

GENETIC VARIABILITY OF SOME PHYSIOLOGICAL TRAITS, YIELD COMPONENTS AND GRAIN QUALITY CHARACTERS IN RICE ENTRIES

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An experiment was performed to evaluate the variability parameters of the quantitative features in fifteen rice genotypes planted during the growing seasons of 2020 and 2021. These genotypes were grown in three replications with a randomized complete block design. For all of the studied characters, analysis of variance revealed that variations between the genotypes were highly significant. Among the studied phenotypic and genotypic parameters, the number of filled grains/panicles showed the highest variations, while grain width had the lowest value in this respect. The highest genotypic coefficient of variation (GCV) was found for grain yield while hulling rice % had the lowest GCV. In yields, the genotypic and phenotypic coefficients were the highest, clarifying the action of additive genes in commanding these traits. Most of the studied traits had a high heritability. The highest genetic advance value (98.06) was determined for the number of filled grains/panicles, while total chlorophyll content had the lowest value (0.11). Five principal components with eigenvalues above 1 were identified using principal component analysis. The first and second principal components were responsible for about 30.34 and 15.24 of the total variation, respectively, indicating that these traits played a larger role in the overall clustering distinction of the populations. Rice enhancement programs can be more successful if selection efforts are focused on these characteristics. Cluster analyses of the fifteen genotypes have grouped the genotypes into five clusters based on the data taken. Genotypes found in Cluster II had the highest thousand-grain weights, grain yield and head rice, and they could be recommended for breeding due to these favourable parameters of height, yield and head rice percentage.

Key words: phenotypic coefficient of variation, total chlorophyll content, leaf area characters, cluster analysis, rice yield

The flag leaf in rice acts an essential part in grain yield and has been studied by some researchers such as Kumar *et al.* (2018). Flag leaf contributes grain weight by 41–43% and is an indicator of the potential yield of grain (Al-Tahir 2014; Yuan *et al.* 2015). Flag leaf area subscribes by increasing chlorophyll content and fresh weight (Kartahadi-maja *et al.* 2021) and contributes to over 50% of

carbohydrate accumulation in grains (Briggs & Aytenfisu 1980; Gladun and Karpov 2015; Niu *et al.* 2022). This character plays a key role in fixing the photosynthetic capacity of the plant, and it has the appearance of a complex trait with two main component factors: flag leaf length and width (Jiantao *et al.* 2017). The grain yield, flag leaf, and grain quality are the traits targeted for the im-

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provement of rice productivity (Paikhomba *et al.* 2013).

A broad range of genetic patterns serving as new bases for plant breeding is provided by genetic variation (Williams *et al.* 2021). The existence of genetic variability for agricultural traits is a key component of breeding programs to expand Rice's gene pool requires credible determines of heritability for planning breeding programs (Akinwale *et al.* 2011). Knowledge concerning the heritability of plant breeders helps to foretell the nature of the following generation, and for selecting and evaluating the extent of genetic improvement by selection (Tuhina-Khatun *et al.* 2007; Ghimire & Hamat 2019). Genetic plant improvement is based on the predictive function of heritability which indicates the transmissibility of various traits descending through generations (Khan & Naqvi 2011). Genetic variability, heritability and selection strength are all factors to consider the genetic advance for different traits (Rahman *et al.* 2015). Rice cultivars with identical characteristics are identified using cluster analysis. Principal component analysis (PCA) as described by Diako *et al.* (2011) was used to define trends and investigate associations between different parameters and rice samples, PCA is a multivariate statistical analysis that uses a linear combination of variables to minimize data with a large number of associated variables into a much smaller collection of new variables that computes most of the variations contained in the original variables (Das *et al.* 2018). PCA aims to find the smallest number of components that can explain the most variance out of all the variables (Nachimuthu *et al.* 2014). This method seeks a linear combination of the column with maximum variance or equivalently (Singh *et al.* 2018).

This study aimed to determine the variability among rice genotypes in flag leaf traits, yield, and grain quality to figure out the extent of variation among genotypes and their genetic diversity. This aids the understanding of the genetic basis of the investigated rice genotypes and their significance in rice breeding. The investigated genotypes with similar traits were organized into groups providing genetic bases for plant breeding programmes. The genetic parameters such as coefficient of genetics advance, variance and heritability were estimated to

select criteria for the improvement of yield components, leaf, and grain quality characters.

MATERIAL AND METHODS

Fifteen local and exotic rice (*Oryza sativa* L.) varieties (Table 1) with variable characteristics of leaves, yield and grain quality characteristics were used as given by the genetic stock of the Rice Research and Training Centre Sakha, Egypt. The varieties were grown in the rice growing seasons of 2020 and 2021 in three replications with randomized complete block design. Each replication had three rows. Plants were individually transplanted at a spacing of 20 × 20 cm between the seedlings and rows in both seasons. The applied agrotechnology was according to the recommended practices.

Five random plants from each entry, at the stage of soft dough, were used to study some parameters. The parameters studied were plant height [cm], flag leaf length [cm], flag leaf width [maximum width, cm], dry weight of flag leaf [g], and flag leaf area [cm²]. At harvest, ten panicles were randomly selected from each guarded hill to determine the number of filled grains. Five guarded square meters were manually harvested and left for three days for air drying. Plants were mechanically threshed after being air dried, and grain yield was measured and balanced to a moisture content of 14%. Grain samples were taken from each plot to determine 1,000-grain weight [g] and yield [g/m²]. Then, for all samples, 150 grams of rough rice (three replications) were taken and thoroughly mixed, and cleaned to test the grain quality characters, milling recovery was estimated according to Adair (1952). Fresh leaves of rice plants at the heading stage were used to determine the chlorophyll content according to the method of Arnon (1949).

All data gathered were statistically analysed according to Steel *et al.* (1997). Phenotypic [σ^2_{ph}] and genotypic [σ^2_g] variances were determined according to the equations by Burton and DeVane (1953): $\sigma^2_g = M1 - M2/r$; $\sigma^2_e = M3$; $\sigma^2_p = \sigma^2_g + \sigma^2_{gy} + \sigma^2_e$, where M1, M2 are the mean squares of the varieties and mean square due to varieties x year interaction,

respectively, $M3$ is the error mean squares, σ^2g is the genotypic variance, σ^2e is the environmental variance, σ^2p is the phenotypic variance, σ^2gy is the genotypes x environmental variance interaction, and r is the number of replications.

Burton (1952) defined the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) as:

$$PCV [\%] = (\sigma^2p / \bar{x}) \times 100; GCV (\%) = (\sigma^2g / \bar{x}) \times 100,$$

where \bar{x} = grand mean of the character under study. Broad sense heritability (h^2_{BS}) for each trait was computed according to Falconer's (1989) equation: $h^2_{BS} = \sigma^2g / \sigma^2p \times 100$. The expected genetic advance (GA) was determined by Allard's (1960) formula:

$$GA = k \times \sigma^2p \times h^2_{BS},$$

where k is the standardized selection differential constant (2.06) at 5% selection intensity. Genetic advance as a percent of the mean (GA [%]) was calculated according to the formula of Comstock and Robinson (1952): GA [%] = genetic advance of particular trait / $\bar{x} \times 100$. Ward's (1963) method was

used to group genotypes into clusters. After preliminary auto-scaling of the variables with the MATLAB 5.1 routine.

Given that our evaluated parameters were measured in different units, we used a correlation matrix which comprises normalizing all variables using division by their standard deviations. PCA was done using the methodology according to Massy (1965) and Jolliffe (1986). Kaiser-Meyer-Olkin (KMO) test was performed during the principal component analysis. The KMO test was mainly used for the data of principal component extraction. Generally speaking, the KMO test coefficient values were distributed between 0 and 1. If the coefficient value was greater than 0.5, the sample was considered to meet the requirements of a reasonable data structure (Yao *et al.* 2021).

All data collected were analysed by using the variance technique by means of the "MSTAT" computer software package. Differences among treatments mean were compared by least significant difference (LSD) at $P \leq 0.05$.

T a b l e 1

Parentage and origin of the investigated entries

No.	Entry	Parentage	Origin
1	Giza 179	GZ1368/GZ6296	Egypt
2	Sakha 101	(Giza 176 / Milyang 79)	Egypt
3	Egyptian Yasmin	IR262-43-8-11/KDML105	Egypt
4	Giza 181	(IR1626-203/IR28//IR22)	Egypt
5	GZ 8455-9-1-1-2	Gz5603-3/Kanto 51	Egypt
6	Koshihikari	na*	Japan
7	IET 1444	(TN 1 / CO 29)	India
8	Gaori	Rajeshwari x Vikaram	India
9	IR 52561-UBN-1-1-2	na	IRRI
10	IR 72944-1-2-2	Norin PL/IR68333-R-R-B-22	IRRI
11	Milyang 54	Milyang 21/IR32//Milyang 23/Milyang 30	Korea
12	Milyang 95	na	Korea
13	Wild Rice 3	na	China
14	WAB 450-T-B-P 3811-B	na	Warda
15	NERICA 4	WAB 450-I-B-P-91/HB	Africa Rice Center

Note: *na – not available.

RESULTS

The mean performance of genotypes for the studied traits is presented in Tables 2 and 3. The results showed a wide range for all characters of the genotypes under study indicating a high genetic variation among them. Plant height characters (Table 2) showed that the highest plant was found for WAB 450-T-B-P 3811-B (125.23 cm) followed by IR 52561-UBN-1-1-2. The highest value for leaf width of 2.58 cm was obtained for Egyptian Yasmin, Giza 181 was the second with 1.70 cm. Also, WAB 450-T-B-P 3811-B gave the longest leaf (42.75 cm) followed by IET 1,444 (40.88 cm). The highest leaf area was found in IET 1,444 compared with the other genotypes under study. Milyang 54 gave the heaviest dry weight of flag leaf (47.80 g), while in the number of filled grains, Milyang 54 out-

performed the other rice cultivars. Gaori gave the highest average of total chlorophyll content (0.34). While Milyang 95 gave the heaviest thousand-grain weight. Results in Tables 2 and 3 showed that Sakha 101, GZ8455-9-1-1-2, Gaori, Milyang 54, and WAB 450-T-B-P 3811-B genotypes recorded the maximum grain yield (1.96). Grain shape ranged between (1.40 to 3.17). Concerning head rice [%], Nerica 4 gave the highest value.

Data in Table 4 present the mean squares (MS) of the five sources of variance for the studied characters (combined). The mean square estimates showed highly significant differences among the fifteen genotypes for these characters. These results clearly showed the amount of variability that existed among the tested genotypes. The variability manifested in statistically significant differences among the genotypes provides a good basis for further plant breeding.

T a b l e 2

Mean performance values for fifteen studied traits in rice entries (combined data)

No.	Entry	Plant height [cm]	Leaf width [cm]	Leaf length [cm]	Leaf area [cm ²]	Dry leaf weight [g]	Total chlorophyll content [μmol/m ²]	No. of filled grains/panicle	1,000-grain weight [g]
1	Giza 179	98.88 ⁺	1.25 ⁺	32.68 ⁺	35.33 ⁺	21.33 ⁺	0.17 ⁺	169.33 ⁺	2.42
2	Sakha 101	102.40	1.37 ⁺	30.31 ⁺	40.05 ⁺	44.17 ⁺	0.22 ⁺	80.00 ⁺	1.55 ⁺
3	Egyptian Yasmin	115.42 ⁺	2.58 ⁺	39.20 ⁺	46.85 ⁺	33.53	0.28 ⁺	181.50 ⁺	2.77
4	Giza 181	114.32 ⁺	1.70 ⁺	36.55 ⁺	28.84 ⁺	33.93	0.26	122.83 ⁺	2.45
5	GZ8455-9-1-1-2	102.71	1.23 ⁺	35.32	31.33	36.45 ⁺	0.23	166.50 ⁺	2.53
6	Koshihikari	100.61 ⁺	1.08 ⁺	29.33 ⁺	19.32 ⁺	28.92 ⁺	0.22 ⁺	112.83 ⁺	2.62
7	IET 1444	113.92 ⁺	1.62 ⁺	40.88 ⁺	49.00 ⁺	24.48 ⁺	0.29 ⁺	164.00 ⁺	2.46
8	Gaori	88.15 ⁺	1.63 ⁺	33.69	28.22 ⁺	43.50 ⁺	0.34 ⁺	106.17 ⁺	2.51
9	IR 52561-UBN-1-1-2	122.02 ⁺	1.45	34.87	29.97 ⁺	28.67 ⁺	0.29 ⁺	177.17 ⁺	2.18
10	IR 72944 -1-2-2	94.33 ⁺	1.27 ⁺	36.78 ⁺	31.74	34.00	0.25	152.67	2.19
11	Milyang 54	111.97 ⁺	1.43	33.55	23.27 ⁺	47.80 ⁺	0.23	211.17 ⁺	2.37
12	Milyang 95	106.38	1.35 ⁺	32.35 ⁺	26.69 ⁺	32.10 ⁺	0.25	123.50 ⁺	3.53 ⁺
13	Wild Rice 3	89.61 ⁺	1.35 ⁺	30.31 ⁺	24.77 ⁺	33.22	0.27	155.33 ⁺	2.62
14	WAB 450-T-B-P 3811-B	125.23 ⁺	1.01 ⁺	42.75 ⁺	26.33 ⁺	31.85 ⁺	0.24	126.17 ⁺	2.30
15	NERICA 4	102.79	1.33 ⁺	33.18 ⁺	33.13 ⁺	34.30	0.21 ⁺	149.50	2.35
<i>LSD</i>		4.28	0.06	1.35	0.722	0.736	0.016	8.66	0.77

Note:⁺Any difference between the mean performance values larger than *LSD* is considered significant; *LSD* – least significant difference at 0.05 level.

T a b l e 3

Mean performance values for fifteen studied traits in rice entries (combined data)

No.	Entry	Grain yield [kg/m ²]	Grain length [mm]	Grain width [mm]	Grain shape	Hulling rice [%]	Milling rice [%]	Head rice [%]
1	Giza 179	1.62	4.62 ⁺	2.86	1.82 ⁺	86.49 ⁺	69.70	41.47 ⁺
2	Sakha 101	1.96	5.59 ⁺	2.88	1.72 ⁺	77.21 ⁺	66.06 ⁺	58.25 ⁺
3	Egyptian Yasmin	1.87	5.56 ⁺	3.25 ⁺	1.94 ⁺	78.00 ⁺	66.28 ⁺	57.81 ⁺
4	Giza 181	1.62	4.62 ⁺	2.78	2.10	81.85 ⁺	73.82 ⁺	54.93
5	GZ8455-9-1-1-2	1.96	5.59 ⁺	2.92	1.91 ⁺	80.31 ⁺	71.37	60.25 ⁺
6	Koshihikari	1.87	5.56 ⁺	2.94	1.93 ⁺	79.31 ⁺	70.71	58.14 ⁺
7	IET 1444	1.62	4.62 ⁺	3.25 ⁺	1.40 ⁺	81.30	67.49 ⁺	43.58 ⁺
8	Gaori	1.96	5.59 ⁺	2.93	2.03	80.54	70.62	52.35
9	IR 52561 -UBN-1-1-2	1.87	5.56 ⁺	2.60 ⁺	2.73 ⁺	80.09 ⁺	64.28 ⁺	50.47 ⁺
10	IR 72944 -1-2-2	1.62	4.62 ⁺	2.23 ⁺	3.34 ⁺	79.42 ⁺	70.94	51.91
11	Milyang 54	1.96	5.59 ⁺	3.16 ⁺	1.89 ⁺	85.19 ⁺	73.25 ⁺	43.25 ⁺
12	Milyang 95	1.87	5.56 ⁺	2.73 ⁺	2.11	80.10 ⁺	65.51 ⁺	56.03 ⁺
13	Wild Rice 3	1.62	4.62 ⁺	2.29 ⁺	3.17 ⁺	81.63 ⁺	73.16 ⁺	57.71 ⁺
14	WAB 450-T-B-P 3811-B	1.96	5.59 ⁺	3.03 ⁺	1.91 ⁺	82.75 ⁺	73.15 ⁺	53.48
15	NERICA 4	1.87	5.56 ⁺	2.82	2.02	80.05 ⁺	69.83	60.47 ⁺
<i>LSD</i>		0.725	0.159	0.103	0.160	0.629	1.850	1.721

Note: ⁺Any difference between the mean performance values larger than *LSD* is considered significant; *LSD* – least significant difference at 0.05 level.

Data in Table 5 show that the number of filled grains/panicles had the highest PCV and GCV, while the lowest values were found for grain width. For all the studied traits, PCV values were higher than GCV values.

The first five principal components with eigenvalues greater than one were determined by PCA. Other principal components showed eigenvalues less than one were deemed non-significant and were therefore overlooked because they were unlikely to have any functional meaning (Figure 1 and Table 7). Then, there were five main components of which the eigenvalues of PC1–PC5 were 4.551, 2.287, 1.849, 1.666, and 1.237, respectively. KMO test was conducted to examine the strength of the partial correlation between the variables. Taking into account that KMO values closer to 1.0 are considered ideal while values less than 0.5 are unacceptable, our results indicated that a KMO value of 0.539 was good enough

for factor analysis to commence. Bartlett's test indicated that the correlation matrix was not an identity matrix prompting the rejection of the null hypothesis (Table 6). The first component can be considered as a measure of the quality of the leaf area similar to the results of Worede *et al.* (2014) and Maji and Shaibu (2012). Rice enhancement programs can be more successful if selection efforts were focused on these characteristics.

The fifteen genotypes (cultivars) were grouped into five clusters (Figure 2). Among the clusters, the maximum number (4) of genotypes were in Cluster I (No. 5, 15, 4, 14) and in Cluster II (No. 6, 12, 8, 2). Three members were in Cluster V (No. 3, 7, 9). Two genotypes were grouped in Cluster III (No. 1, 11) and Cluster IV (No. 10, 13). The dendrogram showed that maximum genetic distance is present between Cluster I and Cluster IV indicating that they had diverse genetic material.

T a b l e 4

Pooled ANOVA for the studied characters in the selected rice genotypes (combined)

No.	Character	SOV					CV [%]
		Replications <i>DF</i> =2	Genotypes <i>DF</i> =14	Year <i>DF</i> =1	G × Y <i>DF</i> =14	Error <i>DF</i> =58	
		MS					
1	Plant height [cm]	41.42 ^{ns}	7369.00 ⁺	442.62 ⁺⁺	279.94 ⁺⁺	13.90	3.43
2	Leaf width [cm]	0.0069 ^{ns}	0.244 ⁺⁺	0.001 ⁺⁺	0.004 ⁺⁺	0.003	3.72
3	Leaf length [cm]	15.99 ^{ns}	90.03 ⁺⁺	884.91 ⁺⁺	68.67 ⁺⁺	1.378	3.38
4	Leaf area [cm ²]	2.048 ^{ns}	417.0 ⁺⁺	126.67 ⁺⁺	2564.6 ⁺⁺	0.396	1.99
5	Dry leaf weight [g]	1.06 ^{ns}	301.84 ⁺⁺	152.36 ⁺⁺	49.12 ⁺⁺	0.412	1.68
6	Total chlorophyll content (SPAD)	0.0004 ^{ns}	0.012 ⁺	0.0001 ^{ns}	0.0022 ⁺⁺	0.0002	5.98
7	No. filled grains/panicle	97.01 ^{ns}	7022.37 ⁺⁺	1013.37 ⁺⁺	733.63 ⁺⁺	56.97	5.14
8	1,000-grain weight [g]	0.046 ^{ns}	14.02 ⁺⁺	0.0348 ⁺	0.0045 ^{ns}	0.453	6.21
9	Grain yield [kg/m ²]	0.050 ^{ns}	15.29 ⁺⁺	0.127 ⁺⁺	0.0565 ⁺⁺	0.398	3.37
10	Grain length [mm]	0.035 ^{ns}	3.60 ⁺⁺	0.650 ⁺⁺	0.001 ^{ns}	0.019	2.50
11	Grain width [mm]	0.0051 ^{ns}	0.509 ⁺⁺	0.077 ⁺	0.031 ^{ns}	0.008	3.10
12	Grain shape	0.022 ^{ns}	23.86 ⁺⁺	1.089 ⁺⁺	0.001 ^{ns}	0.002	2.07
13	Hulling rice [%]	6.752 ^{ns}	37.35 ⁺⁺	2.181 ^{ns}	1.553 ^{ns}	0.301	0.68
14	Milling rice [%]	21.82	58.42 ⁺⁺	0.223 ^{ns}	0.0001 ^{ns}	2.60	2.31
15	Head rice [%]	2.025	226.71 ⁺⁺	3.84 ⁺⁺	0.213 ⁺⁺	2.25	2.68

Note: +, ++ and ns indicate $P < 0.05$, $P < 0.01$ significant and not significant; respectively SOV – statistics of variance; *DF* – degree of freedom; CV – coefficient of variation; MS – mean square; G × Y – genotype × year; ANOVA – analysis of variance.

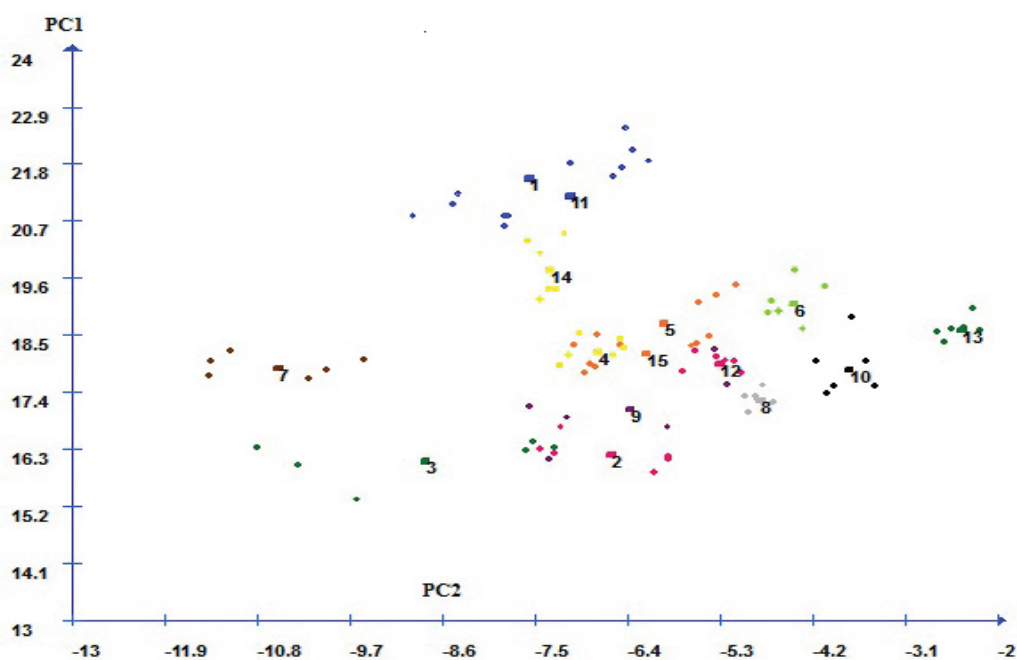


Figure 1. Graphical dispersion of principle components (PC).

Note: 1 – Giza 179; 2 – Sakha 101; 3 – Egyptian Yasmin; 4 – Giza 181; 5 – GZ 8455-9-1-1-2; 6 – Koshihikar; 7 – IET 1444; 8 – Gaori; 9 – IR 5256 UBN-1-1-2; 10 – IR 72944-1-2-2; 11 – Milyang 54; 12 – Milyang 95; 13 – Wild Rice 3; 14 – WAB 450-T-B-P 3811-B; 15 – NERICA 4.

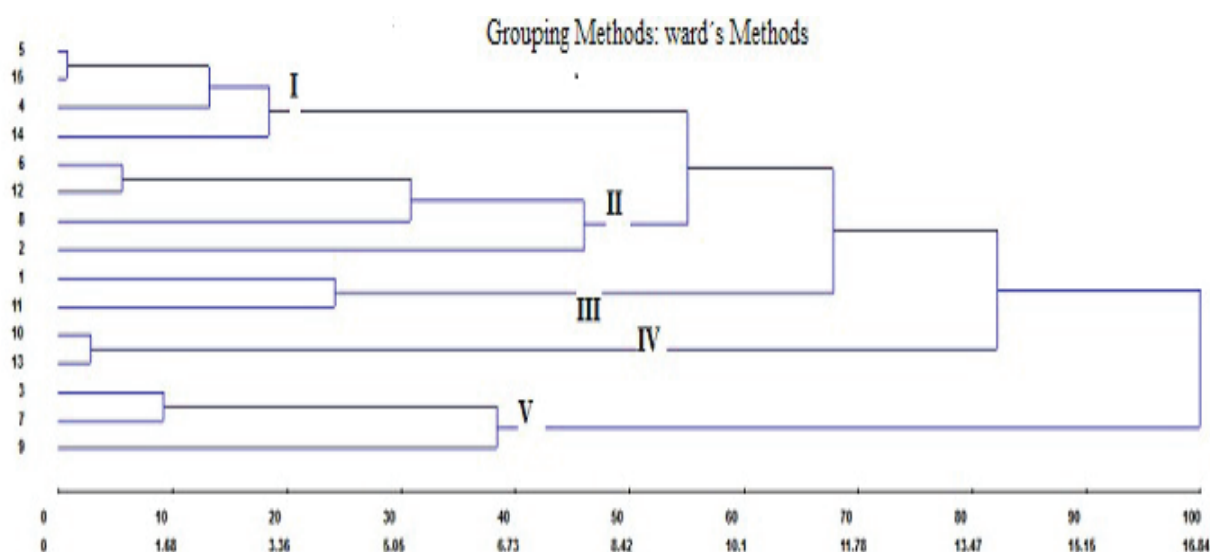


Figure 2. Clustering chart on the studied traits for fifteen cultivars.

Note: 1 – Giza 179; 2 – Sakha 101; 3 – Egyptian Yasmin; 4 – Giza 181; 5 – GZ 8455-9-1-1-2; 6 – Koshihikar; 7 – IET 1444; 8 – Gaori; 9 – IR 5256 UBN-1-1-2; 10 – IR 72944-1-2-2; 11 – Milyang 54; 12 – Milyang 95; 13 – Wild Rice 3; 14 – WAB 450-T-B-P 3811-B; 15 – NERICA 4.

T a b l e 5

Grand mean, variance components, estimates of phenotypic (PCV), and genotypic (GCV) coefficient of variation, heritability and genetic advance for fifteen characteristics in rice

No.	Characters	Grand mean	Genetics components						
			GV	PV	GCV [%]	PCV [%]	h^2_{BS} [%]	GA	GA [%]
1	Plant height [cm]	105.9	241.03	245.66	14.66	14.80	96.29	31.09	29.36
2	Leaf width [cm]	1.37	0.081	0.083	20.68	20.81	97.57	0.57	41.84
3	Leaf length [cm]	34.71	29.55	30.01	14.40	14.52	96.98	10.94	29.00
4	Leaf area [cm ²]	31.59	138.87	139.00	37.30	37.32	99.81	24.24	78.74
5	Dry leaf weight [g]	33.88	100.48	100.61	29.59	29.61	99.72	20.61	60.82
6	Total chlorophyll content [$\mu\text{mol}/\text{m}^2$]	0.249	0.0032	0.0033	22.95	23.19	96.07	0.11	45.89
7	No. of filled grains/panicle	146.58	2321.8	2340.79	32.87	33.01	96.07	98.06	66.90
8	1,000-grain weight [g]	24.55	4.54	4.67	8.68	8.81	98.39	4.21	17.14
9	Grain yield [kg/m ²]	1.42	4.95	5.10	156.66	159.03	94.24	4.38	308.75
10	Grain length [mm]	5.52	1.95	1.20	19.81	19.86	94.24	2.23	40.49
11	Grain width [mm]	2.84	0.19	0.20	15.51	15.62	98.95	0.89	31.31
12	Grain shape	2.13	7.95	7.96	35.14	35.34	97.32	1.57	71.19
13	Hulling rice [%]	80.93	12.35	12.45	4.34	4.36	99.80	7.15	8.84
14	Milling rice [%]	69.74	18.61	19.47	6.19	6.33	98.40	8.32	11.92
15	Head rice [%]	53.3	74.70	75.57	16.26	16.36	97.7	17.5	32.94

Note: GV – genotypic variance; PV – henotypic variance; h^2_{BS} – broad sense heritability; GA – genetic advance; GA% – genetic advance as percent of the mean.

T a b l e 6

The results of the Kaiser-Meyer-Olkin and Bartlett's tests

Kaiser-Meyer-Olkin Measure of Sampling Adequacy		0.556
Bartlett's Test of Sphericity	Approx. Chi-Square	463.226
	Degrees of freedom	91.00
	Significance	0.000

Results in Table 8 show that Cluster V had the plants with maximum height (117.12 cm), while plants with the shortest height (94.33 cm) were grouped in Cluster IV. Genotypes with the highest values of leaf width, leaf length, leaf area, and total chlorophyll content were in Cluster V. Cluster II had genotypes with the highest values of 1,000-grain weight, grain yield, and head rice %. Genotypes in Cluster II provide a better option for breeding.

DISCUSSION

The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all traits to indicate the effect of environmental factors on the expression of the studied characters (Osman *et al.* 2012).

For the number of filled grains/panicle exhibited the highest PCV and GCV, similar results were obtained in rice by Fathima *et al.* (2021), Bhargava *et al.* (2021), Lakshmi *et al.* (2022), and Singh *et al.* (2021). Plant height was moderate PCV and GCV, these results were in accordance with Fathima *et al.* (2021), Bhargava *et al.* (2021), Lakshmi *et al.* (2022), and Nikhitha *et al.* (2020). For the tested traits, there are few variations between PCV and the GCV showing that phenotypic expression is influenced by the environment to some degree.

It also implies that for a future crossing program selection should be based on these characters (Khatun *et al.* 2015). The majority of the studied

T a b l e 7

Sources of variation for the first five principal components (PC)

Character	Eigenvectors of principal component				
	PC1	PC2	PC3	PC4	PC5
Plant height [cm]	0.303	0.133	0.177	0.062	-0.138
Leaf width [cm]	0.295	0.318	-0.221	0.137	0.229
Leaf length [cm]	0.356	0.149	0.058	0.303	0.227
Leaf area [cm ²]	0.327	0.192	-0.202	-0.227	-0.239
Dry leaf weight [g]	-0.144	-0.092	-0.212	0.632	-0.178
Total chlorophyll content [$\mu\text{mol}/\text{m}^2$]	-0.093	0.237	-0.289	-0.039	-0.105
No. filled grains/panicle	0.280	0.224	0.279	0.267	0.275
1,000-grain weight [g]	-0.0075	0.013	-0.225	-0.164	0.787
Grain yield [kg/m ²]	0.331	0.292	0.198	-0.042	-0.227
Grain length [mm]	-0.0309	0.416	0.224	0.038	0.079
Grain width [mm]	0.331	-0.400	-0.104	0.043	0.068
Grain shape	-0.318	0.393	0.279	0.005	-0.010
Hulling rice [%]	0.046	-0.178	0.460	0.389	0.098
Milling rice [%]	-0.124	-0.258	0.380	0.422	0.097
Head rice [%]	0.202	0.189	-0.290	0.042	0.033

T a b l e 8

Cluster means of the investigated characteristics of the 15 rice genotypes

Character	Cluster mean				
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Plant height [cm]	111.26	99.39	105.43	94.33	117.12
Leaf width [cm]	1.32	1.36	1.34	1.27	1.88
Leaf length [cm]	36.95	31.42	33.12	36.78	38.32
Leaf area [cm ²]	29.91	28.57	29.30	31.74	41.94
Dry leaf weight [g]	34.13	37.17	34.57	34.00	28.89
Total chlorophyll content [$\mu\text{mol}/\text{m}^2$]	0.24	0.26	0.20	0.25	0.29
No. of filled grains/panicle	141.25	105.63	190.25	152.67	174.22
1,000-grain weight [g]	2.41	2.55	2.40	2.19	2.47
Grain yield [kg/m ²]	1.85	1.92	1.79	1.62	1.79
Grain length [mm]	5.34	5.58	5.11	4.62	5.25
Grain width [mm]	2.89	2.87	3.01	2.26	3.03
Grain shape	1.99	1.95	1.86	3.26	2.02
Hulling rice [%]	81.24	79.29	85.84	80.53	79.80
Milling rice [%]	72.04	68.23	71.48	72.05	66.02
Head rice [%]	57.28	56.19	42.36	54.81	50.62

traits had a high heritability ranging from 94.24% to 99.81%, with the highest heritability observed for leaf area (99.81%), while the lowest percentage was recorded for grain length. Heritability of plant height was high (96.26%), which was in accordance with Bhargava *et al.* (2021) and Fathima *et al.* (2021), Nikhitha *et al.* (2020) and Singh *et al.* (2021). Burton (1952) proposed that the genetic coefficient of variation when it is combined with heritability provides a straightforward picture of the amount of progress that can be accepted from the selection. Genetic advance (GA) was also measured in this study, with values ranging from 98.06 for the number of filled grains per panicle to 0.11 for total chlorophyll content.

The differences between genotypes on head rice might be due to the genetic variances among tested varieties, environmental influences, or both (Tiruneh *et al.* 2019). Significant differences in the mean square estimates among the fifteen genotypes for these characters showed the amount of

variability among the tested genotypes. This would be advantageous in terms of improving the studied characters (Singh *et al.* 2005). The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all traits to indicate the effect of environmental factors on the expression of the studied characters (Osman *et al.* 2012).

PCA is an important tool to speed up the breeding programme by highlighting desirable genotypes. Screening germplasm of any crop species for genetic diversity in breeding programmes is of great importance for crop improvement, to select diverse and valuable genotypes. PCA is a tool to muzzle genetic divergence among germplasm concerning for characters (Tejaswini *et al.* 2018), because they show up motifs and constrict redundancy in data sets (Amy & Pritts 1991; Adams 1995). PCA reads out all the important components and focuses on their contribution to the total variability.

The first and second principal components were responsible for the highest percentage (30.34% and

15.24%, respectively) of the total variation. Similarly, the overall variation was contributed by the first three major principal components (Altaher & Singh 2003; Subramanian *et al.* 2019; Raiza Christina *et al.* 2021). The first two principal components were plotted to see if there were any relationships between the rice characteristics under study. Generally, the entire variation cannot be explained by a few principal components, the principal component analysis revealed a high degree of variability among the genotypes studied (Tiruneh *et al.* 2019). The first two principal components, which account for 45.58% of the variance, were plotted to see if there were any relationships between the rice characteristics under study (Dehghani *et al.* 2008; Tiruneh *et al.* 2019; Niu *et al.* 2022).

The principal component analysis established five main components, with PC1 contributing the most to the variance in breeding utilization. The features linked with the first three major components were more helpful in differentiating the accessions, even though they are crucial demonstrating the variation patterns among accessions. Genotypes in Cluster II provide better height for breeding in addition to high yield and high head rice %. Instead of focusing on all the features under research, it is helpful for the genetic improvement of essential traits with larger contributions to variability.

CONCLUSIONS

The results of the PCA showed the amount of genetic diversity of varieties under study. The characteristics that contribute to the variability are advised to be taken into consideration for breeding programmes. Genotypes with the highest values of 1,000-grain weight, grain yield and head rice % are found in Cluster II, which had genotypes that provide a better option for breeding. This study confirmed the existence of genotype variability for the majority of the examined variables giving breeders the chance to enhance rice yield and other relevant traits. The overall variation of the population was heavily influenced by the first principal component, which was followed by subsequent components.

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