

## Phenotypic Variation Among Rice (*Oryza sativa* L.) Germplasm Accessions for the Eastern Democratic Republic of Congo and Traits Association Based on Yield and Yield Components.

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### Abstract:

Genetic variation among genotypes and the association between yield with its components are critical information and prerequisite knowledge for a crop yield improvement program. Forty-nine rice genotypes were randomly selected from the germplasm accessions in the Eastern Democratic Republic of Congo for selection in a yield improvement program. The field experiment was conducted following a 7x7 triple lattice design in two locations, each with three replicates. Data were collected on fourteen morphological traits. The variation in the genotypes was explained by four principal components accounting for 78.7% of the total variation. Traits such as panicle length, plant height, number of primary branches/panicles, number of spikelets/panicles, number of filled grains/panicle, panicle weight, number of productive tillers/hill, grain yield, 1000 grains weight, grain length to grain width ratio were the major discriminator traits among the genotypes. High genotypic coefficient of variation than the environmental coefficient of variation was observed among the yield components. Moderate to high heritability and genetic advance exhibited by grain width, number of spikelets/panicles, number of filled grains/panicle, plant height, panicle length, 1000 grains weight, days to flowering, panicle weight, number of productive tillers/hill, and number of primary branches/panicle, indicating that these characters can be improved through selection. Grain yield reflected a significant and positive correlation with the number of productive tillers/hills, panicle weight, number of primary branches/panicle, number of filled grains/panicle, and number of spikelets/panicle. Selection can be based on such traits for grain yield improvement. Breeders should consider this information when selecting parents for grain yield improvement using this germplasm.

**Keywords:** Rice, phenotypic variation, trait selection, correlation, yield components

## 1. Introduction

Rice (*Oryza sativa* L.) is an important cereal among food crops. It feeds more than three billion people worldwide and is a staple food of over 55% of Asia and Africa [1]. An essential source of nutrients, rice contains an average of 80% starch, 12% water, 7.5% protein, and 0.5% ash. Rice grain is also a good source of iron [2] and zinc [3].

Its cultivation triggered the beginning of agriculture almost ten thousand years ago, and since then farmers have made enormous efforts to increase its productivity in tropical and subtropical areas. Currently, around 160 Mha of paddy fields around the world produce around 500 million tons of rice per year. However, this quantity is not enough to feed an ever-growing population, especially in many developing countries in Asia and Africa [4].

Although forecasts vary, the world population is growing significantly and is destined to reach 9.5 billion by 2050. Five out of nine African countries, with over 50% of the population growth between now and 2050 are Nigeria, the Democratic Republic of the Congo, Ethiopia, the United Republic of Tanzania, and Uganda, are in Sub-Saharan Africa (SSA) [1]. Rice is the most rapidly increasing preferred food commodity in these countries, mainly driven by urbanization [5], [6]. In the Democratic Republic of Congo (DRC), rice is the second most-consumed cereal after maize. The estimated consumption of white rice ranges from 7kg to 19.5kg/person/year in 2018 [7].

The DRC has potential of four million ha of irrigable low-land rice production. This potential has been partially limited by the lack of well-adapted and high-yielding varieties [8], [9]. This low level of productivity is attributed to the cultivation of old and low-yielding (0.8 ton/ha) varieties by farmers [7], [9]. With its potential, DRC could play a great role in food security contributing to the availability of rice in the SSA region. However, DRC is one of the SSA countries importing rice to meet its national demand. The marginal increase in local rice production observed between 2008 and 2018 resulted from an increase in harvested area [10]; which implies an increase in the cost of rice production while rice productivity remained stagnant, making rice a non-cash crop for smallholder farmers.

To satisfy the growing demand without affecting the resource base adversely, Ahmadi [10], projects a 50% increase in rice production by 2030 in Africa. Therefore, there is an urgent need to develop high-yielding rice varieties to meet the increasing population and adapt to the current climate conditions, which is the primary goal of crop breeders.

Development of new varieties largely requires availability of genetic variation in the desirable traits within the germplasm accessions [11]. Grain yield is a quantitative trait controlled by several genes and highly influenced by the environment. In rice, yield is determined by the combined action of several traits; the yield components or yield-related traits [12]. Assessing the phenotypic variability using principal component analysis allows the breeders to quantify the relative importance of each trait in discriminating a set of genotypes.

Variation and genetic advance of a population is assessed by estimating genetic parameters, genotypic and phenotypic coefficient of variance and heritability of respective traits to understand genetic and environmental effects on the expression of the traits. The estimated parameters guide the selection of potential parents and suitable characters in a breeding program [13]. Heritability informs the transmission of characters from the parents to future generations, whereas genetic advance helps breeders in the prediction of transmissibility and genetic gain in the improvement process.

Correlation and path analysis help to understand the relationship among the yield related-traits and ultimately in relationship to grain yield. The relationships among the traits informs the breeder in choosing appropriate parameters that are used during breeding and selection. This guides the breeder for the direct and indirect selection for traits that contributes to grain yield [12].

Therefore, this study was undertaken to assess the genetic variation among 49 representative genotypes selected in the Eastern Democratic Republic of Congo for the rice genetic improvement program and to determine the relationship between yield and yield components to enhance efficiency in the selection processes.

## 2. Materials and Methods

### 2.1. Experimental Sites

The experiments were carried out on farmer's rice fields, in two locations; Taba-Congo (S05°50'19" and E029°17'20", at 775m of altitude) and Kabimba (S05°34'19.5", E029°20'03.3" at an elevation of 781m above the sea level) located at 12km and 65km from Kalemie, respectively; in Tanganyika province of the Democratic Republic of Congo. The experimental fields were set up on clayey loam soils.

### 2.2. Plant materials

A random sample of Forty-nine rice genotypes was selected from the germplasm accessions used in the breeding program in the Eastern Democratic Republic of Congo; this sample represents 25% of germplasm. The selected accessions comprised of forty genotypes collected from the National Institute for Agronomic Study and Research (INERA), Gimbi station; five were sourced from the International Rice Research Institute (IRRI-Burundi), and four genotypes obtained from the International Institute of Tropical Agricultural (IITA-DR Congo) (Table 1).

**Table 1.** Rice genotypes used for this study

N°	Genotype name	Source	N°	Genotype name	Source	N°	Genotype name	Source
1	Komboka	IRRI, Burundi	18	ARS168-1-B-3-B	INERA	35	Rukaramu	INERA
2	IR64	IRRI, Burundi	19	ARS851-1-3	INERA	36	Mussekara	IITA, DRC
3	Hubei6	INERA	20	IR87638-10-2-2-4	INERA	37	Yasho Yasho	INERA
4	Giza182	INERA	21	IR98419-B-B-11	INERA	38	Kasozi	IITA, DRC
5	Nipponbare	IRRI, Burundi	22	IR97071-24-1-1-1	INERA	39	IR7525	IITA, DRC
6	Jasmine	INERA	23	ARS803-4-5-4-3	INERA	40	Orylux6	INERA
7	NL59	INERA	24	IR93856-23-1-1-1	INERA	41	ART29	INERA
8	FKR28	INERA	25	ARS790-5-11-1-1	INERA	42	SIPI	INERA
9	08FAN10	INERA	26	IR17015-6-5-3-B1	INERA	43	CRS36	INERA
10	WAB2066-TGR2	INERA	37	IR106359-B-18-5	INERA	44	ARICA2	INERA
11	WAB2066-TGR3	INERA	28	IR95624-B-138-3	INERA	45	NL19	INERA
12	IR99084-B-B-13	INERA	29	IR13A461	INERA	46	NL14	INERA
13	IR127229	INERA	30	Mugwiza	IRRI, Burundi	47	NL17	INERA
14	IR106172-78:1-B-B	INERA	31	Vuninzara	IRRI, Burundi	48	D20-ARS-3-2	INERA
15	ARS848-15-3-2-3	INERA	32	IR97045-24-1-1-1	INERA	49	IR96279-33-3-1-2	INERA
16	IR106364-B-B-CNUS	INERA	33	Kigoma	INERA			
17	ARS844-24-10-2-B	INERA	34	Makasane	IITA, DRC			

### 2.3. Experimental design, layout, and field management

The field experiments in each site were laid out in a 7x7 triple lattice design with three replications. Each replication was comprised of 49 plots representing 49 rice genotypes distributed in seven blocks, each containing seven plots. The experiment had a total of 147 plots on a total space of 40m x 22m. A replicate measured 11m x 22m and the size of an experimental plot was 2m x 1m. A path of 1m was left between the replicates and between the blocks to allow easy movement when collecting data.

The 49 rice genotypes were randomly assigned in each of the three replications by using the FieldHub package in R software.

Each experimental plot had 32 plants at 25cm x 25cm spacing using one plant per hole. The experiments were carried out under irrigated conditions in rice farmer's fields from July to December 2021. The rice seeds were first soaked in warm water for one day, then maintained under warm conditions for another day to accelerate the germination, and subsequently sown in the nursery. After 21 days the seedlings were transplanted to the prepared muddy fields. The rice fields were kept dry for up to two weeks to allow good root development. Then the fields were flooded with water for three days. During the crop cycle, the fields were weeded four times; the first weeding was done eighteen days after transplanting, and the subsequent weeding was done at intervals of one month. Before any weeding operation, the fields were drained to facilitate the operation. For fertilization, urea (46% N) was applied in two fractions; the first fraction was added 20 days after transplanting at the start of the tillering phase at a rate of 60 kg ha<sup>-1</sup> and the second was applied during panicle initiation at a rate of 60 kg ha<sup>-1</sup>. During the reproductive and maturation stages, the fields were protected against birds by covering with a bird mist net and installing scarecrows.

### 2.4. Data Collection

Data were collected on fourteen morphological traits following the Descriptors for Rice [14]; Days to flowering, days to maturity, plant height, panicle length, number of productive tillers/hill, number of primary branches/panicle, number of spikelet/panicle, number of filled grains/panicle, panicle weight, thousand grains weight, and grain yield. Measurements were done from ten selected plants or panicles/hill from the middle of each plot. After harvest, a sample of 10 grains for each genotype was shelled to assess the physical grain's quality, i.e., grain length and grain width, and ratio grain length/grain width was calculated. The mean values of data collected from the two locations were combined and then subjected to statistical analysis.

### 2.5. Statistical Analysis

#### 2.5.1. Analysis of Variance and Genetic parameters

Analysis of variance (ANOVA) was carried out to determine variation among the 49 rice genotypes for yield and yield components. The PBIB.test function from agricolae package was used, following the variance component (VC) model in R software (version 4.1.1) [15]. Genetic parameters were estimated to understand the nature of variation in yield and its components, in determining genetic and environmental effects on the expression of studied traits. The genotypic variance ( $\sigma^2_g$ ) (Equation (1)),

environment variance (Equation (2)), phenotypic variance ( $\sigma^2_p$ ) (Equation (3)) were determined according to Johnson et al. [16].

Genotypic variance ( $\sigma^2_g$ ):

$$\sigma^2_g = \frac{MS_g - MSe}{r} \quad (1)$$

Where  $MS_g$  is the mean square of genotypes,  $MSe$  is the mean square of error, and  $r$  is the number of replications.

Environmental variance ( $\sigma^2_e$ ):

$$\sigma^2_e = MSe \quad (2)$$

Phenotypic variance ( $\sigma^2_p$ ):

$$\sigma^2_p = \sigma^2_g + \sigma^2_e \quad (3)$$

Genotypic and phenotypic coefficients of variation (GCV and PCV, respectively) were calculated according to the formula suggested by [16] as shown in Equations (4) and (5), respectively.

$$GCV = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100 \quad (4)$$

$$PCV = \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100 \quad (5)$$

Where  $\bar{x}$  the experimental mean;

Heritability (Broad sense):

Heritability (Broad sense) was computed following the Standard broad-sense heritability method described by [[16]] as presented in Equation (6).

$$h^2_{bs} = \frac{\sigma^2_g}{\sigma^2_p} \times 100 \quad (6)$$

Genetic advance

Estimation of genetic advance (GA) and genetic advance as percentage of the mean (GAM) were estimated following the formulas [16] as shown in Equation (7) and (8), respectively.

$$GA = \frac{k \times \sqrt{\sigma^2_p} \times \sigma^2_g}{\sigma^2_p} \quad (7)$$

Where:

GA = Expected genetic advance

k = Standardized selection differential at 5% selection intensity (K = 2.063)

$\sigma^2_p$  = Phenotypic variance and  $\sigma^2_g$  = Genotypic variance

$$GAM = \frac{GA}{\bar{X}} \times 100 \tag{8}$$

Where:

GAM = Genetic advance as percentage of mean

GA = Expected genetic advance

X = Grand mean of a character

### 2.5.2. Correlation, Path Analysis, and Principal Components Analysis

Phenotypic correlation analysis was performed to assess the relationship among the studied traits whereas path analysis was conducted to determine the direct and indirect effects of each trait on yield [17]. These were performed in R software (Version 4.1.1) [15], using the variability package.

Principal component analysis was carried out to determine the contribution of the individual genotypes and variables to the total observed variation. This was carried out using the FactoMineR package from Jamovi software (Version 2.3) [18].

### 2.5.3. Cluster Analysis

Cluster analysis was performed using the individuals pairwise Euclidean distance matrix based on the phenotypic traits following the hierarchical method and the dendrogram was constructed using the ward.D2 method. The optimum number of clusters was determined using the R package NbClust.

## 3. Results

### 3.1. Analysis of variance

Analysis of variance of the combined mean values from the two sites (

	DF	DTF	DTM	PH	NPTH	PL	NPBP	NSP	NFGPPW	ThGW	GL	Gw	GLGwR	GY	
<b>variation</b>															
Replication	2	21.9	35.9	28.7	38.3	7.23	4.50	2814	2687	1.424	7.05	0.929	0.253	1.246	0.541
		**	***	ns	***	**	*	***	***	***	*	**	*	**	***

Genotype	48	106.8	127.8	275.9	18.4	8.38	4.07	2159	1910	0.680	12.93	0.256	0.789	2.366	0.185
		***	***	***	***	***	***	***	***	***	***	ns	***	***	***
Block (Replicate)	18	3.5	2.9	13.5	2.3	1.31	1.36	682	642	0.189	0.67	0.109	0.033	0.190	0.066
		ns	ns	ns	ns	ns	ns	**	*	ns	ns	ns	ns	ns	ns
Residual	78	4.4	4.6	12.3	4.6	0.99	1.25	285	330	0.13	1.85	0.18	0.068	0.196	0.056

) revealed highly significant differences among the genotypes for all the studied traits except for grain length.

**Table 2.** Analysis of variance for yield and yield-related traits among 49 rice genotypes

Source of variation	DF	DTF	DTM	PH	NPTH	PL	NPBP	NSP	NFGPP	PW	ThGW	GL	Gw	GLGwR	GY
Replication	2	21.9	35.9	28.7	38.3	7.23	4.50	2814	2687	1.424	7.05	0.929	0.253	1.246	0.541
		**	***	ns	***	**	*	***	***	***	*	**	*	**	***
Genotype	48	106.8	127.8	275.9	18.4	8.38	4.07	2159	1910	0.680	12.93	0.256	0.789	2.366	0.185
		***	***	***	***	***	***	***	***	***	***	ns	***	***	***
Block (Replicate)	18	3.5	2.9	13.5	2.3	1.31	1.36	682	642	0.189	0.67	0.109	0.033	0.190	0.066
		ns	ns	ns	ns	ns	ns	**	*	ns	ns	ns	ns	ns	ns
Residual	78	4.4	4.6	12.3	4.6	0.99	1.25	285	330	0.13	1.85	0.18	0.068	0.196	0.056

DF: Degree of freedom, DTF: Days to flowering, DTM: Days to maturity, PH: Plant height (cm), NPTH: Number of productive tillers/hill, PL: Panicle length (cm), NPBP: Number of primary branches/panicle, NSP: Number of spikelet/panicle, NFGP: Number of filled grains/panicle, PW: Panicle weight (g), ThGW: 1000 Grains weight, GL: Grain length (mm), Gw: Grain width (mm) and GLGwR: Grain length to grain width ratio, GY: Grain yield (kg/m<sup>2</sup>), ns: non-significant; \*, \*\* and \*\*\*: significance at 0.05, 0.01 and 0.001 levels, respectively.

### 3.2. Analysis of genetic parameters

The results of the analysis of the genetic parameters presented in Table 3 revealed that the Phenotypic coefficient of variation (PCV) was higher than the corresponding Genotypic coefficient of variation (GCV) for all the traits.

**Table 3.** Analysis of genetic parameters for yield and yield components in 49 rice genotypes

Character(s)	Mean	MSg	MSe	σ <sup>2</sup> g	σ <sup>2</sup> p	ECV	GCV	PCV	h <sup>2</sup> bs (%)	GA (%)	GAM (%)
Days to flowering	110	106.83	4.40	34.14	38.55	1.90	5.31	5.64	88.58	11.33	10.29
Days to maturity	148	127.83	4.65	41.06	45.71	1.45	4.32	4.55	89.84	12.51	8.43
Plant height (cm)	94.3	275.86	12.27	87.86	100.13	3.72	9.94	10.61	87.75	18.09	19.18
Number of productive tillers/hill	16	18.44	4.61	4.61	9.22	13.46	13.47	19.05	50.04	3.13	19.63
Panicle length (cm)	24.8	8.38	0.99	2.46	3.45	4.02	6.33	7.50	71.31	2.73	11.02
Number of primary branches/panicle	11	4.07	1.25	0.94	2.19	10.62	9.18	14.04	42.75	1.30	12.36
Number of spikelet/panicle	186	2158.54	284.56	624.66	909.22	9.08	13.45	16.23	68.70	42.68	22.97



Number of filled grains/panicle	168	1909.78	330.28	526.50	856.78	10.80	13.64	17.40	61.45	37.05	22.03
Panicle weight (g)	3.44	0.68	0.13	0.18	0.31	10.35	12.50	16.23	59.34	0.68	19.84
1000 grains weight (g)	27.78	12.93	1.85	3.69	5.54	4.90	6.92	8.48	66.64	3.23	11.64
Grain length (mm)	8.85	0.26	0.17	0.03	0.20	4.72	1.85	5.07	13.35	0.12	1.39
Grain width (mm)	2.55	0.79	0.07	0.24	0.31	10.23	19.25	21.80	77.98	0.89	35.02
Grain length to grain width ratio	3.7	2.37	0.20	0.72	0.92	11.95	22.97	25.89	78.69	1.55	41.97
Grain yield (kg/m <sup>2</sup> )	3.6	0.18	0.06	0.04	0.10	6.59	5.75	8.75	43.19	0.28	7.78

According to the categorization of Johnson et al. [16], low PCV and GCV were obtained for days to flowering, days to maturity, panicle length, 1000grains weight, grain length, and grain yield although moderate PCV and GCV were obtained for plant height, number of productive tillers per hill, number of spikelets per panicle, number of filled grains per panicle and panicle weight. The number of primary branches/panicle showed low GCV and moderate PCV while a moderate GCV with a high PCV were obtained for grain width. High PCV and GCV were shown by grain length to grain width ratio. The GCV were greater than the corresponding environmental coefficient of variation (ECV) for days to flowering, days to maturity, plant height, panicle length, number of spikelets/panicle, number of filled grains/panicle, panicle weight, 1000 grains weight, grain width and grain length to grain width ratio while the number of primary branches/panicle, grain length and grain yield showed greater ECV than their corresponding GCV. Although equivalent GCV and ECV were observed for number of productive tillers/hill.

The heritability in broad sense is categorized as low (< 30%), moderate (30% - 60%) and high (> 60%) [19]. For this study, it ranged from 13.35% to 89.84% (Table 3). A low heritability was observed for grain length (13.35%) while a moderate was obtained with panicle weight (59.34%), followed by the number of productive tillers/hill (50.04%), followed by grain yield (43.19%) and the number of primary branches/panicle (42.75%). High heritability was shown by days to maturity (89.84%), followed by days to flowering (88.58%), plant height (87.75%), grain length to grain width ratio (78.69%), grain width (77.98%), panicle length (71.31%), number of spikelet/panicle (68.70%), 1000 grains weight (66.64%), and number of filled grains/panicle (61.45%). Genetic advance as a percent of the mean (GAM) classified as low (<10%), moderate (10%-20%), and high (>20%) [16]. In this study, it ranged from 1.39% to 41.97% (Table 3). A low GAM was shown by the grain length (1.39%), followed by grain yield (7.78%), and days to maturity (8.43%). Moderate GAM was obtained with days to flowering (10.29%), panicle length (11.02%), 1000 grains weight (11.64%), number of primary branches/panicle (12.36%), plant height (19.18%), number of productive tillers/hill (19.63%) and panicle weight (19.84%). High GAM was recorded with Grain length to grain width ratio (41.97%), followed by grain width (35.02%), then the number of spikelet/panicle (22.97%) and the number of filled grains/panicle (22.03%).

### 3.3. Principle Components Analysis

Considering eigen values greater than one, four principal components were considered to be responsible for 78.7% of the total variation (Table 4).



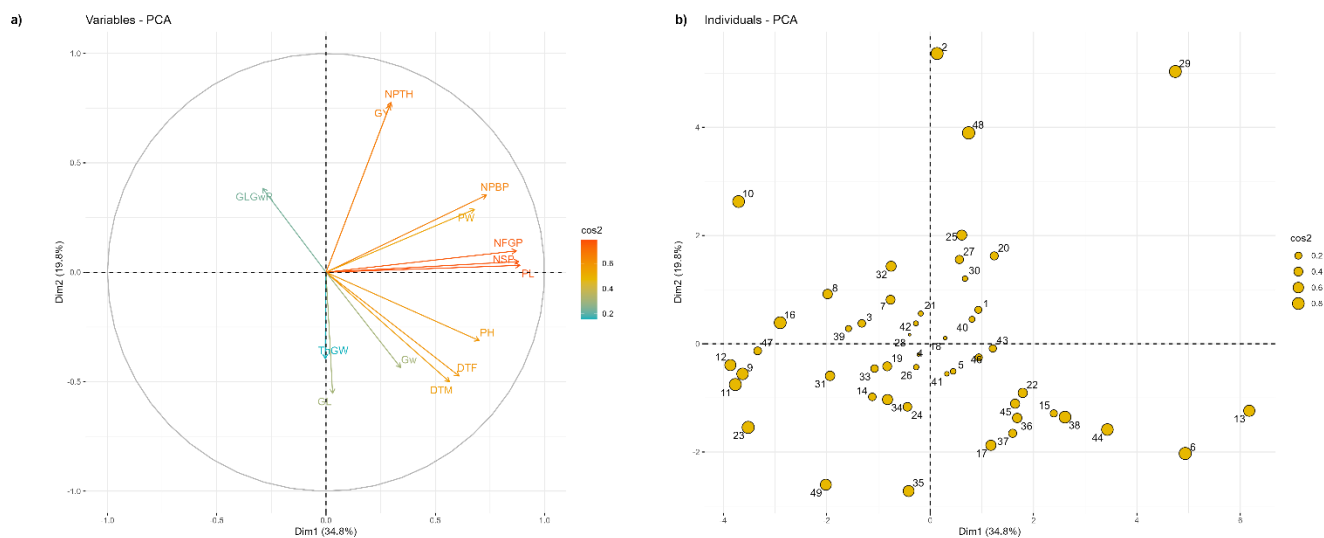
**Table 4.** Contribution of 14 traits to the variation among 49 rice genotypes

Traits	PC1	PC2	PC3	PC4
Days to flowering	0.609	-0.474	-0.017	-0.364
Days to maturity	0.565	-0.500	-0.040	-0.387
Plant height (cm)	0.701	-0.312	0.408	-0.047
Number of productive tillers/hill	0.298	0.777	-0.187	0.095
Panicle length (cm)	0.887	0.032	0.289	0.015
Number of primary branches/panicle	0.734	0.353	-0.086	0.022
Number of spikelets/panicle	0.881	0.049	0.120	-0.083
Number of filled grains/panicle	0.871	0.098	0.076	-0.097
Panicle weight (g)	0.679	0.288	-0.069	0.502
1000 grains weight (g)	-0.004	-0.395	0.512	0.605
Grain length (mm)	0.030	-0.553	0.213	0.606
Grain width (mm)	0.341	-0.436	-0.749	0.314
Grain length to grain width ratio	-0.290	0.384	0.838	-0.147
Grain yield (kg/m <sup>2</sup> )	0.292	0.764	-0.073	0.226
Eigenvalue	4.88	2.78	1.9	1.47
Percentage of variance	34.85	19.84	13.53	10.48
Cumulative percentage of variance	34.85	54.69	68.22	78.71

The eigen values ranged from 4.88 (PC1) to 1.47 (PC4) (Table 4). The first four Principal components accounted for 78.71% of total variation among 49 genotypes based on 14 morphological characters studied. It also indicates that the first principal component contributed 34.85% of the total variation. The second component accounted for 19.84% of the total variation. The third and the fourth principal components accounted for 13.53% and 10.48% of the total variance, respectively. However, all measured traits have positively contributed to the variation in the first principal component except the 1000 grains weight (-0.004) and grain length to grain width ratio (-0.290) which negatively contributed to the variation. Although the major contributors to the variation in the first PC are panicle length (0.887), number of spikelets/panicle (0.881), number of filled grains/panicle (0.871), Number of primary branches/panicle (0.734), plant height (0.701), panicle weight (0.679), days to flowering (0.609), and Days to maturity (0.565). In the second principal component, the number of productive tillers/hill (0.777) and grain yield (0.764) were the most positively contributing characters. In the third principal component traits such as grain length to grain width ratio (0.838) and 1000 grains weight (0.512) explained significant and positive contribution to the variation. The important traits contributing positively and significantly to the variation in the fourth principal component were Grain length (0.606), 1000 grains weight (0.605), and panicle weight (0.502). The PCA plot projection illustrates contribution and association among the variables (

Figure 1a), and illustrates the distribution of the genotypes (

Figure 1b) along with PC1 and PC2.

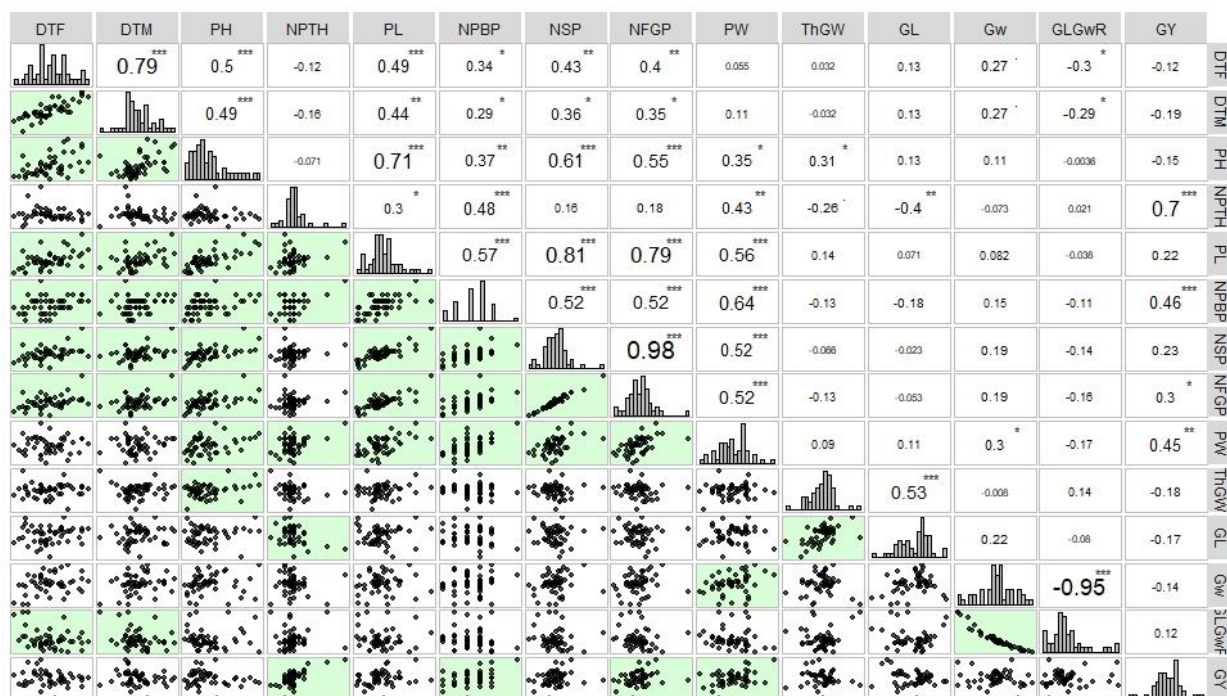


**Figure 1.** Scatter plot showing contribution of the 14 variables (a) and the individuals (b) to the variation observed in PC1 and PC2

3.4. Phenotypic correlation and Path analysis

The phenotypic correlation (

) revealed a significant and positive correlation between grain yield and number of productive tillers per hill (0.7), number of primary branches per panicle (0.46), panicle weight (0.45), and number of filled grains per panicle (0.3). Days to flowering exhibited a highly and positive correlation with days to maturity (0.79), plant height (0.5), panicle length (0.49), number of spikelets per panicle (0.43), number of filled grains per panicle (0.4), and number of primary branches per panicle (0.34), but significant and



negatively correlated with grain length to grain width ratio (-0.3).

**Figure 2.** Association between yield and yield related-traits

DTF: Days to flowering, DTM: Days to maturity, PH: Plant height (cm), NPTH: Number of productive tillers/hill, PL: Panicle length (cm), NPBP: Number of primary branches/panicle, NSP: Number of spikelet/panicle, NFGP: Number of filled grains/panicle, PW: Panicle weight (g), ThGW: 1000 Grains weight, GL: Grain length (mm), Gw: Grain width (mm) and GLGwR: Grain length to grain width ratio, GY: Grain yield (kg/m<sup>2</sup>); \*, \*\* and \*\*\*: significance at 0.05 and 0.01 and 0.001 levels, respectively.

Days to maturity reflected a significant and positive relationship with plant number of filled grains per panicle (0.35), and number of primary branches per panicle (0.29). A significant and negative association was observed between days to maturity and grain length to grain width ratio (-0.29). Plant height showed a highly significant and positive relationship with panicle length (0.71), number of spikelets per panicle (0.61), number of filled grains per panicle (0.55), number of primary branches per panicle (0.37) but significant and positive correlation with panicle weight (0.35) and 1000grains weight (0.31). A positive and highly significant correlation was observed between the number productive of tillers per hill and the number of primary branches per panicle (0.48), panicle weight (0.43) but a significant and positive correlation was exhibited with the panicle length (0.3) while significantly and negatively correlated with grain length (-0.4). Panicle length showed a highly significant and positive relationship with the number

of spikelets per panicle (0.81), the number of filled grains per panicle (0.79), the number of primary branches per panicle (0.57), and panicle weight (0.56). A positive and highly significant correlation was observed between the number of primary branches per panicle with panicle weight (0.64), the number of spikelets per panicle (0.52), and the number of filled grains per panicle (0.52). The number of spikelets per panicle reflected a highly significant and positive correlation with the number of filled grains per panicle (0.98) and panicle weight (0.52). The number of filled grains per panicle exhibited a highly significant and positive association with panicle weight (0.52). Panicle weight showed significant and positive relationship with grain width (0.3). 1000grains weight reflected a highly significant and positive correlation with grain length (0.53) while grain width showed a highly significant and negative correlation with grain length to grain width ratio (-0.95).

Phenotypic path analysis (Table 5) was performed to assess the direct and indirect effects of the yield components on grain yield. It revealed a strong and positive direct effect on grain yield by the number of productive tillers per hill (0.3816), followed by the number of filled grains per panicle (0.3758), and panicle weight (0.3426), while weak and direct effect for days to flowering (0.0810), grain length (0.0795), 1000grains weight (0.0676), and the number of primary branches per panicle (0.0480). While negative direct effects on yield were observed on grain width (-0.5266), grain length to grain width ratio (-0.3471), plant height (-0.2245), panicle length (-0.1459), and days to maturity (-0.1071).

**Table 5.** Phenotypic path analysis of yield and yield related-traits among 49 rice genotypes

	DTF	DTM	PH	NPTH	PL	NPBP	NSP	NFGP	PW	ThGW	GL	Gw	GLGwR
DTF	<b>0.081</b>	-0.08	-0.104	-0.032	-0.063	0.012	-0.01	0.111	0.015	0.003	0.005	-0.109	0.086
DTM	0.061	<b>-0.107</b>	-0.103	-0.06	-0.054	0.011	-0.009	0.097	0.03	-0.003	0.006	-0.132	0.096
PH	0.038	-0.049	<b>-0.225</b>	-0.034	-0.089	0.013	-0.016	0.179	0.096	0.019	0.005	-0.051	-0.001
NPTH	-0.007	0.017	0.02	<b>0.382</b>	-0.04	0.023	-0.005	0.077	0.137	-0.013	-0.024	0.016	0.002
PL	0.035	-0.04	-0.137	0.105	<b>-0.146</b>	0.026	-0.023	0.272	0.2	0.008	0.000	-0.046	0.023
NPBP	0.02	-0.025	-0.059	0.18	-0.08	<b>0.048</b>	-0.016	0.192	0.212	-0.009	-0.016	-0.087	0.06
NSP	0.027	-0.03	-0.12	0.066	-0.112	0.025	<b>-0.03</b>	0.365	0.191	-0.001	-0.005	-0.1	0.053
NFGP	0.024	-0.028	-0.107	0.079	-0.106	0.025	-0.029	<b>0.376</b>	0.187	-0.005	-0.007	-0.092	0.053
PW	0.004	-0.01	-0.063	0.153	-0.085	0.03	-0.017	0.205	<b>0.343</b>	0.003	0.005	-0.146	0.059
ThGW	0.003	0.005	-0.064	-0.075	-0.018	-0.006	0.001	-0.029	0.015	<b>0.068</b>	0.03	0.000	-0.045
GL	0.005	-0.008	-0.015	-0.116	-0.001	-0.01	0.002	-0.032	0.019	0.025	<b>0.08</b>	-0.067	-0.033
Gw	0.017	-0.027	-0.022	-0.011	-0.013	0.008	-0.006	0.066	0.095	0.000	0.01	<b>-0.527</b>	0.319
GLGwR	-0.02	0.03	-0.001	-0.003	0.01	-0.008	0.005	-0.057	-0.058	0.009	0.008	0.483	<b>-0.347</b>

DTF: Days to flowering, DTM: Days to maturity, PH: Plant height (cm), NPTH: Number of productive tillers/hill, PL: Panicle length (cm), NPBP: Number of primary branches/panicle, NSP: Number of spikelet/panicle, NFGP: Number of filled grains/panicle, PW: Panicle weight (g), ThGW: 1000 Grains weight, GL: Grain length (mm), Gw: Grain width (mm) and GLGwR: Grain length to grain width ratio, GY: Grain yield (kg/m<sup>2</sup>).

Considerable positive indirect effects on yield were observed in the number of spikelets per panicle (0.365) and panicle length (0.272) via the number of filled grains per panicle. Positive indirect effect for the number of spikelets via panicle weight (0.191), panicle length (0.2), and the number of filled grains per panicle (0.187) all via panicle weight. A considerable positive indirect effect on yield was also reflected by the number of primary branches per panicle via panicle weight (0.212) and via the number of filled grains per panicle (0.192).

### 3.5. Cluster analysis

The forty-nine rice genotypes in the collection were grouped in three main clusters based on phenotypic traits (Figure ). The three groups have 33, 3, and 13 genotypes, respectively. Mean performance of clusters for all the studied traits presented in Table 6 revealed that Cluster I had the lower plant height mean indicating that this group could be a good source of dwarf parental lines. Whereas cluster II, with high mean performance for number productive tillers/hill, number of primary branches/panicle, panicle weight and number of filled grains/panicle, has gathered high yielding genotypes with major yield contributing traits. Cluster I as well as Cluster II are characterized by early flowering and maturing genotypes. Cluster III has high mean performance for characters such us days to flowering, days to maturity, plant height, 1000grains weight, and grain width.

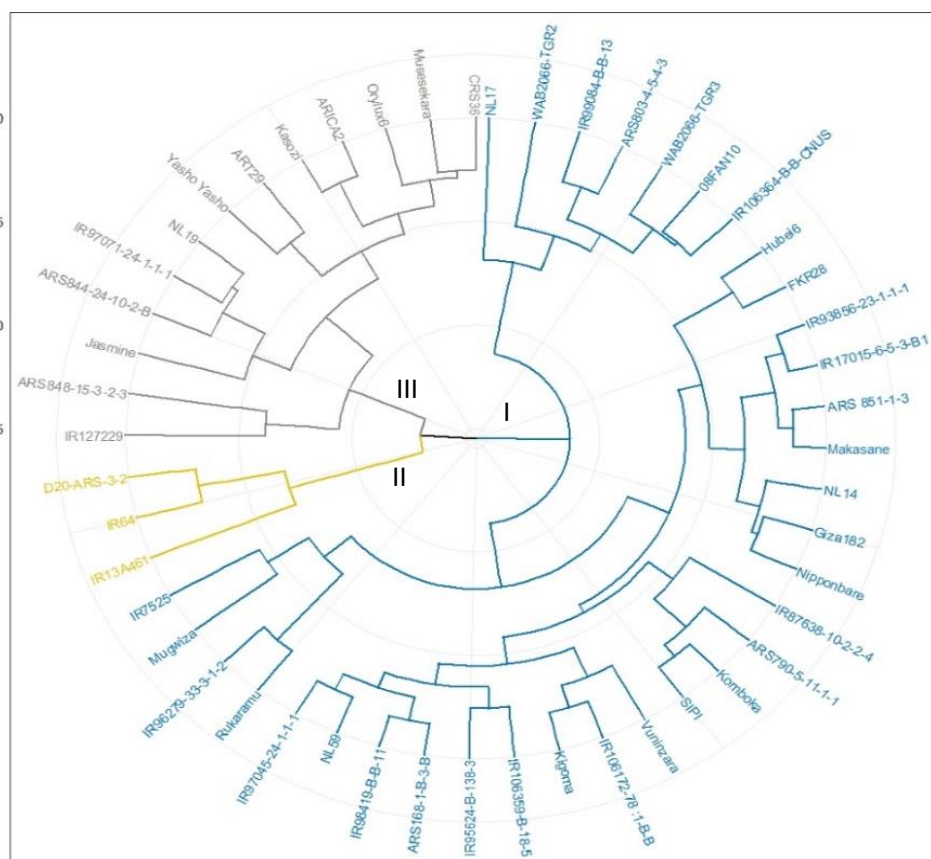


Figure 3. Hierarchical clustering of 49 rice genotypes based on yield and its components



**Table 6.** Mean performance of yield and yield components for clusters

Cluster	Number of genotypes	DTF	DTM	PH	NPTh	PL	NPBP	NSP	NFGP	PW	ThGW	GL	Gw	GLGwR	GY
I	33	108	146	90.8	16	24.1	10	175	159	3.27	27.72	8.87	2.50	3.73	3.56
II	3	106	144	92.4	23	26.4	12	210	191	4.12	26.30	8.33	2.07	4.54	4.15
III	13	116	157	103.5	15	26.2	11	208	187	3.71	28.27	8.94	2.77	3.43	3.58

DTF: Days to flowering, DTM: Days to maturity, PH: Plant height (cm), NPTh: Number of productive tillers/hill, PL: Panicle length (cm), NPBP: Number of primary branches/panicle, NSP: Number of spikelet/panicle, NFGP: Number of filled grains/panicle, PW: Panicle weight (g), ThGW: 1000 Grains weight, GL: Grain length (mm), Gw: Grain width (mm) and GLGwR: Grain length to grain width ratio, GY: Grain yield (kg/m<sup>2</sup>).

Cluster I is comprised of genotypes whose some (NL17, WAB2066-TGR3, WAB2066-TGR2, IR106364-B-B-CNUS, 08FAN10, IR99084-B-B-13, and ARS803-4-5-4-3) had better characters such as for short duration to flowering and to maturity with short plant height characteristic (WAB2066-TGR3, IR106364-B-B-CNUS, WAB2066-TGR2, IR7525 and IR99084-B-B-13). Whereas Cluster II includes genotypes (D20-ARS-3-2, IR64, IR13A461) which performed better for traits such as grain yield and number of productive tillers per hill. Whereas, high performance on other yield components such as number of productive tillers per hill, number of filled grains per panicle, number of spikelets per panicle, panicle weight, number of primary branches per panicle, and panicle weight were observed on IR13A461.

## 4. Discussion

### 4.1. Variance and genetic parameters, Heritability, and Genetic advance analysis

Sustainable development of high-yielding rice varieties is one of the major objectives of rice breeding programs [11]. Improvement of the crop can be achieved when there is wide genetic variation within the germplasm available to the breeder [20]. In this study, a set of 49 representative rice genotypes randomly selected from the germplasm accessions which included genotypes from the National Institute of Study and Agriculture Research (INERA-Kalemie), International Institute for Tropical Agriculture (IITA), and International Rice Research Institute (IRRI-Burundi), were assessed for the genetic variation among them and the association between grain yield and its components.

The genotypes were significantly different ( $P < 0.001$ ) for all studied traits except for grain length. Similar results were reported by Abebe et al.[21], indicating the existence of a wide range of genetic variation within the germplasm and revealing potential for genetic improvement through selection and hybridization for the measured traits. Rashid et al.[22] also found similar results among 34 rice genotypes for all the traits they studied.

The high PCV than the corresponding GCV observed in this study explained the presence of environmental effects on the phenotypic expression of all the studied characters. Similar results were reported by Rashmi et al.[13], Hannan et al.[23], and Htwe et al.[24].

However, the results showed high GCV than ECV for all the traits except for number of primary branches/panicle, grain length, and grain yield. It could be noted the traits in the current study were mainly explained by genetic components and less affected by the environment. Studies reported by Abebe et al.[21] and Girma et al. [12] showed a small environmental influence on most of the yield components. Thus, selection based on the traits like days to flowering, days to maturity, number of

productive tillers per hill, number of spikelets per panicle, number of filled grains per panicle, panicle weight, and 1000 grains weight could be effective in further improvement. These findings were in accordance with the results obtained by Dhakal et al.[25].

Heritability is an important parameter for estimating the proportion of the phenotypic variation in a population that is explained by the genetic components [25]. Heritability informs breeders on the magnitude of transmissibility of a particular trait while genetic advance estimates the measure of genetic gain in selection [23]. In the present study high heritability and genetic advance of the mean (GAM) respectively, were observed for grain length to grain width ratio (78.69% and 41.97%), grain width (77.98% and 35.02%), number of spikelet/panicle (68.70% and 22.97%) and number of filled grains/panicle (61.45% and 22.03%), indicating that these traits are under high genetic control and less influenced by environment in its expression. therefore, improvement can be achieved effectively by direct selection based on these traits [26]. Lipi et al.[27] have also reported high heritability and genetic advance for the number of spikelet/panicle and the number of filled grains/panicle. A similar result was reported by Islam et al.[28] for filled grain per panicle.

High heritability and moderate GAM, respectively, are reflected by days to flowering (88.58% and 10.29%), plant height (87.75% and 19.18%), panicle length (71.31% and 11.02%), and 1000 grains weight (66.64% and 11.64%), revealing that the characters are less influenced by environment in its expression and governed by both additive and non-additive gene action. This indicated a possibility of direct selection for the improvement of these traits [12].

High heritability (89.84%) coupled with low GAM (8.43%) days to maturity, showing non-additive gene action for the expressions of these characters. Direct selection for this trait might not be effective. Moderate heritability coupled with moderate GAM showed by panicle weight (59.34% and 19.84%), the number of productive tillers/hill (50.04% and 19.63%), and the number of primary branches/panicle (42.75% and 12.36%), implies that improvement can be made through simple selection [21]. Grain yield showed moderate heritability (43.19%) and low GAM (7.78%). This informed that this trait is totally governed by non-additive gene action and highly affected by the environment. Thus, heterosis breeding could be used for such traits [12].

Low heritability and low GAM, respectively exhibited by grain length (13.35%, and 1.39%), indicated that direct selection for this trait will not be effective. Therefore, methods of selection based on families and progeny testing are more effective and efficient [21].

#### 4.2. Principal component analysis

Principle component analysis was used to identify the contribution of the variables (traits) towards variation observed in a given population [29]. It is very important in the selection procedure of the breeding program because it helps to identify the traits which have a great impact on the phenotype of the rice germplasm accessions [30].

The results of the principal component analysis showed that the first four principal components with eigen values greater than one accounted for 78.7% of the total variation. The characters associated with these four components are more useful in differentiating the genotypes. Similar results were also reported by Tonegnikes et al.[31]. The major discriminatory characteristics among the genotypes are panicle length, number of spikelets/panicle, number of filled grains/panicle, plant height, and number of productive tillers/hill. This is similar to the findings of Sudeepthi et al.[32] for panicle weight and plant height. Therefore, selection of improved lines can be based on these morphological traits.



#### 4.3. Correlation and path analysis

Grain yield is a complex trait in cereals; controlled by several genes and more influenced by the environment. Rice grain yield is determined by a combination of direct and indirect actions of the yield components [33], [34].

In rice improvement, the direct selection of genotypes based on yield may mislead the breeding program. Determining the direct and indirect effects of various traits on grain yield is critical in determining an appropriate selection criteria for high grain yield [35]. The present study revealed high and positive correlation between grain yield and the number of productive tillers per hill, number of primary branches per panicle, panicle weight, and number of filled grains per panicle. These traits are more reliable components of grain yield. Improvement of these traits through direct selection are more likely to lead to the overall improvement of grain yield. Similar results have been obtained by Akhi et al.[36], and Saleh et al.[37] on the number of productive tillers per hill and the number of filled grains per panicle. Rashmi et al.[13] and Kafi et al.[38] also reported a positive association between grain yield with panicle weight, filled grains per panicle, and grains per panicle. In a study by Tonegnikes et al.[31], in Nigeria using Korean rice germplasm also confirmed positive association between yield and number of productive tillers per hill, panicle weight, number of filled grains per panicle, and number of spikelets per panicle. Andrew et al.[39] have also reported a positive and significant association between grain yield and effective tiller number, grain weight per plant, and the number of grains per panicle. Evaluating Tanzania rice germplasm collections, Suvi et al.[34] found similar results for the association between grain yield and number of productive tillers/hill (number of panicles per plant), number of filled grains/panicle (percentage-filled grains).

Amegan et al.[40] have also reported no relationship between grain yield with plant height and 1000grains weight. This results do not corroborate with findings of Suvi et al. [34] on 1000grains weight.

Path analysis revealed a strong and positive direct contribution of the number of productive tillers per hill, number of filled grains per panicle, and panicle weight to grain yield. Positive indirect effects on grain yield were shown by the number of spikelets per panicle, panicle length and the number of primary branches per panicle. Rashmi et al.[13] have also reported that panicle weight, number of effective tillers per plant, and filled grains per panicle as the major direct contributors to grain yield.

#### 4.4. Cluster analysis

Cluster analysis shows the relationships by grouping together most similar genotypes in the population. Basically, the hybridization of genotypes of the same cluster may not give superior hybrids or segregants, because of the negligible divergence that is among them.

Three major clusters (I, II, and III) were obtained among the 49 genotypes in this study indicating divergence among the breeding material. Shrestha et al.[41] have reported seven clusters in evaluating forty rice genotypes based on growth and yield traits.

Parental lines can be selected from the different clusters identified in this study for crosses to improve various traits such as grain yield, shortening of the plant height, and earliness [41]. Thus, crosses could be directed between high-yielding genotypes (D20-ARS-3-2, IR64, IR13A461) all from cluster II and early maturing genotypes (WAB2066-TGR2, IR106364-B-B-CNUS, and NL17) from cluster I to develop high yielding and early maturing genotypes.

Genotypes such as WAB2066-TGR3, IR106364-B-B-CNUS, WAB2066-TGR2, IR7525 and IR99084-B-B-13 from cluster I could be better parents for breeding for dwarf rice varieties.

Cluster III could be the source of parents for traits such as grain yield, number of productive tillers per hill, number of filled grains per panicle, number of spikelets per panicle, panicle weight, and number of primary branches per panicle and panicle weight.

## 5. Conclusion

This study revealed that wide genetic variation exists in the germplasm for rice breeding program in the Eastern Democratic Republic of Congo, based on a representative set of 49 genotypes, randomly selected from the rice breeding program germplasm. This informs breeders of the opportunity to select better parental types to improve the grain yield using the available germplasm in order to address food security.

Traits such as panicle length, plant height, number of primary branches/panicles, number of spikelets/panicle, number of filled grains/panicle, panicle weight, number of productive tillers/hill, grain yield, 1000 grains weight, and grain length to grain width ratio were identified as the major discriminator traits among the genotypes.

The phenotypic correlation analysis showed that grain yield was significantly and positively correlated with the number of productive tillers per hill, number of primary branches per panicle, panicle weight, and number of filled grains per panicle. Breeders should give priority to these traits during the selection process in rice grain yield improvement program.

Based on fourteen phenotypic traits, the genotypes were grouped into three divergent clusters. The divergence will be useful for the rice improvement program since there is sufficient variation to select for various yield components. Crosses can be made among promising individuals from different clusters for grain yield improvements. Genotypes such as D20-ARS-3-2, IR64, and IR13A461 are promising parents for the development of high-yielding rice varieties. WAB2066-TGR3, IR106364-B-B-CNUS, WAB2066-TGR2, and IR99084-B-B-13 could be included for breeding for dwarf rice varieties, and WAB2066-TGR2, IR106364-B-B-CNUS, and NL17 could be better parents in breeding for early maturing varieties.

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## References

- [1] Campos, H., & Caligari, P. D. S. (2017). Genetic improvement of tropical crops. In *Genetic Improvement of Tropical Crops*. <https://doi.org/10.1007/978-3-319-59819-2>
- [2] Seck, P. A., Diagne, A., Mohanty, S., and Wopereis, M. C. S. (2012) Crops That Feed the World 7: Rice. *Food Sec.*, 4 (1), 7–24. <https://doi.org/10.1007/s12571-012-0168-1>.
- [3] Calayugan, M. I. C., Swamy, M. B. P., Nha, C. T., Palanog, A. D., Biswas, P. S., Descalsota-Empleo, G. I., Min, Y. M. M., and Inabangan-Asilo, M. A. (2021) Zinc-Biofortified Rice: A Sustainable Food Based Product for Fighting Zinc Malnutrition. In: Ali, J. A., Wani, S. H., *Rice Improvement: Physiological, Molecular Breeding and Genetic Perspectives*; Eds.; Springer International Publishing: Gewerbestrasse 11, 6330 Cham, Switzerland, pp 449–470. <https://doi.org/10.1007/978-3-030-66530-2>.
- [4] Wakey, L. (2017) The Challenges of Rice Sustainability: The Increasing World's Population and Climate Change. *SpringerOpen Blog*. <http://blogs.springeropen.com/springeropen/2017/04/19/challenges-rice-sustainability-increasing-worlds-population-climate-change/>
- [5] Bado, V. B., Djaman, K., and Mel, V. C. (2018) Developing Fertilizer Recommendations for Rice in Sub-Saharan Africa, Achievements and Opportunities. *Paddy and Water Environment*, 16 (3), 571–586. <https://doi.org/10.1007/s10333-018-0649-8>.
- [6] Seck, P. A., Touré, A. A., Coulibaly, J. Y., Diagne, A., and Wopereis, M. C. S. (2013) Africa's Rice Economy Before and After the 2008 Rice Crisis. In: Wopereis MCS, Johnson DE, Ahmadi N, Tollens E, J. A. *Realizing Africa's rice promise*, Ed. Boston, pp 24–34.
- [7] FAO, FIDA and PAM. (2019) Analyse des pertes alimentaires: Causes et solutions – Études de cas sur le maïs et le riz en République démocratique du Congo.
- [8] MINAGRI, & CARD. (2013) Stratégie nationale de développement de la riziculture (SNDR) (Secrétariat Général de l'Agriculture Pêche et Elevage, Ed. Kinshasa.
- [9] MINAGRI. (2018) Sécurité alimentaire, niveau de production agricole et Animale, Évaluation de la Campagne Agricole 2017- 2018 et Bilan Alimentaire du Pays.
- [10] Ahmadi, N., Audebert, A., Bennett, M. J., Bishopp, A., de Oliveira, A. C., Courtois, B., Diedhiou, A., Diévert, A., Gantet, P., Ghesquière, A., Guiderdoni, E., Henry, A., Inukai, Y., Kochian, L., Laplaze, L., Lucas, M., Luu, D. T., Manneh, B., Mo, X., Muthurajan, R., Périn, C., Price, A., Robin, S., Sentenac, H., Sine, B., Uga, Y., Véry, A. A., Wissuwa, M., Wu, P., Xu, J. (2014) The Roots of Future Rice Harvests. *Rice*, 7 (1), 29. <https://doi.org/10.1186/s12284-014-0029-y>.
- [11] Bhandari, H., Bhanu, N., Srivastava, K., Singh, M., Shreya, Hemantaranjan, A. (2017) Assessment of Genetic Diversity in Crop Plants - An Overview. *Advances in Plants & Agriculture Research*, 7 (3), 279–286. <https://doi.org/10.15406/apar.2017.07.00255>.
- [12] Girma, B. T., Kitil, M. A., Banje, D. G.; Biru, H. M.; Serbessa, T. B. (2018) Genetic Variability Study of Yield and Yield Related Traits in Rice (*Oryza Sativa* L.) Genotypes. *Adv Crop Sci Tech*, 6 (4), 381.
- [13] Rashmi, D., Saha, S., Loitongbam, B., Singh, S., and Singh, P. K. (2017) Genetic Variability Study for Yield and Yield Components in Rice (*Oryza Sativa* L.). *International Journal of Agriculture, Environment and Biotechnology*, 10 (2), 171. <https://doi.org/10.5958/2230-732x.2017.00020.1>.
- [14] IBPGR-IRRI, Rice Advisory Committee, & I. B. for P. G. R. Descriptors for Rice (*Oryza Sativa* L.) Int. Rice Res. Inst.: Philippines 1980.
- [15] R Core Team (2021) *R: A Language and Environment for Statistical Computing*. <https://cran.r-project.org>
- [16] Johnson, H. W.; Robinson, H. F.; Comstock, R. E. (1955) Estimates of Genetic and Environmental Variability in Soybeans I. *Agronomy Journal*, 47 (7), 314–318. <https://doi.org/10.2134/agronj1955.00021962004700070009x>.
- [17] Silva, T. N., Moro, G. V., Moro, F. V., Santos, D. M. M., and Buzinaro, R. (2016) Correlation and Path Analysis of Agronomic and Morphological Traits in Maize. *Revista Ciência Agronômica*, 47 (2). <https://doi.org/10.5935/1806-6690.20160041>.
- [18] The jamovi project (2022). *Jamovi [Computer Software]*. <https://www.jamovi.org>
- [19] Robinson, H. F., Comstock, R. E., and Harvey, P. H. (1949) Estimates of Heritability and the Degree of Dominance in Corn<sup>1</sup>. *Agronomy Journal*, 41 (8), 353–359. <https://doi.org/10.2134/agronj1949.00021962004100080005x>.

- [20] Ibrahim, S., Alex, T., Maxwell, D. A., Daniel, N., and Richard, A. (2019) Genetic Diversity Analyses of Rice Germplasm Using Morphological Traits. *Journal of Plant Breeding and Crop Science*, **11** (4), 128–136. <https://doi.org/10.5897/jpbcs2018.0786>.
- [21] Abebe, T., Alamerew, S., and Tulu, L. (2017) Genetic Variability, Heritability and Genetic Advance for Yield and Its Related Traits in Rainfed Lowland Rice (*Oryza Sativa* L.) Genotypes at Fogera and Pawe, Ethiopia. *Advances in Crop Science and Technology*, **05** (02), 272. <https://doi.org/10.4172/2329-8863.1000272>.
- [22] Rashid, M., Nuruzzaman, M., Hassan, L., and Begum, S. (2017) Genetic Variability Analysis for Various Yield Attributing Traits in Rice Genotypes. *Journal of the Bangladesh Agricultural University*, **15** (1), 15–19. <https://doi.org/10.3329/jbau.v15i1.33525>.
- [23] Hannan, A., Rana, M., Hoque, M., and Sagor, G. (2020) Genetic Variability, Character Association and Divergence Analysis for Agro-Morphological Traits of Local Rice (*Oryza Sativa* L.) Germplasms in Bangladesh. *Journal of Bangladesh Agricultural University*, No. 0, 1. <https://doi.org/10.5455/jbau.84906>.
- [24] Htwe, N. M., Phyu, S. L., and Thu, C. N. (2019) Assessment of Genetic Variability and Character Association of Myanmar Local Rice (*Oryza Sativa* L.) Germplasm. *Journal of Experimental Agriculture International*, No. September, 1–10. <https://doi.org/10.9734/jeai/2019/v40i330369>.
- [25] Dhakal, A., Sharma, S., Pokhrel, A., and Poudel, A. (2020) Variability and Heritability Estimate of 30 Rice Landraces of Lamjung and Tanahun Districts, Nepal. *Indonesian Journal of Agricultural Science*, **21** (1), 1-10. <https://doi.org/10.21082/ijas.v21n1.2020.p1-10>.
- [26] Iqbal, T., Nazir Ahmad, I. H., Muhammad Zia, M. N., and Ali, F. (2018) Genetic Variability, Correlation and Cluster Analysis in Elite Lines of Rice. *Journal of Scientific Agriculture*, **2**, 85-91. <https://doi.org/10.25081/jsa.2018.v2.900>.
- [27] Lipi, L., Hasan, M., Akter, A., Quddus, M., Biswas, P., Ansari, A., and Akter, S. (2021) Genetic Variation, Heritability and Genetic Advance in Some Promising Rice Hybrids. *SAARC Journal of Agriculture*, **18** (2), 39–49. <https://doi.org/10.3329/sja.v18i2.51107>.
- [28] Islam, M., Raffi, S., Hossain, M., and Hasan, A. (2015) Analysis of Genetic Variability, Heritability and Genetic Advance for Yield and Yield Associated Traits in Some Promising Advanced Lines of Rice. *Progressive Agriculture*, **26** (1), 26–31. <https://doi.org/10.3329/pa.v26i1.24511>.
- [29] Kashyap, A., and Yadav, V. K. (2020) Principal Component Analysis and Character Association for Yield Components in Rice (*Oryza Sativa* L.) Genotypes of Salt Tolerance under Alkaline Condition. *International Journal of Current Microbiology and Applied Sciences*, **9** (10), 481–495. <https://doi.org/10.20546/ijcmas.2020.910.059>.
- [30] Burman, M., Nair, S. K., and Sarawgi, A. K. (2021) Principal Component Analysis for Yield and Its Attributing Traits in Aromatic Landraces of Rice (*Oryza Sativa* L.), *International Journal of Bio-Resource & Stress Management*, **12**(4), **12** (4), 303–308.
- [31] Tonegnikis, S., Efiuse, A., Adetimirin, V., Shittu, A., and Amegan, E. (2019) Evaluation of Korea Rice Germplasm for Yield and Yield Components Adaptable to Nigeria Environmental Conditions, **7** (5), 106–116. <https://doi.org/10.11648/j.jps.20190705.12>.
- [32] Sudeepthi, K., Srinivas, T., Ravi Kumar, B. N., Jyothula, D. P. B., and Nafeez Umar, Sk. (2020) Genetic Diversity and Principal Component Analysis for Yield and Nutritional Traits in Rice (*Oryza Sativa* L.). *International Journal of Current Microbiology and Applied Sciences*, **9** (11), 1916–1928. <https://doi.org/10.20546/ijcmas.2020.911.227>.
- [33] Li, R., Li, M., Ashraf, U., Liu, S., and Zhang, J. (2019) Exploring the Relationships between Yield and Yield-Related Traits for Rice Varieties Released in China from 1978 to 2017. *Frontiers in Plant Science*, **10** (543), 1-12 <https://doi.org/10.3389/fpls.2019.00543>.
- [34] Suvi, W. T., Shimelis, H., Laing, M., Mathew, I., Shayanowako, A. I. T. (2021) Variation among Tanzania Rice Germplasm Collections Based on Agronomic Traits and Resistance to Rice Yellow Mottle Virus. *Agronomy*, **11** (2), 391. <https://doi.org/10.3390/agronomy11020391>.
- [35] Oladosu, Y., Rafii, M. Y., Magaji, U., Abdullah, N., Miah, G., Chukwu, S. C., Hussin, G., Ramli, A., and Kareem, I. (2018) Genotypic and Phenotypic Relationship among Yield Components in Rice under Tropical Conditions. *BioMed Research International*, 2018. <https://doi.org/10.1155/2018/8936767>.
- [36] Akhi, A. H., Miah, M. A. k., Ivy, N. A., Islam, A., and Islam, M. Z. (2016) Association of Yield and Yield Related Traits in Aromatic Rice (*Oryza Sativa* L.). *Bangladesh Journal Agril. Research*, **3** (41), 387–396.

- [37] Saleh, M. M., Salem, K. F. M., and Elabd, A. B. (2020) Definition of Selection Criterion Using Correlation and Path Coefficient Analysis in Rice (*Oryza Sativa* L.) Genotypes. *Bulletin of the National Research Centre*, **44** (1), 1-6
- [38] Kafi, S. H., Abiodun, E. A., Bunmi, O., and Kyung-ho, K. (2021) Correlation Coefficient and Path Analyses of Yield and Yield Related Traits of Korean Double Haploid Rice for Germplasm Improvement in Nigeria. *American Journal of Agriculture and Forestry*, **9** (3), 114–121. <https://doi.org/10.11648/j.ajaf.20210903.13>.
- [39] Andrew, A. E., Bianca, C. U., and Joseph, A. O. (2014) Effects of Yield Components on Yield Potential of Some Lowland Rice (*Oryza Sativa* L.) in Coastal Region of Southern Nigeria. *Journal of Plant Breeding and Crop Science*, **6** (9), 119–127. <https://doi.org/10.5897/jpbcs2014.0449>.
- [40] Amegan, E., Efisue, A., Akoroda, M., Shittu, A., and Tonegnikes, F. (2020) Genetic Diversity of Korean Rice (*Oryza Sativa* L.) Germplasm for Yield and Yield Related Traits for Adoption in Rice Farming System in Nigeria. *IJGG*, **8** (1), 19. <https://doi.org/10.11648/j.ijgg.20200801.13>.
- [41] Shrestha, J., Subedi, S., and Kushwaha, U. K. S. (2021) Maharjan, B. Evaluation of Growth and Yield Traits in Rice Genotypes Using Multivariate Analysis. *Heliyon*, **7** (9), 1-6. <https://doi.org/10.1016/j.heliyon.2021.e07940>.