

ASSESSMENT OF VARIABILITY, GENETIC PARAMETERS AND CLUSTER ANALYSIS OF SOME RICE GENOTYPES USING QUANTATIVE TRAITS

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ABSTRACT: Rice is the most important crop for many countries around the world, being the main cash crop for farmers. This research was carried out at the experimental farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt during 2022 and 2023 rice seasons to investigate the variability for desired quantitative traits and genetic parameters i.e. phenotypic and genotypic coefficients of variation, broad sense heritability and correlations among 11 rice genotypes for some agronomical characteristics. Randomized complete block design, with three replications were used in the both seasons. The analysis of variance of 11 studied traits revealed highly significant differences between the genotypes indicating into a wide range of variation among the tested rice genotypes in their genetic background. The genotypes Sakha 101, SKC23824-422, GZ9362-34-2-1-3and Sakha 104 showed the highest mean values for grain yield plant⁻¹ (59.90, 59.50, 59.40 and 59.00 g, respectively).The widest and thickest grains were observed in IR51672-62-2-1 with mean value 4.10 -2.60mm. The highest PCV and GCV were observed in panicle weight, number of filled grains panicle⁻¹ and1000-grain weight. The positive correlation coefficients between grain yield and number of panicles plant⁻¹, panicle length, panicle weight, number of filled grains panicle⁻¹ and 1000-grain weight. High heritability observed for all studied traits except panicle length trait were low. The dendrogram analysis divided the studied genotypes into two main clusters based on the mean values of the studied traits. Out of the 11 rice genotypes, seven genotypes proved to be high yield and its components and these genotyped could be candidate for progress evaluations for developing new varieties with desirable traits.

Key words: Rice - genetic components - correlation analysis

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the main cereal crops worldwide. More than half of the world's population depends on rice as staple food, especially in developing countries. As a widely cultivated cereal, rice is an important source of carbohydrates in the diet of the average person. The primary objective of all breeding programs worldwide is to produce high-yielding varieties (Ehdaie and Waines 1989) of high quality that can be distributed to farmers. Finding a significant degree of variability is necessary to select the desirable lines for further manipulation to achieve this goal. Analysis of trait variability and how one trait relates to other traits. Rice yield increasing on existing land remains the primary strategy for increasing production to match future food demand for a growing population. Globally, an additional 176 million tons of rice will be need by 2035, which could be

met by increasing yield potential from 10 to 12.3 tons per hectare (Khush, 2013). Yield is still the main objective of rice development; however, rice grain quality is now receiving more attention due to increasing awareness of its importance (Riyanto *et al.* 2021). According to Sumanth *et al.* (2017), phenotypic variability refers to the variations in the members of a population caused by their genetic makeup and environment during growth. The amount of genetic diversity affects how breeding programs are planned and implemented to improve quantitative traits. As a result, the availability of genetic diversity with concerning to desirable traits and the selection expertise of plant breeders are very necessary for the success of plant breeding efforts (Adhikari *et al.*, 2018). Therefore, an important basis for the genetic improvement of the trait is variability, genetic diversity, expected genetic improvement and heritability of the trait. Heritability measures

how much of a trait were passed on to subsequent generations by comparing the variance due to genetic differences to all other phenotypic variation for a trait in a population. Higher heritability and genetic advance estimates for each trait suggest that these traits could be used more effectively through selection in subsequent generations (Haider *et al.*, 2012). Number of grains panicle⁻¹, days to maturity, plant height and paddy yield gave the highest heritabilities, while number of tillers plant⁻¹ had the lowest. According to Akhtar *et al.* (2011), paddy yield showed a high genetic association with number of grains panicle⁻¹, days to maturity and 1000- grain weight. Rice grain length and shape are important physical characteristics that affect both the price and the acceptance of a variety. Information on the genetic basis of these traits were need to improve rice length and shape (Agus Riyanto *et al.*, 2023). Genetic factors have a greater influence on the length and shape of grain rice than environmental factors (Quamruzzaman *et al.*, 2020). Babu *et al.* (2012) studied the correlation and path analysis in twenty-one popular hybrids of rice. They found some character association of the yield attributing traits revealed significantly positive association of grain yield per plant with number of productive tillers plant⁻¹. To create acceptable genotypes the current study aimed to evaluate the genotypic and phenotypic of rice genotypes and the relationship between traits in rice genotypes. Anis *et al* 2022 reported that positive correlation coefficients between grain yield and number of panicles and number of filled grains panicle⁻¹ indicated that the better exploration of these

traits could be used to develop desired rice varieties / lines.

MATERIALS AND METHODS

During the two summer rice growing seasons of 2022 and 2023, the experimental research trial carried out at the experimental farm of Sakha Agricultural Research Station, Kafrelsheikh, Egypt. The plant materials consisted of 11 rice genotypes (Table 1). The seeds were sown in the nursery on 20May and transplanted into the field after 30 days. Individual seedlings of each variety were planted in 3 rows with 20 cm spacing between rows and a 20 cm distance between mounds within rows. Experiments were conducted under normal irrigated conditions using a randomized complete block design (RCBD). All genotypes were replicated three times. Nitrogen fertilizers were added as recommended (IRRI 1996). Insect and weed control were applied periodically as required. Analysis of variance was evaluated according to Steel *et al.* (1997). Ten plants from each replicate selected randomly were measure characters including days to heading (day), plant height (cm), number of panicles plant⁻¹, panicle length (cm), panicle weight, No. of filled grains panicle⁻¹, 1000 grain weight(gm), grain yield plant⁻¹(gm), grain length(mm), grain width(mm) and grain thickness (mm). Genetic advance (GA) and heritability in broad sense meaning(H) were computed according whom Allard (1960). The relationship between the examined traits across experimental factors was better understood using the correlation coefficient Gomez and Gomez (1983).

Table (1). List of the studied genotypes and their parentage and origin.

No.	Genotypes	Parentage	Origin
1	Giza177	Giza 171/Yomjo No. 1//PiNo.4	Egypt
2	Sakha101	Giza 176/Milyang 79	Egypt
3	Sakha104	GZ 4096-8-1/GZ 4100-9-1	Egypt
4	Sakha105	GZ 5581-46-3/GZ 4316-7-1-1	Egypt
5	GZ9362-34-2-1-3	Sakha101/AC2342	Egypt
6	IR51672-62-2-1-1-2-3	IR24594-204-1-3-2-6-2//IR28222-9-2-2-2-2	IRRI
7	YUNJING 23	-----	China
8	SKC 23819-184	Giza 177/M 204	Egypt
9	SKC 23819-192	Giza 177/M 204	Egypt
10	SKC 23819-194	Giza 177/M 204	Egypt
11	SKC 23824-422	Giza178 // M202	Egypt

RESULTS AND DISCUSSION

Performance of the studied genotypes

Data in Tables 2 and 3 showed that the mean performance of the eleven genotypes for all studied agro- morphological traits. The early maturity dates were observed for the genotypes SKC23824-422, Sakha 105 and Giza 177 with mean values of 85.70, 89.00 and 89.70 days, respectively. For plant height, highly differences were found among all genotypes with mean values ranged from 89.70 and 107.00 cm for the

Sakha 101 and Yun Jing 23 genotypes respectively, indicating that these genotypes growth rates varied. The greatest numbers of panicle plant⁻¹ measured by SKC23824-422. Meanwhile, IR51672-62-2-1-1-2-3 and Sakha 104 genotypes scored the highest mean values for panicle length trait. meanwhile, the highest panicle weight and No. of filled grains panicle⁻¹ mean value were scored by YUNJING 23 genotype.

Table 2. Mean values for some agro-morphological traits of the studied 11 genotypes of rice.

Genotypes	Days to heading (days)	Plant height (cm)	No. of panicles Plant ⁻¹	Panicle length (cm)	Panicle weight (g)	No. of filled grains panicle ⁻¹
Giza177	89.7	97.3	20.7	20.3	3.9	138.7
Sakha101	108.7	89.7	22.3	22.4	4.1	146.7
Sakha104	100.0	106.0	20.3	23.2	5.1	170.3
Sakha105	89.0	100.3	19.0	21.4	4.0	147.3
GZ9362-34-2-1-3	93.7	92.3	19.3	23.3	3.7	143.0
IR51672-62-2-1-1-2-3	92.3	100.7	17.0	20.7	5.2	126.0
YUNJING 23	101.0	107.0	18.0	21.3	5.6	185.0
SKC 23819-184	103.3	90.7	20.0	20.0	5.1	94.0
SKC 23819-192	99.7	91.0	18.0	19.7	5.4	104.0
SKC 23819-194	96.0	94.3	22.0	20.0	5.1	124.0
SKC23824-422	85.7	104.0	23.3	22.3	5.4	155.0
LSD 0.05 %	1.06	1.90	1.63	2.17	0.12	23.01
0.01 %	1.56	2.78	2.39	3.18	0.17	33.72

Table 3. Mean values for some agro-morphological traits of the 11 studied genotypes of rice.

Genotypes	1000-grain weight (g)	Grain yield plant ⁻¹ (g)	Grain length (mm)	Grain width (mm)	Grain thickness (mm)
Giza177	27.7	51.7	7.6	3.3	2.3
Sakha101	27.1	59.9	8.0	3.4	2.1
Sakha104	28.3	59.0	7.9	3.5	2.2
Sakha105	28.6	47.0	8.1	3.4	2.3
GZ9362-34-2-1-3	27.9	59.4	7.7	3.3	2.2
IR51672-62-2-1-1-2-3	38.4	47.6	7.9	4.1	2.6
YUNJING 23	32.0	56.3	7.8	3.7	2.4
SKC 23819-184	38.4	53.5	9.1	3.6	2.4
SKC23819-192	40.2	45.4	9.9	3.8	2.3
SKC23819-194	38.2	54.3	9.6	3.9	2.4
SKC23824-422	33.8	59.5	7.7	3.6	2.2
LSD 0.05 %	1.01	3.94	0.17	0.17	0.10
0.01 %	1.48	5.77	0.24	0.25	0.14

Data presented in Table 3 showed that the genotypes Sakha 101, SKC23824-422, GZ9362-34-2-1-3 and Sakha 104 scored the highest mean values for grain yield plant⁻¹ (59.90, 59.50, 59.40 and 59.00 respectively). While the highest mean values for grain length were found in the genotypes SKC 23819-192, SKC23819-194 and SKC23819-184 (9.90m, 9.60m and 9.10 m respectively). The widest and thickness grains were found in genotype IR51672-62-2-1-1-2-3 with mean values of 4.10 -2.60mm respectively. All the obtained results will be considered in the next hybridization programs to get the most preferred traits in rice plants.

Analysis of variance (ANOVA)

The analysis of variance (Table 4) for all evaluated genotypes showed highly significant differences for all studied agro- morphological traits. This suggested that there were sufficient amounts of genetic variability among the evaluated genotypes for each trait. Hence, selection is potential to identify the beneficial genotypes. These results are in agreement with

those obtained by Seedek 2009 and Anis *et al* 2022. This showed that genotypes were determine for grain production, days to flowering, panicle length, and plant height all had vital genetic diversity. As a result, there is a chance for genetic improvement through selection and hybridization of tested genotypes for important features. This finding is extremely comparable with those of Gyawali *et al.* (2018), Rashid *et al.* (2017), Sumanth *et al.* (2017), Abebe *et al.* (2017), and Bandi *et al.* (2018) they revealed significant genetic diversity across rice genotypes for yield and main yield contributing variables.

Estimation of genetic variability

Phenotypic coefficient of variance (PCV) was generally higher than genotypic coefficient of variance (GCV) for all studied traits indicating the environmental influence on the expression of these traits, but a bigger portion of PCV was contribute by the genotypic component, than by the environmental component.

Table 4. Mean squares for some quantitative traits of the 11 studied genotypes of rice.

Traits	Replications (<i>df</i> =2)	Genotypes (<i>df</i> =10)	Error (<i>df</i> =20)	CV (%)
Days to heading	0.64	144.79**	0.57	7.21
Plant height (cm)	2.21	122.94**	1.81	6.55
No. of panicles/plant	0.27	11.87**	1.34	9.91
Panicle length (cm)	4.81	5.15**	2.38	6.13
Panicle weight (cm)	0.01	1.47**	0.01	14.69
No. of filled grains/panicle	590.18	2141.95**	266.82	19.15
1000-grain weight (gm)	1.08	80.68**	0.51	15.81
Grain yield/plant (gm)	3.37	88.36**	7.83	10.04
Grain length (mm)	0.04	1.99**	0.01	9.93
Grain width (mm)	0.01	0.22**	0.01	7.13
Grain thickness (mm)	0.01	0.06**	0.01	5.95

** significant at 0.01 levels of probability.

Breeding programs for any crop may be better and more effective by taking into account the genetic diversity of the genotypes that are selected for further changes in order to achieve the breeding aim. To begin an effective breeding program, a genetic survey using suitable parameters is required. These parameters include genotypic (GV) and phenotypic (PV) variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (H) in a broad sense and genetic advance (GA%) which were displayed in Table 5. Phenotypic variation frequently exceeded genotypic variance in all the studied traits, as would be predicted. It is important to keep in mind that total variability depends on both heritable and non-heritable components when computed the variance in yield components responsible for variations in yield among different genotypes. While compute of heritability and genetic advance are essential first steps in any breeding program because they provide information needed to design the most efficient breeding program and the relative usefulness of selection, while coefficients of variation measure the level of variability present in a population.

Largest genotypic variation (GV) and phenotypic variance (PV) for total no. of filled grains panicle⁻¹ (625.05), days to headings (48.07), plant height (40.38), grain yield (26.84) and 1000- grain weight (26.72). As well as high heritability (H) values, showed by days to heading (98.83), plant height (95.70), Panicle weight (98.69), Grain length (97.94), Grain width (82.15) and grain yield (87.43). The results revealed significant phenotypic and genotypic variances among the genotypes for the traits under consideration. The PCV values were higher than GCV values for most studied traits, which reflect the influence of environment on the expression of these traits. High heritability and genetic progress are essential factors for

determining the result of picking the best candidates. Days to heading, plant height and 1000-grain weight had high heritability and high genetic advance. Similar results were obtained by Sedeek *et al.* (2009) and El-Namaky (2012). The genotypic coefficient of variation demonstrated how much genetic diversity was present in the genotypes for different phenotypes, but it did not fully allow for the assessment of heritable variation. Permanent genetic enhancement benefits from heritable variation (Singh 2000). The potential of heritability to predict the accuracy of phenotypic value as a guide to breeding value is its most crucial role in the genetic study of quantitative traits. Reliable estimates of the amount of genetic advancement to be anticipated through phenotypic selection are provided by the genotypic coefficient of variation and heritability estimations. Gaballah (2009) also published the findings, which were consistent with the ones presented here. Genetic progress and heritability are crucial selection criteria. The genetic advance estimates are useful for comprehending the sort of gene activity involved in the production of diverse polygenic traits. In contrast to low values, which are indicative of non-additive gene activity, high values of genetic progress indicate additive gene action (Singh and Narayanan, 1993). Thus, if there is significant genetic advancement, heritability estimates will be accurate. The results of this study suggest that some traits, for most studied traits, showed high heritability and high genetic advance, indicating selection will be 100 percent highly effective. For all characteristics under study, the phenotypic coefficient of variance was found to be larger than the genotypic coefficient of variance, indicating the effect of the environment on the expression of these traits. (Malimar *et al.*, 2015; Rashid *et al.*, 2017; Gyawali *et al.*, 2018) revealed similar findings.

Table 5. Assessment of genetic parameters for some quantitative of the 11 studied genotypes of rice.

Traits	Mean	G.V	P.V	G.C.V	P.C.V	Hbs	GA	GA%
Days to heading	96.3	48.07	48.64	7.20	7.24	98.83	14.20	14.75
Plant height (cm)	97.6	40.38	42.19	6.51	6.66	95.70	12.81	13.12
No. of panicles plant ⁻¹	20.0	3.51	4.85	9.37	11.01	72.37	3.28	16.41
Panicle length (cm)	21.3	0.92	3.30	4.50	8.52	27.94	1.05	4.90
Panicle weight (cm)	4.8	0.49	0.50	14.59	14.69	98.69	1.43	29.84
No. of filled grains panicle ⁻¹	139.5	625.05	891.86	17.93	21.41	70.08	43.12	30.92
1000-grain weight (g)	32.8	26.72	27.24	15.77	15.92	98.11	10.55	32.18
Grain yield plant ⁻¹ (g)	54.0	26.84	34.67	9.60	10.91	87.43	9.39	17.40
Grain length (mm)	8.3	0.66	0.67	9.77	9.88	97.94	1.66	19.92
Grain width (mm)	3.6	0.07	0.08	7.24	7.99	82.15	0.49	13.52
Grain thickness (mm)	2.3	0.02	0.03	5.76	6.48	78.88	0.24	10.54

The correlation coefficient

The correlation coefficient statistically estimated as reported by Gomez and Gomez (1983). Regarding the correlation between studied traits presented in Table 6. Grain yield plant⁻¹ was highly significant and positively correlated with No. of panicles plant⁻¹ and Panicle length, while the correlation between grain yield and panicle weight, 1000-grain weight (gm) and Grain width was significant and positively correlated. Negatively correlated between thousand grain weight and no. of panicles/plant and Panicle length, Cyprien and Kumar (2011) and Anis *et al* (2022) found that panicle number, panicle weight, 1000-grain weight, days to 50% flowering and seed to seed days were considered as causal factors and effects grain yield. For grain dimensions, results in table 6 showed that high positively significant correlation were observed between grain length and each of grain width and grain thickness. Negatively correlated to days to heading with plant height, panicle length and grain thickness. Generally, The positive correlation coefficients between grain yield and number of panicles plant⁻¹, panicle length, panicle weight, number of filled grains panicle⁻¹ and 1000-grain weight

indicate that better exploration of these traits could be used to develop desired rice varieties/lines.

Cluster Analysis Based on Mean Performance of Traits

The mean performance of the 11 agromorphological traits employed to calculate the euclidean distances among eleven genotypes. The dendrogram constructed using these values as indicated in Figure (1). This dendrogram divided the eleven genotypes into two main clusters. Among the two cluster, cluster 1 had two genotypes SKC 23819-184 and SKC 23819-192 that were characterized by early maturing and short Plant stature. Cluster 2 comprised two sub groups, first sub group had seven genotypes (Sakha 105, Giza 177, GZ9362-34-2-1-3, SKC23824-422 IR51672-62-2-1-1-2-3, SKC 23819-194 and Sakha 101) these genotypes almost similar in yield and component traits, second sub group had two genotypes (Sakha 104 and YUNJING 23) similar in panicle length, panicle weight and no. of filled grains panicle⁻¹. Similar findings were reported in rice by Chandra *et al.* (2007), Rajesh *et al.* (2010) and Anis *et al.* (2022).

Table 6. Correlation coefficients estimates of the 11 studied traits.

Traits	HD	PH	NPP	PL	PW	NFGP	1000-GW	GYP	GL	GW	GT
Days to heading	0										
Plant height (cm)	-0.397	0									
No. of panicles plant ⁻¹	-0.041	-0.12	0								
Panicle length (cm)	-0.011	0.305	0.254	0							
Panicle weight (cm)	0.141	0.391	-0.143	-0.321	0						
No. of filled grains panicle ⁻¹	-0.102	0.754**	0.105	0.671**	-0.023	0					
1000-grain weight (gm)	0.044	-0.198	-0.256	-0.714**	0.711**	-0.666**	0				
Grain yield plant ⁻¹ (gm)	0.236	0.128	0.625**	0.729**	0.493*	0.526*	0.492*	0			
Grain length (mm)	0.326	-0.536*	-0.064	-0.672**	0.381	-0.715**	0.743**	-0.439*	0		
Grain width (mm)	0.024	0.125	-0.351	-0.517*	0.753**	-0.303	0.844**	-0.417*	0.467*	0	
Grain thickness (mm)	-0.166	0.168	-0.605**	-0.64	0.436*	-0.327	0.656**	-0.6	0.229	0.764**	0

* & ** significant at 0.05 and 0.01 levels of probability, respectively.

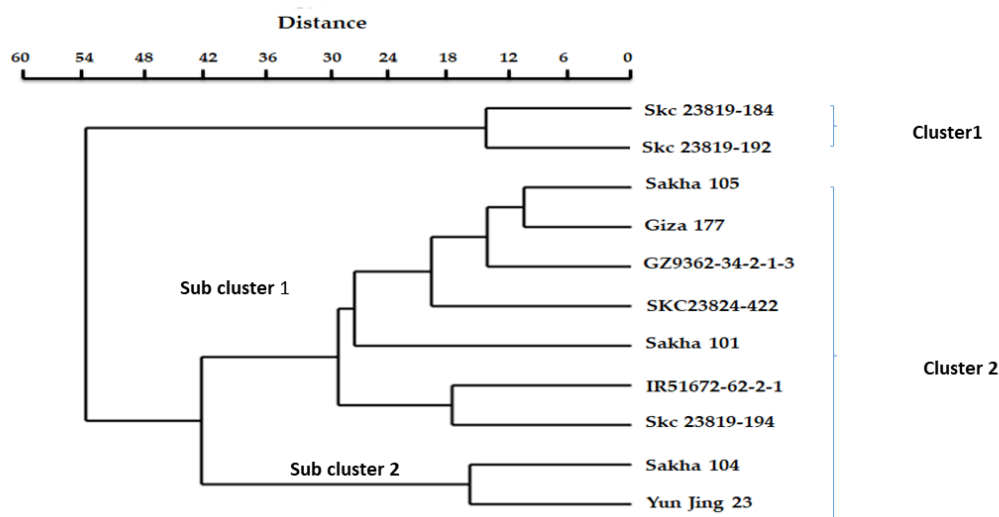


Figure 1: Cluster analysis based on mean performance of studied traits

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تقدير التباين، المكونات الوراثية وتحليل القرابة لبعض التراكيب الوراثية من الأرز باستخدام الصفات الكمية

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الملخص

يعتبر محصول الأرز من المحاصيل الاستراتيجية باعتباره من المحاصيل الأساسية المستخدمة في الغذاء. في هذه الدراسة تم تقييم أحد عشر تركيب وراثي للتباين في الصفات الكمية المرغوبة وتقدير المقاييس الوراثية (معامل إختلاف الشكل الظاهري والوراثي للتباين، ونسبة التوريث بالمعنى الواسع)، والإرتباط لهذه الصفات. أجريت الدراسة خلال عامي 2022 و 2023 في المزرعة البحثية بمحطة بحوث سخا التابعة لمركز البحوث الزراعية، مصر. استخدم تصميم القطاعات كاملة العشوائية في ثلاثة مكررات. وقد أظهر تحليل التباين إختلافات معنوية بين الطرز الوراثية لجميع الصفات المدروسة وسجلت الأصناف سخا 101 و SKC23824-422 و GZ9362-34-2-1-30 و سخا 104 أعلى محصول للنبات 59.00 و 59.40 و 59.50 و 59.90 على التوالي بينما أكبر عرض وسمك للحبة وجد مع IR51672-62-2-1 بقياس يتراوح ما بين (4.10) و -2.60mm .

وأضحت النتائج أن التباين المظهري دائما يكون أعلى من التباين الوراثي لكل الصفات المدروسة وهذا يشير إلى تأثير الصفات بالبيئة. في هذه الدراسة لوحظ أن أعلى تباين مظهري ووراثي في صفات وزن السنبل، عدد الحبوب الممتلئة بالسنبل، وزن الألف حبة.

أيضا لوحظ معامل إرتباط موجب بين محصول الحبوب وعدد السنابل/ النبات، طول السنبل، وزن السنبل، عدد الحبوب الممتلئة ووزن الألف حبة. درجة التوريث كانت عالية في كل الصفات ما عدا طول السنبل فكانت منخفضة. من خلال تحليل درجة القرابة بين التراكيب الوراثية باستخدام قيم المتوسطات وجد أن سبعة من هذه التراكيب مرتبطة معا لصفات المحصول ومكوناته ويمكن إستخدام هذه التراكيب في برامج التربية.