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Original article

Estimation of heterosis, heritability and genetic parameters for some agronomic traits of rice using the line × tester method

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ABSTRACT

Twelve F1 hybrids generated from Line × Tester and their seven parents were tested in a randomised full block design with three replications during the 2017 and 2018 growing seasons. The primary goal of this study was to analyze the genetic diversity and relationships of seven rice genotypes and their children from the first generation (F1) by analyzing heterosis, wide and narrow sense heritability, correlation coefficient, and cluster analysis. The best combinations for duration, plant height, and sterility percentages were Al – AHSA-1 × Giza177, Al – AHSA-2 × Giza177, Al – AHSA-2 × Shin2, and BL1 × IET1444. These paternal lines have the potential to be employed in future breeding projects. In contrast, there is a high positive heterosis for the number of tillers per plant, 1000-grain weight, number of full grains per panicle, and grain production per plant. Among the best crosses were Al-AHSA-2 × IET1444, Al-AHSA-1 × Giza177, Al-AHSA-1 × IET1444, and Al-AHSA-2xGiza177. This study concludes as except for panicle weight, all attributes tested had the maximum broad-sense heritability, while the lowest narrow-sense heritability values were noted for sterility percentage (1.76) followed by duration (3.03), panicle length (3.61), and 1000-grain weight (3.62) accordingly.

1. Introduction

Rice (Oryza sativa L.) is a key crop in the world, with more than half of the world's population relying on it as a staple diet. Rice grains, on the other hand, give calories to more than three billion people worldwide (Amirjani, 2011). Rice production is increasing every year to cover the rising demand, which is due to the rapid world population increase (Khush, 2005; Gregory and George, 2011). Increasing yield productivity plays a major role in decreasing the gap between production and consumption. It also uses advances in production technologies for high-yielding and early-maturing varieties (Swain, 2005). Exploring heterosis in self-pollinated crops, particularly rice, is necessary for enhanced yield and yield attributes (Alam et al., 2004). The negative heterosis found to be desirable for plant height and duration, while positive heterosis was desirable in other yield characters (Jelodar, 2010). The use of heterosis will increase the production yield from 15 to 30% higher than inbred varieties (Virmani et al., 1997; Cheng et al., 2007). Knowledge of heterosis, heritability, and genetic components for any crop, on the other hand, will give breeders with the information needed to select optimal breeding strategies for hybrid variety creation programs (Ammaret al., 2014). Information on the genetic diversity of the parents might help lessen exposure to stressors and give raw material for plant breeders. The similarity of the number of quantitative characteristics estimated in people and populations can be used to quantify the quantitative morphological traits estimated in individuals and populations (Dingkhun and Asch, 1999; Bahraman et al., 1999, and El-Malky et al., 2008). The aim of this study is to estimate the heterosis with mild and better parents, estimate the genetic parameters and heritability, and assess the correlation coefficients among the studied characters.

2. Materials and methods

During the 2017 and 2018 seasons, King Faisal University collaborated with the International Rice Research Institute (IRRI) in the Philippines and the Rice Research & Training Center (RRTC) in Sakha, Egypt. Seven rice types (Oryza sativa L.) were employed, including two varieties from the Kingdom of Saudi Arabia, Al-AHSA-1 and Al-AHSA-2, as well as BL1, IRBLTCT2, Giza177, IET

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1444, and Shin2. Four cultivars/lines, Al-AHSA-1, Al-AHSA-2, BL1 and IRBLTCT2, were used as "Lines" in a line × tester mating technique, and three varieties, IET1444, Giza177, and Shin2, were stock in the International Rice Research Institute (IRRI) gene bank in the Philippines. During the 2017 season, a line × tester cross among seven parents was employed to produce twelve crosses. In 2018, parental varieties and F1 first generation seeds were planted in rows 20 × 20 cm apart. In a randomized complete block design, three replicates were used in the experiment (RCBD). The parents and F1 plants were transplanted in 2018, and nine agronomic characteristics were recorded. Sensitivity to rice blast reaction, plant height (cm), duration (day), number of panicle length (cm), tiller/plant, number of panicle weight (g), panicle/plant, 1000-grain weight (g), number of filled grain yield/plant (g), grain/panicle, and sterility percentage were among the agronomic characteristics studied.

2.1. Cluster diagram

The Numerical Taxonomy and Multivariate Analysis system, Version 2.1, was used for the analysis (Rolhf, 2000). An agglomerative hierarchical clustering algorithm with a complete linkage strategy was used to assess the output. To begin, the data was analyzed to generate a matrix of dissimilarity values, and the phenotypic distance between each pair of varieties was calculated as a Euclidean distance. The Euclidean distance matrix was then clustered using the un-weighted pair-group method based on arithmetic average (UPGMA) to generate a dendogram.

2.2. Statistical investigation

The analysis of variance technique (Khan et al., 2019) was used with the "MSTATC" computer software program to accomplish the analysis of variance.

3. Results

The mean square among genotypes was found to be extremely significant in the current study for all of the analyzed traits (Table 1), showing that rice genotypes differed in their genetic potential for such qualities. Parents vs crossings were also found to be highly significant for all traits. For blast, duration, plant height, number of panicles per plant^{-1}, panicle weight, 1000 grain-weight, spikelet fertility percent, and grain yield^{-1}, line variance was extremely significant. For all of the qualities investigated, the interaction of line × tester was likewise extremely significant. For blast reaction, all the genotypes were resistant except the two varieties (Al–AHSA-1and Al–AHSA-2) which were susceptible to blast. Moreover, the crosses BL1 × Shin2, BL1 × IET 1444, Al-AHSA-2 × IET 1444 andAl-AHSA-1 × Shin2 were high yielding combinations (52.47, 52.37, 50.33 and 49.13 gm/plant) respectively.

3.1. Analysis of variance for agronomic traits

There were highly significant differences between genotypes for the traits under examination (Table 2). Agronomic properties were assessed in twelve hybrid combinations, four lines, and three testers. Parental lines and crosses revealed highly significant variances in all of the investigated traits. As parents vs. crosses mean square was displayed, the average heterosis was highly significant in all crosses. Furthermore, the male testers demonstrated highly substantial differences in all agronomic characteristics.

3.2. Estimation of heterosis

Heterosis is expressed as a percentage difference from the F1 mean values and the values of the better and mid-parents. The results revealed a substantial positive heterotic effect relative to either better-parent or mid-parent values for panicle number per plant -1, panicle length, panicle weight, 1000 grain weight, number of filled grains per panicle, and grain yield per plant -1. In contrast, a substantial negative heterotic effect for duration and plant height relative to better-parent and mid-parent values was seen, which could be advantageous in breeding efforts. For overall duration, nine of the twelve hybrid combinations demonstrated negative heterosis relative to the mid-parent, ranging from (-2.99) for the cross Al-AHSA-2 × Giza177 to (-8.70) for Al-AHSA-2 × IET1444. It is worth noting that some of the rice varieties used in these crosses were found to be the finest combiners, while others were among the worst combiners for earliness (Table 3). In terms of plant height, four crossings demonstrated significantly substantial negative heterosis, ranging from (-3.92) for BL1 × IET1444 to (-12.74) for Al-AHSA-2 × Shin2 (Table 4). These crosses could be used in plant height increase breeding efforts. According to the data in (Table 5), six hybrid combinations for panicle length recorded substantial and extremely significant positive estimations of heterosis at mid-parent, ranging from 1.66 to 6.52. The best hybrid combinations, on the other hand, were IRBLTCT2 × Giza177, Al-AHSA-1 × Shin2, and IRBLTCT2 × IET1444. While the number of panicles/plants ranged from 7.02 to 36.73, eight hybrid combinations were highly statistically positive. Furthermore, the most successful crosses were Al-AHSA-2 × Giza177, Al-AHSA-1 × Giza177, Al-AHSA-2 × Shin2, Al-AHSA-1 × IET1444, and Al-AHSA-1 × IET1444 (Table 4). These findings suggest that specific crosses can be utilized to increase the amounts of panicles per plant in rice. In the panicle weight, nine hybrid combinations had highly significant and favorable heterosis estimations when compared to mid and better-parents. Al-AHSA-1 × IET1444, Al-AHSA-2 × IET1444, and Al-AHSA-2 × IET1444 had the highest estimations (Table4). In terms of 1000-grain weight, seven combinations demonstrated a significantly significant positive heterotic value in comparison to the mid-parent and better-parent. Al-AHSA-2 × IET1444, Al-AHSA-1 × IET1444, IRBLTCT2 × IET1444, and Al-AHSA-1 × Giza177 are the hybrid combinations (Table 4). To develop this characteristic, these parent pairings could be employed in a hybrid breeding program. Eight hybrid combinations, on the other hand, demonstrated significantly significant positive heterosis compared to the mid-parent and better-parent in the number of filled grains/panicle, which ranged from 6.22 to 39.66. The best combinations, however, were Al-AHSA-1 × Giza177, Al-AHSA-1 × IET1444, and Al-AHSA-2 × Giza177 (Table 4). In contrast, significant negative heterosis for sterility percent was reported in eight hybrids relative to the-mid parent. (See Table 4). In the same characteristic, however, eight hybrids showed highly substantial positive heterosis relative to the mid-parent. The crosses Al-AHSA-1 × IET1444 (17.75), Al-AHSA-2 × IET1444 (15.53), and Al-AHSA-1 × Giza177 had the highest estimations (12.49). These findings imply that the parents involved in these crosses could be used in hybrid vigor deployment for grain production per plant.

3.3. Genetic variance components for agronomic attribute

Table 4 shows the genetic factors (additive and dominance effects) and heritability estimates for agronomic features (duration, plant height, number of tiller plants, panicle length, and number of panicles per plant-1). Except for panicle weight, the additive genetic variance (12D) was lower than the dominance genetic variance (14H), indicating that the dominant component of genetic

Table 1
Mean performance of parents and their F1 hybrids in terms of agronomic traits.

Genotypes	Blast	Duration (days)	Plant Height (cm)	No. of tiller /plant	Panicle Length (cm)	No. of panicle /plant
Al –AHSA-1 × IET 444	1.67	141.67	119.00	25.33	23.60	22.00
Al –AHSA-1 × Giza177	1.33	133.33	116.67	23.00	19.23	20.00
Al –AHSA-1x Shin2	2.00	132.67	110.33	29.67	23.97	26.67
Al –AHSA-2 × IET1444	1.67	133.00	129.33	22.33	25.07	20.33
Al –AHSA-2 × Giza177	2.00	135.33	121.00	24.67	22.53	22.33
Al –AHSA-2 × Shin2	2.00	131.33	107.33	26.67	20.93	23.67
BL1x IET 1444	1.33	129.67	98.00	27.67	22.70	23.33
BL1x Giza177	2.00	124.67	116.33	23.67	20.43	20.00
BL1x Shin2	1.67	135.00	101.67	29.33	23.23	26.00
IRBLTCT2x IET1444	2.00	131.00	97.33	24.00	24.37	20.67
IRBLTCT2x Giza177	2.00	128.33	111.00	19.00	22.33	18.33
IRBLTCT2x Shin2	2.00	124.33	98.00	28.00	23.77	25.67
Al –AHSA-1	6.67	156.33	144.00	16.00	28.00	14.00
Al –AHSA-2	6.67	154.33	142.00	21.00	28.10	14.00
BL1	2.67	137.00	104.00	24.67	21.77	24.00
IRBLTCT2	2.00	137.00	96.00	20.33	23.50	19.67
IET1444	2.00	137.00	100.00	25.00	22.63	24.00
Giza177	2.00	124.67	99.00	19.00	18.43	18.67
Shin2	2.00	122.33	104.00	26.00	23.57	25.00
LSD 0.05	0.57	2.78	3.74	1.88	1.47	2.28
LSD 0.01	0.75	3.66	4.92	2.47	1.93	3.01

No	Panicle Weight (gm)	1000-grain Weight (gm)	No. of filled grains/panicle	Sterility %	Grain yield/plant (gm)
Al –AHSA-1 x IET 444	3.90	23.83	186.33	24.33	53.07
Al –AHSA-1 x Giza177	4.07	27.30	176.67	14.33	43.37
Al –AHSA-1x Shin2	4.33	27.23	158.67	13.67	49.13
Al –AHSA-2 x IET1444	3.47	24.83	151.67	9.33	50.33
Al –AHSA-2 x Giza177	3.73	22.43	151.67	10.67	41.50
Al –AHSA-2 x Shin2	4.00	27.87	142.33	12.67	44.57
BL1x IET 1444	3.97	24.43	170.00	9.00	52.37
BL1x Giza177	4.10	28.40	148.00	6.67	41.93
BL1x Shin2	4.47	27.67	141.33	14.33	52.47
IRBLTCT2x IET1444	4.38	22.60	161.67	7.00	51.30
IRBLTCT2x Giza177	4.60	28.00	150.00	10.00	47.77
IRBLTCT2x Shin2	4.70	26.63	138.00	14.33	46.30
Al –AHSA-1	2.90	25.00	109.00	51.00	38.87
Al –AHSA-2	2.73	25.33	109.00	51.00	35.87
BL1	4.04	29.51	134.67	12.13	52.40
IRBLTCT2	4.60	26.48	148.33	14.79	50.60
IET1444	3.60	18.55	173.33	11.23	51.27
Giza177	4.71	26.52	144.00	5.25	41.23
Shin2	4.71	28.67	143.00	6.41	50.00
LSD 0.05	0.27	0.98	6.79	5.06	2.71
LSD 0.01	0.35	1.29	8.93	6.66	3.56

Table 2
Variance analysis (ANOVA) and mean square from line × testers for the investigated characters.

S.O.V	d.f	Blast	Duration (days)	Plant height (cm)	No. of tiller /plant	Panicle length (cm)	No. of panicle /plant
Replication	2	0.07	3.53	1.95	5.28	1.09	3.7
Genotypes	18	8.71**	245.72**	618.14**	40.85**	17.98**	39.75**
Parents	6	16.43**	514.05**	1205.86**	40.16**	35.26**	65.41**
Pa. vs Crosses	1	55.82**	592.99**	341.12**	168.42**	14.17**	83.69**
Crosses	11	0.21	67.79**	322.76**	29.63**	8.90**	21.77**
Lines	3	0.25	114.25**	589.52**	18.70**	3.49**	4.62**
Testers	2	0.19	41.69**	427.58**	103.86**	24.30**	91.58**
Lines × Testers	6	0.19	53.25**	154.44**	10.34**	6.48**	7.06**
Error	36	0.14	3.43	6.19	1.56	0.95	2.31

S.O.V	d.f	Panicle weight (gm)	1000-grain weight (gm)	No. of filled grains/panicle	Sterility %	Grain yield/plant (gm)
Replication	2	0.04	0.02	0.65	1.14	0.14
Genotypes	18	1.00**	21.48**	1191.87**	519.22**	83.06**
Parents	6	2.14**	38.16**	1553.11**	1235.21**	140.85**
Pa. vs Crosses	1	0.78**	0.60**	4802.01**	1195.04**	58.16**
Crosses	11	0.40**	14.28**	666.63**	67.24**	53.80**
Lines	3	1.03**	5.01**	1261.81**	111.44**	22.94**
Testers	2	0.60**	38.40**	1496.78**	33.78**	198.73**
Lines × Testers	6	0.01	10.88**	92.33**	56.30**	20.92**
Error	36	0.03	0.42	20.45	11.37	3.24

**, Significant at 0.01 level.

Table 3
Estimates of heterosis for mid-parent and better parent in F_1 hybrids.

Cross	Duration (days)		Plant height (cm)		No. of tiller /plant	
	M.P	B.P	M.P	B.P	M.P	B.P
Al –AHSA-1 × IET 444	−3.41**	3.41*	−2.46	19.00**	23.58**	1.33
Al –AHSA-1 × Giza177	−4.42**	6.95**	−10.60**	−1.96	15.00**	21.05**
Al –AHSA-1x Shin2	2.31	8.45**	6.09**	6.09**	17.11**	14.10**
Al –AHSA-2 × IET1444	−8.70**	−2.92*	6.89**	29.33**	−2.90**	−10.67**
Al –AHSA-2 × Giza177	−2.99*	8.56**	−7.28**	1.68	23.33**	17.46**
Al –AHSA-2 × Shin2	−5.06**	7.36**	−12.74**	3.21	13.48**	2.56**
BL1x IET 1444	−5.35**	−5.35**	−3.92*	−2.00	11.41**	10.67**
BL1x Giza177	−4.71**	0	4.33**	11.86**	8.40**	−4.05**
BL1x Shin2	4.11**	10.35**	−2.24	−2.24	15.79**	12.82**
IRBLTCT2x IET1444	−4.38**	−4.38**	−0.68	1.39	5.88**	−4.00**
IRBLTCT2x Giza177	−1.91	2.94*	3.26*	15.63**	−3.39**	−6.56**
IRBLTCT2x Shin2	−4.11**	1.63	−2.00	2.08	20.86**	7.69**
LSD 0.05	2.41	2.78	3.24	3.74	1.62	1.88
LSD 0.01	3.17	3.66	4.26	4.92	2.14	2.47

*, Significant at 0.05 and **, Significant at 0.01 levels.

Table 4
Estimates of genetic parameters for agronomic traits.

Genetic paramentes	Duration (days)	Plant height (cm)	No. of tiller /plant	Panicle length (cm)	No. of panicle plant
Dominance of genetic variance	16.61	49.42	2.93	1.84	1.58
Additive Genetic variance	0.63	7.26	0.83	0.1	0.63
Genetic variance	17.23	56.68	3.76	1.95	2.22
Environmental variance	3.43	6.19	1.56	0.95	2.31
Phenotypic variance	4.55	7.93	2.31	1.7	2.13
Ratio of GCAvar. /SCAvar.	1.04	1.15	1.28	1.06	1.4
Narrow-sense heritability	3.03	11.55	15.64	3.61	14
Broad-sense heritability	83.38	90.16	70.7	67.14	48.95
Expected Genetic advance	0.28	1.89	0.74	0.13	0.61
Dominance of genetic variance	0.01	3.49	23.96	14.98	5.89
Additive Genetic variance	0.02	0.15	24.77	0.47	1.42
Genetic variance	0.03	3.63	48.74	15.45	7.31
Environmental variance	0.03	0.42	20.45	11.37	3.24
Phenotypic variance	0.03	2.01	8.32	5.18	3.25
Ratio of GCAvar./SCAvar.	1.54	1.04	2.03	1.03	1.24
Narrow-senseheritability	39.69	3.62	35.81	1.76	13.44
Broad-senseheritability	24.04	89.55	70.45	57.61	69.27
Expected Genetic advance	0.17	0.15	6.14	0.19	0.9

Table 5
Estimates of the correlation coefficient for agronomic characters.

Characters	Blast	Duration (says)	Plant height (cm)	No. of tiller /plant	Panicle length (cm)	No. of panicle /plant	Panicle weight (gm)	1000-grain weight (gm)	No. of filled grains / panicle	Sterility %	Grain yield/ plant (gm)
Blas**t**	–										
Duration **(days)**	0.83*	–									
Plant height **(cm)**	0.85*	0.86*	–								
No. of tiller /plant	−0.37	−0.53	−0.53	–							
Panicle length **(cm)**	0.69	0.84	0.86*	−0.3	–						
No. of panicle /plant	−0.61	−0.75*	−0.80*	0.87**	−0.6	–					
Panicle weight **(gm)**	−0.81*	−0.93**	−0.88**	0.34	−0.80*	0.64	–				
1000-grain weight (gm)	0.17	−0.26	−0.06	0.02	−0.13	0.07	0.41	–			
No. of filled grains /panicle	−0.86*	−0.67	−0.87**	0.57	−0.68	0.77*	0.59	−0.42	–		
Sterility %	0.84*	0.94**	0.97**	−0.59	0.90**	−0.85*	−0.90**	−0.13	−0.82*	–	
Grain yield /plant	−0.56	−0.58	−0.80*	0.72*	−0.49	0.91**	0.6	0.05	0.75*	−0.76*	–

variance was dominating in the expression of these traits. The number of panicles/plants, number of full grains/panicles, and sterility percent attributes had the greatest estimated values of environmental variance.

Except for panicle weight and the number of filled grains/panicle, all of the tested traits had high broad-sense heritability values, while all of the studied traits had low to moderate narrow-sense heritability estimates. The sterility percent (1.76) had the lowest estimates of narrow-sense heredity, followed by duration (3.03), panicle length (3.61), and 1000-grain weight (3.62). Furthermore, the ratio of general combining ability (GCA) to specific combining ability (SCA) variances was equal or greater than one for all traits studied, indicating that non-additive gene action predominated over additive gene action for all traits studied. It is useful to be

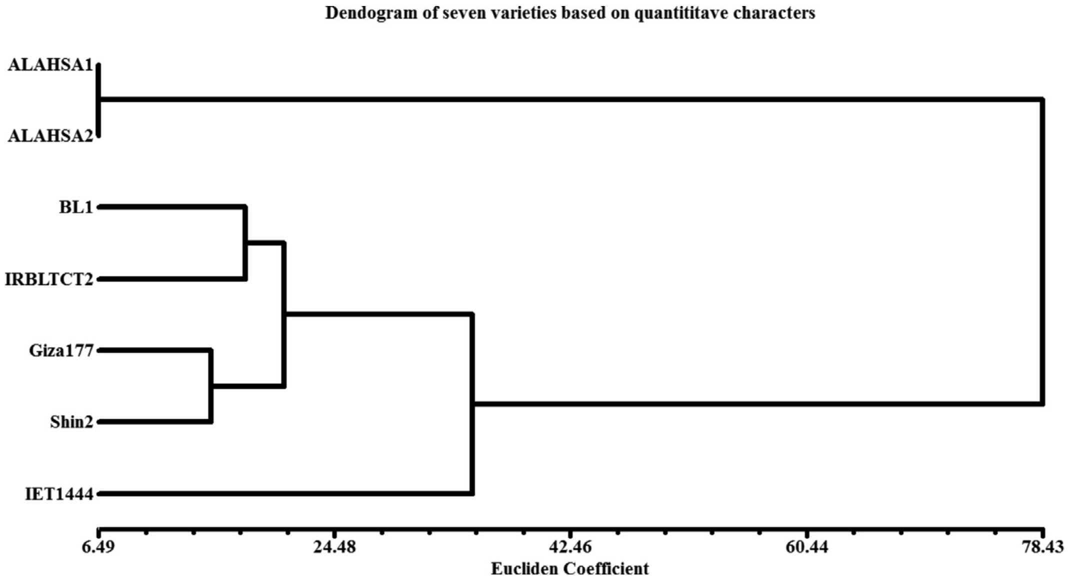

Fig. 1. Cluster diagram for seven kinds defined by nine morphological characteristics.

aware of the genetic progress made by applying selection pressure to a population while developing an effective breeding program. In all of the variables investigated, low estimations of genetic advance (Gs%) expressed as percentages of the mean were perceived (Table 4). Furthermore, the majority of the studied traits had low narrow-sense heritability estimates and low genetic advance, implying that improvement in these traits could be obtained through heterosis breeding or by a single plant selection in later generations following hybridization or intermeeting of selected segregates via recurrent selection.

3.4. Clustering of cultivars according to agronomic characteristics

The dendrogram indicated two groups by employing agronomic features to find clustering tendencies between the genotypes investigated (Fig. 1). The first group consisted of Al-AHSA-1 and Al-AHSA-2, which were similar in terms of blast reaction, duration, plant height, 1000-grain weight, number of filled grains panicle, and sterility percentages. The second group consisted of BL1, IRBLTCT2, IET 444, Giza177, and Shin2. The second group, on the other hand, broke into two subgroups, with the variation IET1444 branching out of the groupings. This cultivar had the fullest grains per panicle, the least in 1000-grain weight, and belonged to the Indica-Japonica type. The second subgroup was divided into two branches, the first of which contained Giza177 and Shin2, which were similar in duration, panicle weight, and the number of filled grains panicle. The second branch, on the other hand, includes the BL1 and IRBLTCT2 variants.

4. Discussion

When heterosis is used for yield improvement in rice, it has an advantage of about 10–15% over the best-inbred varieties. The increased yield benefit of rice hybrids is due to higher spikelet number, increased biomass and to some extent higher grain weight. The heterosis of these yield traits found in the F1 hybrid is owing to the cumulative impact of net-positive heterotic effects after the negative ones are eliminated (Gang Zhou et al., 2012). The combined influence of these components may be sufficient to explain the genetic foundation of heterosis in the hybrid. As a result, the current study used a line × tester mating strategy with four different female parents and three male parents to determine the extent to which heterosis and genetic characteristics improve yield qualities and their relationships with grain production. The qualities considered were the most important in rice yield breeding (Panwar 2005; Fahmi et al., 2017). The current study findings revealed that ANOVA for agronomic traits revealed significant variations among all genotypes for all attributes tested and genotypes. This revealed a significant level of heterogeneity among genotypes for many attributes, as well as a significant amount of heterosis among hybrids. The extremely significant mean squares of lines and testers for all agronomic traits revealed an interaction and surprisingly distinct combining ability impacts, which may be attributed to the enormous genetic variety of lines and testers. Similarly, Hammoud (2004), El-Diasty et al., (2008), Sedeek (2015).

The indicated lines differed significantly for all traits, implying a superior representation and selection for this investigation. Furthermore, it revealed a highly significant line × tester interaction, which could be attributed to the substantial genetic variability among lines and testers (Sunil 2006, and El-Malky and Elamawi 2013.). Simultaneously, the mean performance of yield traits revealed that a separate genetic system was engaged in influencing yield features, emphasizing the need of studying these qualities (Anis et al 2016). However, the best combinations were Al –AHSA-1 × IET 444, Al –AHSA-1 × Giza177, Al-AHSA-2 × IET1444, Al-AHSA-2 × Giza177, Al –AHSA-2 × IET1444, Al –AHSA-2 × Giza177 and IRBLTCT2 × Giza177, which suggest a possible inclusion of these hybrids in high panicle weight in rice breeding programs Latha et al., (2013), Abdel-Moneam, et al., (2016). The genetic component estimates showed that non-additive variance or dominance governed in all traits. Heritability estimates indicated a predominance of tester's influences for these traits (Saidaiah et al., 2010). These results are consistent with those of Sultan et al., 2013. Heterosis is the process through which the performance of an F1 produced by crossing two genetically distinct individuals outperforms that of the parents' mean. Negative heterosis is a favorable trait for the earliness traits because it aids in the development of new early mature rice varieties. The best promising hybrid combinations were Al–AHSA-2 × IET1444, BL1 × IET 1444, Al–AHSA-2 × Shin2, BL1 × Giza177, and Al–AHSA-1 × Giza177. For the number of tiller plant^{-1}, ten out of twelve crosses demonstrated substantial and favorable heterosis effects relative to both mid-parent and better-parent, with the best hybrid combinations being Al-AHSA-1 × IET1444, Al-AHSA-2 × Giza177, IRBLTCT2 × Shin2 and BL1 × Shin2 (Table 4). These findings agreed with those of Tiwari et al. (2011), Latha et al. (2013).

Finally, a thorough understanding of the interrelationships between plant qualities such as earliness and other characters is critical for the breeder when attempting to increase a complicated quantitative character such as earliness for which direct selection is ineffective. As a result, association analysis was performed to establish the direction of selection and the number of characters that demonstrated to be important in enhancing earliness. The correlation coefficient between the qualities was calculated. The relationship between the qualities revealed a substantial positive link between the earliness traits. This suggests that these component features had a significant positive relationship with crucial earliness characteristics. As a result, these four characteristics directly contribute to the character of earliness. Although the number of panicles per plant, spikelet fertility, thousand grain weight, and grain yield did not show a positive significant association, their role in grain yield could not be overlooked because these component traits did show a positive significant association with important yield attributes (Babu et al., 2012, Lakshmi et al., 2014, and Fahmi et al., 2017). As a result, these qualities may be believed to play an indirect role in determining grain yield via other traits. It is critical to separate the observed phenotypic connection into direct and indirect impacts of the component variables on grain yield. The number of panicles per plant was related to the number of days to heading, the number of days to maturity, and the length of panicle initiation. This shows that these features make direct contributions to yield components.

Estimate the genetic distance among cultivars through quantitative characters under the studied genotypes is diagrammatically illustrated in Fig. 1. The genotypes are classified to three different origins four from IRRI, one from Egypt and two from Saudi Arabia. The results showed that the two Saudi Arabia varieties were in group one, reflected that the classified of these genotypes according to the genetic diversity of their geographical origin and pedigree. The rice breeder can use the parents between clusters as parents for future hybridization rather than within cluster for a successful breeding progarmme selection of genetically diverse parents as an important pre-requisite so as to obtain better and desirable recombinants. These results concur with those of documeneted studies (Fahmi et al 2012; Tejaswini et al 2016).

5. Conclusion

In this study, it is shown that it is possible to improve quantitative traits genetically by gaining a better understanding of the genetic variability and the degree to which desired features can be inherited. Breeders will be able to create more suited cultivars faster if they have access to information on heterosis and genetic characteristics such as heritability, genetic progress, and the effect of environment on the expression of these traits.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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