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STUDY OF COMBINING ABILITY OF SOME IMPORTANT TRAITS IN SOME HYBRID RICE COMBINATIONS

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ABSTRACT: The investigation was carried out at the experimental farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt, during 2018, 2019 and 2020 rice growing seasons. The aim of this study was to estimate the genetic statistics of the important traits in some hybrid rice combinations, 24 hybrids were produced by crossing six CMS lines with four testers and then evaluated in two seasons. Line x tester analysis showed highly significant difference in mean squares for genotypes of most traits. The best genotype was the hybrid PR78/IR58025A for grain yield indicating that it can be used in breeding program to improve grain yield. Furthermore, concerning the (GCA) the good combiners for studied traits were PR78 and IR58025A for grain yield, PR78 and IR69625A for biomass. These genotypes can transfer the superiority to their offspring in hybrid combinations. In addition, the most promising hybrids which have the highly significant SCA effects for grain yield wasPR2/IR69625A and could be used in breeding program.

Key words: Hybrid rice, line x tester, combining ability and grain yield

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important cereal crops in the world, contributing significantly to global food security by providing food for more than half of the world's population (Chauhan *et al.* 2017). It is very important to enhance rice production to satisfy the needs of this important crop. One of the ways to increase rice yield is hybrid rice. It is easy to obtain 15-20% higher yield just growing hybrid rice compared with the common varieties (Faiz *et al.* 2006). Line x Tester analysis is a way to estimate combining ability effects helping to identify the desirable parents and crosses required for breeding programs (Rashid *et al* .2007). Also, it provides information about general combining ability and specific combining ability effects of parents and the best way to estimate different types of gene actions. The differences in GCA are mainly due to additive gene action while the differences in SCA are attributed to non-additive gene effects (Fasahat *et al.* 2016). Therefore, the knowledge of combining ability provides information on the nature and magnitude of gene effects that regulate grain yield and yield characters hence enabling the breeder to design an effective breeding method for genetic enhancement of grain yield and yield components (Yuga *et al.* 2018). Thus, the main objective of the present study was to estimate combining ability values for yield and its component characters and to know the best hybrid combinations for breeding programs.

MATERIALS AND METHODS

The present investigation was conducted during 2018, 2019 and 2020 rice growing seasons at the Rice Research and Training Center (RRTC) farm, Sakha, Kafr El-Sheikh, Egypt. The studied experimental materials were six lines and four testers, selected out of the elite germplasm collection maintained at RRTC (Table 1). Crosses were made according to line x tester mating design (Kempthorne, 1957) by pollinating the six CMS lines with the aforementioned testers (four restorer lines) during 2018 summer season. The resulting 24 F_1 hybrid combinations were grown in a randomized complete block design with three replications where, all genotypes, parents and crosses were evaluated at the research field during the summer 2019 and 2020 seasons. Thirty-day old seedlings were transplanted with one seedling hill^{-1} adopting spacing of 20 cm between rows and plants. Each test entry consisted of 14 rows of 5 m length. All agronomical practices were followed as

recommended. The analysis of variance (ANOVA) was carried out using the means for all traits. The variances of general combining ability (GCA) and specific combining ability (SCA) were computed as described by (Kempthorne, 1957). The principal component and cluster were performed using SPSS 22.0 (IBM, Armonk, NY, USA). The studied traits were duration(days to harvest), plant height, panicle length(cm), panicle weight(g), grain yield(t ha^{-1}), biomass (t ha^{-1}), filled grains /panicle, number of spikelets/panicle, fertility $= \frac{No.of\ filled\ grains/panicle}{No.of\ spikelets/\ panicle} \times 100\%$, and hulling (%), milling(%) and head rice (%).

RESULTS AND DISCUSSION

Analysis of variance:

Data in Table 2 revealed significant and highly significant differences among evaluated genotypes for all traits of study except for milling in both seasons and hulling in 2020 growing season. This result indicated that the genotypes had wide genetic diversity among themselves. The analysis of variance indicated that not significant differences between replication in most traits indicating low influence of environment and homogeneity of the experimental land on these traits. On the other hand, significant and highly significant replication differences were observed in biomass, filled grains/panicle and number of spikelet's/panicle in both studied seasons in addition for plant height, milling, fertility and head rice in 2019 and duration in 2020,

indicating the high influence of the environment and heterogeneity of the experimental land in these trait. Significant variances due to lines x testers interaction for all the traits studied in both seasons except for milling also, grain yield was not significant in 2019 and head rice in 2020, suggesting the presence of significant variances for SCA among hybrids which have a significant and highly significant lines x testers interaction. These results coincide with the findings of (El-Mowafi *et al.* 2012). The significant differences between lines x testers interaction for these traits suggested that specific combining ability is widely attributed to the expression of these traits and gives significance of dominance or non-additive genetic variances for all these traits (Ghidan and Khedr, 2021). Furthermore, the analysis of variance revealed significant differences among parents, crosses, lines, and lines x testers interaction for all the studied traits (Table 2), except for that of hulling, milling and head rice in both seasons and panicle weight in 2019 which were non-significant among parents. Whereas variance of parent's *vs*. crosses for plant height and hulling in both seasons and milling in 2019 growing season, were found to be non-significant. These data are in harmony with those reported by Salgotra *et al.* (2009). While, the analysis of variance revealed non-significant values among testers for milling and head rice in both seasons, grain yield and hulling in 2019 season and panicle length and panicle weight in 2020 growing season.

Table 1. Cytoplasmic male sterile (CMS) and restorer lines used for producing the hybrids.

Genotypes	Cytoplasmic source	Grain type	Origin
CMS line			
IR58025A/B	Wild abortive (WA) CMS line	Indica long grain	IRRI
IR68902A/B	Wild abortive (WA) CMS line	Indica long grain	IRRI
IR69625A/B	Wild abortive (WA) CMS line	Indica long grain	IRRI
IR70368A/B	Wild abortive (WA) CMS line	Indica long grain	IRRI
Pusa3A/B	Wild abortive (WA) CMS line	Indica long grain	Egypt
Pusa13A/B	Wild abortive (WA) CMS line	Indica long grain	Egypt
Restorer line			
PR1	Restorer line	Indica long grain	Egypt
PR2	Restorer line	Indica long grain	Egypt
PR78	Restorer line	Indica long grain	Vietnam
G.181	Restorer line	Indica long grain	Vietnam

Table 2. Analysis of variance for rice yield and its components.

S.O.V	d.f	Duration (day)		Plant height (cm)		Panicle length(cm)		Panicle weight(g)		Grain yield (t ha^{-1})		Biomass (t ha^{-1})	
		2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020
Replications	2	0.186ns	3.30*	38.48*	8.21ns	0.012ns	0.07ns	0.004ns	0.036ns	2.83ns	2.14ns	45.17**	102.5***
Genotypes	33	42.36***	43.05***	292.8***	212.4***	6.735***	10.38***	0.526***	0.108***	7.30**	9.20***	398.8***	509.6***
Parents	9	79.24***	83.15***	470.5***	473.6***	4.283***	4.19***	0.032ns	0.143***	11.70***	12.90***	128.1***	116.6***
Crosses	23	29.31***	28.97***	234.8***	119.3***	4.703***	5.45***	0.305***	0.096***	2.30*	4.30**	301.4***	434.1**
Par.vs.Crosses	1	10.58**	5.99*	28.8ns	3.579ns	75.54***	179.68***	10.05***	0.065***	82.60***	87.30***	5075.1***	5786.0***
Lines	5	48.90***	46.56***	171.7***	39.7***	8.606***	16.60***	0.119***	0.259***	3.16*	2.80***	244.6***	156.4***
Testers	3	107.50***	105.94***	354.6***	395.4***	2.602***	0.18ns	0.723***	0.021ns	3.45ns	2.5*	1037.0***	1333.0***
LinesxTesters	15	7.14**	7.71***	231.9***	90.65***	3.822***	2.78***	0.284***	0.056***	1.82ns	5.19***	173.2***	346.6***
Error	66	0.62	0.99	10.85	4.28	0.168	0.29	0.019	0.012	1.33	0.81	1.74	3.97

Table 2.Continue…

| S.O.V	d.f	Filled grains/panicle		Number of Spikelets/panicle		Fertility(%)		Hulling(%)		Milling(%)		Head rice(%)	
		2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020
Replications	2	662.9***	446.5***	509.2**	505.55***	16.48***	0.80ns	34.9ns	20.86ns	89.90*	58.8ns	163.5**	75.46ns
Genotypes	33	3503.9***	3065.2***	3808.2***	362.2***	27.65***	25.02***	36.7**	28.7ns	26.8ns	29.4ns	46.9*	56.8ns
Parents	9	4677.6***	4079.5***	4841.1***	4194.7***	40.28***	37.70***	9.9ns	10.6ns	22.1ns	20.1ns	20.5ns	20.2ns
Crosses	23	3085.9***	2102.5***	3377.8***	2267.4***	23.10***	16.75***	47.4***	36.9*	27.6ns	25.8ns	43.3*	40.4ns
Par.vs.Crosses	1	2554.6***	16079.5***	4410.2***	14450***	18.45*	101.19***	38.13ns	1.92ns	50.8ns	197.4***	365.3***	763.6***
Lines	5	1126.8***	1043.5***	1097.7***	1037.8***	25.32***	16.17***	78.5**	11.7ns	36.5ns	38.0ns	34.8ns	76.7*
Testers	3	1273.1***	2584.9***	1965.3***	3137.3***	58.70***	10.03*	28.1ns	63.9*	25.9ns	35.1ns	5.6 ns	19.4ns
Lines xTesters	15	4101.6***	2359.0***	4420.4***	2503.4***	15.24***	18.29***	40.9**	39.8*	24.9ns	19.9ns	53.7*	32.4ns
Error	66	21.15	17.85	21.84	18.24	2.75	2.89	12.8	19.57	19.60	19.58	24.3	31.79

Among lines, significant and highly significant differences were observed, in the two years, for all studied characters except for milling in both growing seasons, hulling in 2020 and head rice in 2019 growing seasons. These results were agreed with Panwar (2005).

Multivariate Analysis

Principal components analysis (PCA) is a mathematical procedure that transforms several (possibly) correlated variables into a (smaller) number of uncorrelated variables (PC). The first PC accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible. The first five components in the principal component analysis (Figs. 1 and 2) with Eigenvalues > 1 contributed (75.42 and 79.03 %) variability existing in the genotypes for yield component traits in both seasons, respectively. The remaining components with Eigenvalues < 1 contributed (24.58 and 20.97%) variability in both seasons, respectively. The eigenvalues in PC1 had the highest variance (24.10 and 25.10 %) followed by the PC2 were (17.52 and 18.09 %) in two seasons, respectively. Thus, the results of principal component analysis used in the study have revealed the traits contributing for the variation. These scores can be utilized to make precise selection indices whose intensity can be decided by variability explained by each of the principal component. To identify and classify maximum variability into total variability for

grouping the accessions by taking into account several traits and relationship among them (Dhakal *et al.* 2020 and Christina *et al.* 2021).

The results in Table (3) showed that the value of the panicle length (0.09 and 0.24), panicle weight (0.25 and 0.05), fertility (0.02 and 0.06), grain yield (0.37 and 0.38), biomass (0.40 and 0.35) and milling (0.18 and 0.02) which showed positive loading in PC1 in first and second seasons, respectively while other traits showed negative loadings in one or in both seasons. In PC2, the parameters viz., grain yield (0.06 and 0.10) and head rice (0.02 and 0.31) showed positive loading in both seasons, respectively while other traits showed negative loadings in one or in both seasons. As for PC3, the traits like plant height, filled grains, number of spikelets, grain yield and head rice showed positive loading in both seasons whereas, further traits showed negative loadings in one year at least. These traits are largely engaged in the divergence and they also carry most of the variability. In PC4, the parameters viz., plant height, filled grains, fertility, grain yield and hulling showed positive loading in both seasons. In addition to PC5, the traits duration, panicle weight, grain yield and hulling showed positive loading in both seasons. Hence, the selection of traits with high variability will be rewarding for future breeding programs (Dhakal *et al.* 2020 and Christina *et al.* 2021).
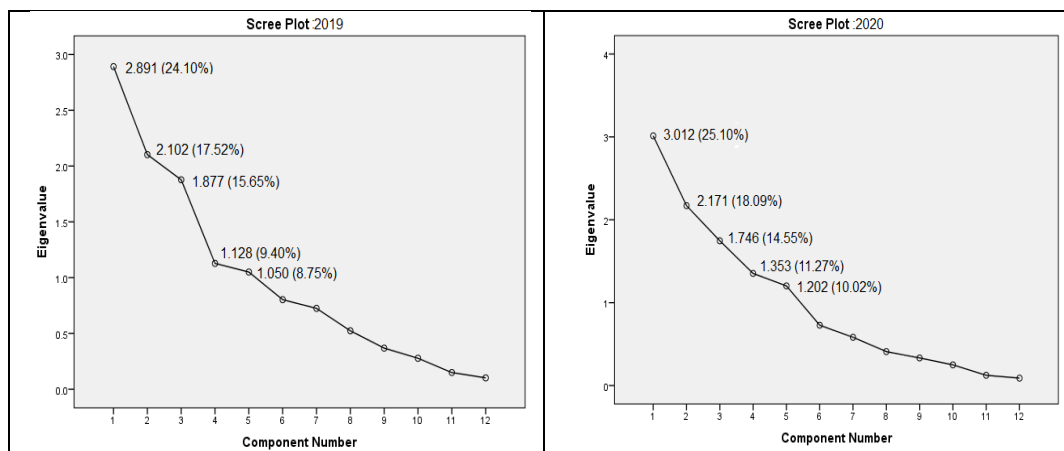
Figures 1, 2: Scree plot of principal component analysis among eigenvalue and principal components in the two seasons.

Table 3. Contribution of first five principal components to variation in rice genotypes.

Traits	PC1		PC2		PC3		PC4		PC5	
	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020
Duration	-0.18	0.00	0.19	0.00	-0.28	0.11	-0.24	0.64	0.15	0.11
Plant height	-0.05	0.23	-0.06	-0.05	0.06	0.07	0.69	0.01	0.08	-0.40
Panicle length	0.09	0.24	-0.05	-0.14	-0.29	-0.03	-0.04	-0.09	0.21	-0.01
Panicle weight	0.25	0.05	0.05	0.00	-0.28	0.01	-0.24	0.04	0.23	0.70
Filled grains	0.05	-0.02	0.43	-0.02	0.03	0.45	0.03	0.09	-0.09	0.06
No. of spikelets	0.00	-0.05	0.40	-0.06	0.06	0.30	-0.12	-0.39	-0.01	0.31
Fertility%	0.02	0.06	0.29	-0.01	-0.02	0.42	0.41	0.07	0.02	-0.16
Grain yield	0.37	0.38	0.06	0.10	0.03	0.04	0.01	0.22	0.01	0.15
Biomass	0.40	0.35	-0.02	0.13	0.10	-0.04	-0.02	-0.19	-0.18	-0.01
Hulling%	-0.05	0.22	-0.04	0.41	0.03	-0.06	0.09	0.16	0.85	0.06
Milling%	0.18	0.02	-0.02	0.40	0.37	-0.03	-0.14	-0.05	0.13	-0.01
Head rice%	0.00	-0.09	0.02	0.31	0.38	0.04	0.09	-0.11	0.15	-0.05

The distribution and nature of diversity for quantitative traits were described in the diagram (Figs. 3 and 4) between PC1 and PC2 to identify the relationship among studied traits and grain yield. The diagram indicated that there is significant correlation between the variation of grain yield and panicle weight, panicle length, biomass and plant height and then filled grain and fertility since these traits are very closed to grain yield. On the other hand the growth duration was representing a negative effect on grain yield in 2st season.

Mean performance.

Evaluation of six CMS lines, four testers and their F$_1$ hybrid combinations for some yield and its component characters are presented in Table (4). Data showed significant and highly significant differences among the genotypes for plant height, duration, grain yield (t ha^{-1}), biological yield, panicle weight, panicle length, number of filled grains/panicle, number of spikelets/panicle, fertility, milling, hulling and head rice characters during the two seasons of study. Results in Table (4) showed that mean performances varied from one combination to another. For duration, CMS line IR58025A and

IR70368 Agave the lowest mean values (134.67 and 135.67) and (135.33 and 136.33 days) in 2019 and 2020 seasons, respectively. While the durations of early testers PR78 and G.181 were (132.67 and 133.00) and (133.67 and 134.33 days) in the first and second seasons, respectively. In addition, the hybrid combinations PR1/Pusa13A and PR2/Pusa13A showed the following duration (132.33 and 133.67) and (130.67 and 131.67days) in 2019 and 2020 seasons, respectively. For the breeder, the most desirable mean values are towards the shortest durations. Similar findings were reported by Hammoud (1996). Concerning plant height, most CMS lines showed the shortest plants that recorded by IR69625A (136.67 and 138.67cm) and IR68902A (148.33 and 150.00cm) in both seasons, respectively. The tester line PR2 exhibited plants with mean height of 150cm and 151.67cm in the two seasons, respectively. The most desirable mean value is towards short stature that was found in the F$_1$ hybrids G.181/IR69625A (150.00 and 148.33cm) and G.181/IR70368A (151.67 and 151.67cm) in both seasons, respectively. Even if both parents are semi dwarf, their F$_1$ hybrid often showed tall stature and lodging (Virmani, 1994). Data in

Table (4) showed that there were significant differences between plant height, duration, grain yield (t ha^{-1}), biomass (t ha^{-1}), panicle weight, panicle length, filled grains, number of spikelets/panicle, fertility% and milling quality characters during the two season of study. Furthermore, the best and stable values in both seasons for grain yield (t ha^{-1}) were for PR78/IR58025A (16.37 and 16.83), for biomass were PR78/IR69625A (68.17and71.00), for panicle weight were PR2/IR58025A (4.33 and 3.42g) and for panicle length were PR1/IR70368A (28.14 and 27.17), respectively. However, there were highly significant differences among these traits such as filled grains with mean values of 210.67 and 201.33. For number of spikelets/panicle was with mean values of 226.53 and 241.00 and for fertility% with mean values of 87.32 and 86.87 in both seasons, respectively for the same hybrid G.181/Pusa3A these findings are in accordance with El- Mowafi *et al.* (2015). Regarding to milling quality characters, results in Table (4) showed that the highest hulling percentage (91.67% and 85.00%) were obtained for the hybrid PR78/IR68902A for the two seasons 2019 and 2020, respectively. Data in Table (4) revealed significant differences among the tested genotypes. Concerning milled rice and head rice, the tested genotype G.181/IR69625A gave the highest values 72.19 and 71.55 % for the two seasons, respectively while for head rice the tested genotype G.181/IR70368A gave the best

mean values (63.87 and 67.78) for the two seasons respectively. Similar observations were reported by Lokaprakash *et al.* (1991).

Phylogenetic analysis of parental lines:

The dendrogram analysis of ten parental lines relied on their morphological data and showed two main clusters with internal sub-clusters revealing varying degrees of diversity (Figs. 5 and 6). The first cluster, in 1st season contains five parental lines (three CMS lines i.e. Pusa3a, Pusa13a and IR68902A and two restorer lines PR1 and G.181), while the other five parental lines listed in the second cluster (three CMS lines IR69625A, IR58025A and IR70368 and two restorer lines PR78 and PR2).

In 2st season there are three parental lines listed in first cluster (PR1, G.181 and Pusa13A), while the second cluster contains the rest seven parental lines. In both seasons some parental lines listed in the same group, the first group contains PR78, IR58025A and IR70368A, while the second group contains G.181 and Pusa13A and the third group contains PR2 and IR69625A. The current results indicated that the parental lines listed in the same groups have the best findings for specific combining ability as in PR78, IR70368A and PR78/IR70368 hybrid combination in many traits (El- Mowafi *et al.* 2021).
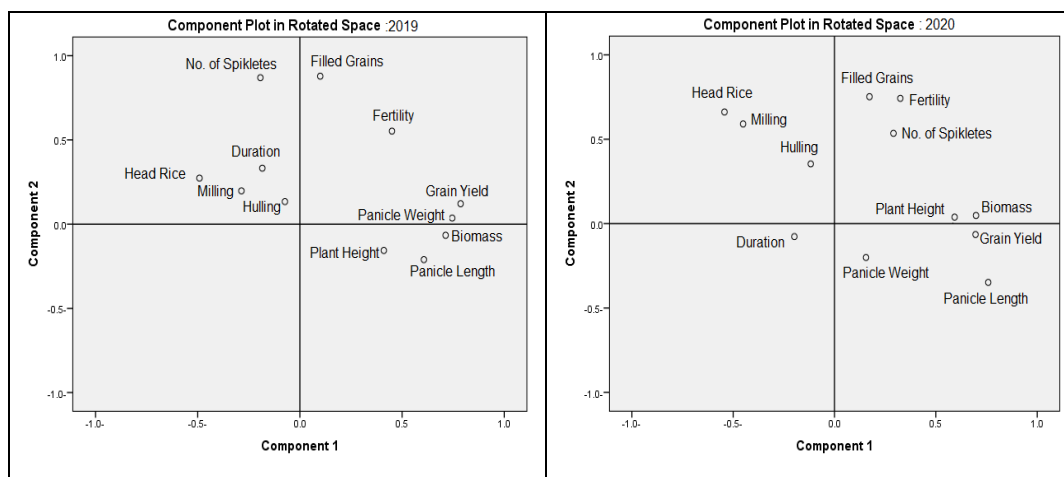
Figures 3 and 4: The diagram of principal components 1 and 2

Table 4. Mean performance of parents and its hybrids for yield and its component.

Genotype	Duration (day)		Plant height (cm)		Panicle length(cm)		Panicle weight(g)	
	2019	2020	2019	2020	2019	2020	2019	2020
Line								
IR58025A/B	134.67	135.67	170.00	172.00	24.07	24.30	2.93	3.04
IR68902A/B	138.67	140.00	148.33	150.00	23.43	22.73	2.80	2.90
IR69625A/B	136.67	138.00	136.67	138.67	22.69	22.47	3.03	3.13
IR70368A/B	135.33	136.33	165.00	167.00	24.03	23.98	2.95	3.06
Pusa3A/B	151.00	152.00	168.33	170.00	23.58	23.23	2.94	3.05
Pusa13A/B	136.00	136.33	168.33	170.00	24.20	23.89	2.92	3.03
Tester								
PR1	137.63	138.30	170.00	172.00	25.79	25.62	2.91	3.02
PR2	136.60	137.60	150.00	151.67	26.36	25.73	2.89	3.00
PR78	132.67	133.00	171.67	173.67	25.90	25.39	2.86	2.96
G.181	133.67	134.33	173.33	175.33	24.61	24.95	3.18	3.28
Crosses								
PR1/IR58025A	137.67	139.00	158.33	161.67	25.85	27.10	3.62	3.67
/IR68902A	135.67	136.67	155.00	156.67	24.24	26.66	3.88	3.29
/IR69625A	134.67	136.00	163.33	161.67	25.67	25.28	3.94	3.48
/IR70368A	135.67	136.67	170.00	165.00	28.14	27.17	3.13	3.26
/Pusa3A	136.33	137.00	161.67	161.67	26.10	29.56	3.40	3.40
/Pusa13A	132.33	133.67	170.00	171.67	25.69	27.50	3.55	3.33
PR2/IR58025A	136.67	137.67	175.00	173.33	27.31	27.28	4.33	3.42
/IR68902A	135.67	136.33	170.00	168.33	27.00	27.78	3.50	2.85
/IR69625A	134.67	136.00	168.33	171.67	26.38	24.78	3.97	2.92
/IR70368A	135.67	136.67	166.67	166.67	25.13	27.23	3.82	2.88
/Pusa3A	136.67	137.33	163.33	165.00	25.79	27.74	3.08	3.01
/Pusa13A	130.67	131.67	173.33	171.67	26.42	27.00	3.41	3.07
PR78/IR58025A	136.67	138.00	163.67	168.33	25.56	28.89	3.38	2.96
/IR68902A	134.67	135.67	165.00	165.00	26.50	28.33	3.75	2.98
/IR69625A	134.67	135.67	166.67	165.00	25.22	28.27	3.47	3.01
/IR70368A	136.67	138.00	171.67	168.33	23.22	27.64	3.23	3.09
/Pusa3A	138.33	139.33	170.00	170.00	27.72	27.76	3.94	3.02
/Pusa13A	133.33	134.33	161.67	163.33	27.89	27.53	3.52	2.95
G.181/IR58025A	142.67	143.67	155.00	158.33	26.50	28.92	3.90	3.02
/IR68902A	143.67	144.33	171.67	170.00	27.11	27.90	3.47	3.15
/IR69625A	136.67	137.67	150.00	148.33	28.21	24.50	4.09	3.15
/IR70368A	137.00	138.00	151.67	151.67	26.01	24.89	3.76	3.23
/Pusa3A	143.67	145.00	163.33	163.33	26.50	26.00	3.74	3.26
/Pusa13A	137.67	138.67	161.67	160.00	28.32	25.71	3.24	3.25
L.S.D 0.05	1.01	1.61	17.69	6.99	0.67	0.87	0.22	0.18
L.S.D 0.01	1.35	2.13	23.39	9.23	0.89	1.16	0.30	0.24

Table 4. Continue…

Genotypes	Grain yield (t ha^{-1})		Biomass (t ha^{-1})		Filled grains/panicle		Number of Spikelets/panicle	
	2019	2020	2019	2020	2019	2020	2019	2020
Line								
IR58025A/B	11.87	12.08	29.33	31.13	169.67	171.33	195.33	199.00
IR68902A/B	11.33	11.88	28.58	29.61	204.00	242.00	277.67	181.33
IR69625A/B	11.20	11.41	27.67	28.69	182.67	184.67	226.67	230.67
IR70368A/B	11.73	11.94	28.34	29.62	162.33	164.00	180.33	184.00
Pusa3A/B	13.17	13.70	32.25	33.53	253.00	255.00	268.33	172.00
Pusa13A/B	12.65	12.86	35.02	36.04	214.33	216.33	240.67	24.67
Tester								
PR1	11.30	11.43	28.50	29.76	251.00	253.67	276.47	280.67
PR2	11.12	11.35	27.25	28.28	184.33	186.00	210.00	213.67
PR78	11.67	12.20	36.50	37.78	146.00	167.67	170.40	193.67
G.181	17.67	18.27	48.42	48.51	234.00	236.00	259.67	263.67
Crosses								
PR1/IR58025A	14.35	14.67	38.92	39.08	197.67	208.33	226.53	241.00
/IR68902A	13.00	14.00	35.83	34.75	264.33	177.00	291.60	210.00
/IR69625A	15.60	15.37	51.25	62.08	174.33	192.33	208.33	220.67
/IR70368A	12.97	13.97	36.42	34.83	169.00	213.67	192.13	245.67
/Pusa3A	13.78	13.28	58.00	57.42	145.33	229.00	174.33	257.33
/Pusa13A	14.10	14.37	49.58	55.00	160.67	147.67	177.87	177.67
PR2/IR58025A	15.17	14.93	48.17	60.42	171.33	128.67	186.53	163.33
/IR68902A	14.63	13.93	45.83	45.08	162.00	166.00	180.73	196.33
/IR69625A	14.82	14.70	52.75	52.17	204.67	184.00	225.00	214.33
/IR70368A	14.05	15.63	48.83	49.00	197.33	174.67	215.33	204.67
/Pusa3A	13.38	13.52	45.83	45.50	193.67	172.33	215.80	202.00
/Pusa13A	15.43	15.13	57.83	58.67	185.67	225.00	202.00	258.67
PR78/IR58025	16.37	16.83	63.67	64.83	200.33	187.33	216.93	213.33
/IR68902A	15.55	16.75	57.92	75.83	223.00	186.33	245.67	220.67
/IR69625A	14.80	13.50	68.17	71.00	208.67	179.67	237.00	250.67
/IR70368A	14.63	15.50	61.25	61.42	254.67	261.33	181.17	198.33
/Pusa3A	13.52	15.32	41.25	41.67	269.33	284.33	183.83	197.67
/Pusa13A	14.20	12.87	48.92	47.83	238.33	237.33	255.27	253.33
G.181/IR58025A	13.53	14.47	36.00	37.33	168.67	151.33	190.00	181.67
/IR68902A	14.80	16.83	32.50	33.75	167.00	171.33	191.07	205.67
/IR69625A	14.47	13.53	52.50	39.92	174.67	205.67	205.67	236.00
/IR70368A	13.52	13.57	37.83	49.58	259.67	198.00	288.20	228.33
IR58025A/B	14.18	16.83	37.50	39.00	210.67	201.33	241.27	231.33
/Pusa13A	13.43	14.33	37.25	39.67	225.00	176.00	254.67	205.67
L.S.D 0.05	2.17	1.32	2.84	6.48	34.48	29.10	35.61	29.73
L.S.D 0.01	2.89	1.75	3.75	8.57	39.31	38.48	38.17	39.31

Table 4. Continue…

| Genotypes	Fertility (%)		Hulling(%)		Milling(%)		Head rice(%)	
	2019	2020	2019	2020	2019	2020	2019	2020
Line								
IR58025A/B	86.90	86.13	83.33	81.67	64.33	66.33	59.00	60.40
IR68902A/B	86.65	86.22	81.63	80.13	70.00	71.67	64.81	66.48
IR69625A/B	80.58	80.09	80.60	78.93	73.33	74.83	67.98	69.38
IR70368A/B	89.78	88.93	81.93	80.43	66.23	67.90	60.16	61.90
Pusa3A/B	94.32	93.77	82.60	80.27	67.71	69.37	61.67	63.33
Pusa13A/B	89.06	88.42	82.73	81.23	71.17	72.67	64.31	65.71
Tester								
PR1	90.79	90.33	84.00	82.33	70.30	71.97	65.44	67.11
PR2	87.70	86.98	86.97	85.47	69.84	71.34	62.76	64.16
PR78	85.33	86.45	84.98	83.32	69.77	71.43	63.38	65.04
G.181	89.92	89.34	82.63	80.63	72.17	73.67	64.03	65.43
Crosses								
PR1/IR58025A	87.16	86.41	77.64	75.31	70.49	65.86	60.20	60.38
/IR68902A	90.61	84.34	88.73	79.40	64.95	64.95	54.28	54.28
/IR69625A	83.55	87.18	85.54	85.29	68.89	68.89	60.00	60.00
/IR70368A	87.89	87.02	80.55	77.57	67.65	66.31	56.90	56.44
/Pusa3A	83.27	88.98	77.72	79.73	65.94	64.49	53.36	56.67
/Pusa13A	90.52	83.03	82.95	83.41	66.36	66.66	67.38	62.30
PR2/IR58025A	91.85	78.69	82.09	82.07	62.33	71.10	54.02	59.79
/IR68902A	89.59	84.61	80.00	77.54	69.32	69.16	56.54	55.16
/IR69625A	91.04	85.92	80.33	80.00	70.89	69.67	64.03	61.78
/IR70368A	91.61	85.41	83.00	81.12	66.06	66.67	60.78	56.75
/Pusa3A	89.60	85.15	72.82	73.06	61.02	60.67	55.46	52.80
/Pusa13A	91.41	88.97	81.43	81.60	71.02	69.74	61.75	61.62
PR78/IR58025A	92.29	87.62	82.22	83.42	71.44	70.00	62.56	63.33
/IR68902A	90.78	89.43	91.67	85.00	70.28	71.39	62.28	59.72
/IR69625A	88.07	87.36	81.92	78.89	70.14	68.89	61.61	58.89
/IR70368A	85.30	88.82	81.08	83.42	72.74	68.89	53.97	60.00
/Pusa3A	91.93	89.51	80.55	82.48	65.26	68.29	57.81	60.17
/Pusa13A	93.35	89.59	77.31	76.93	67.51	66.11	60.49	59.95
G.181/IR58025A	88.80	83.31	82.93	82.40	66.36	70.15	59.49	62.15
/IR68902A	87.49	83.22	83.85	78.00	68.10	67.00	61.62	51.00
/IR69625A	84.92	87.12	85.30	84.89	72.19	71.55	59.67	59.67
/IR70368A	90.12	86.60	76.16	86.10	68.35	74.89	63.87	67.78
/Pusa3A	87.32	86.87	83.99	85.11	68.61	66.69	59.43	56.11
/Pusa13A	88.40	85.38	83.41	84.63	64.56	65.57	53.33	56.59
L.S.D 0.05	4.49	4.71	5.83	7.22	7.21	7.23	8.40	9.19
L.S.D 0.01	5.93	6.22	7.72	9.54	9.53	9.04	10.63	12.15
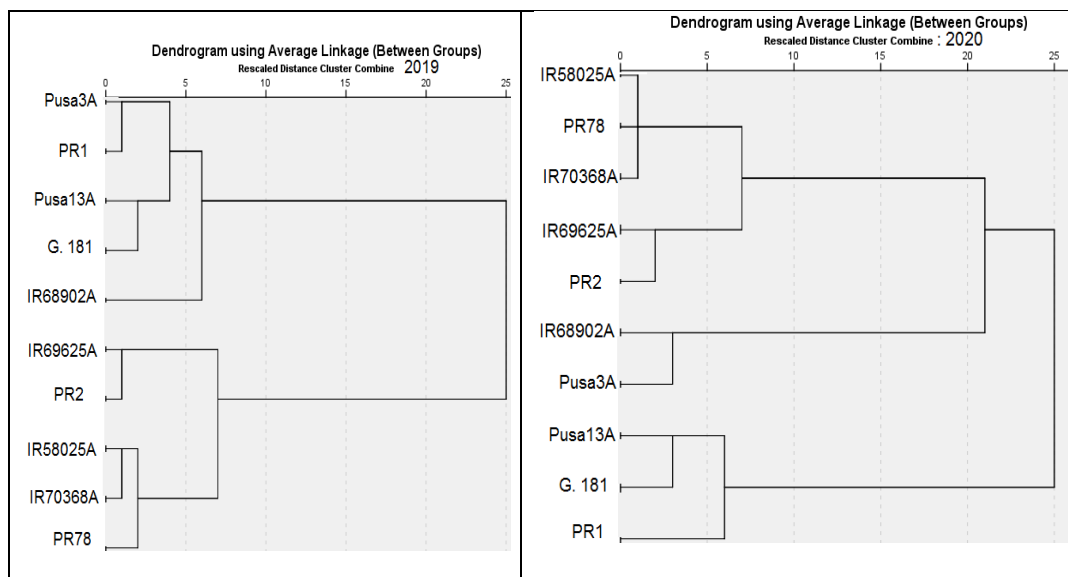
Figure 5 and 6: UPGMA dendrogram analysis of cytoplasmic male sterile (CMS) and restorer lines based on the data of their yield and its component.

Proportional contribution of the line, tester and line × tester

The proportional contribution of lines, testers and their interaction to the total variance are presented in Table 5. The testers played important role towards duration (47.84 and 47.71%) in both seasons and biomass (44.88%) in 2019 growing seasons indicating predominant paternal influence for these traits.

On the contrary, maternal lines contributed most panicle length (66.24%) and panicle weight (58.88%) in 2020 growing seasons, which indicated that the testers contributed by more positive alleles in these characters and prevalence of additive gene action. Similar observations were reported by El- Mowafi *et al.* (2015). The contribution of maternal and paternal interactions (line x tester) were found much more than lines and testers, individually. Hence, line × tester interactions provide much more variation for the appearing of the traits. It is remarkable that hybrid combinations had higher values than their parents with respect to plant height, filled grains/panicle, number of spikelet's/panicle, fertility, grain yield, hulling, milling and head rice in both studied seasons in addition to panicle length and panicle weight in 2019 and biomass in 2020 growing seasons,

indicating that these traits are influenced by non-additive gene action. Similar findings were reported by Hassan *et al.* (2016).

General combining ability effects (GCA):

The general combining ability given in Table 6revealed the differences among the CMS female lines and the male testers exhibited highly significant differences for most studied characters. This is indicating that they interacted and produced markedly different combining ability effects, and this might be due to the wide genetic diversity of lines and testers. Significant differences of GCA effects were observed among the male sterile lines (CMS) for all characters as shown in Table 6.The IR69625A and Pusa13A showed significantly high and negative estimates of GCA effects for duration. It was the highest in case of Pusa13A (-3.0 and -3.04), and the lowest in IR69625A with mean values (-1.42 and -1.29) in both seasons, respectively. These CMS lines appeared to be good parental combiners in hybrid combination for duration besides all the testers except G.181. Concerning plant height (Table 6) the results showed that G.181 was the best combiner by highly significant and negative estimates of GCA effects in both studied seasons followed by PR1 and IR58025A in one studied

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season. However, the negative values of GCA effects lead to decreased plant height that could be useful to breed short stature rice cultivars. These data are in agreement with those reported by El- Mowafi *et al.* (2018). Data in Table 6revealed that the estimates of GCA effects of grain yield were significant and highly significant for PR78 (0.94 and 0.38) and IR58025A (0.85 and 0.48) in the two seasons, respectively. Similar results were recorded by El-Refaee (2002). In case of biomass, there were significant positive and negative estimates of GCA effects. The tester PR78 gave highly significant positive ones with mean values of 9.19 and 10.60 in the two seasons, respectively. Besides, the CMS lines gave highly significant positive effects IR69625A gave highly significant positive one with mean values of 8.50 and 6.46 in the two seasons respectively. Panicle weight significant positive and negative GCA for male parental lines. The tester lines; PR1, PR2 and PR78 were gave significant and positive

estimates of GCA effects in the first year and not significant in second year. In case of CMS lines, the Pusa13A gave highly significant positive (0.288) values for the second year. For panicle length, the male parental line, PR1 and G.181 gave the highest significant positive values (0.28 and 0.35) in first season, respectively. However, the CMS line Pusa3A gave highly significant positive GCA values of 0.95 and 0.89 in both years, respectively. Number of spikelets/panicle, gave highly significant and positive estimates for the parental line PR1 (15.21). GCA of the CMS IR68902A and Pusa13A showed highly significant positive in only one year. Furthermore, the estimates of GCA effects of fertility% were significant positive (Table 6) for parental line PR2 with values of 1.81 and 1.92, in the two years, respectively. On the other side, the CMS line exhibited highly significant positive GCA for the CMS Pusa13A (1.88 and 1.76) in the two years, respectively.

Table 5. Proportional contribution of Lines, Testers and Lines x testers.

Proportional contribution		Lines	Testers	Lines x testers
Duration(day)	2019	36.27	47.84	15.90
	2020	34.94	47.71	17.35
Plant height(cm)	2019	15.9	19.7	64.40
	2020	7.24	43.22	49.54
Panicle Length(cm)	2019	39.78	7.22	53.00
	2020	66.24	0.44	33.32
Panicle Weight(g)	2019	8.51	30.90	60.60
	2020	58.88	2.90	38.22
Grain yield (t ha^{-1})	2019	29.61	19.38	51.01
	2020	14.29	7.45	78.27
Biomass (t ha^{-1})	2019	17.64	44.88	37.47
	2020	7.83	40.08	52.08
Filled grains/panicle	2019	7.94	5.38	86.68
	2020	10.79	16.04	73.17
Number of Spikelets/panicle	2019	7.06	7.59	85.35
	2020	9.95	18.05	72.00
Fertility(%)	2019	23.82	33.14	43.03
	2020	20.98	7.81	71.21
Hulling(%)	2019	36.01	7.72	56.27
	2020	6.92	22.62	70.45
Milling(%)	2019	28.75	12.23	59.03
	2020	32.04	17.74	50.22
Head rice(%)	2019	17.45	1.68	80.87
	2020	41.3	6.28	52.42

Table 6. Estimates of GCA effects (gi) of each tester and line for yield and its component characters.

Genotypes	Duration(day)		Plant height(cm)		Panicle length(cm)		Panicle weight(g)		Grain yield (t ha^{-1})		Biomass(t ha^{-1})	
	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020
Tester												
PR1	-1.19**	-1.13**	-0.28ns	-1.99*	0.28***	-0.05ns	0.103**	0.047ns	-0.38ns	-0.47*	-2.67**	-2.63**
PR2	-1.58***	-1.68***	6.81**	5.00**	-0.44***	-0.12ns	0.083*	0.002ns	0.24ns	-0.10ns	2.21**	1.98*
PR78	-0.86***	-0.79***	-1.39ns	2.22*	-0.19*	0.11ns	0.113***	-0.021ns	0.94***	0.38*	9.19***	10.60**
G.181	3.64***	3.59***	-5.44***	-5.83***	0.35***	0.06ns	-0.300**	-0.029ns	-0.36ns	0.18ns	-8.74**	-9.95**
SE	0.15	0.23	2.56	1.00	0.10	0.13	0.032	0.026	0.31	0.19	0.41	0.94
LSD 0.05	0.30	0.46	5.10	1.99	0.19	0.25	0.064	0.052	0.62	0.38	1.17	1.87
LSD 0.01	0.40	0.61	6.76	2.64	0.26	0.34	0.086	0.070	0.82	0.50	1.87	2.48
Line												
IR58025A/B	1.83***	1.96***	-7.08*	0.97ns	-0.38***	-0.59**	0.012ns	-0.120**	0.85*	0.48*	-0.97ns	0.59ns
IR68902A/B	0.83***	0.63*	2.08ns	0.56ns	0.17ns	0.89**	0.065ns	0.001ns	0.15ns	0.64**	-4.65**	-2.47*
IR69625A/B	-1.42***	-1.29**	-1.25ns	-2.78ns	-0.42***	-0.45**	-0.060ns	-0.025ns	0.58ns	-0.47*	8.50**	6.46**
IR70368A/B	-0.33ns	-0.29ns	1.67ns	-1.53ns	-1.23**	1.14***	-0.173**	-0.070*	-0.55ns	-0.08ns	-1.58*	-1.11ns
Pusa3A/B	2.17***	2.04***	1.25ns	0.56ns	0.95***	0.89**	0.077ns	-0.073*	-0.63ns	-0.00ns	-2.02**	-3.93**
Pusa13A/B	-3.00***	-3.04**	3.33ns	2.22ns	0.91***	-1.87**	0.077ns	0.288**	-0.05ns	-0.57*	0.73ns	0.47ns
SE	0.18	0.29	3.13	2.47	0.12	0.15	0.039	0.032	0.38	0.23	0.50	1.15
LSD 0.05	0.36	0.56	6.23	4.92	0.24	0.31	0.079	0.064	0.78	0.46	1.41	2.29
LSD 0.01	0.48	0.74	8.30	6.52	0.32	0.41	0.105	0.085	1.03	0.61	1.87	3.04

Table 6. Continue...

Genotypes	Filled grains/panicle		Number of Spikelets/panicle		Fertility(%)		Hulling(%)		Milling(%)		Head rice(%)	
	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020
Tester												
PR1	-9.53*	14.56**	-4.32ns	15.21**	-1.87**	0.68ns	0.39ns	-1.02ns	-0.56ns	-1.78ns	-0.51ns	-0.54ns
PR2	-6.97ns	-5.0ns	-11.89*	-3.66ns	1.81**	1.92**	-1.85*	-2.19*	-1.16ns	-0.23ns	-0.44ns	-0.91ns
PR78	16.31**	-13.39**	3.86ns	-16.05**	1.29*	0.41ns	0.66ns	0.55ns	2.06*	0.86ns	0.58ns	2.64*
G.181	8.19ns	3.83ns	12.36*	4.50ns	-1.19ns	-0.06ns	1.81*	2.38*	0.09ns	2.02*	0.37ns	-0.00ns
SE	4.99	5.15	5.15	4.30	0.65	0.68	0.84	1.04	1.02	1.01	1.16	1.33
LSD 0.05	9.93	8.36	10.25	8.56	1.29	1.35	1.67	2.07	2.02	2.00	2.31	2.65
LSD 0.01	13.17	11.09	13.59	11.35	1.72	1.80	2.22	2.75	2.69	2.66	3.06	3.51
Line												
IR58025A/B	-8.25ns	-11.19*	-13.12*	-10538*	0.99ns	-1.74*	-0.58ns	-0.34ns	-0.28ns	1.21ns	-014ns	3.52*
IR68902A/B	12.33*	-14.94**	14.14*	12.10*	0.59ns	-1.33ns	4.26**	-1.16ns	0.23ns	0.06ns	-0.52ns	-3.85*
IR69625A/B	-2.17ns	10.31*	2.88ns	8.97ns	-2.14ns	1.64*	2.47*	2.13*	2.59*	2.68*	2.83*	1.19ns
IR70368A/B	2.42ns	6.81ns	3.10ns	7.52ns	-0.31ns	0.23ns	-1.60ns	0.91ns	0.76ns	1.12ns	-0.32ns	1.35ns
Pusa3A/B	-13.00*	7.64ns	-12.61*	7.35ns	-1.01ns	0.39ns	-3.03ns	-1.04ns	-2.73*	-3.03*	-2.69*	-2.45ns
Pusa13A/B	9.67ns	-8.61ns	6.33ns	-11.37*	1.88*	1.76*	-0.53	0.50ns	-0.57	-1.05ns	1.54ns	1.23ns
SE	6.11	5.15	6.31	5.27	0.79	0.83	1.03	1.27	1.28	1.27	2.85	1.63
LSD 0.05	12.14	10.25	12.56	10.49	1.57	1.65	2.05	2.55	2.55	2.53	2.83	3.24
LSD 0.01	16.10	13.60	16.66	13.91	2.09	2.19	2.72	3.38	3.38	3.35	3.75	4.30

For milling quality, the hulling percentage had significant positive GCA for parental line G.181 with values of 1.81 and 2.38 in the two years, respectively. However, the CMS line IR69625A gave significant positive one in both years (2.47 and 2.13) respectively (El- Mowafi *et al.* 2015). Furthermore, the CMS line IR69625A was a good combiner for milling and head rice followed by the male parent PR78.

Estimates of specific combining ability effects (SCA):

Estimates of SCA effects for each F_1 hybrid combination for the studied characters are shown in Table 7. For duration, there were significant negative SCA effects for the hybrids PR2/IR58025A with mean values of (-1.89 and -1.79), PR2/Pusa13A (-2.14 and -2.26), PR78/IR70368A (-2.89 and -2.93) and PR78/Pusa3A (-1.22 and -1.54) in the two years, respectively. Negative values would be useful for breeder. This agreed with Anis *et al.* (2016). Also for plant height, 2 out of 24 crosses were found to be negatively significant for SCA effects in first season and three hybrids in second season. The useful negative significant (desirable) values of SCA effects were shown by PR1/IR69625A with mean value of (-18.19) and PR1/Pusa3A with mean value of (-13.14) in 2019 growing season and could be useful to breed short stature cultivars (El- Mowafi *et al.* 2012). For second year, the significant negative values for SCA effects ranged between (-5.00 and –7.50). In case of grain yield, significant positive and negative SCA effects were recorded.

Positive significant was recorded for PR2/IR69625A (1.06 and 1.56) in the two seasons, respectively. As for biomass there were significant positive SCA effects for five hybrid combinations. The highest values were that of the PR78/Pusa3A (15.02 and 14.15), in both seasons, respectively.

Concerning panicle weight, high positive and significant estimates were recorded for the hybrid combination G.181/IR69625A with values of0.279 and0.197inboth years, respectively. Regarding filled grains/panicle, there were significant positive SCA effects for the hybrid PR1/Pusa3A which exhibited largest (67.78) values. The similar findings were reported by El- Mowafi *et al.* (2015).For number of spikelets/ panicle: results showed that nine hybrid rice combinations exhibited positive and significant SCA effects ranging from 28.96 for G.181/Pusa3A to 68.66 for PR1/Pusa3A but in only one season. In case of fertility%, significant positive SCA effects were recorded for the three hybrid rice combinations, PR1/IR68902A, PR1/IR69625A and PR1/Pusa3A in only one season. On the other side, there were significant positive SCA effects for milling quality characters. For hulling percentage, the hybrid PR2/IR58025A showed the best value (4.95 and 5.16) in both seasons respectively. But for milling percentage, the hybrid G.181/70368A gave the highest positive significant value (5.08) in second season. In case of head rice the combination PR78/70368A give the highest mean values of 5.68 and 7.54 in the two years, respectively.

Table 7. Estimates of SCA effects (sij) of each hybrid for yield and its component characters.

Genotypes	Duration(days)		Plant height(cm)		Panicle length(cm)		Panicle weight(g)		Grain yield (t ha^{-1})		Biomass (t ha^{-1})	
	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020
PR1/IR58025A	0.44ns	0.54ns	2.36ns	-2.36ns	-0.41ns	0.60ns	-0.126ns	-0.055ns	-0.13ns	-0.090ns	-5.10**	-8.70**
/IR68902A	-0.17ns	-0.24ns	12.64*	2.92ns	-1.29***	0.23ns	0.154ns	0.070ns	0.08ns	-0.19ns	-0.73ns	8.02***
/IR69625A	-0.89ns	-0.79ns	-18.19***	0.69ns	-0.12ns	-1.38**	0.184*	0.023ns	1.05**	1.26***	7.78***	4.81*
/IR70368A	0.61ns	0.49ns	3.19ns	-1.25ns	1.82**	0.56ns	-0.212***	-0.038ns	-0.96*	-0.94*	-1.95*	-3.13ns
/Pusa3A	-0.56ns	-0.46ns	-13.14*	-6.94ns	-0.71***	1.57**	-0.398***	-0.165*	-1.12**	-0.95*	-4.52**	-9.97**
/Pusa13A	-0.17ns	0.24ns	1.53ns	-1.67ns	-0.39ns	-0.41ns	-0.228**	0.010ns	-0.10ns	1.34**	0.60ns	-4.25*
PR2/IR58025A	-1.89***	-1.79***	0.97ns	-2.22ns	0.97***	-0.86***	0.522***	0.033ns	0.55ns	0.99	5.70**	17.88***
/IR68902A	2.61**	2.49**	13.69*	13.83*	0.13ns	-0.31ns	0.105ns	0.122ns	0.66ns	1.27**	-1.78*	-3.65ns
/IR69625A	0.69ns	0.79ns	1.53ns	1.39ns	0.16ns	-1.87**	0.297***	0.100ns	1.06**	1.56**	-2.25*	8.42**
/IR70368A	1.08***	1.35*	0.14ns	5.00*	-0.35ns	0.66*	0.167*	0.135*	-0.34ns	0.53ns	-5.62**	-6.10**
/Pusa3A	0.36ns	0.13ns	5.97ns	1.11ns	0.05ns	0.95**	-0.603***	-0.052ns	-0.62ns	-1.16*	2.81***	4.10*
/Pusa13A	-2.14**	-2.26**	-7.64ns	-7.50**	0.14ns	0.25ns	0.140ns	-0.183**	0.10ns	-0.95*	5.10**	-6.42**
PR78/IR58025A	0.61ns	0.46ns	5.28ns	3.47ns	0.15ns	0.65*	-0.181*	0.015ns	0.45ns	-0.23ns	-7.00**	-11.24**
/IR68902A	1.00**	1.15*	-4.44ns	-1.25ns	1.82***	0.17ns	0.209***	-0.010ns	0.02ns	1.07*	0.54ns	-1.69ns
/IR69625A	1.28**	1.46*	-8.06ns	3.19ns	0.28ns	-0.12ns	-0.101ns	0.003ns	0.34ns	0.45ns	5.97**	2.10ns
/IR70368A	-2.89***	-2.93**	-8.89ns	-5.42*	-2.25**	-0.70*	0.073ns	-0.008ns	0.08ns	-1.28**	0.49ns	10.83***
/Pusa3A	-1.22**	-1.54***	-2.64ns	-1.94ns	0.14ns	-0.22ns	0.129ns	-0.092ns	0.45ns	-0.99*	15.02**	14.15***
/Pusa13A	-0.50ns	-0.65ns	-7.36ns	-5.00*	1.03**	-0.38ns	-0.271***	-0.067ns	-0.57ns	-1.12*	-2.02ns	-2.38ns
G.181/IR58025A	0.44ns	0.46ns	6.81ns	2.78ns	-0.62*	0.79ns	0.079ns	-0.084ns	-0.69ns	0.19ns	-13.59***	-14.83***
/IR68902A	1.28**	1.74***	3.19ns	4.17ns	-0.55*	-0.19ns	0.063ns	0.244***	0.82*	1.91**	0.59ns	3.06ns
/IR69625A	0.028ns	0.21ns	3.61ns	6.39*	0.67***	-0.73*	0.279***	0.197***	0.19ns	0.66ns	3.85ns	7.34**
/IR70368A	1.25**	-1.24*	0.56ns	0.00ns	-0.81**	-0.27ns	-0.031ns	-0.138*	0.91*	1.06*	7.23***	6.39**
/Pusa3A	0.69ns	0.54ns	3.61ns	-5.56*	-0.57*	0.62*	-0.081ns	0.076ns	0.59ns	-1.69**	8.67***	-13.06**
/Pusa13A	0.53ns	0.49ns	0.56ns	0.83	0.71**	0.38ns	-0.167*	-0.136*	0.50ns	-0.03ns	2.41*	-0.67ns
SE	0.36	0.57	6.27	2.47	0.24	0.31	0.079	0.064	0.77	0.47	1.00	2.29
LSD 0.05	0.72	1.13	12.48	4.92	0.47	0.62	0.157	0.128	0.78	0.94	1.99	4.56
LSD 0.01	1.00	1.50	16.55	6.52	0.63	0.82	0.209	0.171	1.03	1.24	2.64	6.05

Table 7. Continue…

Genotype	Filled grains/panicle		No. of spikelets/panicle		Fertility (%)		Hulling(%)		Milling(%)		Head rice (%)	
	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020
PR1/IR58025A	24.69*	24.86*	25.86*	26.07*	-0.99ns	1.72ns	-3.97ns	-4.46ns	3.39ns	-1.54ns	1.64ns	-0.49ns
/IR68902A	6.19ns	-35.25*	-6.58ns	-32.84*	0.011ns	4.29 **	2.72ns	3.17ns	-4.16ns	2.05ns	-4.61ns	0.71ns
/IR69625A	9.53ns	31.81**	8.08ns	29.60**	1.02ns	3.20*	0.35ns	2.07ns	2.16ns	-0.14ns	2.91ns	0.46ns
/IR70368A	-24.30*	-21.42*	-27.36*	-22.83*	-0.033ns	-0.63ns	0.90ns	-0.78ns	-1.39ns	-0.37ns	0.06ns	0.74ns
/Pusa3A	67.78***	-12.72ns	68.66***	-13.35ns	4.86**	-0.48ns	2.28ns	0.44ns	-2.66ns	1.30ns	-3.88ns	0.21ns
/Pusa13A	-35.11**	4.17ns	-34.64**	-8.078ns	-1.84ns	1.48ns	-4.21*	-0.53ns	2.32ns	1.26ns	-1.70ns	1.025ns
PR2/IR58025A	12.61ns	24.56***	14.54ns	28.57***	-0.10ns	-0.13ns	4.95*	5.16*	0.48ns	2.40ns	3.01ns	3.22ns
/IR68902A	-45.28***	-7.67ns	-48.56**	-7.15ns	-0.93ns	-0.86ns	-3.02ns	-4.36ns	-0.15ns	-2.36ns	2.57ns	4.03ns
/IR69625A	-8.72ns	-12.64ns	-6.34ns	-13.67 ns	-1.47ns	-0.39ns	1.88ns	4.05ns	-1.08ns	1.01ns	-0.81ns	0.46ns
/IR70368A	25.06*	-1.41ns	17.89ns	1.20ns	2.33ns	0.048ns	-1.09ns	-0.35ns	1.52ns	0.14ns	3.13ns	2.60ns
/Pusa3A	12.78*	2.64ns	14.14ns	2.52ns	-0.08ns	0.055ns	-2.01ns	-3.93ns	-2.01ns	-1.72ns	-0.29ns	2.64ns
/Pusa13A	-24.41*	11.41ns	-25.69*	12.36ns	-0.78ns	0.29ns	1.22ns	0.24ns	1.57ns	0.56ns	-2.03ns	0.41ns
PR78/IR58025A	-18.64ns	12.19ns	-22.75ns	12.70ns	1.03ns	0.63ns	-0.035ns	-3.46ns	-0.49ns	-1.00ns	1.46ns	3.25ns
/IR68902A	9.14ns	-7.25ns	8.01ns	-9.42 ns	1.06ns	0.72ns	4.66*	0.97ns	-1.48ns	-2.28ns	2.33ns	2.58ns
/IR69625A	-46.8***	-12.19ns	-41.89**	-9.36 ns	-4.68**	-2.29ns	0.23ns	0.82ns	2.42ns	-1.16ns	-5.94*	1.69ns
/IR70368A	56.3**	7.25ns	56.64**	6.07ns	2.58ns	0.95ns	-4.84*	1.66ns	-0.44ns	5.05*	5.68*	7.54*
/Pusa3A	-26.99**	26.69**	-25.15*	24.53*	-2.89ns	2.42ns	-1.44ns	0.66ns	1.28ns	1.33ns	-2.64ns	0.77ns
/Pusa13A	24.99*	-10.42ns	23.88ns	-11.92ns	0.25ns	0.29ns	-4.09*	-5.12*	-3.02ns	-4.13ns	-0.61ns	2.73ns
G.181/IR58025A	-26.72*	-26.02**	-23.84ns	-21.86 *	2.65ns	-3.77*	1.13ns	1.83ns	-1.58ns	2.39ns	0.71ns	2.28ns
/IR68902A	24.72*	9.75ns	25.10*	9.24 ns	0.49ns	1.05ns	4.42*	2.63ns	3.31ns	0.41ns	2.55ns	0.32ns
/IR69625A	-34.22***	-38.39***	-40.26**	-36.27**	1.47ns	-3.89*	1.29ns	2.79ns	-0.45ns	1.51ns	7.55*	2.72ns
/IR70368A	-9.88ns	58.50**	-8.56ns	63.46**	-1.32ns	1.75ns	2.01ns	1.86ns	5.08*	2.95ns	1.45ns	2.41ns
/Pusa3A	29.61**	-20.78***	28.96*	-29.47**	1.18ns	2.93ns	-4.62*	-5.26*	-1.48ns	-1.77ns	-0.83ns	1.61ns
/Pusa13A	14.39ns	0.67ns	19.86ns	2.29ns	-1.33ns	-0.79ns	1.33ns	0.61ns	-2.89ns	-2.69ns	-7.77*	3.52ns
SE	12.22	10.31	12.61ns	10.53ns	1.59ns	1.67ns	2.07ns	2.55ns	2.55ns	2.56ns	2.85	3.26
LSD 0.05	24.29	20.52	25.09	18.85	3.16	3.32	4.12	5.07	5.07	5.05	5.67	6.49
LSD 0.01	32.23	27.22	33.29	-27.80	4.20	4.41	5.46	6.73	6.73	6.71	7.52	8.61

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دراسة القدرة على الائتلاف لبعض الصفات الهامه في بعض تراكيب الأرز الهجين

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الملخص العربى

تم إجراء البحث بالمزرعة التجريبية بمحطة أبحاث سخا ، كفر الشيخ ، مصر ، خلال مواسم زراعة الأرز ٢٠١٨ و ٢٠١٩ و ٢٠٢٠. هدفت الدراسة إلى تقدير القدرة العامة والخاصة على الائتلاف لبعض تراكيب الأرز الهجين ، وتم إنتاج ٢٤ هجينًا عن طريق تهجين ستة امهات عقيمه الذكر مع أربعة اباء معيدين للخصوبه في موسم ٢٠١٨ ثم تقييمها في موسمى ٢٠١٩ و ٢٠٢٠. أظهر تحليل Line x tester اختلافات عاليه المعنويه بين التراكيب الوراثيه المستخدمه فى الدراسه لكل الصفات. كان أفضل تركيب وراثي هو الهجين PR78/IR58025A لمحصول الحبوب (طن/هكتار) مما يشير إلى امكانيه استخدامه في برنامج التربية لتحسين محصول الحبوب. علاوة على ذلك ، وبالنسبة للقدرة العامة على الائتلاف فقد كانت أفضل الآباء على النحو التالي ؛ PR78 و IR58025A لمحصول الحبوب / نبات ؛ PR78 و IR69625Aللمحصول البيولوجى ؛ PR1 و IR58025A لوزن السنبله ؛ يمكن لهذه الطرز الجينية نقل التفوق إلى نسلها في التهجينات الناتجه عنها.بالإضافة إلى ذلك كان الهجين PR2/IR69625Aمن أكثر الهجن الواعدة والتى حصلت على قيم عاليةة المعنوية فى القدرة الخاصة على الائتلاف ويمكن ان تستخدم فى برامج التربية .