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Genetic Variability, Multivariate and Association Analysis for Agronomic Traits in Different Rice Genotypes

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ABSTRACT

The current study aimed to evaluate the presence of variability for desired traits and to estimate genetic parameters (phenotypic and genotypic coefficients of variation, broad sense heritability), correlations and principal component analysis for such traits. The study was conducted in 2020 and 2021 at the Rice Research Department Farm of the Sakha Research Station of the Agricultural Research Centre, Egypt. In a randomized complete block design with three replications, fifteen rice genotypes were evaluated for yield and yield components, including days to flowering, plant height, number of panicles per plant, panicle length, total spikelets per panicle, panicle density index, grain length, width, thickness, shape and 1000 grain weight and grain yield per plant. The analysis of variance showed significant differences between the genotypes for all the studied traits. The genotypes Egyptian Yasmine, IRRI 154, Sakha 101, Giza 178, IR 65600-77-4-2-1, and IRRI 147 were found to have the highest mean values for grain yield/plant (53.47, 55.07, 52.32, 52.07, 50.02, and 46.60, respectively). The widest grains, measuring 3.31 to 3.63 mm, were found in the genotypes WAB-96-1-1, IR 65600-77-4-2-1, Sakha 105, GZ 10101-5-1-1-1, and IRRI 147. IR 65600-77-4-2-1 recorded the thickest grain (2.37 mm). All the results obtained will be considered in the next hybridization programs to get the most preferred traits in rice plants.

Keywords: Genetic variability, multivariate analysis, association analysis, agronomic traits, rice



INTRODUCTION

Rice, the second most important cereal crop after wheat, grows effectively at a wide range of temperatures. 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. Increasing rice yields on existing land remains the primary strategy for increasing production to meet future food demand for a growing population. Globally, an additional 176 million tons of rice will be needed by 2035, which can 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 is passed on to subsequent

generations by comparing the variance due to genetic differences to all other phenotypic variation for a trait in a population.

At the genotypic level, yield per plant was positively and significantly correlated with thousand kernel weight and spikelet fertility. The largest positive direct effect was observed for thousand grain weight. Higher heritability and genetic advance estimates for each trait suggest that these traits can 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 were shown to have 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 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 is needed to improve rice length and shape (Agus Riyanto et al., 2023). Genetic factors have a greater influence on the length and shape of rice than environmental factors (Quamruzzaman et al., 2020). To create acceptable genotypes, the current study aimed to evaluate the genetic diversity of rice genotypes and the relationship between traits in rice genotypes.

MATERIALS AND METHODS

In this study, we examined the morphological traits of 15 rice genotypes in the 2021 and 2022 rice seasons. The plants were grown on a farm at the Sakha Research Institute of the Egyptian Agricultural Research Center, Department of Rice Research. The seeds were sown in the nursery on May 20 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

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within rows. Experiments were conducted under fully irrigated conditions using a randomized complete block design (RCBD). All genotypes were replicated three times.

Nitrogen fertilizers were added as recommended (RRTC 2020). Insect and weed control were applied periodically as required. Analysis of variance was done using the combined analysis by Steel et al. (1997).

Table 1. List of 22 rice genotypes used in this study

Genotypes	pedigree	origin	type
Giza 178	Giza175 / Milyang49	Egypt	Indica/Japonica
Giza 182	Giza181/IR39422-161-1-3-1/Giza181	Egypt	Indica
Sakha 101	(Giza 176/ Milyang 79)	Egypt	Japonica
Sakha 105	GZ5581-46-3/GZ4316-7-1-1	Egypt	Japonica
Egyptian Yasmine	(Jasmin85) IR841-67	Egypt	Indica
GZ 9399-4-1-1-3-2-2	Giza178/IR65844-29-1-3-1-2	Egypt	Indica/Japonica
GZ 10101-5-1-1-1-1	Sakha 103 / IRI 385	Egypt	Indica/Japonica
IRRI 142	Jinmiby eo/ Cheolweon 46	IRRI	Indica
IRRI 152	IR77863-95-2-3/HR15490-34	IRRI	Japonica
IRRI 154	IR73012-137-2-2-2/IRRI104	IRRI	Indica
IRRI 147 (IR63307-4B-4-3)	IR51511-B-B-34-B/ TCCP266-2-49-BB-3	IRRI	Indica/Japonica
IRAT 112	IRAT 13/ Dourado Precoce	Côte d'Ivoire	Japonica
WAB-96-1-1	TA 257/YS 121	WARDA	Indica
IR14P1016	KH68/BPI 76	IRRI	Indica
IR 65600-77-4-2-1	Shen Nung 89-366/Ketan Lumbu	IRRI	Indica

The measured characters on nine plants from each genotype included days to heading (DTH) (day), plant height (PH) (cm), panicle length (PL) (cm), panicle weight (PW), panicle density index (PDI), number of panicles/plant (NPP), 1000-grain weight (TGW), total spikes (TS), fertility percentage (FP), grain yield (GYP), grain length (GL), grain width (GW), grain thickness (GTH) and grain shape (GS). Genetic advance (GA), expected genetic advance (EGS) and heritability in the broad sense meaning (H) were computed. The relationship between the examined traits across experimental factors was better understood using the correlation coefficient and principal component analysis (PCA). PCA was performed using a computer software program SPSS version 25. PCA analysis was done using the methodology given by Massy (1965) and Jolliffe (1986).

RESULTS AND DISCUSSION

The days to heading, plant height (cm), number of panicles/plant, 1000-grain weight (g), fertility percentage, and grain yield among the evaluated genotypes showed highly significant differences in the analysis of variance (Table 1), which would indicate overall wide differences among the genotypes studied. Except for panicle density index, which reflects unaccounted-for variation between the two years of study and suggests that each genotype's performance in one environment will not change from year to year, mean squares due to genotypes by years interaction were not significant for all studied traits. The

significant differences among rice genotypes in the investigation indicate the presence of genetic variability in the material used and provide a good opportunity for yield improvement.

Since the genotype year interaction was not significant and the variations across genotypes were noticeable, grain yield and other parameters showed stability throughout the seasons (Table 1). This appears to demonstrate the potential for future improvement through selection of all characters studied. This showed that genotypes that were assessed for grain production, days to flowering, panicle length, and plant height all had intrinsic genetic diversity. As a result, there is a chance for genetic improvement through selection and hybridization of tested genotypes for important features. With Poudel *et al.* (2014) and Gyawali *et al.* (2018), this finding is extremely comparable. Poudel *et al.* (2014), Gyawali *et al.* (2018), Bekele *et al.* (2013), Rashid *et al.* (2017), Sumanth *et al.* (2017), Abebe *et al.* (2017), and Bandi *et al.* (2018) all revealed significant genetic diversity across rice genotypes for yield and main yield contributing variables.

Performance of the used genotypes:

Table 2 shows the average results of the genotypes under study for the combined data. For days to heading (day), the genotypes IRRI 142, GZ 9399-4-1-1-3-2-2 and GZ 10101-5-1-1-1 were 85.67, 91.67 and 93 days, respectively, and behaved as the earlier for heading dates.

Table 1. The combined analysis of variance for studied agronomic characteristics.

S. O. V	df	DTH1	PH1	PL1	PW	PDI	NPP	TGW
Blocks	2	3.21	28.93	0.33	0.18	1.28	2.71	0.15
Treatments	14	515.73**	1274.07**	41.53**	3.27**	38.94**	54.4**	55.56**
Years	1	3.6ns	0.01ns	0.02ns	0.001ns	8.91**	1.11ns	0.02ns
T x Y	14	0.15ns	0.8ns	0.011ns	0.02ns	0.62ns	0.75ns	0.01ns
Error	58	0.91	18.38	1.72	0.15	0.79	0.96	0.03
Mean		101.82	100.90	22.43	3.37	7.95	18.24	26.91
CV (%)		0.94	4.25	5.84	11.33	11.18	5.38	0.60
S. O. V	df	TS	FP	GYP	GL	GW	GTH	GS
Blocks	2	68.54	11.92	0.79	0.28	0.001	0.01	0.01
Treatments	14	2666.84***	145.64**	325.86**	4.27**	0.71**	0.09**	1.71**
Years	1	0.030	6.29ns	0.14ns	0.01ns	0.002ns	0.021ns	0.02ns
T x Y	14	0.570	3.83ns	2.08ns	0.012ns	0.003ns	0.001ns	0.014ns
Error	58	12.88	2.86	1.87	0.07	0.01	0.001	0.02
Mean		143.00	91.14	44.01	8.50	3.10	2.15	2.79
CV (%)		2.51	1.86	3.11	3.10	2.66	3.12	5.12

Where DTH: days to heading (day), PH: plant height (cm), PL1: panicle length (cm), PW: panicle weight, panicle density index (PDI), NPP: number of panicles/plant, TGW: 1000-grain weight, TS: total spikelet, FP: fertility percentage, GYP: grain yield per plant, GL: grain length, GW: grain width, GTH: grain thickness and GS: grain shape.

*, ** and ns indicate ($p \leq 0.05$) significant, high a significant ($p \leq 0.01$) and non-significant, Y = year, and T = treatment

The rice genotypes under study showed considerable variances in plant height, indicating that these genotypes' growth rates varied. The genotypes GZ 10101-5-1-1-1, Sakha101, GZ 9399-4-1-1-3-2-2, Sakha105, IR 65600-77-4-2-1, and IRRI 142 had the most favorable mean values for dwarfism.

Data given in Table 2 showed that the genotypes IR14P1016, IRRI 147, IRRI 154, and Egyptian Yasmine had the largest mean panicle lengths. The greatest panicle weights were measured by WAB-96-1-1, Egyptian Yasmine, and IRRI 154 (5.07, 4.4, and 4.17 g, respectively). While WAB-96-1-1, IRRI 154, and IR14P1016 earned the greatest panicle density index.

The genotypes IRRI 154, WAB-96-1-1, Egyptian Yasmine, and Giza178 have the greatest number of total spikelets in a panicle (191.41, 170.01, 166.67, and 160.68 spikelets, respectively). The genotypes IRAT 112, WAB-96-1-1, IR14P1016, IRRI 147, and Sakha 105 had the highest mean values for 1000-grain weight, ranging from 32.03 to 28.13g. The genotypes GZ 10101-5-1-1-1, GZ 9399-4-1-1-3-2-2, Sakha 105, Giza 182 and Giza 178 showed the greatest mean values of fertility percentage, which were 95.78, 95.58, 95.43, 95.03 and 94.62%, respectively.

Table 2. Mean performances of agronomic and yield traits of the used rice genotypes

Genotypes	DTHI	PHI	PLI	PW	PDI	NPP	TGW
Giza 178	102.17	101.67	21.67	2.80	7.33	21.50	22.43
Giza 182	102.67	93.50	21.33	2.37	4.96	19.33	26.03
Sakha 101	108.50	84.83	23.33	3.13	6.24	21.00	26.38
Sakha 105	96.17	89.83	20.67	3.04	6.41	19.67	28.13
Egyptian Yasmine	115.67	106.83	24.83	4.20	8.35	20.33	26.08
GZ9399-4-1-1-3-2-2	91.67	87.17	19.67	2.43	5.44	18.50	26.57
GZ 10101-5-1-1-1	93.00	80.17	20.33	2.60	6.28	17.00	27.03
IRRI 142	85.67	91.00	21.33	3.43	8.19	18.67	23.45
IRRI 152	93.17	96.83	21.50	3.23	8.20	17.00	27.85
IRRI 154	109.00	124.83	25.87	4.17	10.08	20.50	21.40
IRRI 147	99.67	114.50	26.33	3.50	7.20	18.83	28.70
IRAT 112	97.67	110.83	18.67	3.07	7.21	16.67	32.00
WAB-96-1-1	102.83	124.17	20.20	5.07	15.48	10.67	32.03
IR14P1016	112.67	117.00	27.37	3.60	10.07	13.17	29.53
IR 65600-77-4-2-1	116.83	90.33	23.30	3.90	7.86	20.83	26.06
Genotypes	TS	FP	GYP	GL	GW	GTH	GS
Giza 178	160.68	94.62	52.07	7.35	2.77	1.93	2.66
Giza 182	128.28	95.03	42.78	9.32	2.66	2.11	3.51
Sakha 101	143.04	93.60	52.32	7.94	3.07	2.14	2.59
Sakha 105	123.94	95.43	43.92	8.32	3.41	2.25	2.44
Egyptian Yasmine	166.67	90.33	55.07	9.94	2.55	2.08	3.91
GZ9399-4-1-1-3-2-2	131.95	95.58	43.05	7.81	3.10	2.11	2.52
GZ 10101-5-1-1-1	132.73	95.78	42.37	8.11	3.40	2.26	2.39
IRRI 142	145.31	87.85	38.68	8.03	3.16	2.18	2.54
IRRI 152	132.41	80.35	34.55	7.78	3.29	2.27	2.37
IRRI 154	191.41	91.13	53.47	8.19	2.89	1.92	2.84
IRRI 147	133.41	86.80	46.60	7.89	3.31	2.23	2.39
IRAT 112	111.58	82.62	34.27	9.55	2.99	2.13	3.20
WAB-96-1-1	170.01	94.45	37.52	9.34	3.63	2.14	2.57
IR14P1016	126.94	94.53	33.43	9.83	2.63	2.09	3.75
IR 65600-77-4-2-1	146.71	88.92	50.02	8.15	3.58	2.37	2.28

DTH: days to heading (day), PH: plant height (cm), PLI: panicle length (cm), PW: panicle weight, panicle density index (PDI), NPP: number of panicles/plant, TGW: 1000-grain weight, TS: total spikelet, FP: fertility percentage, GYP: grain yield per plant, GL: grain length, GW: grain width, GTH: grain thickness and GS: grain shape.

The genotypes Giza178, Sakha 101, IR 65600-77-4-2-1, IRRI 154, and Egyptian Yasmine produced the greatest results for the quantity of panicles per plant (21.5, 21, 20.83,

20.5, and 20.33, respectively). The genotypes Egyptian Yasmine, IRRI 154, Sakha 101, Giza 178, IR 65600-77-4-2-1, and IRRI 147 were found to have the highest mean values for grain yield/plant (53.47, 55.07, 52.32, 52.07, 50.02, and 46.60, respectively). The genotypes Egyptian Yasmine, IR14P1016, IRAT 112, WAB-96-1-1, and Giza 182 produced the greatest mean values for grain length, with respective mean values of 9.94, 9.83, 9.55, 9.34, and 9.32 mm. While the widest grains, measuring 3.31 to 3.63 mm, were found in the genotypes WAB-96-1-1, IR 65600-77-4-2-1, Sakha 105, GZ 10101-5-1-1-1, and IRRI 147. IR 65600-77-4-2-1 (2.37 mm) recorded the thickest grain, whereas IRRI 154 (1.92 mm) recorded the thinnest grain. The Indica rice genotypes Egyptian Yasmine, IR14P1016, Giza 182, and IRAT 112 had the greatest grain shape values (3.91, 3.75, 3.51, and 3.2, respectively). The japonica genotypes had the lowest results.

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Principal components analysis:

The study of principle components (PCA) of variability for the two years' utilized rice genotypes comprised all studied agronomic and yield variables. 74.37 percent of the cumulative total variance is made up of the first three components. According to Table 3 and Fig. 1, the components' eigenvalues account for 4.34, 3.67, and 2.40 percent of the variation in the average values of the examined treatments. The PC1 had a high positive correlation with panicle weight, number of panicles / plant, and harvest index traits. The PC2 was strongly correlated with 1000 grain weight and fertility percentage. The PC3 was highly correlated with number of panicles / plant. The PC1 accounted for highest value of the total variance of all analyzed variables, followed by PC2 and PC3. The variables analyzed by PCA which contributed the highest for the total variance could be manipulated during yield improvement programs in rice as suggested by El-Mageed, T.A.A *et al.*, 2022, Khan, F. *et al.*, 2017 and Shaaban, A. *et al.*, 2022. Bii *et al.* (2020) found that first three principal components having Eigen value more than one are cumulatively contributing 68.69% to the total variability. PC1 has the contribution from the traits days to heading (0.34), panicle weight (0.45) and panicle density index (0.29) which accounted 31% of total variability indicating these traits contributed more to the total variance.

The correlation coefficient:

The relationships among the studied traits represented as correlation coefficient are presented in Table (4). The correlation coefficient was statistically estimated as reported by Gomez and Gomez (1983). Regarding the correlation between studied traits, grain yield was highly significant and positively correlated with each of number of panicles (0.778),

thousand grain weight (0.641), total spikelet number (0.60) and days to heading (0.50). Panicle weight was highly significant and positively correlated with total spikelet number (0.88), plant height (0.69) and panicle density index (0.65). While number of panicles was significant and negatively correlated to thousand grain weight (-0.73) and panicle density index (-0.68). Cyprien and Kumar (2011) 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. Babu et al. (2012) studied the correlation and path analysis in twenty one popular hybrids of rice (*Oryza sativa* L.) whereas, character association of the yield attributing traits revealed significantly positive association of grain yield per plant with number of productive tillers per plant.

For grain dimensions results in table 4 showed that high positively significant correlation were found between grain length and each of grain shape (0.83) and thousand grain weight (0.51). Grain thickness was high positively significant correlated to grain width (0.71) and negatively correlated to total spikelet number (-0.51). For grain shape there were high negatively significant correlation with grain width (-0.84) and grain thickness (-0.47).

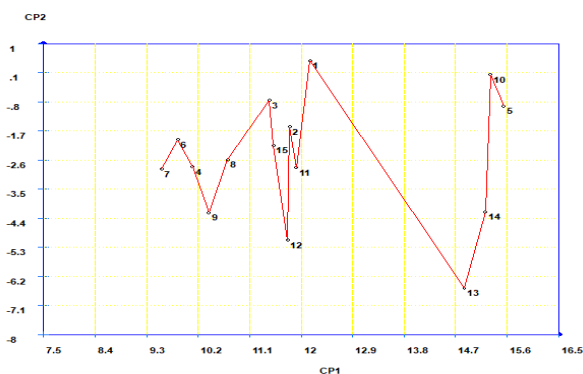


Figure 1. Principal components multivariate analysis for used genotypes

Table 3. Principal components multivariate analysis for used genotypes

	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigenvalue	4.34	3.67	2.40	1.29	1.07	0.58	0.34
Importance (%)	31.00	26.21	17.16	9.25	7.65	4.14	2.46
% Accumulated	31.00	57.22	74.37	83.62	91.27	95.41	97.87
DTH1	0.34	0.40	0.29	0.35	0.32	-0.13	0.01
PH1	0.13	-0.14	0.16	-0.16	-0.26	0.46	-0.46
PL1	0.00	0.08	0.04	0.35	0.30	0.02	-0.14
PW	0.45	-0.10	0.39	0.12	-0.19	0.23	0.17
PDI	0.29	-0.30	-0.10	0.01	0.03	-0.13	0.16
NPP	-0.06	0.16	0.73	-0.19	-0.01	-0.25	-0.04
TGW	0.20	0.46	-0.15	-0.17	-0.16	0.14	0.55
TS	-0.70	0.22	0.23	0.21	-0.21	0.16	0.11
FP	0.17	0.51	-0.15	-0.10	-0.08	0.30	-0.48
GYP	0.06	0.22	-0.02	-0.51	-0.30	-0.46	-0.04
GL	0.07	-0.32	0.22	0.08	-0.33	-0.11	-0.03
GW	0.06	0.06	-0.04	0.32	-0.49	0.20	0.28
GTH	-0.08	-0.12	0.20	-0.48	0.42	0.49	0.31
GS	-0.01	0.07	-0.04	0.02	0.01	-0.02	0.00

Where DTH: days to heading (day), PH: plant height (cm), PL1: panicle length (cm), PW: panicle weight, panicle density index (PDI), NPP: number of panicles/plant, TGW: 1000-grain weight, TS: total spikelet, FP: fertility percentage, GYP: grain yield per plant, GL: grain length, GW: grain width, GTH: grain thickness and GS: grain shape.

Genetic variability:

Breeding programs for any crop may be made better and more successful 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 (GS %). Estimates of genetic (GV) and phenotypic (PV) variance, genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability (H) broadly construed, and genetic advance (GA%) were displayed in Table 5. Phenotypic variation frequently exceeded genotypic variance in all the studied growth characteristics, as would be predicted. It is important to keep in mind that total variability depends on both heritable and non-heritable components when determining the variance in yield components responsible for variations in yield among different genotypes. While estimates 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.

The results demonstrated the largest genotypic variation (GV) and phenotypic variance (PV) in total spikelet (884.65), plant height (418.56), days to headings (171.61), grain yield, fertility % (47.59), thousand grain weight (18.51), and number of panicles per plant (17.81). The largest anticipated genetic advance (EGA), as well as high heritability (H) values, were shown by the panicle density index, grain shape and grain yield.

The results revealed considerable phenotypic and genotypic variances among the genotypes for the traits under consideration. The estimates of GCV were high for plant height (20.28) number of panicles/plant (23.18), panicle weight (30.26) and grain yield (23.61), panicle density index (44.86), total spikelet (20.8) and grain shape (26.9). The remaining traits recorded moderate to low GCV estimates. The PCV values were higher than GCV values for most studied traits, which reflect the influence of environment on the expression of these traits.

Most genotypes displayed appreciable variations for the traits under investigation (Table 5). Higher estimates of heritability for the number of days before heading (1), plant height (0.97), grain yield (0.99), and total spikelets (0.99) along with strong genetic progress suggest the existence of additive genes. High heritability and genetic progress are essential factors for determining the result of picking the best candidates. Days to heading and plant height had high heritability and high genetic advance, whereas panicle length (cm), panicle weight, number of panicles per plant, 1000-grain weight, TGW, fertility percentage, GL, GW, GTH, and GS had high heritability and low genetic advance. 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.

Table 4. Correlation analysis among the studied growth and yield characters

	DTH	PH	PL	PW	PDI	NPP	TGW	TS	FP	GYP	GL	GW	GTH
PH	0.36												
PL	0.63*	0.45											
PW	0.48	0.69**	0.38										
PDI	0.25	0.73**	0.18	0.88**									
NPP	0.13	-0.44	0.13	-0.38	-0.68**								
TGW	-0.04	0.22	-0.24	0.17	0.29	-0.73**							
TS	0.40	0.44	0.34	0.65**	0.55*	0.14	-0.53						
FP	0.15	-0.19	0.00	-0.15	-0.03	-0.01	-0.18	0.17					
GYP	0.50	-0.09	0.36	0.10	-0.21	0.778**	-0.64**	0.60*	0.28				
GL	0.43	0.45	0.13	0.36	0.35	-0.49	0.51*	-0.07	0.04	-0.28			
GW	-0.32	-0.20	-0.37	0.21	0.23	-0.24	0.33	-0.08	-0.12	-0.20	-0.40		
GTH	-0.18	-0.48	-0.20	-0.05	-0.16	-0.12	0.42	-0.51*	-0.29	-0.30	-0.12	0.71**	
GS	0.47	0.37	0.33	0.09	0.05	-0.13	0.10	0.01	0.10	-0.02	0.83**	-0.84**	-0.47

Where DTH: days to heading (day), PH: plant height (cm), PL: panicle length (cm), PW: panicle weight, PDI: panicle density index (PDI), NPP: number of panicles/plant, TGW: 1000-grain weight, TS: total spikelet, FP: fertility percentage, GYP: grain yield per plant, GL: grain length, GW: grain width, GTH: grain thickness and GS: grain shape.

Table 5. Genetic variability Parameters

	Mean	PV	GV	EV	PCV	GCV	GA	EGA	H
DTH	101.82	171.91	171.61	0.3	12.88	12.87	26.91	26.43	1
PH	100.9	424.69	418.56	6.13	20.42	20.28	41.25	40.88	0.97
PL	22.43	13.84	13.27	0.57	16.59	16.24	7.05	31.45	0.92
PW	3.37	1.09	1.04	0.05	30.98	30.26	1.96	58.22	0.91
PDI	7.95	12.98	12.72	0.26	45.32	44.86	7.13	89.64	0.96
NPP	18.24	18.13	17.81	0.32	23.35	23.14	8.47	46.42	0.97
TGW	26.91	18.52	18.51	0.01	15.99	15.99	8.86	32.91	1
TS	143	888.95	884.65	4.29	20.85	20.8	60.83	42.54	0.99
FP	91.14	48.55	47.59	0.95	7.64	7.57	13.8	15.14	0.96
GYP	44.01	108.62	108	0.62	23.68	23.61	21.22	48.23	0.99
GL	8.5	1.42	1.4	0.02	14.04	13.92	2.38	27.98	0.97
GW	3.1	0.24	0.23	0.001	15.69	15.58	0.97	31.43	0.97
GTH	2.15	0.03	0.03	0.001	8.06	8.06	0.36	16.6	1
GS	2.79	0.57	0.56	0.01	27.06	26.9	1.52	54.46	0.98

DTH: days to heading (day), PH: plant height (cm), PL: panicle length (cm), PW: panicle weight, NPP: number of panicles/plant, TGW: 1000-grain weight, TS: total spikelets, FP: fertility percentage, GYP: grain yield per plant, GL: grain length, GW: grain width, GTH: grain thickness and GS: grain shape.

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, like days to heading, showed high heritability and high genetic advance, indicating selection will be 100 percent highly effective, while other traits, like number of panicles/plant and fertility percentage, showed high genetic advance with low or medium heritability, indicating they would also show a positive response to selection. 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.

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التباين الوراثي و تحليل المتغيرات المتعددة والارتباط للصفات الزراعية لتراكيب وراثية مختلفة في الأرز

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مركز البحوث والتدريب في الارز- معهد بحوث المحاصيل الحقلية - مركز البحوث الزراعية - الجيزة - مصر

المخلص

الدراسة الحالية كان الهدف منها هو تقييم وجود التباين في الصفات المرغوبة وتقدير الصفات الوراثية (معامل اختلاف الشكل الظاهري والوراثة للتباين، ونسبة التوريث بالمعنى الواسع)، والارتباطات وتحليل المكونات الرئيسية لهذه الصفات. أجريت الدراسة في عامي ٢٠٢٠ و ٢٠٢١ في مزرعة قسم بحوث الأرز بمحطة بحوث سخا التابعة لمركز البحوث الزراعية، مصر. في تصميم القطاعات الكاملة العشوائية بثلاثة مكررات، تم تقييم خمسة عشر تركيباً وراثياً من الأرز لصفات المكونات المحصولية ومحصول الحبوب، بما في ذلك أيام التزهير، وارتفاع النبات، وعدد السنابل لكل نبات، وطول السنبل، وإجمالي السنبلات لكل سنبل، ومؤشر كثافة السنبل، وطول الحبوب، العرض والسماكة والشكل ووزن ١٠٠٠ حبة، وحاصل الحبوب لكل نبات. أظهر تحليل التباين اختلافات معنوية بين الطرز الوراثية لجميع الصفات المدروسة. سجلت الأصناف ياسمين المصري و IRRI 154 وسخا ١٠١ وجيزة ١٧٨ و IR 65600-77-4-2-1 و IRRI 147 أعلى محصول للنبات 53.47 (46.60، 50.02، 52.07، 52.32، 55.07) بالترتيب. بينما أكبر عرض للحبوب والذي يتراوح ما بين ٣،٣١ إلى ٣،٦٣ مم وجد في الأصناف WAB- 65600-77-4-2-1 و IR 96-1-IR 65600-77-4-2-1 وسخا 96-1-IR 65600-77-4-2-1، بينما سجل أكبر سمك للحبة في الصنف IR 65600-77-4-2-1 (م ٢،٣٧). ستؤخذ جميع النتائج التي تم الحصول عليها في الاعتبار في برامج التهجين التالية للحصول على أفضل الصفات المرغوبة في نبات الأرز.

الكلمات الدالة: الاختلاف الوراثي، التحليل متعدد المتغيرات، تحليل الارتباط، الأرز