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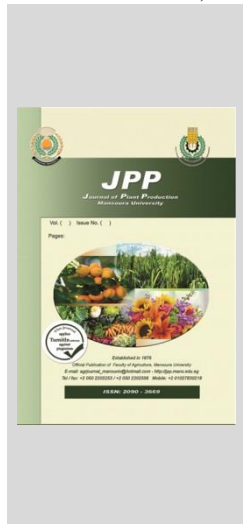
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Genetic Analysis for Grain Yield and its Components of some New Rice Restorer Lines in Early Generations

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ABSTRACT

The present investigation was carried out at the experimental farm of Rice Research Department, Sakha Agriculture Research Station, FCRI, ARC, Egypt, during three seasons of 2016, 2017 and 2018. To assess the genetic parameters and phenotypic correlation coefficients for the studied traits of promising restorer lines had earliness and high yielding during F₃ and F₄ generations in hybrid rice program. Twenty populations used for each two crosses IR69625A x Giza 178R and G46A x Giza 178R evaluated in F₃ and F₄ generations. Seventy five plants divided to five groups for each population. F₃ and F₄ generations showed highly significant and positive variation among populations for the studied traits during two seasons. The means values for the studied traits in F₄ population were higher than of F₃ populations except days to heading, indicating the effectiveness of selection for these traits. The two crosses combinations recorded high heritability coupled with high genetic advance as percent of mean indicating to the presence of non-additive gene action in both populations. There were positive and significant associations between grain yield and the studied traits of all populations in both generations, indicated that, selections for seed set % and grain yield were effective in later generations. It could be concluded the presence of genetic diversity for two generations for the studied traits, high heritability in broad sense which indicated that genotypic variance effect play an important role in inheritance of these traits for developing new plant types using as a restorer lines in hybrid rice program.

Keywords: Rice, genetic variability, heritability, genetic advance, correlation.

INTRODUCTION

Rice (*Oryza sativa* L.) is the main food crop of more than one-half of the world's population and grows worldwide. Rice production has to be increased 1% per annum to deliver sufficient rice for an ever growing population of rice-consuming countries (Lafarge and Bueno 2009). According to the Food and Agriculture Organization (FAO), hybrid rice technology is the key approach for the increase of global rice production (Virmani, 1999). It has a 15–30% advantage in yield over modern inbred rice varieties (Julfiquar, 2009), but does not frequently exhibit higher yield potential (Horie *et al.*, 2003). Higher grain yield of hybrid rice is an intricate outcome of genotype and environment interaction.

Hence, increasing rice yields on existing land remains the primary strategy for increasing production, to meet the future demand for food, for increasing population. Globally additional 176 million tons rice is required by 2035, which can be fulfilled by increase yield potential from 10 to 12.3 tons per hectare (Khush, 2013). Rice breeders are interested in developing cultivars with improved yield and other desirable agronomic characters. To achieve this goal, breeders have the option of selecting desirable genotypes in early generations or delaying intense selection until advanced generations are reached, when progenies are now nearly homozygous. To increase grain yield would be most effective if the components involved were highly heritable and genetically independent or positively correlated. The selection criterion for production may be yield, which correlated with one or more of the yield components, i.e, number of panicles per unit area, number of grains per panicle, and 1000 grain weight.

Phenotypic variability is the differences between individuals in a population due to genetic composition and growing environment (Sumanth *et al.*, 2017). Therefore, success on plant breeding activities entirely depends on the existence of genetic variability with respect to desired traits and selection skill of plant breeder (Adhikari *et al.*, 2018). Variability, genetic diversity, expected genetic advances and heritability of the traits are therefore key basis for genetic improvement of the trait. Heritability is the ratio of variation due to differences between genotypes to the total phenotypic variation for a trait in a population and shows the component of a character transmitted to future generations. Genetic advance shows the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance is more precise in predicting the genetic gain under selection than heritability alone. In addition to relationship between yield and yield attributing traits are prime important for direct and indirect selection of traits to which contributes to yield (Aditya and Bhartiya, 2013). Estimates of heritability and genetic advance will help in knowing the nature of gene action affecting the concerned trait (Sravan, 2012). Yield component traits show association among themselves and with yield. Plant breeder have to find significant correlations among yield and yield component traits, and effect of yield component traits on grain yield to predict the superior cross combinations and to select ideal plant type with yield increased (Nagarajun *et al.*, 2013).

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Therefore, the main objectives to assess the genetic parameters and correlation phenotypic coefficient for some yield components of some promising rice genotypes in early generations to select new restorer lines with earliness and high yielding.

MATERIALS AND METHODS

As a complement to previous studies Talha (2015), the F₂ seeds of the two crosses were multiplied in 2016 season and selected twenty populations with highly seed set% and multiplied in the third and fourth generation during 2017 and 2018 seasons. The materials used in the present investigation were for two crosses involving two cytoplasmic male sterile *i.e.*, IR69625A and G46A and one restorer line called Giza 178R. The experiment was conducted during 2017 and 2018 seasons in the experimental farm of Rice Research and Training Center, Sakha, KafreElsheikh, Egypt. All recommended standard cultural practices for rice cultivation were applied of RRTC (2016). Individual plant selections were made for the F₃ and F₄ generations. Based on their performance the selections were made on days to heading, number of panicles per plant, seed setting %, 1000-grain weight and grain yield per plant as recommended by Standard Evaluation System (SES) of IRRI (2008). 75 recombinant plants divided in five groups (within family) were selected, their data were recorded, harvested individually and carried forwarded to the next generation.

F₃ generation

F₃ generation was raised during May 1st 2017 season. 20 F₃ families were planted at a rate of 75 plants per family. The families after 30 days were transplanted in 5 rows having 15 hills per row with 20 × 20 cm spacing between and within rows in randomized complete block design with four replications. The observations were recorded from 60 random plants (12 plants per replicate) from each F₃ family as in F₂ population. Progeny mean, maximum, minimum and selected populations for selected individuals for each population were estimated irrespective of crosses. Mean values were used to estimate the parent offspring correlation and regression between F₂ and F₃ generation using Past and SPSS16. The desirable 75 plants divided in five groups (within family) of each family were selected and forwarded to F₄ generation.

F₄ generation

Twenty families selected from F₃ population were raised in plant progeny rows 75 plants (five groups) per family. The families were grown at May 1st during 2018 in 5 rows having 15 hills per row with the same spacing as in F₃ generation. Data were recorded from 75 randomly selected plants from each family as in F₃ generation. Progeny mean, range and percentage of F₄ population mean of selected individuals were estimated. Progeny mean of F₄ generation and their corresponding mean of individual plant selections in F₃ generation were used to study the parent offspring correlation and regression as in between F₂ and F₃ generation.

Statistical analysis

The F₃ generation analysis for all corresponding characters was conducted using one-way ANOVA based on the (Kearsey and Pooni 1996) method. There were 4 parameters, namely V_A (additive component of genetic variance), V_D (dominant component of genetic variance), V_{EC} (common environmental variance), and V_E (environmental component of variance), but only 2

statistics, σ^2w and σ^2B . Therefore, it was necessary to ignore 2 parameters, and as the environmental variation (V_E) was clear, V_E and V_{EC} were set at 0 (Kearsey and Pooni 1996 and Amiri-Fahliani *et al.*, 2010). In the ANOVA Table of the F₃ generation, the between (MSB) and the within (MSW) families variance sources of variation had expectations $\sigma^2w + r \sigma^2B$ and σ^2w , respectively, in which r was equal to the number of individuals per family. Using the expectation values of σ^2w and σ^2B given for the F₃ generation (Kearsey and Pooni, 1996), $\sigma^2B = MSB - MSW / r$ and $\sigma^2w = MSW$ (Amiri-Fahliani *et al.*, 2010). Supposing V_D and V_{EC} were zero, then V_A = σ^2B and V_E = $\sigma^2w - 1/2 V_A$ (Kearsey and Pooni, 1996). Weighted least squares (WLS) were used in multiple variable regression methods to estimate the standard errors (SE) of parameters Amiri-Fahliani *et al.* (2010). Heritability and genetic advance were measured using the formula given by (Singh and Chaudhary 1985) and (Allard 1960). Genotypic and phenotypic co-efficient of variation were calculated by the formula of (Burton 1952). Genotypic and phenotypic correlation coefficient was obtained using the formula suggested by (Johnson *et al.*, 1955). Narrow sense heritability of characters was evaluated as the ratio of additive genetic variance (V_A) to phenotypic variance (V_P) (Falconer and MacKay 1997) and (Singh 2005) as $h^2_n = V_A / V_P$.

RESULTS AND DISCUSSION

Analysis of variance and heritability% of parents and F₁, F₂ hybrids:

Three parents, two F₁ hybrids and two F₂ crosses were studied during 2015 and 2016 seasons. Different agronomic characteristics were studied and enlisted in Table 1. Analysis of variance revealed highly significant difference among the parents and F₁ hybrids for the studied traits. Among the yield component in F₂, days to heading, number of panicles per plant, seed set %, 1000 grain weight and grain yield per plant exhibited significant difference. The estimates of genotypic coefficient of variation (GCV) were lower than the respective phenotypic coefficient of variation (PCV) (Table 2), indicating the influence of environmental factors on the expression of the traits studied which are in agreement with the findings of (Chaubey and Singh 1994) and (Abebe *et al.*, 2017) indicated that there was very little environmental influence on these traits and cannot be improved by providing favorable environment. In general, high coefficient of variability shows scope of selection in favour of traits of interest and low coefficient of variability indicates the need for creation of variability and selection. The estimates of the heritability (h²) values were highly, range from 95.01% for number of panicles per plant % to 99.69% for grain yield per plant, demonstrating that the largest proportion of the phenotypic expression of traits in parents and F₁, F₂ hybrids is genetic variance. High to medium level heritability for grain yield was reported by (Gyawali *et al.*, 2018) and (Bandhi *et al.* 2018) may be due to the influence of the environment on the yield as it is polygenic trait.

Data in Table 2 showed that Mean performance genotypes indicated strong of genetic variability for the improvement of days to heading, number of panicles per plant, seed setting (%), 1000-grain weight (g) and grain yield per plant, which are important in hybrid rice yield. There were the line G46B recorded the desirable values for days to

heading and 1000 grain weight, while, the F₁ generation of cross IR69625A x Giza 178 recorded the highest values for number of panicle per plant and grain yield per plant, the line IR69625B recorded the desirable value for seed set%, according (Mirarab *et al.*, 2011). Grain yield per plant between F₁ and F₂ generation shows the highest inbreeding

depression (18.36%) of cross II. Lowest inbreeding depression (2.18) was observed for days to heading between F₁ and F₂ generation of cross I. (Raju *et al.*, 2005) studied heterosis and inbreeding depression in rice for yield components and grain characteristics.

Table 1. Estimates of the mean square and genetic parameters of variation for the studied traits of parents, F₁ and F₂ generation during 2016 season.

Genetic parameters	Studied Traits									
	Days to heading (day)		No. of panicles per plant		Seed set (%)		1000- grain weight (g)		Grain yield per plant (g)	
	Par. + F ₁	F ₂	Par. + F ₁	F ₂	Par. + F ₁	F ₂	Par. + F ₁	F ₂	Par. + F ₁	F ₂
σ ² G	75.16**	42.93*	19.09**	12.76*	5.45**	56.36*	9.17**	6.10*	156.50**	16.43*
σ ² E	1.26	0.79	0.63	0.67	0.59	1.63	0.19	0.30	0.48	0.74
σ ² ph	76.42	43.72	19.72	13.43	6.04	57.99	9.36	6.40	156.98	17.17
GV	24.63	14.05	6.15	4.03	1.62	18.24	2.99	1.93	52.01	5.23
PV	25.89	14.84	6.78	4.70	2.21	19.87	3.18	2.23	52.49	5.97
GCV	8.89	6.91	23.03	17.20	2.44	8.39	12.33	10.33	27.86	9.56
PCV	8.97	6.97	23.41	17.64	2.57	5.51	12.46	10.85	27.90	9.78
h ²	98.35	98.19	96.81	95.01	90.23	97.19	97.97	95.31	99.69	95.69
GA	17.71	13.37	8.86	7.17	4.57	15.25	6.17	4.97	25.73	8.17

Table 2. Mean performance and inbreeding depression (%) for five yield traits of three parents and two crosses of rice in the F₁ and F₂ populations during 2015 and 2016 seasons.

Genotypes	Studied Traits				
	Days to heading (day)	No. of panicles per plant	Seed set (%)	1000- grain weight (g)	Grain yield per plant (g)
IR69625B*	102.59	18.33	97.52	24.33	37.78
G46B*	90.32	15.81	95.21	26.62	37.23
Giza 178	100.39	19.17	96.06	22.13	46.26
Cross I (F ₁)	99.67	22.83	96.27	23.87	53.40
Cross II (F ₁)	94.39	18.70	93.88	25.80	49.89
LSD 0.05	2.11	1.49	1.44	0.82	1.30
Cross I (F ₂)	97.50	18.87	92.52	22.90	44.04
Cross II (F ₂)	92.15	15.95	86.39	24.92	40.73
LSD 0.05	3.13	2.87	4.48	1.92	3.03
ID (%) Cross I	2.18	17.35	3.90	4.06	17.53
ID (%) Cross II	2.37	14.71	7.98	3.41	18.36

* B line (Maintainer line) ID: Inbreeding depression % Cross I: IR69625A x Giza 178R Cross II : G46A x Giza 178R

Analysis of Variance of F₃ and F₄ generations:

The analysis of variance data for yield and its component between families for F₃ and F₄, the two crosses (IR69625Ax Giza 178R and G46A x Giza 178R) were highly significant, these referred to the high magnitude of genetic effect and low environmental effect, indicated the extant of significant differences among the genotypes examined revealing that sufficient variability was present and selection would be potential to develop new type of the restorer lines as shown in Table (3). Similar results were obtained by of (Sumanth *et al.*, 2017); (Oniya *et al.*, 2017); (Jambhulkar and Bose 2014) and (Mural *et al.*, 2012). This indicates that the genotypes are highly variable especially those traits which showed significant difference, Thus, the possibility genetic improvement through selection is highly promising.

Mean performance:

Mean performance values for the studied characters of twenty families to two hybrid combinations as F₃ and F₄ generations during 2017 and 2018 seasons are presented in Tables 4 and 5. The yield performance of F₃ families raised from the selected F₂ populations on the basis of phenotypic performance of the crosses which showed much encouraging results. The mean performance values of F₃ and

F₄ populations for all studied characters as shown in (Table 4). Out of 20 families only 8-15 families, could be isolated as promising families to continue in next generation in cross 1 for the studied characters. Thus there was practically good relationship between the seed set% of individual F₂ selected and the mean yield of corresponding F₃ families. This is also proved by the evidence of a significant correlation and regression as shown in Fig 1. Similar type of finding was reported by (Sharma and Choubey 1985). Thus selection based on phenotypic performance for yield in early generation is effective. The F₄ families mean was earlier than the F₃ population which recorded 96.55 day for days to heading trait, compared to the means of F₃ population's mean 100.07 day in cross 1. On the other hand, The F₄ families means were recorded 19.19, 96.35%, 25.92g and 50.54g higher than the means of F₃ families 17.73, 94.56, 23.99 and 47.47 for number of panicles per plant, seed set%, 1000 grain weight and grain yield per plant in cross 1, respectively, indicated to the selection will be effective in next generation.

Table 3. Analysis of variance (ANOVA) for yield and its related characters of 20 populations in F₃ and F₄ generations in crosses IR69625A x Giza 178R and G46 x Giza 178R during 2017 and 2018 seasons.

Cross 1	F ₃	F ₄	F ₃	F ₄
	Between families		Within families	
D.F	19		57	
Days to heading (day)	22.62**	7.59**	2.11	0.95
No. of panicles per plant	9.34**	6.39**	1.77	0.84
Seed set %	9.34**	6.04**	1.36	1.49
1000 grain weight (g)	7.71**	3.04**	1.04	0.63
Grain yield per plant (g)	46.53**	12.49**	6.64	1.75
Cross 11	F ₃	F ₄	F ₃	F ₄
D.F	19		57	
Days to heading (day)	20.78**	6.25**	6.05	1.34
No. of panicles per plant	13.78**	9.68**	1.39	0.97
Seed set %	46.89**	12.09**	5.75	1.19
1000 grain weight (g)	3.92**	3.66**	0.73	0.35
Grain yield per plant (g)	84.56**	39.93**	8.96	3.98
Cross I: IR69625A x Giza 178R	Cross II: G46A x Giza 178R			

In addition to, out of 20 families only 8-12 families could be selected as promising families for next generation.

Thus there was practically good relationship between the seed set% of individual F₂ selection and the mean yield of corresponding F₃ families. The F₄ families mean was 94.78 for days to heading trait which were lower than the means of F₃ population's mean 96.20 in cross II. On the other hand, The F₄ families means were 18.96, 95.21, 25.79 and 52.67 higher than the means of F₃ families 16.55, 91.99%, 24.63g and 45.28g for number of panicles per plant, seed set%, 1000 grain weight and grain yield per plant in cross II,

respectively, indicating to improvement in grain yield for F₄ families means in crosses 1 and 2 respectively which were higher than F₃ families means in the two crosses. Thus F₄ generation inherited and retained their parental characteristics under considerations such as days to heading , number of panicles per plant, seed set%, 1000 grain weight and grain yield and as revealed by the F₃-F₄ correlation and regressions as shown in Fig 1.

Table 4. Mean performance of yield and yield contributing characters for 20 F₃ and F₄ rice families during 2017 and 2018 seasons.

Genotypes	Days to heading		No. of panicles per plant		Seed set %		1000 grain weight		Grain yield per plant	
	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄
Cross I										
Pop.1	102.20	98.50	15.32	18.53	90.83	92.92	22.86	25.90	44.46	47.13
Pop. 2	100.20	98.50	16.83	18.21	93.97	94.64	24.98	25.60	45.17	51.47
Pop. 3	99.00	98.00	19.63	20.00	96.41	97.37	24.44	24.68	51.89	51.11
Pop. 4	96.40	95.00	19.14	21.53	96.80	97.14	23.96	23.92	47.65	47.21
Pop. 5	99.40	97.50	19.63	19.60	95.05	97.48	23.19	26.75	51.52	52.36
Pop. 6	100.20	97.25	17.40	18.63	96.14	97.08	22.81	26.25	52.01	51.20
Pop. 7	100.80	97.25	16.83	18.43	94.55	95.49	24.81	25.66	44.91	47.21
Pop. 8	101.20	95.50	17.99	18.31	94.41	97.06	21.85	25.58	41.88	52.05
Pop. 9	93.60	94.75	18.58	18.53	93.61	96.74	24.01	25.10	51.33	52.35
Pop. 10	99.00	98.75	18.00	19.56	94.69	96.46	24.13	27.09	44.89	52.58
Pop. 11	102.00	95.25	16.79	18.58	93.56	96.56	26.66	26.85	49.31	52.05
Pop. 12	100.40	98.25	16.35	16.69	93.57	97.09	24.78	26.50	49.55	50.74
Pop. 13	103.20	95.75	16.78	20.31	97.15	96.69	21.70	26.33	47.90	51.82
Pop. 14	99.40	97.75	18.18	18.44	94.62	94.74	26.15	27.31	44.58	48.69
Pop. 15	100.60	97.25	14.34	17.60	93.39	94.84	23.26	26.73	41.88	50.73
Pop. 16	102.20	95.50	20.84	21.79	92.48	97.44	23.83	25.84	51.30	51.11
Pop. 17	101.20	95.75	18.88	19.73	93.48	96.41	21.93	25.50	44.66	50.15
Pop. 18	99.40	95.00	17.88	19.28	95.15	96.70	24.48	25.11	46.83	49.94
Pop. 19	100.00	95.50	17.24	20.22	94.26	97.84	25.53	24.96	50.19	50.39
Pop. 20	101.00	95.75	18.03	20.35	96.00	96.37	25.34	26.14	51.16	52.19
Minimum	93.60	94.75	14.34	16.69	90.83	92.92	21.70	23.92	41.88	47.13
Maximum	103.20	98.75	20.84	21.79	97.15	97.84	26.66	27.31	52.01	52.58
Mean	100.07	96.64	17.73	19.21	94.50	96.35	24.03	25.89	47.65	50.62
LSD 0.05	0.321	0.477	1.282	0.544	0.851	1.349	0.638	0.805	1.807	0.896
Cross II										
Pop.1	96.75	95.25	15.06	20.25	86.28	93.98	23.51	24.10	39.03	50.33
Pop. 2	97.75	93.25	16.82	17.00	93.62	95.12	25.41	26.68	49.60	49.87
Pop. 3	98.25	96.50	17.13	18.95	94.84	95.98	25.58	27.05	46.17	54.49
Pop. 4	97.75	95.25	16.15	17.18	94.26	95.60	24.36	25.16	39.70	48.63
Pop. 5	97.75	95.25	19.33	20.11	94.68	95.49	22.89	25.75	44.92	46.02
Pop. 6	91.50	95.25	17.00	17.18	94.68	95.20	23.50	24.91	44.74	52.29
Pop. 7	93.50	93.75	17.40	21.20	92.10	95.73	22.76	25.64	43.70	54.65
Pop. 8	97.50	94.00	17.81	18.00	91.73	92.56	24.28	25.57	35.21	53.98
Pop. 9	94.50	92.75	18.20	19.08	88.73	94.99	25.10	25.16	53.18	57.03
Pop. 10	95.00	93.50	18.63	19.35	86.68	90.43	26.65	26.39	40.85	52.21
Pop. 11	97.75	94.50	17.71	18.90	91.50	94.85	24.90	26.04	43.56	55.01
Pop. 12	95.50	94.00	17.50	18.40	85.75	96.40	23.80	24.65	48.69	54.92
Pop. 13	98.00	93.50	18.81	18.91	94.27	96.14	24.45	26.18	46.18	54.90
Pop. 14	97.50	97.50	14.90	17.14	91.41	94.39	24.71	24.81	46.53	51.09
Pop. 15	97.25	95.00	13.81	20.63	91.72	95.45	24.07	25.43	45.70	54.94
Pop. 16	94.50	95.00	16.13	17.14	95.60	95.80	25.42	26.78	47.48	49.51
Pop. 17	96.00	96.25	14.24	17.70	90.59	96.42	23.98	26.64	42.39	55.27
Pop. 18	93.25	94.25	13.88	19.38	95.78	97.64	25.61	25.62	51.96	51.94
Pop. 19	95.50	94.50	14.63	16.21	93.76	95.90	25.52	26.79	46.54	52.98
Pop. 20	98.75	96.00	15.60	17.00	92.55	95.81	24.95	26.88	45.59	51.27
Minimum	91.50	92.75	13.81	16.21	85.75	90.43	22.76	24.10	35.21	46.02
Maximum	98.75	97.50	19.33	21.20	95.78	97.64	26.65	27.05	53.18	57.03
Mean	96.21	94.76	16.54	18.48	92.03	95.19	24.57	25.81	45.08	52.56
LSD 0.05	3.746	1.568	1.112	0.850	2.726	1.061	0.156	0.511	2.787	0.968

Cross I: IR69625A x Giza 178

Cross II: G46A x Giza 178

Table 5. Mean performance Maximum, minimum and selected families values for yield and yield contributing characters of 20 F₃ and F₄ generations during 2017 and 2018 seasons.

Genotypes	Studied traits											
	Population No.		Days to heading (g)		No. of panicles per plant		Seed set %		1000-grain weight (g)		Grain yield per plant (g)	
	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄
Cross (I)												
Max. Pop.	13	10	103.20	98.75	20.84	21.79	97.15	97.84	26.66	27.31	52.01	52.58
	3	9	99.50	95.75	18.18	19.60	95.15	96.69	24.78	26.33	49.31	51.11
Selected Pop	4	13	99.25	95.50	17.99	19.56	95.05	96.56	24.48	26.14	47.90	50.74
	18	20	98.75	95.25	17.88	19.28	94.62	96.37	24.13	25.90	47.65	50.73
Min. Pop.	14	4	93.50	94.75	14.34	16.69	90.83	92.92	21.70	23.92	41.88	47.13
Pop. Mean	-	-	100.07	96.64	17.73	19.21	94.50	96.35	24.03	25.89	47.65	50.62
Differ	-	-	9.50**	4.00**	6.50**	5.10**	6.32**	4.92**	4.96**	3.39**	10.46**	5.45**
LSD 0.05	-	-	0.321	0.980	0.594	0.405	0.500	0.895	0.592	0.550	2.409	1.145
Cross (II)												
Max. Pop.	20	9	98.75	97.50	19.33	21.20	95.78	97.64	26.65	27.05	53.18	57.03
	3	7	96.00	94.50	17.13	18.95	93.76	95.81	24.95	26.64	46.17	54.49
Selected Pop	9	13	95.50	94.25	17.00	18.91	93.62	95.60	24.90	26.39	46.17	53.98
	16	19	95.00	94.00	16.82	18.90	92.55	95.49	24.71	26.18	45.59	52.98
Min. Pop.	8	5	91.50	92.75	13.81	16.21	85.75	90.43	22.76	24.10	35.21	46.02
Pop. Mean	-	-	96.21	94.76	16.54	18.48	92.03	95.19	24.57	25.81	45.08	52.56
Differ	-	-	7.54**	4.75**	5.52**	4.99**	10.03**	7.21**	3.89**	2.95**	17.97**	11.01**
LSD 0.05	-	-	2.693	1.160	0.494	0.399	1.612	0.405	0.804	0.180	1.491	0.778
Giza 178 (check)			100.39		19.17		96.06		22.13		46.26	

Cross I: IR69625A x Giza 178R

Cross II: G46A x Giza 178R

Genetic parameters:

Genetic parameters involved additive, dominance, environmental variance, heritability in both broad and narrow

senses and genetic advance estimates of two hybrid combinations as F₃ and F₄ generations during 2017 and 2018 seasons for studied characters as shown in Table 6.

Table 6. Estimation of genetic parameters for yield related traits of 20 populations F₃ and F₄ rice population during 2017 and 2018 seasons.

Genetic parameters	Days to heading (day)		No. of panicles per plant		Seed set %		1000 grain weight (g)		Grain yield per plant (g)	
	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄
Cross I										
Mean	100.00	96.64	17.73	19.21	94.50	96.35	24.03	25.89	47.65	50.62
σ ² A	5.56	2.22	2.52	1.85	2.66	1.52	2.22	0.80	13.30	3.58
σ ² D	6.22	3.14	9.16	3.04	5.59	8.87	3.87	3.42	26.49	6.82
σ ² E	0.08	0.12	0.83	0.15	0.37	0.92	0.21	0.33	1.65	0.41
σ ² G	11.78	5.36	11.68	4.89	8.25	10.39	6.09	4.22	39.79	10.40
σ ² ph	11.86	5.48	12.51	5.04	8.62	11.31	6.30	4.55	41.44	10.81
GV	2.80	1.17	2.78	1.06	1.72	2.37	1.46	1.00	9.71	2.53
PV	3.39	1.86	3.35	1.71	3.11	3.27	1.73	1.23	10.67	2.80
GCV %	1.43	1.12	9.40	5.36	1.39	1.60	5.03	3.86	6.54	3.14
PCV %	1.84	1.41	10.32	6.81	1.87	1.88	5.47	4.28	6.86	3.31
H ₂ b	99.31	97.81	93.36	97.04	95.75	91.87	96.73	92.81	96.02	96.25
H ₂ N	46.88	40.51	20.14	36.66	30.87	13.43	35.30	17.66	32.09	33.12
GA	7.05	4.72	6.80	4.49	5.72	6.36	5.00	4.08	12.73	6.52
GA (%)	7.05	4.88	38.35	23.36	6.05	6.61	20.81	15.75	26.72	12.88
Cross II										
Mean	96.21	94.76	16.54	18.48	92.03	95.19	24.57	25.81	45.08	52.56
σ ² A	2.56	1.34	3.24	2.24	10.07	2.59	1.18	0.82	16.42	8.87
σ ² D	59.25	11.28	8.23	5.16	40.10	7.13	1.28	1.87	47.82	12.66
σ ² E	7.09	1.24	0.62	0.36	3.75	0.57	0.01	0.13	3.92	0.47
σ ² G	61.81	12.62	11.47	7.40	50.17	9.72	2.46	2.69	64.24	21.53
σ ² ph	68.90	13.86	12.09	7.76	53.92	10.29	2.47	2.82	68.16	22.00
GV	15.28	2.95	2.71	1.69	12.32	2.19	0.56	0.62	15.82	5.02
PV	15.97	3.78	3.36	2.32	13.22	3.17	0.79	0.84	16.79	6.49
GCV %	4.06	1.81	9.95	7.03	3.81	1.55	3.05	3.05	8.82	4.26
PCV %	4.15	2.05	11.08	8.24	3.95	1.87	3.62	3.55	9.09	4.85
H ₂ b	89.71	91.04	94.84	95.30	93.04	94.48	99.51	95.33	94.24	97.85
H ₂ N	3.71	9.69	26.78	28.87	18.68	25.17	47.77	28.97	24.09	40.33
GA	15.56	6.98	6.79	5.47	14.07	6.24	3.22	3.30	16.03	9.45
GA (%)	16.18	7.37	41.07	29.60	15.29	6.56	13.11	12.78	35.55	17.99

Cross I: IR69625A x Giza 178R

Cross II: G46A x Giza 178R

Dominance variance appears in the studied characters for cross I and cross II.

Heritability is a fraction of variance in phenotypic expression that gets from genetic effect. The nature of

selection units and sampling errors also influences greatly the magnitude of heritability estimates. The heritability estimates in segregating generation helps to know genetic variance of genotype and environmental interaction and genetic

component to be expected from selection in the next generation. Heritability in broad sense was low for all the studied characters and ranged from 93.52% and 90.67 for seed set% and days to heading as F₄ and F₃ generations to 99.44% and 98.95% for days to heading and 1000 grain weight in F₃ and F₄ generation of crosses I and II, respectively. On the other side, Heritability in narrow sense was high for all the studied characters and ranged from 8.01% and 20.84% for days to heading and seed set% of crosses I and II as F₃ and F₄ generation to 47.47% and 45.27 % for days to heading and 1000 grain weight traits of crosses I and II as F₃ and F₄ generations. So selection for these traits might be regarding. High heritability with high genetic advance was reported by (Chakraborty and Chakraborty 2010).

Data on variability, heritability, genetic advance and genetic advance percent mean are presented for F₃ and F₄ families is shown in Table 6. The estimates of GCV were lower than that of PCV for all the studied characters, indicating some light influence of environment on the traits. However, relatively small differences between GCV and PCV for these characters indicated that these were predominantly governed by the genetic factors. In cross I, maximum GCV was observed for number of panicles per plant (15.65%), whereas, the phenotypic coefficient of variation (PCV) was maximum for grain yield plant per plant (19.95%) in F₃ generation. In cross II, maximum GCV was observed for number of panicles per plant (16.92%), while, the phenotypic coefficient of variation (PCV) was maximum for number of panicle per plant (17.09%) in F₃ generation. Similar findings were also reported by (Pandy and Anurag 2010); (Mulugeta *et al.* 2012); (Venkanna *et al.*, 2014) and (Warkad *et al.*, 2014). These indicate the presence of slight environmental influence to some degree in the phenotypic expression of the characters.

According to (Johnson *et al.*, 1955), heritability estimates along with genetic advance would be more useful than the former alone in predicting the effectiveness of selection. Therefore, it is essential to consider the predicted genetic advance along with heritability estimate as a tool in selection programme for better efficiency. In this investigation, high heritability coupled with moderate or high genetic advance was observed for most of the studied characters. High heritability and moderate genetic advance suggested the predominant role of non-additive gene action in their inheritance and selection in later generation would be more effective. (Suman *et al.*, 2005) and (Shukla *et al.*, 2005) indicated the same result.

Phenotypic coefficient correlation: Correlation coefficient analysis has been used by breeders to reveal a positive relationship between yield and other traits that enhance yield in rice genotypes. Grain yield, being a quantitative trait, is a complex character of any crop. Various morphological and physiological plant traits contribute to yield. These yield-contributing components are interrelated with each other showing a complex chain of relationship and highly influenced by the environmental conditions (Prasad *et al.*, 2001). Phenotypic correlation result indicated that yield (g/ plant) correlated positively and significantly with number of panicles plant⁻¹, seed set% and 1000 grain weight between families in F₃ generation. In addition to seed set% and 1000 grain weight between families in F₄ generation for the cross IR69625A x Giza178R, whereas grain yield correlated positively and significantly with 1000 grain weight between families in F₃ generation for the cross G46A x Giza 178R as shown in Table 7. These results signified that if thousand seed weight increased then yield per hectare would be increased mostly through the positive indirect effect of thousand seed weight with other characters. (Ghosal *et al.*, 2010) denoted that thousand seed weight had direct positive effect on yield ton per hectare.

Table 7. Phenotypic correlation coefficients among growth, yield and its component traits of 20 families in F₃ and F₄ generations of crosses IR69625A x Giza 178R and G46A x Giza 178R.

Traits	Cross I DTH	Cross II DTH	Cross I NOP	Cross II NOP	Cross I SS	Cross II SS	Cross I TGW	Cross II TGW
NOP	-0.227*	0.030						
	-0.355**	-0.177						
SS	-0.177	0.025	0.220*	-0.068				
	-0.323**	0.104	0.332**	-0.049				
TGW	-0.143	0.077	0.017	-0.109	-0.040	0.015		
	0.365**	-0.004	-0.348**	-0.240*	-0.192	0.067		
GY	-0.184	-0.215	0.450**	-0.112	0.255*	0.185	0.226*	0.233*
	-0.094	-0.177	0.027	0.165	0.341**	0.060	0.288**	-0.001

DTH: Days to heading NOP: Number of panicles per plant SS: Seed set TGW: Thousand grain weight GY: Grain yield per plant

Moreover all the traits showed medium and strong correlation and regression between F₃ and F₄ generation. The intergeneration correlation and regression for yield component traits are shown in Table 8, there were positive correlation and regression of the F₃ generation with F₄ generation for the studied traits The highest correlation was noticed in number of panicles per plant and seed set% (0.677 and 0.498) and lowest value for 1000 grain weight (0.111) of cross IR69625Ax Giza 178R.

With respect to, the intergeneration correlation and regression for yield component traits are shown in Table 8 and Figure 1, there were positive and negative correlation and regression of the F₃ generation with F₄ generation for the studied traits except number of panicles per plant and grain yield per plant

traits. The highest correlation was noticed in 1000-grain weight and seed set% (0.537 and 0.494) and lowest value for grain yield per plant (0.152) of cross G46Ax Giza 178R.

The findings were consistent with the findings (Suwanto *et al.*, 2015), (Barman and Borah 2012). This indicated the effectiveness of selection for these traits. These results were also consistent with the mean performance of the F₃ and F₄ progeny mean performance. Tables 8 and Figure 1). This indicates that selection for grain yield on the basis of phenotypic performance in early generation may not be advisable. This indicated the effectiveness of selection for these traits in later generation. This study will help the breeders to select for yield and its component to select desirable genotypes for developing new types lines of rice.

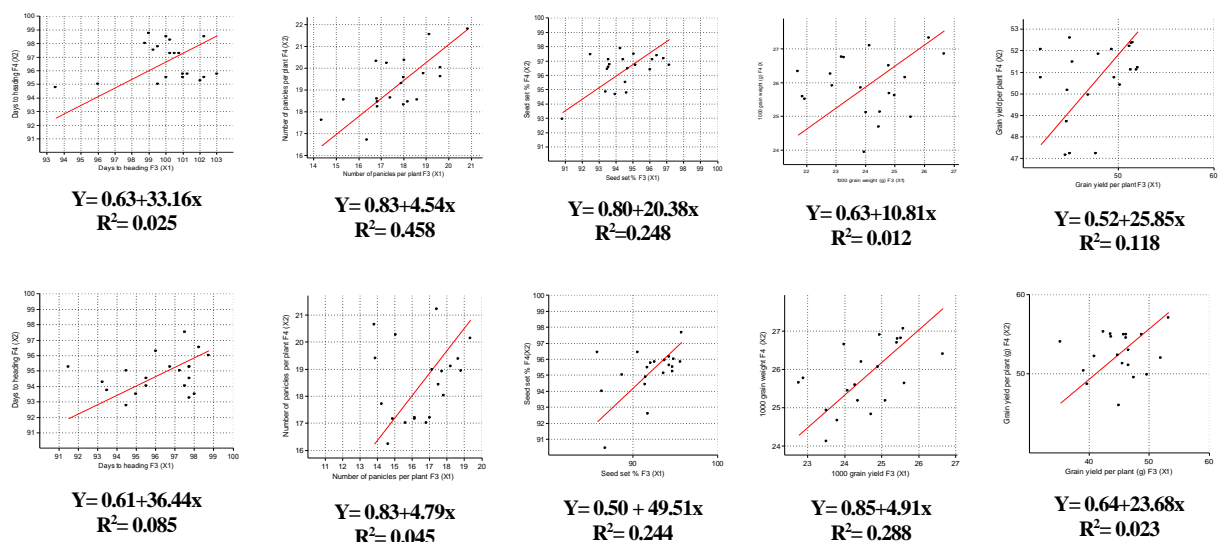


Fig. 1. Parent progeny relationship in different traits based on (F₃ and F₄) for crosses IR69625A x Giza 178 and G46A x Giza 178.

Table 8. Parent offspring correlation and regression in F₃ and F₄ of the crosses over segregating generation for different characters of crosses IR69625A x Giza 178R and G46A x Giza178R .

Trait	Correlation Coefficient		Regression Coefficient	
	Cross I	Cross II	Cross I	Cross II
Days to heading(day)	0.158	0.292	33.16	36.44
No. of panicle/ plant	0.677**	0.212	4.54	4.79
Seed set (%)	0.498*	0.494*	20.38	49.51
1000-grain weight(g)	0.111	0.537*	10.81	4.91
Grain yield/ plant (g)	0.343	0.152	25.94	23.68

*and ** Significant at 5% and 1% level of probability

CONCLUSION

It could be concluded that presence of genetic diversity among the mean performance of two generations for the studied traits. The mean performance values indicated the improvement for the most traits by selection, high heritability in broad sense which indicated that, genotypic variance effect play an important role inheritance of these traits for developing new type plants (NPTs) using a restorer lines from segregation generations.

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التحليل الوراثي لمحصول الحبوب ومكوناته لبعض سلالات الأرز المعيدة للخصوبة في الأجيال الإنعزالية المبكرة إبراهيم عبد النبي عبدالعظيم طلحة*

قسم بحوث الأرز- معهد بحوث المحاصيل الحقلية- مركز البحوث الزراعية

أجريت هذه الدراسة في حقل التجارب لقسم بحوث الأرز، محطة البحوث الزراعية بسبخا، معهد بحوث المحاصيل الحقلية، مركز البحوث الزراعية، مصر خلال ثلاثة مواسم 2016 – 2017 – 2018 م وتهدف إلى تقدير الثوابت الوراثية والارتباط المظهري للصفات المدروسة لبعض سلالات المعيدة للخصوبة المبكرة التي تمتاز بالتبكير والمحصول العالي في الأجيال الإنعزالية المبكرة الثالث والرابع لإستخدامها كسلالات معيدة للخصوبة في برامج الأرز الهجين. تم استخدام عشرون عشيرة من كلا الهجينين IR69625A x Giza 178R و G46A x Giza 178R وتقبيهم في كلا الجيلين الثالث والرابع. تم تطبيق كافة التوصيات الفنية طبقاً لمركز البحوث والتدريب في الأرز وتسجيل البيانات على 75 نبات لكل عشيرة تم تقسيمهم إلى خمس مجموعات. أوضحت النتائج أن عائلات الجيلين الثالث والرابع معنوية عالية لصفات عدد الأيام حتى التزهير وعدد الداليات / نبات ونسبة العقد ووزن الألف حبة ومحصول الحبوب خلال الموسمين. كذلك سجلت متوسطات عشائر الجيل الرابع أعلى من عشائر الجيل الثالث لكل الصفات المدروسة عدا صفة عدد الأيام حتى التزهير مما يشير إلى فعالية الانتخاب لتلك الصفات لإنتاج نباتات جديدة (NPTs) يمكن إستخدامها كسلالات معيدة للخصوبة في برامج تربية الأرز الهجين. سجل كلا من الهجينين مكافئ وراثي وتحسين وراثي كنسبة من المتوسط عالي وهذا يدل على تقدم الفعل الجيني الغير المضيف (السبادي) لكل من عشائر الجيلين الثالث والرابع. أوضحت النتائج وجود ارتباطات موجبة لعشائر الجيلين وهذا يدل على أن الانتخاب لنسبة العقد ومحصول الحبوب يكون فعال في الأجيال المتأخرة. وتوصي الدراسة بوجود تنوع وراثي بين متوسط سلوك كل من الجيلين للصفات والمكافئ الوراثي العالي في الجيل الثالث والرابع هذا دليل على أن التباين الوراثي يلعب دوراً كبيراً في توريث تلك الصفات لإنتاج طرز نباتات جديدة (NPTs) لإستخدامها كسلالات معيدة للخصوبة من الأجيال الإنعزالية في برنامج الأرز الهجين.