

# Journal of Plant Production

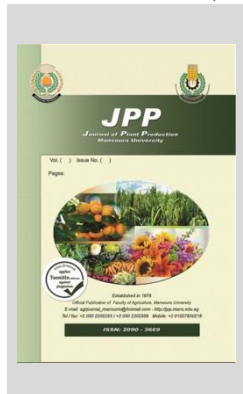
Journal homepage & Available online at: [www.jpp.journals.ekb.eg](http://www.jpp.journals.ekb.eg)

## Studies on Correlation and some Morphological, Yield and its Components Traits in some Rice Hybrids

Arafat, E. F. A.; M. E. Negm\* and Dalia E. Elsharnobi



Rice Research Section, Field Crops Research Institute, Agricultural Research Center, Giza, Egypt



### ABSTRACT

Fourteen rice hybrids were grown in the two successive seasons 2020 and 2021 in Kafr El-Sheikh, Egypt, at the Experimental Farm of Rice Research and Training Center to evaluate the presence of variation for investigated traits and to estimate correlations for the studied traits with the grain yield. Every analyzed trait revealed substantial variations between hybrids, indicating a wide range of genetic variability controlling the studied traits. Grain yield ( $t\ ha^{-1}$ ) and 100-grain weight attributes with IR69625A×GZ6296, IR58025A×GZ6296 and G46A×GZ6296 hybrids achieved the highest estimated values and the hybrids IR70368A×PR78 and Pusa13A×Giza181 in the grain yield only. Five hybrids showed surpass over standard check variety, EHR1 for grain yield and some other traits. A strong positive correlation and regression was found between grain yield ( $t\ ha^{-1}$ ) and the following variables: panicle length, number of spikelets panicle<sup>-1</sup>, harvest index and biological yield ( $t\ ha^{-1}$ ) and it can be dependent on these trait to select the best genotypes in breeding program to improve the grain yield.

**Keywords:** Hybrid rice, grain yield, correlation, regression.

### INTRODUCTION

The world's population is expected to reach 9.1 billion people by the year 2050, but agricultural production is not growing at a similar rate. To feed an additional 3.2 billion people by 2050, the global agricultural production of grains must increase from 2.1 billion tons to 3 billion tons (FAO, 2015). Expanding rice production through increases in yield potential is necessary to address the issues of population expansion, climate change, and a lack of arable land (Cordero-Lara, 2020). In tropical, subtropical, and temperate climates, rice (*Oryza sativa* L.) is frequently grown (Huang *et al.*, 2021). The enormous variety of ecological settings in which rice can flourish is proof the crop's cultivars' high genetic variability. Every breeder in the world strives to create cultivars that are higher producing and of higher quality. Finding a sufficient level of variability in the targeted genotypes that will be chosen for additional manipulation to reach the target is a requirement for achieving this goal. Planning a successful breeding program will require careful consideration of the variability of the qualities and their relationships to other variables that affect crop output (Mary and Gopalan, 2006). The creation of high-yielding cultivars necessitates a detailed understanding of the genetic diversity for yield currently present and its constituent parts. Measurement of rice genotype genetic variability was one of the study's goals and estimates the correlation among morphological, yield and its components traits to determine the most suitable breeding methods to get new rice hybrids with more adaptable and improved traits.

### MATERIALS AND METHODS

In the current study, 14 rice hybrids were examined to determine their morphological, yield, and component

qualities as well as their associations with grain production. The 2020 and 2021 rice consecutive seasons saw the cultivation of rice hybrids at the Research Farm of Rice Research and Training Center, Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt. On May 5<sup>th</sup>, the nursery was planted for each hybrids, and after 30 days, it was transferred to the field. For each hybrid, there were planted in five rows. Individual seedlings were transplanted. Seedling-to-seedling and row-to-row spacing were kept at 20 and 20 cm, respectively. A randomized complete block design (RCBD) with three replications was used to design the experiments in each season. Three divides of nitrogen fertilizer application were added. At the time of seeding, phosphorus and potash were treated in full doses. Regular applications of weed and insect control were made as necessary. All of the traits' variance was examined using combination analysis in accordance with Steel *et al.* (1997). The correlation estimates according to Kown and Torrie (1964). The outcome variable taken into consideration was grain yield, and the causal variables were the other variables. The traits that were noticed were plant height (cm) and heading date (day), panicle length (cm), panicle weight (g), number of tillers plant<sup>-1</sup>, number of filled grains panicle<sup>-1</sup>, spikelets panicle<sup>-1</sup>, seed set percentage, 100-grain weight (g), grain yield ( $t\ ha^{-1}$ ), biological yield ( $t\ ha^{-1}$ ), and harvest index %, were measured according to (IRRI, 1996).

### RESULTS AND DISCUSSION

Table 1 shows the results of the analysis of variance for the investigated traits. For heading date (day), panicle weight (g), and 100-grain weight, mean squares due to years were significant and highly significant. Meanwhile, all the investigated traits showed highly significant for genotypes mean squares for both and across years; it suggests that the

\* Corresponding author.

E-mail address: mahrousnegm9@gmail.com

DOI: 10.21608/jpp.2022.158046.1161

genotypes exhibit substantial genetic variability (Hadifa et al., 2018). Therefore, this is the basic requirement to complete the study, as genetic diversity enables the plant breeder to choose the best genotypes and include them in

breeding programs to obtain the best promising and high genotypes in the grain yield. Ponnuswamy et al. (2018) and Huang et al. (2021) studied the combined analysis and the interaction between genotypes and year.

**Table 1. Mean squares of fourteen rice hybrids for studied morphological, yield and its components traits in both and across the two studied years.**

SOV	df		Heading date (day)			Plant height (cm)			Panicle length (cm)			Panicle weight (g)		
	Single	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.
year		1			78.11*			10.36 <sup>ns</sup>			0.46 <sup>ns</sup>			1.29 <sup>**</sup>
Replication × year	2	4	0.60**	0.72 <sup>ns</sup>	4.66	40.30*	7.04 <sup>ns</sup>	23.67	0.89 <sup>ns</sup>	1.11 <sup>ns</sup>	1.00	0.02 <sup>ns</sup>	0.08 <sup>ns</sup>	0.05
Genotypes	13	13	79.53**	77.51**	155.9**	351.7**	285.23**	622.68**	5.37**	4.38**	7.74**	1.14**	1.30**	2.41**
year × Genotypes		13			1.18 <sup>ns</sup>			14.21*			2.02**			0.03 <sup>ns</sup>
Error	26	52	0.88	0.83	0.86	7.87	3.26	5.57	0.37	1.15	0.76	0.04	0.02	0.03
Total	41	83												
cv %			0.94	5.03	3.55	5.68	3.66	3.89	1.23	2.17	1.44	6.00	4.82	6.40

**Table 1. Continued:**

SOV	df		No. of tillers plant <sup>-1</sup>			Filled grains panicle <sup>-1</sup>			No. of spikelets panicle <sup>-1</sup>			Seed set %		
	Single	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.
year		1			19.05 <sup>ns</sup>			27.43 <sup>ns</sup>			2.33 <sup>ns</sup>			7.31 <sup>ns</sup>
Replication × year	2	4	12.17 <sup>ns</sup>	5.37 <sup>ns</sup>	8.77	96.50 <sup>ns</sup>	120.98 <sup>ns</sup>	108.74	162.17 <sup>ns</sup>	135.60 <sup>ns</sup>	148.88	7.53**	0.09 <sup>ns</sup>	3.81
Genotypes	13	13	26.37**	13.21**	28.45**	3009**	2903**	5894**	3705**	3615**	7294**	27.2**	26.4**	53.22**
year × Genotypes		13			11.12*			17.53 <sup>ns</sup>			24.44 <sup>ns</sup>			0.36 <sup>ns</sup>
Error	26	52	3.88	5.50	4.69	80.14	80.48	80.31	97.78	84.13	90.96	0.57	0.53	0.55
Total	41	83												
cv %			9.21	11.47	9.03	18.12	18.16	19.79	6.65	6.15	5.85	0.82	0.79	0.79

**Table 1. Continued:**

SOV	df		100-grain weight (g)			Grain yield (t ha <sup>-1</sup> )			Biological yield (t ha <sup>-1</sup> )			Harvest index %		
	Single	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.
year		1			0.81*			0.001 <sup>ns</sup>			19.74 <sup>ns</sup>			96.50 <sup>ns</sup>
Replication × year	2	4	0.01 <sup>ns</sup>	0.037*	0.025	0.03 <sup>ns</sup>	1.73**	0.881	2.25 <sup>ns</sup>	9.02*	5.63	3.03 <sup>ns</sup>	70.46**	36.74
Genotypes	13	13	0.15**	0.186**	0.31**	11.72**	11.59**	23.24**	43.89**	58.62**	99.60**	47.55**	43.21**	79.14**
year × Genotypes		13			0.02**			0.07 <sup>ns</sup>			2.91*			11.62**
Error	26	52	0.005	0.009	0.007	0.16	0.103	0.13	0.767	1.34	1.06	1.74	3.82	2.78
Total	41	83												
cv %			.14	0.197	0.18	0.81	.65	0.80	1.77	2.35	2.27	2.67	3.95	3.68

where, \* and \*\* indicate (p ≤ 0.05) significant and high a significant (p ≤ 0.01)

Mean squares due to year x genotypes were significant or highly significant for plant height (cm), panicle length (cm), tillers plant<sup>-1</sup>, 100-grain weight (g), biological yield (t ha<sup>-1</sup>), and harvest index, this showed that the tested genotypes were changed and were ranked differently from year to year for the aforementioned traits. It might be said that certain hybrids exceed the others if the mean squares of genotypes were highly significant than the interaction mean squares of genotypes with years and therefore we can identify the most superior hybrids. The investigation's significant variances amongst rice hybrids show that the material was genetically variable and present a promising possibility for increased output. Grain yield and other characters exhibited stability across the seasons since no significance of year × genotype interaction was detected and the differences among hybrids were apparent. Contrarily, Shrestha et al. (2020) found significant interaction between genotypes and year in grain yield.

**Mean performance:**

The mean performances of the studied hybrids at both and across years are presented in Table 2. For days to heading, the hybrids G46A×GZ6296, IR69625A×Giza179, IR70368A×Giza179 and IR69625A×GZ6296 were the shortest duration hybrids, their estimated values were 88.33, 91.33, 94.00 and 96.33 day, respectively for the first year, 87.67, 89.00, 91.00 and 95.33 day, respectively for the second year and 88.00, 90.17, 92.50 and 95.83 day,

respectively for combined data. These findings concur strongly with those made public by Guan et al. (2010), Tiwari (2015) and Gaballah (2016).

Significant differences in plant height trait were recorded between the rice hybrids studied; the hybrids IR70368A×Giza179, IR69625A×Giza179 and IR69625A×GZ6296 produced the most ideal mean values for dwarfism, their estimated values were 77.00, 84.00 and 85.17 cm, respectively for the first year, 82.17, 82.17 and 84.33 cm, respectively for the second year and 79.58, 83.08 and 84.75 cm, respectively for combined data. These outcomes concur with those attained by Abd Allah et al. (2010), Kumar et al. (2013), Bhati et al. (2015) and Gaballah (2016).

The hybrids, Pusa13A×Giza181, IR70368A × Giza 181, Pusa 13A×PR78 and G46A×GZ6296 gives the highest means with values of 24.80, 25.00, 25.00 and 24.40 cm in the first year, 25.00, 25.50, 23.00 and 24.00 cm in the second year and 24.88, 24.77, 24.02 and 24.22 cm for combined data, respectively, for panicle length (cm).

Regarding panicle weight, the hybrids, G46A × GZ6296, IR69625A ×GZ6296, Pusa13A×PR78 and IR 69625A × Giza181 recorded the highest mean values (4.72, 4.52, 3.99 and 3.91 g, respectively) in the first year, (4.63, 4.48, 3.64 and 3.51 g, respectively) in the second year and (4.68, 4.50, 3.81 and 3.71 g, respectively) for the combined data (El-Mowafi et al., 2021).

With concerning number of tillers plant<sup>-1</sup> the highest mean values obtained from hybrids, G46A×GZ6296 and IR58025A×GZ6296, their values were 26.67 and 25.33 tillers plant<sup>-1</sup> in the first season, 23.67 and 22.67 tillers plant<sup>-1</sup> in the second season and 25.17 and 24.00 tillers plant<sup>-1</sup> for combined data (El- Mowafi *et al.*, 2021, El- Mowafi *et al.*, 2022 and Elsharnobi *et al.*, 2022).

Regarding number of filled grain panicle<sup>-1</sup> the superior values resulted from hybrids, G46A×GZ6296 (209.0, 207.3 and 208.2 grains) in both seasons one and two and combined data, respectively and IR69625A×GZ6296 (195.3, 192.7 and 194.0 grains) in the first and second season and their combined data, respectively (Elsharnobi *et al.*, 2022).

**Table 2. Mean performances of morphological, yield and its components of fourteen rice hybrids of 2020 and 2021 seasons and their combined data.**

Genotypes	Heading date (day)			Plant height (cm)			Panicle length (cm)			Panicle weight (g)			Tillers plant <sup>-1</sup>			Filled grains panicle <sup>-1</sup>		
	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.
EHR1	99.33	97.00	98.17	95.67	95.30	95.50	23.20	21.70	22.42	2.58	2.27	2.42	19.00	19.67	19.33	93.70	95.7	94.67
IR70368A×Giza178	98.67	97.00	97.83	87.67	91.50	89.58	21.90	23.30	22.60	3.69	3.21	3.45	21.67	18.33	20.00	136.0	137.7	136.8
Pusa13A×Giza178	101.0	99.00	100.0	92.67	97.83	95.25	22.70	23.30	23.00	2.95	2.73	2.84	20.33	22.67	21.50	129.3	128.0	128.7
IR69625A×GZ6296	96.33	95.33	95.83	85.17	84.33	84.75	23.20	23.30	23.25	4.52	4.48	4.50	22.00	22.00	22.00	195.3	192.7	194.0
IR58025A×GZ6296	98.67	98.00	98.33	109.0	108.3	108.7	23.30	23.70	23.50	2.93	2.87	2.90	25.33	22.67	24.00	147.3	157.3	152.3
G46A×GZ6296	88.33	87.67	88.00	105.7	103.3	104.5	24.40	24.00	24.22	4.72	4.63	4.68	26.67	23.67	25.17	209.0	207.1	208.2
IR69625A×Giza179	91.33	89.00	90.17	84.00	82.17	83.08	21.80	20.50	21.13	3.56	3.17	3.37	16.33	20.33	18.33	121.3	124.7	123.0
IR70368A×Giza179	94.00	91.00	92.50	77.00	82.17	79.58	20.40	22.50	21.47	3.11	2.71	2.91	23.33	21.00	22.17	108.0	107.3	107.7
IR69625A×PR78	102.0	99.67	100.8	88.33	90.17	89.25	22.50	22.30	22.43	3.40	3.38	3.39	19.33	17.67	18.50	133.0	135.3	134.2
IR70368A×PR78	102.7	99.33	101.0	96.33	95.83	96.08	23.40	22.00	22.72	3.05	2.83	2.94	18.33	20.33	19.33	116.0	117.3	116.7
Pusa13A×PR78	102.7	99.67	101.2	115.7	115.5	115.6	25.00	23.00	24.02	3.99	3.64	3.81	22.00	23.00	22.50	135.3	136.7	136.0
IR69625A×Giza181	102.3	100.0	101.2	85.67	91.50	88.58	23.80	24.20	23.97	3.91	3.51	3.71	20.67	17.67	19.17	149.0	147.0	148.0
IR70368A×Giza181	104.0	102.7	103.3	90.00	87.50	88.75	25.00	24.50	24.77	3.59	3.30	3.44	19.33	18.00	18.67	132.0	136.7	134.3
Pusa13A×Giza181	107.0	106.0	106.5	101.7	98.83	100.3	24.80	25.00	24.88	3.14	2.93	3.04	25.33	19.33	22.33	110.7	108.3	109.5
LSD 0.05	1.90	9.82	7.71	5.71	29.12	17.10	1.23	2.17	1.44	0.43	0.32	0.41	3.99	4.75	4.78	18.12	18.16	19.79
CV %	0.94	5.03	3.55	3.00	14.94	9.54	2.62	4.6	3.71	6.00	4.82	6.40	9.21	11.47	9.03	6.54	6.5	5.88

**Table 2. Continued**

Genotypes	Spikelets panicle <sup>-1</sup>			Seed set (%)			100-grain weight (g)			Grain yield (t ha <sup>-1</sup> )			Biological yield (t ha <sup>-1</sup> )			Harvest index (%)		
	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.	Year1	Year2	Comb.
EHR1	101.3	102.0	101.7	92.44	93.79	93.11	2.82	2.51	2.67	12.02	11.67	11.84	32.13	30.15	31.14	37.4	41.53	39.46
IR70368A×Giza178	143.7	144.0	143.8	94.67	95.61	95.14	2.61	2.30	2.46	9.56	9.67	9.61	31.02	29.48	30.25	30.9	36.59	33.74
Pusa13A×Giza178	139.0	137.0	138.0	93.06	93.43	93.24	2.25	2.13	2.19	11.63	11.91	11.77	29.54	29.81	29.68	39.4	39.94	39.66
IR69625A×GZ6296	213.3	209.0	211.2	97.05	95.73	96.39	2.83	2.80	2.81	14.54	14.70	14.62	34.15	34.63	34.39	42.6	42.46	42.51
IR58025A×GZ6296	157.7	168.7	163.2	95.40	96.84	96.12	2.95	2.87	2.91	14.72	14.91	14.81	33.33	33.74	33.54	44.2	44.18	44.19
G46A×GZ6296	232.3	230.7	231.5	95.44	96.39	95.91	3.02	2.97	2.99	14.24	13.89	14.06	33.98	35.33	34.66	41.9	39.42	40.68
IR69625A×Giza179	127.3	130.3	128.8	95.29	95.65	95.47	2.79	2.43	2.61	9.59	9.43	9.51	26.98	25.44	26.21	35.5	39.95	37.73
IR70368A×Giza179	114.7	112.3	113.5	94.19	95.55	94.87	2.66	2.30	2.48	9.33	9.67	9.50	26.30	24.07	25.19	35.5	40.32	37.91
IR69625A×PR78	144.0	146.0	145.0	92.37	92.69	92.53	2.63	2.52	2.58	12.98	12.83	12.91	33.24	30.74	31.99	39.1	41.92	40.49
IR70368A×PR78	127.7	127.7	127.7	95.83	96.61	96.22	2.50	2.33	2.42	14.56	14.63	14.59	35.85	32.78	34.31	37.8	44.85	41.33
Pusa13A×PR78	150.3	150.7	150.5	90.03	90.71	90.37	2.78	2.47	2.63	11.44	11.22	11.33	37.04	36.67	36.85	30.9	30.61	30.76
IR69625A×Giza181	155.3	152.7	154.0	95.93	96.29	96.11	2.31	2.21	2.26	11.85	11.89	11.87	34.91	33.15	34.03	34.0	35.98	34.97
IR70368A×Giza181	143.0	147.7	145.3	92.31	92.55	92.43	2.56	2.32	2.44	12.80	12.78	12.79	34.91	33.15	34.03	36.7	38.59	37.63
Pusa13A×Giza181	132.0	127.7	129.8	83.84	97.39	90.62	2.60	2.40	2.50	14.63	14.61	14.62	40.65	41.30	40.97	36.0	35.46	35.73
LSD 0.05	20.02	18.57	21.06	2.00	1.99	2.18	0.13	0.19	0.18	0.81	0.56	0.76	1.82	2.54	2.41	2.67	3.95	3.68
CV %	6.65	6.2	5.85	1.06	1.0	1.03	2.42	3.98	2.83	3.25	2.24	2.32	2.73	3.99	3.25	3.54	5.00	3.77

With respect to the number of spikelets panicle<sup>-1</sup> the superior values resulted from hybrids, G46A×GZ6296 (232.3, 230.7 and 231.5 spikelets) in the first and second seasons, as well as the combined data, and IR69625A×GZ6296 (213.3, 209.0 and 211.2 spikelets) in both seasons one and two and combined data, respectively. The most desirable mean values of seed set percentage were exhibited by the hybrids, IR69625A×GZ6296, IR70368A×PR78 and IR69625A×Giza181, which gave the highest values, (97.10, 95.80 and 95.90 %, respectively) in the first year, (95.70, 96.60 and 96.30 %, respectively) in the second year and (96.39, 96.22 and 96.11 %, respectively) for the combined data. These results agree with Elsharnobi *et al.* (2022) they reported similar findings.

With respect to 100-grain weight, the hybrids, G46A × GZ6296, IR58025A × GZ6296 and IR69625A×GZ6296 gave the highest mean values, which were (3.02, 2.95 and 2.83 g) in the first and second season and combined data, respectively, (2.97, 2.87 and 2.80 g) in the first and second season and combined data, respectively and (2.99, 2.91 and 2.81 g) in the first and second season and their combined data, respectively. Elshenawy *et al.* (2018) reported similar results.

With respect to grain yield (t ha<sup>-1</sup>), The hybrids were able to identify the best desired mean values, IR58025A × GZ6296, IR69625A × GZ6296, Pusa13A × Giza181, IR70368A×PR78 and G46A×GZ6296 which gave the grain yield ranged from 14.24 to 14.72 t ha<sup>-1</sup>, 13.89 to 14.91 and 14.06 to 14.81 t ha<sup>-1</sup>, in the first

and second season and combined data, respectively. The highest mean biological yield ( $t\ ha^{-1}$ ) significant values were obtained by IR69625A  $\times$  GZ6296, IR58025A $\times$ GZ6296, G46A  $\times$  GZ6296, IR 69625A  $\times$ PR78 and IR70368A $\times$ PR78 hybrids, which gave the best values ranged between ( $37.80$  and  $44.20\ t\ ha^{-1}$ ) in the first season, ( $39.42$  and  $44.85\ t\ ha^{-1}$ ) in the second season and ( $40.49$  and  $44.19\ t\ ha^{-1}$ ) for the combined data, respectively. For Harvest index percentage the hybrids, IR69625A $\times$ PR78, G46A $\times$ GZ6296, IR70368A  $\times$  PR78, IR69625A $\times$ GZ6296 and IR58025A $\times$ GZ6296 provided mean values that ranged from  $37.8$  to  $44.2\ \%$ ,  $39.42$  to  $44.85\ \%$  and  $40.49$  to  $44.19\ \%$ , in the seasons and their combined data, respectively. These findings agree with the results found by Abd El-Hadi *et al.* (2013) and Elshenawy *et al.* (2018).

**Phenotypic correlations coefficients among characters:**

When simultaneously selecting between multiple traits in plant breeding programs, especially

when a trait's heritability is low or it is challenging to quantify or detect, the correlation between traits is crucial. Thus, choosing plants based on traits that are connected with the primary variable is one of the mechanisms employed. Knowing the degree of the correlation between an explanatory variable and the primary variable allows one to evaluate the effect on the primary variable. A third party's influence on them or a group of characters could be the cause of the close bond between two characters (Júnior *et al.*, 2021). There were 4 significant phenotypic correlations that might be used to establish whether there was a linear link between features. The grain yield and biological yield showed the highest degree of significant positive connection ( $0.730$ ), corroborating with El-Mowafi *et al.* (2022), who discovered a strong positive correlation. However the lowest magnitude of significant positive correlation ( $0.062$ ) was observed between grain yields with seed set percentage.

**Table 3. Estimation of phenotypic correlation coefficient among different morphological, yield and its components characteristics for combined data of two studied seasons of rice.**

	GY	HD	PH	PL	PW	TIL	FG	SPK	SS	GW	BY
GY	1										
HD	0.314 <sup>ns</sup>	1									
PH	0.422 <sup>ns</sup>	0.232 <sup>ns</sup>	1								
PL	0.598*	0.521*	0.545*	1							
PW	0.200 <sup>ns</sup>	-0.373 <sup>ns</sup>	0.057 <sup>ns</sup>	0.344 <sup>ns</sup>	1						
TIL	0.370 <sup>ns</sup>	-0.288 <sup>ns</sup>	0.571*	0.361 <sup>ns</sup>	0.335 <sup>ns</sup>	1					
FG	0.404 <sup>ns</sup>	-0.419 <sup>ns</sup>	0.163 <sup>ns</sup>	0.354 <sup>ns</sup>	0.888**	0.517*	1				
SPK	0.472*	-0.376 <sup>ns</sup>	0.227 <sup>ns</sup>	0.422 <sup>ns</sup>	0.891**	0.569*	0.992**	1			
SS	0.062 <sup>ns</sup>	-0.586*	-0.353 <sup>ns</sup>	-0.355 <sup>ns</sup>	0.245 <sup>ns</sup>	0.063 <sup>ns</sup>	0.448 <sup>ns</sup>	0.372 <sup>ns</sup>	1		
GW	0.389 <sup>ns</sup>	-0.509*	0.368 <sup>ns</sup>	0.069 <sup>ns</sup>	0.428 <sup>ns</sup>	0.567*	0.558*	0.586*	0.222 <sup>ns</sup>	1	
BY	0.730**	0.596*	0.621*	0.868**	0.279 <sup>ns</sup>	0.305 <sup>ns</sup>	0.241 <sup>ns</sup>	0.332 <sup>ns</sup>	-0.388 <sup>ns</sup>	0.169 <sup>ns</sup>	1
HI	0.572*	-0.272 <sup>ns</sup>	-0.111 <sup>ns</sup>	-0.176 <sup>ns</sup>	-0.061 <sup>ns</sup>	0.181 <sup>ns</sup>	0.294 <sup>ns</sup>	0.286 <sup>ns</sup>	0.525*	0.424 <sup>ns</sup>	-0.135 <sup>ns</sup>

Where, GY= Grain yield ( $t\ ha^{-1}$ ), HD= Heading date (day), PH= Plant height (cm), PL= Panicle length (cm), PW= Panicle weight (g), TIL=Tillers plant<sup>-1</sup>, FG= Filled grains panicle<sup>-1</sup>, SPK= Spikelets panicle<sup>-1</sup>, SS= Seed set (%), GW=100-grain weight (g), BY= Biological yield ( $t\ ha^{-1}$ ), HI= Harvest index (%).

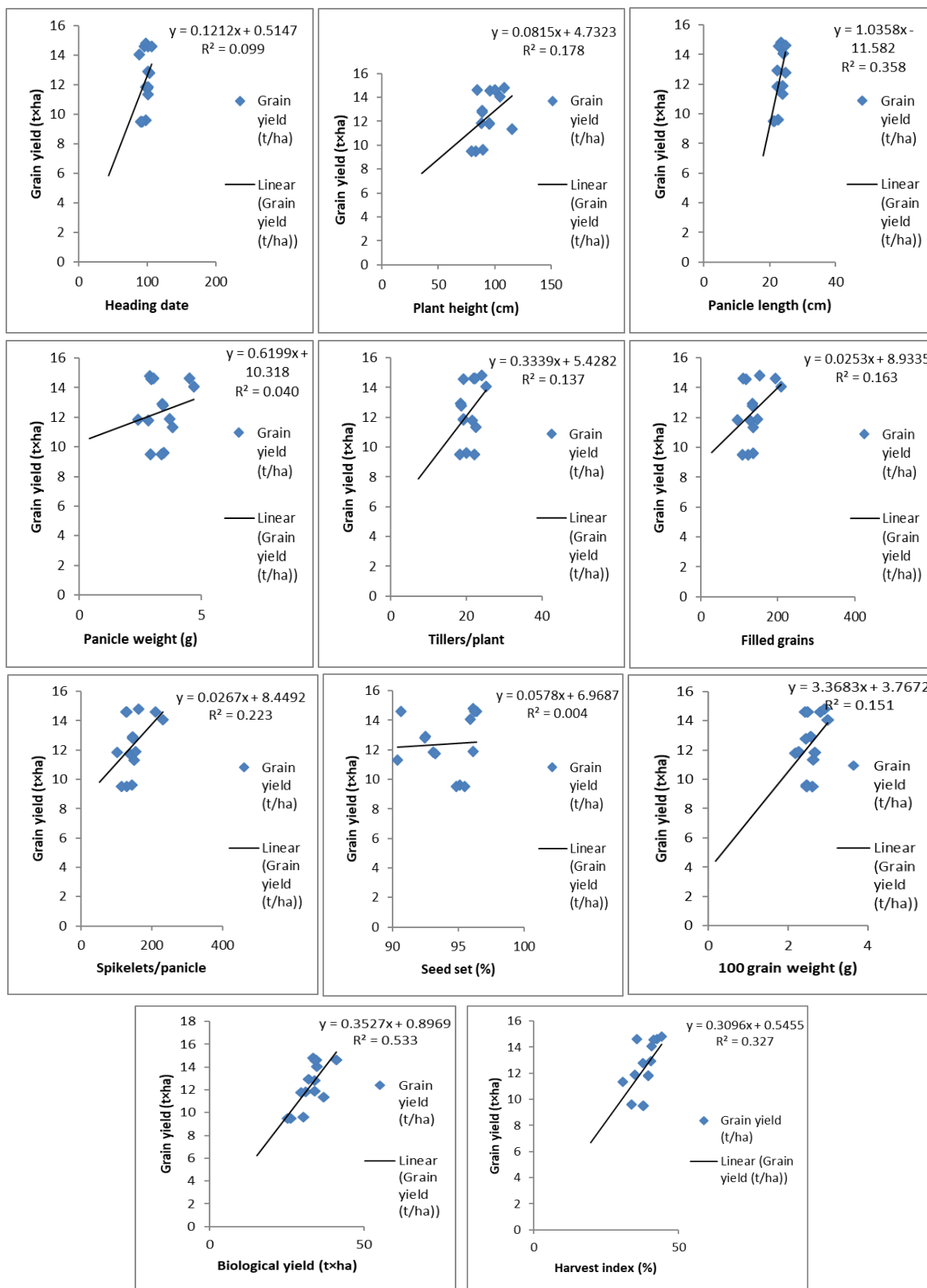
The phenotypic correlations estimates for morphological and yield and its related traits for combined data of two studied seasons are presented in Table 3. Duration showed significant and positive phenotypic correlated with panicle length and biological yield. On the contrary, it was negative correlated with seed set percentage and 100-grain weight. Plant height exhibited significant and positive phenotypic correlation with number of tillers plant<sup>-1</sup>, panicle length and biological yield.

The phenotypic correlation coefficients between panicle length and biological yield were found to be significantly significant and positive. Panicle weight showed positive and highly significant correlation with each of number of filled grains panicle<sup>-1</sup> and number of spikelets panicle<sup>-1</sup>. Number of tillers plant<sup>-1</sup> showed positive and significant correlation with number of filled grains panicle<sup>-1</sup>, number of spikelets panicle<sup>-1</sup> and 100-grain weight. The number of filled grains panicle<sup>-1</sup> showed significant and highly significant and positive phenotypic correlation with 100-grain weight and number of spikelets panicle<sup>-1</sup>, respectively. Number of spikelets panicle<sup>-1</sup> showed significant and positive phenotypic correlation with 100-grain weight. Seed set percentage showed significant and positive phenotypic correlation with harvest index

percentage. The degree of phenotypic correlation and several researchers Bhati *et al.* (2015), Gaballah (2016) and Touhiduzzaman *et al.* (2016) had stated that it was used in the selection.

**Linear regression**

The direct influence variables on yield's linear regression analysis (Figure 1) revealed a linear effect for the variables heading date, plant height (cm), panicle length (cm), panicle weight (g), number of tillers plant<sup>-1</sup>, filled grains panicle<sup>-1</sup>, number of spikelets panicle<sup>-1</sup>, 100-grain weight (g), biological yield ( $t\ ha^{-1}$ ) and harvest index (%). Furthermore, highly dependence of grain yield on biological yield, panicle length, harvest index and number of spikelet's panicle<sup>-1</sup>, was evident from the significant positive correlation with regression functions, accounting for  $R^2 = 0.533$ ,  $R^2 = 0.358$ ,  $R^2 = 0.327$  and  $R^2 = 0.223$  explained variability in grain yield, respectively. On the other hand the least traits which grain yield dependent on were seed set ( $0.004$ ) and panicle weight ( $0.040$ ). According to Streck *et al.* (2018), the variable that showed the best linear response with rice grain yield in a no-tillage system was the number of viable spikelets per panicle. A direct linear behavior and the model explained around 68% of the variation in rice yield.



**Figure 1. Analysis using linear regression of direct effect factors on grain production in several hybrids of rice.**  
 \*\* Significant at 1% probability by F test

**CONCLUSION**

For the analysis of variance, every trait under investigation showed distinct differences across hybrids. The highest estimated values were recorded with IR 69625 A × GZ6296, IR58025A×GZ6296 and G46A × G Z 6296 hybrids in the grain yield (t ha<sup>-1</sup>) and 100-grain yield (g) traits and the

hybrids IR70368A×PR78 and Pusa 13A × Giza181 in the grain yield only. Five hybrids showed superiority over standard check variety, EHR1 for grain yield and some other traits. Grain yield (t ha<sup>-1</sup>) showed significant and highly significant positive correlation with panicle length, number of spikelets panicle<sup>-1</sup>, harvest index and biological yield.

## REFERENCES

- Abd Allah, A.A., M.H. Ammar and A.T. Badawi (2010). Screening rice genotypes for drought resistance in Egypt. *J. Plant Breeding and Crop Sci.*, 2(7): 205-215.
- Abd El-Hadi, A. H., Kawser S. Kash, H.F. El-Mowafi and G.B. Anis (2013). The utilization of cytoplasmic male sterile (CMS) and restorer lines in the developing of hybrid rice *J.Agric.Chem.and Biotechn., Mansoura Univ.* 4(7): 263 – 274.
- Bhati, M., B. G. Suresh and S. R. Aishwarya (2015). Genetic variability, correlation and path coefficient for grain yield and quantitative traits of elite rice (*Oryza Sativa* L.) Genotypes at Uttar Pradesh. *Elect. J. Plant Breed.*, 6(2):586-591 .
- Cordero-Lara, K.I. (2020). Temperate japonica rice (*Oryza sativa* L.) breeding: History, present and future challenges. *Chil. J. Agric. Res.*, 80: 303–314.
- El-Mowafi, H.F.; AlKahtani, M.D.F.; Abdallah, R.M.; Reda, A.M.; Attia, K.A.; El-Hity, M. A.; El-Dabaawy, H.E.; Husnain, L.A.; Al-Ateeq, T.K.; EL-Esawi, M.A.(2021). Combining Ability and Gene Action for Yield Characteristics in Novel Aromatic Cytoplasmic Male Sterile Hybrid Rice under Water-Stress Conditions. *Agriculture*, 11, 226.
- El-Mowafi, H. F. ; E. F. A. Arafat ; M. E. Negm\*; Mariam T. Wissa and Dalia E. Elsharnobi (2022). Study of Heterosis and Genetic Parameters for Yield and its Components Traits in Hybrid Rice (*Oryza sativa* L.) using line x tester mating system. *J. of Plant Production, Mansoura Univ., Vol. 13 (7):297 – 303.*
- Elsharnobi, D.E., E.F.A. Arafat, R.M. Abdallah and M.E. Negm (2022). Study of combining ability of some important traits in some hybrid rice combinations. *Menoufia J. Plant Prod.*, (7) : 57 – 74
- Elshenawy, M.M., G.B. Anis, W.H. Elgamal and E.A. Ramadan(2018). Genetic basis of combining ability for various quantitative traits using cms lines of rice (*Oryza sativa* L.). *The Serbian Journal of Agricultural Sciences.* 67(2): 125-135.
- FAO (Food and Agriculture Organization of the United Nations) (2015). FAOSTAT Database; High level expert forum-How to feed the world 2050, Oct. 12-13, Rome, Italy.
- Gaballah, M. M. (2016). Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components of rice genotypes. *Egypt. J. plant breed.*, 20 (1):73-87.
- Guan, Y.S., R. Serraj, S.H. Liu, J.L. Xu, J. Ali, W.S. Wang, E. Venus, L.H. Zhu and Z.K. Li (2010). Simultaneously improving yield under drought stress and non-stress conditions: A case study of rice (*Oryza sativa* L.). *J. Exper. Botany*, 61(15): 4145-4156.
- Hadifa, A. A. ; Mervet M.A. Osman and M.M. Abdelhameed (2018). Genetic Divergence of Some Rice Genotypes under Normal and Saline soil Conditions. *J. Plant Production, Mansoura Univ.*, 9 (1): 117 – 127.
- Huang, X., S. Jang, B. Kim, Z. Piao, E. Redona and H.J. Koh (2021). Evaluating Genotype × Environment Interactions of Yield Traits and Adaptability in Rice Cultivars Grown under Temperate, Subtropical and Tropical Environments. *Agriculture*, 11: 1-12.
- IRRI (International Rice Research Institute) (1996). Stander evaluation system for rice. International Rice Research Institute (IRRI), P.O Box 933, 1099 Manila, Philippines.
- Júnior, A.C.S., V.Q. Carneiro, I.G. dos Santos, R.D.S. Rosado, C.D. Cruz and P. C. Soares (2021). Genetic progress over twenty-three years of irrigated rice breeding in southeastern Brazil. *Acta Scientiarum. Genetics and plant breeding*, 43: 1-12.
- Kown, S.H. and J.H. Torrie (1964). Heritability and interrelationship among traits of two soybean populations. *J. Crop Sci.*, 4: 196-198.
- Kumar, A., N. R. Rangare and V. Vidyakar.(2013). Study of genetic variability of indian and exotic rice germplasm in allahabad agroclimate. *Supplement on Genetics & Plant Breeding*, 8(4): 1445-1451.
- Mary, S. S. and A. Gopalan (2006). Dissection of genetic attributes yield traits of fodder cowpea in F<sub>3</sub> and F<sub>4</sub>. *J Applied Sci. Res.*, 2: 805-808.
- Ponnuswamy, R., A. Rathore, A. Vemula, R.R. Das, A.K. Singh, D. Balakrishnan, H.S. Arremsetty, R.B. Vemuri and T. Ram (2018). Analysis of Multi-location Data of Hybrid Rice Trials Reveals Complex Genotype by Environment Interaction. *Cereal Research Communications.* 46(1), pp. 146–157.
- Shrestha, J.; U.K.S. Kushwaha, B. Maharjan, M. Kandel, S.B. Gungur, A.P. Poude, M.K.L. Karna and R. Acharya (2020). Grain Yield Stability of Rice Genotypes. *Indonesian Journal of Agricultural Research.* 3(2): 116 – 126.
- Steel, R. G. D., J. H. Torrie and D. A. Dickey (1997). Principles and Procedures for Statistics. M.c. Graw Hill Book Co., New York, USA.
- Streck, E.A., G.A. Aguiar, P.H.K. Facchinello, L. Perin, T.K. Krüger, A.M.M. Júnior (2018). Correlations and path analysis for yield components in irrigated rice. *Comunicata Scientiae.* 9(2): 154-161.
- Tiwari, G.C. (2015). Variability, heritability and genetic advance analysis for grain yield in rice. *International Journal of Engineering Research and Applications*, 5(7):46-49.
- Touhiduzzaman, R.K., M.I.A. Sikder, H. Mehraj, A.F.M.J. Uddin (2016) Correlation and genetic distance on sixteen rice varieties grown under SRI. *Advances in Plants & Agric. Res.*, 3(3):1-5.

دراسات على الارتباط وبعض القياسات المورفولوجية و المصولة و مكوناتها في بعض هجن الأرز  
السيد فاروق علي عرفات ، محروس السيد نجم و داليا السيد الشرنوبى  
قسم بحوث الأرز – معهد بحوث المحاصيل الحقلية – مركز البحوث الزراعية

## المخلص

تمت زراعة أربعة عشر هجياً من الأرز في الموسمين المتعاقبين ٢٠٢٠ و ٢٠٢١ في المزرعة البحثية لمركز البحوث والتدريب في الأرز بسخا ، كفر الشيخ ، مصر لتقييم التباين وتقدير الارتباط بين الصفات المدروسة ومحصول الحبوب. أظهرت جميع الصفات المدروسة اختلافات عالية المعنوية بين الهجن لتحليل التباين ، مما يشير إلى وجود مدى واسع من التباين الوراثي المتحكم في الصفات المدروسة. تم تسجيل أعلى القيم المقدر باستخدام الهجين التاليه IR69625A × GZ6296 و IR58025A × GZ6296 و IR70368A × PR78 و IR70368A × PR78 و Pusa13A × Giza181 في محصول الحبوب فقط. وكذلك أظهرت خمسة أنواع هجينة تفوقها على الصنف هجين مصري ١ لمحصول الحبوب وبعض الصفات الأخرى. تم العثور على ارتباط إيجابي وانحدار قوي بين محصول الحبوب (طن/هكتار) والمتغيرات التالية: طول الدالية (سم) ، عدد السنبلات لكل سنبل ، دليل الحصاد والمحصول البيولوجي (طن/هكتار) ويمكن أن يعتمد على هذه الصفات لاختيار أفضل الطرز الوراثية في برنامج التربية لتحسين محصول الحبوب.