21.0	0.8	171	74	74	1341	22	5.9	2.1	2.4	57
Range _ higher value			124	146	134	23	29	49	1.6	284	98	347	8121	35	9.4	2.8	4.0	75
Mean			112	134	97	14	25.5	27.55	1.15	203	85	148	5255	28	8.1	2.5	3.2	65.7
LSD			13.5	16.1	14.3	6.8	3.3	8.644	0.364	68.8 1	13.4	103. 3	3816	7.47	1.51	0.30	0.66	9.5
Fpr.			0.24 1	0.26 9	<.00 1	<.00 1	<.00 1	0.026	0.019	0.60 3	0.13 4	0.09 6	<0.006	0.57 4	0.00 5	0.05 6	0.079	0.427
SE			6.83	8.21 3	8.9	4.2	2.1	5.385	0.227	34.9	7	52	2160	3.8	0.77	0.30	0.41	4.85
CV%			7.5	7.5	9.1	29.5	8.2	19.5	19.6	21.1	9.8	43.4	41.3	16.2	11.5	7.5	12.7	9.1

References

- Abade, A., Bokosi, J. M., Mwangwela, A. M., Mzengeza, T. R., & Abdala, A. J. (2016). Characterization and evaluation of twenty rice (*Oryza sativa* L.) genotypes under irrigated ecosystems in Malawi and Mozambique. *African Journal of Agricultural Research*, 11(17), 1559–1568. <https://doi.org/10.5897/AJAR2016.10895>
- Abd El-Mohsen, A. A., & Abo-Hegazy, S. R. (2013). Comparing the relative efficiency of two experimental designs in wheat field trials. *Scientific Research and Review Journal*, 1(3), 101–109. Science Explorer Publications. <https://doi.org/10.12816/0003974>
- Agri-tech Seeds. (2024). Thousand seed weight protocol: Post-harvest grain classification method. Agri-tech Seeds. Retrieved December 24, 2025, from <https://www.agritechseeds.com>
- Akter, N., Khalequzzaman, M., Islam, M. Z., Mamun, M. A. A., & Chowdhury, M. A. Z. (2018). Genetic variability and character association of quantitative traits in jhum rice genotypes. *SAARC Journal of Agriculture*, 16(1), 193–203. Retrieved October 25, 2025, from <https://paperity.org/p/254052142/genetic-variability-and-character-association-of-quantitative-traits-in-jhum-rice>
- Anumalla M, Khanna A, Catolos M, Ramos J, Cruz M. S. T, Venkateshwarlu C, Konijerla J, Pradhan S. K, Dash S. K, Das Y, Chowdhury D, Chetia S. K, Das J, Nath P, Merugumala G. R, Roy B, Pradhan N, Jana M, Dana I, Hussain W (2025). Future flooding tolerant rice germplasm: resilience afforded beyond Sub1A gene. *The Plant Genome*, 18, e70040. <https://doi.org/10.1002/tpg2.70040>
- Bakode, Sandhya, Sanjay Kumar Singh, G. K. Koutu, Shailendra Sagar Prajapati, and Pushpa Jharia. 2025. "Phenotypic Characterization and Association Analysis of Morphological Traits in Diverse Rice Genotypes (*Oryza Sativa* L.)". *International Journal of Plant & Soil Science* 37(6): 548-60. <https://doi.org/10.9734/ijpss/2025/v37i65534>
- Burman M, S. K., Nair, S. K. and Sarawgi, A. K. 2019. Genetic diversity analysis in unique Rice (*Oryza sativa* L.) of Chattisgarh, India. *International Journal of Microbiology and Applied Sciences*, 8(11): 1096 1099.
- Bhangar, N. A., Arain, F., Pandrani, M. I., Khan, N., Soomro, G., Rao, F., Rao, N., Pandrani, I. A., & Jamro, A. H. (2024). Correlation and heritability estimation for agronomic traits in rice (*Oryza sativa* L.) genotypes. *Kashmir Journal of Science*, 3, 74–82. <https://doi.org/10.61450/kjs.v3i3.79>
- Bhor, T. J., Kashid, N. V., & Kadam, S. M. (2020). Genetic variability, character association and path analysis studies for yield components traits in promising rice (*Oryza sativa* L.) genotypes. *Journal of Pharmacognosy and Phytochemistry*, 9(4), 1953–1956. <https://www.phytojournal.com/archives/2020/vol9issue4/PartAA/9-3-184-255.pdf>
- Cobb JN, Juma RU, Biswas PS, Arbelaez JD, Rutkoski J, Atlin G, Hagen T, Quinn M, Ng EH (2019) Enhancing the rate of genetic gain in public-sector plant breeding programs: lessons from the breeder's equation. *Theor Appl Genet* 132(3): 627–645. <https://doi.org/10.1007/s00122-019-03317-0>
- Demeke, B., Dejene, T., & Abebe, D. (2022). Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (*Oryza sativa* L.) genotypes at Pawe, Northwestern Ethiopia. *Cogent Food & Agriculture*, 8(1), 2157099. <https://doi.org/10.1080/23311932.2022.2157099>
- Farrow, E. M., Wang, J., Shi, H., Yang, J., Hua, B., & Deng, B. (2024). Selected Trace Element Uptake by Rice Grain as Affected by Soil Arsenic, Water Management and Cultivar—A Field Investigation. *Frontiers in Environmental Science*, 12, Article 1347330. <https://doi.org/10.3389/fenvs.2024.1347330>

- [13] Food and Agriculture Organization of the United Nations (2025) FAOSTAT Statistical Database. FAO, Rome. Available at: <https://www.fao.org/faostat> on 8/8/2025
- [14] Gomez KA, Gomez AA (1984). Statistical procedures for agricultural research (2 ed.). John Wiley and Sons, New York 680 p.
- [15] Gunasekaran, A; Seshadri G, Ramasamy, Muthurajan S, and Karuppasamy K. S, (2023) Identification of Newer Stable Genetic Sources for High Grain Number per Panicle and Understanding the Gene Action for Important Panicle Traits in Rice. *Plants* 2023, 12(2), 250; <https://doi.org/10.3390/plants12020250>
- [16] Hariharan, B., Mahendran, R., Jegadeeswaran, M., Nagajothi, R., Vanitha, J., & Thirugnanakumar, S. (2025). Analysis of genetic variability and association for yield traits in rice (*Oryza sativa* L.) germplasm lines. *Agricultural Science Digest*. Advance online publication. <https://doi.org/10.18805/ag.D-6331>
- [17] He, Q., Wu, H., Zeng, L., LMMM Caiyun Yin, Wang, Li, Tan, Y., Wanqing Lv, Liao Z, Zheng, X., Zhang, S., Han, Q., Wang, D., Zhang, Y., Xiong, G., Wang Q., (2025), OsKANADI1 and OsYABBY5 regulate rice plant height by targeting GIBEREL-LIN 2-OXIDASE6, *The Plant Cell*, Volume 37, Issue 1, koae276, <https://doi.org/10.1093/plcell/koae276>
- [18] Jadhav, S., Balakrishnan, D., Shankar, V. G. et al (2022). Genetic diversity analysis and population structure in a rice germplasm collection of different maturity groups. *J. Plant Biochem. Biotechnol.* 31, 524–532 (2022). <https://doi.org/10.1007/s13562-021-00699-5>
- [19] Kempton, R. A., Kleinknecht, K., & Singh, R. K. (2012). Statistical methods for plant variety trials (Vol. 2). Los Baños, Philippines: International Rice Research Institute (IRRI). <https://doi.org/10.1017/CBO9781139028737>
- [20] Kumar, M. S. C., Sundaram, R. M., Reddy, A. V., Gireesh, C., Mahender Kumar, R., Krishnamurthy, S. L., Anantha, M. S., & Sekhar, M. R. (2025). Selection of traits for yield improvement in rice through interactions of yield-related traits in F₂ population. *Biochemistry and Biotechnology Research Journal*, 9(2S), 154–160. Available at: <https://www.biochemjournal.com/archives/2025/vol9issue2S/PartG/S-9-2-52-154.pdf> (Accessed: 26 October 2025).
- [21] Li, T., Yang, Z., Ang, Y. et al (2025). Genome-wide association study identifies elite alleles of FLA2 and FLA9 controlling flag leaf angle in rice. *BMC Genomics* 26, 280. <https://doi.org/10.1186/s12864-025-11487-z>
- [22] Luong, N. H., Balkunde, S. G., Shim, KC. et al. (2022). Characterization of Domestication Loci Associated with Awn Development in Rice. *Rice* 15, 61 (2022). <https://doi.org/10.1186/s12284-022-00607-y>
- [23] Meena, D., Kumar, M., Chawla, R., Koli, H. K., & Meena, N. K. (2023). Principal component analysis for yield and related attributes in rice genotypes. *Biological Forum – An International Journal*, 15(6), 174–178. Retrieved from <https://www.researchtrend.net/bfij/pdf/Principal-component-analysis-for-yield-and-related-attributes-in-rice-genotypes-Deepak-Meena-29.pdf>
- [24] Mohapatra, P. K., Sarkar, R. K., Panda, D., & Kariali, E. (2025). *Tillering behavior of rice plant* (Vol. 11). Singapore: Springer Nature. <https://doi.org/10.1007/978-981-99-6163-0>
- [25] Molla K. A, (2022). Flowering time and photoperiod sensitivity in rice: Key players and their interactions identified, *The Plant Cell*, Volume 34, Issue 10, October, Pages 3489–3490, <https://doi.org/10.1093/plcell/koac230>
- [26] Mounika, J., Krishna Veni, B., Chapara, R., & Bhuvaneswari, V. (2024). Genetic variability and association studies in rice (*Oryza sativa* L.). *The Andhra Agricultural Journal*, 71(1), 23–28. <https://doi.org/10.61657/aaj.2024.88>
- [27] Nakamura, S., Satoh, A., Aizawa, M., and Ohtsubo, K. (2022). Characteristics of physicochemical properties of chalky grains of Japonica rice generated by high temperature during ripening. *Foods* 11, 97. <https://doi.org/10.3390/foods11010097>
- [28] Nguyen, V. H., Morantte, R. I. Z., Lopena, V. et al., (2023). Multi-environment Genomic Selection in Rice Elite Breeding Lines. *Rice* 16, 7 (2023). <https://doi.org/10.1186/s12284-023-00623-6>
- [29] Osman, K. A., Kang, K. H., El-Siddg, A. A., Ahmed, Y. M., & Abdalla, S. M. (2020). Assessment of genetic variability for yield and attributed traits among rice doubled haploid (DH) lines in semi-arid zone Sudan. *African Journal of Agricultural Research*, 16(7), 939–946. <https://doi.org/10.5897/AJAR2019.14496>
- [30] Pachauri, K. A., Sarawgi, A. K., Bhandarkar, B., and SK Nair, S. K., (2020). Characterization and variability analysis of rice germplasm accessions for morphological traits. *Journal of Pharmacognosy and Phytochemistry*. E-ISSN: 2278-4136 P-ISSN: 2349-8234 JPP 2020; 9(5): 1407-1413 www.phytojournal.com
- [31] Patterson, H. D., & Williams, E. R. (1976). A new class of resolvable incomplete block designs. *Biometrika*, 63(1), 83–92. <https://doi.org/10.1093/biomet/63.1.83>
- [32] Prabhu B. M, and Abhishree R, (2024). Plant height in rice: Yield booster or barrier? ISSN (E): 2277-7695 ISSN (P): 2349-8242 TPI 2024; 13(2): 155-160 © 2024 TPI The Pharma Innovation Journal; 13(2): 155-160. www.thepharmajournal.com
- [33] Pragnya, K., K. V. Radha Krishna, L. V. Subba Rao and Suneetha, K. 2018. Studies on Morphological Characterization in Soft Rice (*Oryza sativa* L.) Genotypes. *Int. J. Curr. Microbiol. App. Sci.* 7(05): 1348-1374. <https://doi.org/10.20546/ijcmas.2018.705.162>
- [34] Rahangdale, S., Singh, Y., Koutu, G. K., & Tiwari, S. (2019). Genetic variability, correlation and path coefficient studied for yield and quality traits in JNPT lines of rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences*, 8(10), 1025–1037. <https://doi.org/10.20546/ijcmas.2019.810.120>
- [35] Reddy N. R, Babu G. S, Lavanya G. R (2020). Genetic diversity studies in elite rice (*Oryza sativa* L.) germplasm for yield and quality traits. *Journal of Pharmacognosy and Phytochemistry* 2020; 9(3): 316-320. E-ISSN: 2278-4136 P-ISSN: 2349-8234 www.phytojournal.com

- [36] Shrestha, P., Kandel, B. P., Shrestha, P. et al., (2024). Characterization of rice landraces of Lamjung and Tanahun districts. *Genet Resour Crop Evol* 71, 4669–4683 (2024). <https://doi.org/10.1007/s10722-024-01929-0>
- [37] Standard Evaluation System for Rice (IRRI, 2013), 5th Edition, P. O. Box 933, 1099 Manila, Philippines.
- [38] Shanmugam, S., Samonte, S. O. P. B., Sanchez, D. L. et al. Genetic assessment of diverse rice germplasm for yield-related and stress tolerance traits. *Genet Resour Crop Evol* 72, 885–904 (2025). <https://doi.org/10.1007/s10722-024-02004-4>
- [39] Tadiboyina Surya, K. Amudha, P. Sivasakthivelan, S. Geetha, D. Uma and M. Sudha (2024). Therapeutic potential of anthocyanin rich deep pigmented rice landraces and its genetic improvement: A review. *Ann. Phytomed.*, 13(2): 282–290. <http://dx.doi.org/10.54085/ap.2024.13.2.27>
- [40] Thakur, N., Katiyar, P., Banjare, B., & Magar, A. S. (2024). Correlation studies in long duration rice genotypes (*Oryza sativa* L.). *The Pharma Innovation Journal*, 13(8), 157–159. <https://www.thepharmajournal.com/archives/2024/vol13issue8/PartC/13-8-59-159.pdf>
- [41] Wang, X., Liu, Y., Zhang, Y., & Li, Y. (2022). Field rice panicle detection and counting based on deep learning. *Frontiers in Plant Science*, 13, 966495. <https://doi.org/10.3389/fpls.2022.966495>
- [42] Zeng, D., Qin, R., Tang, L., Jing, C., Wen, J., He, P., & Zhang, J. (2025). Enrichment of rice endosperm with anthocyanins by endosperm-specific expression of rice endogenous genes. *Plant Physiology and Biochemistry*, 219, Article 109428. <https://doi.org/10.1016/j.plaphy.2024.109428>