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Research Article

Studies of Genetic Parameters and Cluster analysis of some Quantitative Characters through Diallel analysis of rice (*Oryza Sativa* L.)

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Abstract

General combining ability (GCA), specific combining ability, (SCA) and genetic analysis were used in this study for F, generation obtained from half diall cross among six rice parents namely; Toride1, Fuknishiki Giza172, Sakha101, IR83526-38-3-3-1, and Sakha105. The results showed that both (GCA) and (SCA) variances were found to be highly significant for all nine characters studied in F, generations. This would indicate the importance of both additive and non-additive genetic variance in determining the performance of these nine characters. The best cross combinations for earliness were (IR 83526-38-3-3-1 x Sakha105), (Giza172 x Fuknishiki), (IR 83526-38-3-3-1 x Toride1), (IR 83526-38-3-3-1 x Fuknishiki), and (Sakha101 x Fuknishiki) for earliness and grain yield per plant, it could be used in breeding program. Analysis by components of variation showed that additive (D) genetic variances were significant for all characters in F1 generation except number of panicle/plant, grain yield/plant, and 1000-grain weight. The two dominant components H1 and H2 were found to be highly significant for all traits studied in the F₁ generations. Also, the magnitudes of these components were found to be larger than those of the additive genetic variance. These results indicated that the dominance genetic variation had greater role in the inheritance of these traits, F value was positive in F, for all traits except for number of panicles/plant and grain yield/plant. This indicates more dominant alleles present in the parental lines than recessive alleles in the F, generation. Dominance variation overall heterozygous loci (h²) was significant in the 1000-grain weight and panicle weight in the F_1 generation. The estimates of average degree of dominance (H1/D)^{1/2} were found to be higher than unity for all traits under investigation in the F_1 , indicating the presence of over dominance for these traits at F_1 generations. Clustering varieties, based on similarity of quantitative characters, produced two broad groups. The first one included IR83526-38-3-3-1 alone in one branch due to the highest value in plant height, the number of field grains per panicle and this variety from Indica types. While, the second group was divided into two sub-groups, the first sub-group included Giza172 and Sakha 101, which were similar in the number of tiller per plant and number of panicles per plant. The second sub group including Fuknishiki in one branch, while, Toride1 and Sakha 105 varieties were very near due to similarity in grain yield/plant, number of field grains per panicle and 1000-grain weight.

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Keywords

Combining ability; additive variance; Genetic analysis; Quantitative characters; Cluster analysis; Rice (Oryza Sativa L).

Introduction

Rice (Oryza sativa L.) is one of the most staple food and good source for all human stages and more than one-half of the world's population is dependent on rice [1]. In Egypt, rice is the second major field crop after wheat. Egyptian rice production at 5.8 million tons rough rice, which produced about 4.0 million tons milled from about 0.8 million hectares planted by rice [2]. Increasing the yield is the main target for plant breeding programs via selecting the superior genotypes, which will transfer their desirable characteristics to next generations. Genetic improvement for rice was studied worldwide through diallel cross analysis, which helps to identify the best parents and their combinations for further selection and suggests the breeder that the appropriate stage for selection as some traits are fully expressed after generations become uniform [3]. Thus, the combining ability and heterosis analysis, which is derived from a diallel mating design, is usually the appropriate method for choosing the parents and progenies with high general combining ability (GCA) and high specific combining ability (SCA), respectively. The GCA and SCA can further determine the heritability and also provide information on additive and dominance variance [4-7]. In breeding programs, information on combining ability assess to know the nature of gene action, desirable parents and important quantitative traits may be found [8].

Consequently, the main objective of this research is to study combining ability (general and specific), study of the heterosis and inheritance of some quantitative characters in F_1 generations in rice and study the genetic relationships among individuals and populations. This was measured by similarity of number of quantitative characters as reported by Zhang et al., Dingkhun et al., and El-Malky [9-11]. Analysis was conducted using the Numerical Taxonomy and Multivariate Analysis system, Version 2.1 [12]. The output was analyzed using an agglomerative hierarchical clustering method with complete linkage strategy. Firstly, a matrix of dissimilarity values was produced and the phenotypic distance between each pair of lines was estimated as Euclidean distance. Secondly, cluster analysis was then conducted on the Euclidean distance matrix with un-weighed pairgroup method based on arithmetic average (UPGMA) to develop a dendogram.

Materials and Methods

Breeding materials and crossing program

Six rice varieties viz, Toride1, Fuknishiki (Japanese Deferential Varieties), Giza172, Sakha101, IR83526-38-3-3-1, and Sakha105 were crossed in all possible combinations excluding reciprocals in 2014-2015 seasons. The hybridization technique using the hot water method for emasculation was utilized [13,14]. The six parents and 15 F1 were evaluated at the Experimental Farm of Rice Research and Training Center, Sakha, Kafr El-Sheikh Governorate, Egypt, during the rice growing season of 2015. Parents and hybrids were grown in a RCBD with three replication. Each plot contained three rows and each

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row contained 25 plants. The growing space was 20x20 cm. Seeds were sown at 30 days and transplanted to the permanent field. Parentage and country released under investigation are given in Table 1.

Also, averages of two years of nine quantitative characters under study were used for constructing genetic relationships among rice varieties.

Experimental design and analysis of field experiments data

Combining ability effects for F₁ were analyzed according to Griffing et al. [15] using Method 2 and Model one fixed model. The data obtained were also subjected to analysis as described by Hayman et al. [16] to obtain more information about the genetic behavior of the traits under study. All statistical parameters and analysis of variance were computed by IRRISTAT and MSTAT-Cpc software. Genetic relationships among individuals and populations were measured by similarity of number of quantitative characters as reported by Zhang et al., Dingkhun et al. and El-Malky [9,10,11]. Clustering analysis were conducted using the Numerical Taxonomy and Multivariate Analysis system, Version 2.1 [12]. The output was analyzed using an agglomerative hierarchical clustering method with complete linkage strategy. Firstly, a matrix of dissimilarity values was produced and the phenotypic distance between each pair of lines was estimated as Euclidean distance. Secondly, cluster analysis was then conducted on the Euclidean distance matrix with un-weighed pairgroup method based on arithmetic average (UPGMA) to develop a dendrogram.

Results

Analysis of variance

Table 2 presents the mean square values among F, generations. The data showed that both general combining ability (GCA) and specific combining ability (SCA) variance were highly significant for all nine characters studied in F₁ generation. This would indicate the importance of both additive and non-additive genetic variance in determining the performance of these nine characters. The GCA/SCA ratio in F, were found to be greater than unity for heading date, plant height, number of tillers/ plant, number of panicles/plant, grain yield/plant and number of field grains/panicle. Indicating that, additive and additive x additive types of gene action were of greater importance in the inheritance of these characters. The results concluded that selection procedures based on the accumulation of additive effects would be successful in improving these traits. These results were in agreements with those obtained by Abd El-Aty et al., Aidy et al, Anandakumar et al, Asfaliza et al. and Sedeek [4,17-20].

Variety	Parentage	Country of release
Toride1	TKM1/NORIN 8*5	Japan
Fuknishiki	KINKIUS45/KINKIUS11// ZENTH/3/KINKIUS45/ KINKIUS11/4HATSUNISHIKI	Japan
Giza 172	Nahda / Kinmaza	Egypt
Sakha 101	Calrose 76/Giza 172//Gz 242	Egypt
IR83526-38-3-3-1	Exotic	IRRI
Sakha 105	Giza177 / Suwwon349	Egypt

Table 1: Parentage, country of release and main characters of six parental lines.

Mean performance of parents and their F₁ generation

Conspicuously, Table 3 shows that the shortest plants that are favorite for rice breeders under study were observed in Sakha 101 followed by Sakha 105 and Toride1. While, the tallest ones were exhibited in Fuknishiki, IR83526-38-3-3-1 and Giza 172 rice varieties. Sakha 105 followed by Fuknishiki and Toride1. Were the earlier rice cultivars, otherwise, Giza 172, IR83526-38-3-3-1 and Sakha 101 were the latest rice cultivars compared with other rice cultivars. Quite a number of tillers/plant and number of panicles/plant were detected for Giza 172 and Sakha 101. In addition, Sakha 101 and IR83526-38-3-3-1 were found to be the rice cultivar with heavy grain and panicle and high number of filled grains with superior grain yield (58.39 and 55.43 g /plant), respectively. Sakha 105 and Giza 172 has a longest panicle (25.40 and 24.66 cm), respectively. The parental mean values of grain yield were ranged between 44.33 - 58.39 g/plant for Fuknishiki and Sakha 101, respectively.

In addition, the F1 mean values of plant height were ranged between 106.40 for (Giza 172 X Sakha 101) and 141.50 cm for (Fuknishiki X Giza 172) rice crosses. Plant height of six rice crosses were ranged between 106.40-115.00 cm. This agrees with the target of rice breeders for selected ideal plant height for resistance. This was done for lodging and suitable for mechanical harvesting. Moreover, Fuknishiki X IR83526-38-3-3-1 and Giza 172 X Sakha 101 rice crosses were earlier in heading than 125 days. This was suitable for selecting early maturing rice genotypes. About seven rice crosses were found to have longer panicle than the longest panicle parent, their estimated values of panicle length ranged between 23.80 cm for Sakha 101 X IR83526-38-3-3-1 and 26.50 cm for IR83526-38-3-3-1 X Sakha103. In addition, ten crosses had heavier 1000-grain than the heaviest 1000-grain parent. For number of panicles/ plant, two crosses, Toride1 X IR83526-38-3-3-1 and Fuknishiki X Sakha 101 were superior than the highest parent (Toride1 and Sakha 101, respectively) in number of panicles/ plant. Many number of filled grains/panicle were exhibited for Fuknishiki X Sakha 101 and Sakha 101 X IR83526-38-3-3-1, which included Sakha 101 as a female or male parent, it was a good donor for improving these traits. Furthermore, the highest estimated values of panicle weight were showed for eight rice crosses, Toride1 X Fuknishiki, Toride1 X Sakha 101, Toride1 X IR83526-38-3-3-1, Toride1 X Sakha 105, Fuknishiki X Sakha 101, Fuknishiki X IR83526-38-3-3-1, Fuknishiki X Sakha 105 and IR83526-38-3-3-1 X Sakha103. Grain yield/plant was found to be higher than the highest parent for thirteen rice crosses, indicating that over-dominance played a remarkable role in the inheritance of these traits in these mentioned crosses. Moreover, grain yield/plant was controlled by partial dominance in Fuknishiki X Giza 172 and Giza 172 X Sakha 101. Their F, mean values located between the values of their parental lines.

General combining ability effects

Estimates of general combining ability effects for F_1 generation are presented in Table 4. Highly significant negative values of GCA for heading date and plant height would be of interest from the plant breeder point of view. However, the positive value of GCA effects would be useful for the other traits and could be used as a good donor for transferring these characters to their offspring.

As for heading date, the three rice varieties Toride1, Fuknishiki and Sakha103 showed highly significant negative estimates of GCA. GCA effects in F1 generation proved to be

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Table 2: Mean squares of general and specific combining ability and GCA/SCA for nine character.

S.O.V.	d.f	Grain yield/plant	1000-grain weight	Panicle weight	No. of filled grains/panicle	Panicle length	
Replication	2	14.21	1.55	0.1	9.38	0.085	
Genotypes	20	136.43**	8.57**	0.6904**	1409.08**	5.735**	
Error	40	7	1.1	0.04	17.83	0.2354	
GCA	5	100.98**	1.22**	0.09**	612.01**	1.4352**	
SCA	15	26.98**	3.4021**	0.28**	422.25**	2.0751**	
Error	40	2.33	0.37	0.01	5.94	0.08	
GCA/SCA		3.74	0.36	0.31	1.45	0.69	
S.O.V.	d.f	Heading date (days)	Plant height (cm)	No. of tillers/plant	No. of panicles/plant		
Replication	2	1.63	1.28	1.97	0.55		
Genotypes	20	395.73**	474.30**	22.13**	13.24**		
Error	40	0.63	4.77	1.53	0.73		
GCA	5	341.23**	358.56**	14.41**	5.36**		
SCA	15	62.14**	91.28**	5.03**	4.10**		
Error	40	0.21	1.59	0.51	0.25		
GCA/SCA		5.49	3.93	2.86	1.31		

Table 3: Mean performance of parent and crosses for the studied traits.

Genotypes	Durations (day)	Plant height (cm)	No. of Tillers/ plant	Panicle Length (cm)	No. of Panicles/ plant	1000-grain weight (g)	Panicle Weight (g)	No. of filled grains/ panicle	Grain yield/ plant (g)
Toride1	133.55	113.20	20.66	22.90	19.75	23.73	2.26	159.00	53.52
Fuknishiki	121.77	138.80	21.33	22.93	20.20	23.96	2.20	126.33	44.33
Giza 172	155.29	133.73	27.00	24.66	21.66	26.06	2.51	141.66	54.44
Sakha 101	144.61	103.47	27.00	21.33	23.20	23.06	3.35	166.00	58.39
IR83526-38-3-3-1	155.30	135.82	22.00	22.13	23.02	23.13	3.39	187.66	55.43
Sakha 105	120.95	109.43	22.33	25.40	20.69	22.46	2.43	161.66	52.47
Toride1 X Fuknishiki	135.00	113.70	23.40	25.30	19.60	27.40	4.91	155.90	67.78
Toride1 X Giza 172	143.00	135.00	21.80	23.20	19.60	24.10	2.99	163.00	55.90
Toride1 X Sakha 101	146.30	123.70	24.20	22.90	23.60	24.40	3.50	145.50	75.80
Toride1 X IR83526-38-3-3-1	136.80	125.70	26.30	24.00	24.00	26.70	3.88	165.00	60.30
Toride1 X Sakha 105	138.10	112.90	23.50	25.80	21.50	27.20	3.80	186.70	62.30
Fuknishiki X Giza 172	136.00	141.50	23.00	24.10	22.20	24.20	2.90	166.00	53.20
Fuknishiki X Sakha 101	133.60	129.70	29.00	25.50	27.80	26.00	3.80	219.00	65.56
Fuknishiki X IR83526-38-3-3-1	120.00	115.00	22.40	25.60	20.90	27.30	3.80	185.00	89.60
Fuknishiki X Sakha 105	135.90	131.00	24.20	23.50	23.20	22.40	4.00	142.00	91.30
Giza 172 X Sakha 101	123.10	106.40	19.50	22.20	17.50	25.30	3.10	98.60	55.90
Giza 172 X IR83526-38-3-3-1	144.30	107.00	26.80	23.00	22.70	25.00	3.10	173.40	61.00
Giza 172 X Sakha105	145.70	131.40	23.20	21.20	22.30	26.40	3.30	132.00	72.20
Sakha 101 X IR83526-38-3-3-1	141.00	132.04	25.00	23.80	23.00	24.20	3.20	198.20	68.40
Sakha 101 X Sakha 105	149.00	110.70	25.80	24.20	21.70	28.00	3.10	175.00	72.22
IR83526-38-3-3-1 X Sakha103	145.00	121.50	23.50	26.50	22.00	26.40	4.43	175.00	63.00
LCD 0.05 0.01	0.67 1.05	1.86 2.93	1.05 1.65	0.41 0.65	0.87 1.34	0.88 1.40	0.14 0.23	3.58 5.64	2.24 3.53

good general combiners for developing early genotypes. The rice varieties Sakha101, Toride1 and Sakha105 exhibited highly significant desirable negative estimates of GCA effects for plant height in F_1 generation there by proving to be good general combiners for developing short stiff genotypes.

Concerning number of tillers per plant and number of panicles per plant, Sakha101 proved to be good general combiners in both the F_1 generation. Desirable highly significant GCA effects were detected by Giza172 and Sakha101 for grain yield per plant, by Fuknishiki for 1000-grain weight, by IR83526-38-3-1 for panicle weight and Sakha105 for number of filled grains per panicle. Sakha105 for panicle length in F_1 proved to be good general combiners in this respect.

Specific combining ability effects

Estimates of specific combining ability effects from F_1 generation are shown in Table 5. SCA for heading date was negative and highly significant in seven crosses in F_1 generation. The best cross combinations for earliness were (IR 83526-38-3-3-1 x Sakha105), (Giza172 x Fuknishiki), (IR 83526-38-3-3-1 x Toride1) and (IR 83526-38-3-3-1 x Fuknishiki). This indicated that one of these combinations could be useful for selecting early maturing lines. Concerning plant height, seven crosses were highly significant and negative in F_1 and the best crosses were (Giza172 x Sakha101) and (Fuknishiki x Sakha105) in F_1 generation. While, for number of tillers per plant the best cross

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was (Sakha101 x Toride1), which gave highly significant positive estimates of SCA effects.

As for grain yield per plant, six crosses showed highly significant positive SCA effects in F, and ranged between 1.887 and 8.369. The best cross was (Sakha101 x Fuknishiki). As for 1000-grain weight, the crosses (IR 83526-38-3-3-1 x Sakha105) and (Giza172 x Sakha101) showed highly significant positive SCA effects. Concerning panicle weight, the best hybrids were (Sakha101 x Toride1), (Sakha101 x Fuknishiki), (Sakha101 x Sakha105) and (IR 83526-38-3-3-1 x Fuknishiki) where highly significant positive SCA effects were detected. While in number of filled grains per panicle, the best crosses were (Giza172 x Fuknishiki), (Giza172 x Sakha105) and (Sakha101 x Toride1). This gave highly significant positive SCA effects than in panicle length the best hybrids was (Giza172 x Fuknishiki), (Sakha101 x Fuknishiki) and (IR 83526-38-3-3-1 x Toride1). From the previous data it has been observed that the best genotypes showed desirable SCA effects. This could be obtained from crossing good by good, good by low and low by low general combiners. Similar conclusions were drawn by [4,6,11,19,21,22].

Estimates of mid and better parent heterosis

A large number of crosses exhibited high estimates of heterosis in a desirable direction for different traits under study. The estimates of mid-parent and better parent heterosis for different traits are presented in Table 6. A greater magnitude of heterosis when it measured as a deviation from mid-parent and better parent was observed in Fuknishiki X Sakha 105 (88.64 and 74.00%), Fuknishiki X IR83526-38-3-3-1 (79.63 and 61.65%), Giza 172 X Sakha105 (35.07 and 32.62 %), Toride1 X Fuknishiki (38.54 and 26.64 %), Toride1 X Sakha 101 (35.47 and 29.82 %) and Sakha 101 X. Sakha 105 (30.29 and 23.69 %) rice crosses for grain yield /plant, respectively. The availability of sufficient hybrid vigor in several crosses in respect of grain yield suggests that a hybrid breeding program. The crosses Fuknishiki X IR83526-38-3-3-1, Giza 172 X Sakha 101, Giza 172 X IR83526-38-3-3-1 and Sakha 101 X IR83526-38-3-3-1 exhibited highest negative heterosis for duration when it measured as a deviation from midparent and better parent. Appearance of significant and negative heterosis for duration indicated the possibility of exploiting heterosis for earliness. For plant height, two crosses, Fuknishiki X IR83526-38-3-3-1 and Giza 172 X IR83526-38-3-3-1 recorded significant mid and better parent heterosis in a desirable negative direction. Approximately, high estimated values of mid and better parent heterosis were reported in Toride1 X Fuknishiki, Toride1 X IR83526-38-3-3-1, Toride1 X Sakha 105, Fuknishiki X Sakha 101, Fuknishiki X IR83526-38-3-3-1, Fuknishiki X Sakha 105 and IR83526-38-3-3-1 X Sakha105 exhibited high significant and positive estimates of heterosis for number of tillers/plant. Often, among the studied crosses including Sakha 105 as a male parent exhibited highly significant positive estimates of better parent heterosis for number of tillers/plant. Moreover, highly significant and positive estimates of mid and better parent heterosis were observed for panicle length in about eight crosses, the highest estimated values were observed in Fuknishiki X Sakha 101 (15.23% and 11.21%), Fuknishiki X IR83526-38-3-3-1 (13.63% and 11.64%) and Toride1 X Fuknishiki (10.41% and 10.34%), respectively.

In addition, high estimated values of mid and better parent heterosis were observed in Fuknishiki X Sakha 101 (28.11% and 19.83%) followed by Fuknishiki X Sakha 105 (13.48% and 12.13%), Toride1 X IR83526-38-3-3-1 (12.23% and 4.26%), and Giza 172 X Sakha105 (5.31% and 2.95%), respectively. Exhibited high significant and positive estimates of heterosis for a number of panicles/plant. From 15 crosses, ten crosses recorded significant positive mid and better parent heterosis for 1000-grain weight.

All studied crosses recorded significant positive either mid or better heterosis for panicle weight, while, the other remaining crosses recorded highly significant magnitude of mid and better heterosis in negative direction for such trait. The crosses Toride1 X Sakha 105, Fuknishiki X Sakha 101, Sakha 101 X IR83526-38-3-3-1 and Sakha 101 X Sakha 105 exhibited highly positive heterosis for number of filled grains/panicle when it measured as a deviation from mid-parent and better parent. Similar results were reported by several scientists like Chitra, Sedeek, Hassan, Saravanan, Senguttuvel, Shanthala, EL-Abd, Ganapath, Amudha and Ammar [5,20,22,23-29]

Table 4: Estimate of GCA effects for the parental lines at F ₁ generation for nine characteristic states and the parental lines at F ₁ generation for nine characteristic states and the parental lines at F ₁ generation for nine characteristic states and the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at F ₁ generation for nine characteristic states at the parental lines at the parental	cters in rice.
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Paranta	Heading data (daya)	Plant baight (om)	No. of tilloro/plant	No. of popialog/plant		
Farents	Heading date (days)	Flant neight (cm)	No. of tillers/plant	No. of particles/plant		
Toride1	-2.64**	-3.66**	0.01	-0.16		
Fuknishiki	-9.674**	3.60**	-1.07**	-1.07**		
Giza 172	5.27**	3.88**	1.18**	0.16		
Sakha 101	6.62**	-7.20**	2.01**	1.32**		
IR83526-38-3-3-1	4.35**	9.60**	-0.82**	0.32**		
Sakha 105	-4.29**	-6.22**	-1.32**	-0.56**		
L.S.D. at 0.05	0.148	0.407	0.318	0.16		
at 0.01	0.229	0.631	0.492	0.247		
Parents	Grain yield/plant	1000-grain weight	Panicle weight	No. of filled grains/ panicle	Panicle length	
Toride1	3.16**	0.42**	-0.07**	-2.72**	0.28**	
Fuknishiki	-5.32**	0.31**	-0.09**	-2.31**	0.46**	
Giza 172	2.70*	0.15	-0.04*	-10.56**	-0.15**	
Sakha 101	3.21**	-0.60**	0.08**	-5.51**	-0.53**	
IR83526-38-3-3-1	-2.14**	-0.31**	0.17**	12.19**	-0.42**	
Sakha 105	-1.61**	0.03	-0.06**	8.90**	0.35**	
L.S.D. at 0.05	0.493	0.195	0.036	0.787	0.09	
at 0.01	0.764	0.302	0.057	1.219	0.14	

Analysis by components of variation

The estimated genetic components of variation for all characters studied in F_1 generations are shown in Table 7. Additive (D) genetic variances were significant for all characters in F_1 generation except number of panicle/plant, grain yield/plant and 1000-grain weight. The two dominance components H1 and H2 were found to be highly significant for all traits studied. Also, the magnitudes of these components were found to be larger than those of the additive genetic variance. These results indicated that the dominance genetic variation had greater role in the inheritance of these traits. Similar results for different traits were reported by Abd El-Aty, Saravanan, Senguttuvel, Shanthala and EL-Abd [4,23,24,25,26].

A positive F value indicates an excess of dominant genes, while negative value indicates an excess of recessive genes. In this study F value was positive in F_1 for all traits except number of panicles/plant and grain yield/plant. This indicated that more dominant alleles are present in the parental lines than recessive alleles in the F_1 generation.

These results indicated that the excess of dominant genes controlling these traits. Dominance variance over all heterozygous loci (h^2) was significant in the 1000-grain weight and panicle weight in the F_1 generation. In conclusion, significant values of (h^2) indicating the prevalent of dominance effect over all loci in all crosses, while insignificant values indicating the absence of the dominance effect over all loci in the heterozygote's. This could be due to the presence of a considerable amount of canceling dominance effects in the parental varieties. The results agreed with Asfaliza and Ganapathy [19,27].

The estimates of average degree of dominance $(H1/D)^{1/2}$ were found to be greater than unity for all traits under investigation in the F₁, indicating the presence of over dominance in the inheritance of these traits at F₁.

The estimates of H2/4H1 ratio did not reach the ratio 0.25 for all characters and ranged from 0.17 to 0.23 in F_1 , indicating

that genes having positive and negative effects were not equally distributed in the parents.

The proportion of dominant and recessive alleles in the parents (KD/KR) was greater than unity in all characters except number of tillers/plant, grain yield/plant and 1000-grain weight, indicating that the proportions of dominant alleles were greater for these characters in F, generation [19,26] found similar results.

The environmental component (E) was insignificant indicating that these characters were affected by the environmental components with different degrees.

The correlation coefficients (r) between the parental lines (Yr) and the parental order of dominance (Wr+Vr) for all the characters studied according to Hayman are given in Table 6. The results showed that correlation coefficients were highly significant and positive for heading date and number of filled grains/panicle in F_1 , indicating that the decreaser genes were dominant over the increaser ones. On the other hand, number of panicle/plant was highly significant and negative, this means that the dominance genes were associated with high mean expression. According to Hayman [16], if the correlation between parental mean values and Wr+Vr is small, it means that the genes with positive and negative effects in the parental lines could be in equal proportions.

Heritability in narrow sense value is an indicator of the efficiency of selection in identifying the best genotypes. Heritability in both broad and narrow senses in F_1 generation is shown in Table 6. Heritability estimates in broad sense were found to be high for all characters. While, heritability in narrow sense were found to be lower than those of broad sense, indicating the importance of non-additive genetic variance in the inheritance of these characters. Therefore, it could be concluded from Hayman [16] analysis and combining ability analysis that selection procedures which are known to be effective in shifting gene frequency when both additive and non-additive genetic variation are involved would be successful in improving the most traits under examination. These results agreed with those obtained by Asfaliza, EL-Abd, Rather, El-Hissewy and Main [19,26,30-33].

 Table 5: Specific combining ability (SCA) of 15 crosses for nine agronomic characters.

Crosses	Heading	Plant height (cm)	No. of tillers /plant	No. of panicles	Grain yield	1000-grain weight (g)	Panicle weight	No.of filled grains	Panicle
	uale (uays)			/plant	/plant (g)		(g)	/panicle	length (cm)
Toride1 X Fuknishiki	-0.97**	-5.58**	-1.74	-2.24**	8.37**	2.20**	0.67**	-19.42**	0.72**
Toride1 X Giza 172	8.21**	-0.77	-3.07**	-0.88**	5.85**	-0.87**	-0.11*	-19.17**	-0.68**
Toride1 X Sakha 101	-1.10**	12.28**	1.42	0.38	-0.26	2.09**	0.49**	37.79**	-0.52**
Toride1 X IR83526-38-3-3-1	-10.93**	-8.07**	1.06	1.68**	-2.77**	0.69**	-0.53**	-13.25**	0.90**
Toride1 X Sakha 105	-0.33	6.80**	1.11	3.83**	1.73**	-0.91**	0.61**	-19.96**	0.79**
Fuknishiki X Giza 172	-12.24**	11.62**	12.47**	1.05**	-4.44**	2.14**	-0.36**	5.42**	2.15**
Fuknishiki X Sakha 101	2.478**	-6.56**	10.33**	-1.34**	3.15**	-2.87**	0.49**	-11.29**	0.37**
Fuknishiki X IR83526-38-3-3-1	-6.47**	-6.70**	0.91	1.51**	-10.09**	0.36	0.70**	-31.33**	-0.88**
Fuknishiki X Sakha 105	6.59**	-10.29**	-5.51**	-0.75**	0.38	0.49	-0.33**	10.29**	-0.52**
Giza 172 X Sakha 101	-3.83**	-14.76**	-12.40**	1.89**	2.66**	1.32**	0.19**	-8.71**	.87**
Giza 172 X IR83526-38-3-3-1	2.28**	5.64**	5.14**	0.3	-0.72	-1.24**	-0.03	-16.08**	1.86**
Giza 172 X Sakha105	7.32**	-7.97**	4.59**	1.14**	1.89**	0.12	-0.16**	7.88**	-0.25
Sakha 101 X IR83526-38-3-3-1	8.00**	13.58**	-6.07**	1.58**	3.68**	-1.45**	-0.47**	11.21**	0.98**
Sakha 101 X Sakha 105	4.42**	5.40**	5.95**	-0.73**	-5.85**	1.35**	0.53**	-8.83**	-0.63**
IR83526-38-3-3-1 X Sakha103	-13.25**	7.10**	2.66**	-4.18**	-2.23**	3.15**	0.17**	17.79**	-2.91**
L.S.D. at 0.05	0.407	1.118	1.986	0.439	1.354	0.536	0.1	2.161	0.248
at 0.01	0.459	1.261	2.24	0.495	1.528	0.604	0.113	2.438	0.279

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Ganatypas	Duration	s (day)	Plant hei	ght (cm)	No. of Tille	ers/ plant	Panicle Le	ength (cm)			
Genotypes	M.P	B.P	M.P	B.P	M.P	B.P	M.P	B.P			
Toride1 X Fuknishiki	5.75**	10.86**	-9.76**	0.44	11.46**	9.70**	10.41**	10.34**			
Toride1 X Giza 172	-0.98**	7.08**	9.34**	19.26**	-8.52**	-19.26**	-2.44**	-5.92**			
Toride1 X Sakha 101	5.19**	9.55**	14.18**	19.55**	1.55**	-10.37**	3.55**	0	0		
Toride1 X IR83526-38-3-3-1	-5.28**	2.43**	0.96	11.04**	23.30**	19.55**	6.60**	4.80**			
Toride1 X Sakha 105	8.53**	14.18**	1.42*	3.17**	9.33**	5.24**	6.83**	1.57**			
Fuknishiki X Giza 172	-12.10**	11.69**	1.86*	5.81**	-11.73**	-14.81**	-1.28**	-2.27**			
Fuknishiki X Sakha 101	0.31	9.72**	7.07**	25.35**	20.01**	7.41**	15.23**	11.21**			
Fuknishiki X IR83526-38-3-3-1	-13.38**	-1.45**	-16.25**	-15.33**	3.39**	1.82**	13.63**	11.64**			
Fuknishiki X Sakha 105	11.98**	12.36**	5.55**	19.71**	10.86**	8.37**	-2.75**	-7.48**			
Giza 172 X Sakha 101	-17.91**	-14.87**	-10.29**	2.83*	-27.78**	-27.78**	-3.46**	-9.98**			
Giza 172 X IR83526-38-3-3-1	-7.08**	-7.08**	-20.61**	-19.99**	9.39**	-0.74	-1.69**	-6.73**			
Giza 172 X Sakha105	5.49**	20.46**	8.08**	20.08**	-5.94**	-14.07**	-15.30**	-16.54**			
Sakha 101 X IR83526-38-3-3-1	-5.97**	-2.50**	10.36**	27.61**	2.04**	-7.41**	9.53**	7.55**			
Sakha 101 X Sakha 105	12.22**	23.19**	3.99**	6.99**	4.60**	-4.44**	3.57**	-4.72**			
IR83526-38-3-3-1 X Sakha103	4.98**	19.88**	-0.92	11.03**	6.02**	5.24**	11.51**	4.33**	4.33**		
LCD 0.05	0.47	0.67	1.3	1.86	0.74	1.05	0.29	0.41	0.41		
0.01	0.74	1.05	2.05	2.93	1.17	1.65	0.46	0.65	0.65		
Genotypes	No. of Pa Plant	lo. of Panicles/ 10 lant (g		1000-grain weight (g)		Panicle Weight (g)		no. of filled grains/ panicle			
	M.P	B.P	M.P	B.P	M.P	B.P	M.P	B.P	M.P	B.P	
Toride1 X Fuknishiki	-1.88**	-2.97**	14.91**	14.36**	120.18**	117.26**	9.28**	-1.95	38.54**	26.64**	
Toride1 X Giza 172	-5.34**	-9.51**	-3.19**	-7.52**	25.37**	19.12**	8.43**	2.52	3.56**	2.68*	
Toride1 X Sakha 101	9.90**	1.72**	4.30**	2.82**	24.78**	4.48**	-10.46**	-12.35**	35.47**	29.82**	
Toride1 X IR83526-38-3-3-1	12.23**	4.26**	13.96**	12.52**	37.35**	14.45**	-4.81**	-12.08**	10.69**	8.79**	
Toride1 X Sakha 105	6.33**	3.91**	17.77**	14.62**	62.05**	56.38**	16.45**	15.49**	17.56**	16.41**	
Fuknishiki X Giza 172	-3.49**	2.49**	-3.24**	-7.14**	23.14**	15.54**	-5.72**	17.18**	-10.24**	-2.28*	
Fuknishiki X Sakha 101	28.11**	19.83**	10.59**	8.51**	36.94**	13.43**	49.83**	31.93**	27.65**	12.28**	
Fuknishiki X IR83526-38-3-3-1	-3.29**	-9.21**	15.95**	13.94**	35.96**	12.09**	17.84**	-1.42	79.63**	61.65**	
Fuknishiki X Sakha 105	13.48**	12.13**	-3.49**	-6.51**	72.79**	64.61**	-1.39	-12.16**	88.64**	74.00**	
Giza 172 X Sakha 101	-21.98**	-24.57**	3.01**	-2.92**	5.80**	-7.46**	-35.90**	-40.60**	-0.91	-4.26**	
Giza 172 X IR83526-38-3-3-1	1.61**	-1.39**	1.65**	-4.07**	5.08**	-8.55**	5.31**	-7.60**	11.04**	10.05**	
Giza 172 X Sakha103	5.31**	2.95**	8.82**	1.30*	33.60**	31.47**	-12.96**	-20.48**	35.07**	32.62**	
Sakha 101 X IR83526-38-3-3-1	-0.48	-0.86	4.78**	4.63**	-5.04**	-5.60**	12.09**	5.62*	20.19**	17.14**	
Sakha 101 X Sakha 105	-1.12**	-6.47**	23.02**	21.42**	7.27**	-7.46**	6.82**	5.42*	30.29**	23.69**	
IR83526-38-3-3-1 X Sakha103	0.66*	-4.43**	15.81**	14.14**	52.23**	30.68**	0.19**	-6.75**	16.77**	13.66**	
LCD 0.05	51	0.87	0.36	0.88	0.09	0.14	2.53	3.58	1.59	2.24	
0.01	0.8	1.34	0.99	1.4	0.14	0.23	3.99	5.64	2.51	3.53	

Table 6: Estimates of heterosis as a deviation from mid-parents (MP) and better-parents (BP) for all traits in the studied rice crosses.

Estimates of phenotypic correlation coefficients

The phenotypic correlation coefficients among all possible pairs of grain yield component traits are presented in Table 8. Lucidly, grain yield was positively and strongly correlated with each of 1000-grain weight (0.26) number of panicles/plant (0.26), 1000-grain weight (0.55) and number of filled grains/panicles (0.57). This result indicated that these traits were found to be the principle yield components. Therefore, any selection based on these traits will bring the desired improvement in grain yield. Panicle Length showed significant either positive correlation with 1000-grain weight (0.45), Panicle Weight (0.52) and number of filled grains/panicle (0.55). Among yield related traits, Durations was significantly and positively associated with number of tillers/ plant (0.56). However, a highly significant and positive estimate of phenotypic correlation coefficient (0.574) was recorded between number of tillers/plant and each of panicle length (0.44), number of panicles/plant (0.74) and number of filled grains/panicle (0.45). Present findings coincide with the results of Hassan, Ganapathy, Deng, Patil and Satyanarayana [22,27,34-36]. However, the current results do not coincide with the findings of Chauhan [30], they reported that grain yield per plant was positively correlated with plant height. The difference in results may be attributed to the difference in genetic material and environmental conditions of the experiment.

Clustering of the varieties based on agronomic characters

The characters used for this purpose in the present study were the same agronomical quantitative characters (Table 9 and 10), which were studied in the previous two analyses. Normality was checked for all traits, which indicated that all traits had good approximations of normal distributions [3,38].

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Source of variance	Heading date (days)	Plant height (cm)	No. of tillers/plant	No. of panicles/plant			
H,	271.37 ± 57.04**	388.40 ± 85.41**	20.88 ± 4.92**	16.39 ± 5.13**			
H ₂	218.88 ± 50.95**	334.32 ± 76.30**	16.06 ± 4.40**	14.72 ± 4.59**			
h ₂	16.74 ± 34.29	0.171 ± 51.35	2.30 ± 2.96	1.45 ± 3.08	1.45 ± 3.08		
(F) Gene distribution	37.46 ± 54.89	117.17 ± 82.19	0.30 ± 4.74	-0.26 ± 4.94			
(E) Environmental effects	0.226 ± 8.493	1.535 ± 12.716	0.518 ± 0.733	0.241 ± 0.765	0.241 ± 0.765		
(H1/D) ^{1/2}	1.266	1.282	2.149	3.356			
H2/4H ₁	0.2016	0.2151	0.1922	0.2245			
KD/KR	1.191	1.479	1.0314	0.947	0.947		
r	0.776**	0.348	0.355	0.156	0.156		
H.ns	62.62	50.41	49.93	30.12	30.12		
H.bs	99.84	99.1	94.27	95.69			
Source of variance	Grain yield/plant	1000-grain weight	Panicle weight	No.of filled grains/panicle	Panicle length		
(D) Additive effect	21.82 ± 14.09	1.35 ± 0.94	0.22 ± 0.11*	1198.0 ± 415.79**	2.642 ± 1.20**		
H,	118.01 ± 35.77*	11.90 ± 2.38**	1.11 ± 0.28**	3825.62 ± 1055.54**	9.30 ± 3.04**		
H ₂	86.28 ± 31.96*	11.34 ± 2.13**	0.87 ± 0.25**	3268.18 ± 942.94**	6.63 ± 2.72**		
h ₂	-1.09 ± 21.51	6.29 ± 1.43**	0.51 ± 0.17**	2191.55 ± 634.66**	0.73 ± 1.83		
(F) Gene distribution	-13.20 ± 34.43	-0.18 ± 2.29	0.42 ± 0.27	548.95 ± 1015.79	4.60 ± 2.93		
(E) Environmental effects	2.447 ± 5.326	0.372 ± -0.355	1.368 ± 4.237	65.937 ± 157.157	7.558 ± 0.454		
(H1/D) ^{1/2}	2.325	29.676	2.223	1.786	1.876		
H2/4H ₁	0.1827	0.2382	0.1959	0.237	0.1782		
KD/KR	0.769	0.623	2.492	1.294	2.735		
r	0.342	0.0184	0.398	0.349	0.388		
H.ns	58.15	10.58	71.11	30.31	16.84		
H.bs	95.73	89.61	94.54	95.27	96.37		

 Table 8: Phenotypic correlation coefficient among all possible pairs of all studied traits.

No.	Traits	1	2	3	4	5	6	7	8
1	Durations (day)								
2	Plant height (cm)	-0.15							
3	No. of tillers/plant	0.56**	0.03						
4	Panicle Length (cm)	0.13	-0.06	0.44**					
5	No. of panicles/plant	0.27	0.27	0.74**	0.14				
6	1000-grain weight (g)	0.01	-0.20	0.20	0.45**	0.04			
7	Panicle weight (g)	-0.06	0.02	0.23	0.52**	0.22	0.56**		
8	No. of filled grains/panicle	-0.13	0.25	0.45**	0.55**	0.45**	0.19	0.19	
9	Grain yield/ plant (g)	-0.03	-0.09	0.15	0.15	0.26*	0.26*	0.55**	0.57**

Clustering varieties, based on similarity of quantitative characters, produced two large groups (Figure 1). The first one included IR83526-38-3-3-1 alone in one branch due to the highest value in plant height, number of field grains per panicle and this variety from Indica-Japonica types. While, the second group was divided into two sub-groups, the first sub-group included Giza172 and Sakha 101, which were similar in number of tellers per plant and number of panicles per plant. On the other hand, Giza 172 was used as a parent to produced Sakha 101. The second sub group including Fuknishiki in one branch, while, Toride1 and Sakha 105 varieties were very near due to were similar in grain yield/ plant, number of field grains per panicle and 1000-grain weight (Table 9).

Discussion

The information on combining ability assess to know the nature of gene action, desirable parents and important quantitative traits may be found Borgohain [8] and useful in breeding programs. In this study GCA and SCA were highly significant for all traits this would both additive and non-additive are important. Also, GCA/SCA ratio were greater than unity indicating that, additive and additive X additive were played in the inheritance of these characters. It could be concluded that the selection will be useful in the late generation. However, the genotype with negative GCA values is preferred for duration and plant height traits it considered as a good combiner for

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Parents	Heading date (days)	Plant height (cm)	No. of tillers	No. of panicles	Grain yield	1000-grain weight	Panicle weight	No. of filled grains	Panicle length
			/plant	/plant (g)	/plant (g)	(g)	(g)	/panicle	(cm)
Toride1	133.55	113.2	20.66	19.75	53.52	23.73	2.26	159	22.9
Fuknishiki	121.77	138.8	21.33	20.2	44.33	23.96	2.2	166	22.93
Giza 172	155.29	133.73	27	23.02	54.44	26.06	3.35	141.66	24.66
Sakha 101	144.61	103.47	27	23.2	58.39	23.06	2.51	126.33	21.33
IR83526-38-3-3-1	155.61	135.82	22.33	21.66	55.43	23.13	3.39	187.66	22.13
Sakha 105	120.95	109.43	22	20.69	52.47	22.46	2.43	161.66	25.4

Table 9: Six Parental rice cultivars and mean of different traits (Average of two years).

Table 10: Similarity matrix for six variants based on nine morphological characters.

Varieties	Toride1	Fuknishiki	Giza 172	Sakha 101	IR83526-38- 3-3-1	Sakha 105		
Toride1	0							
Fuknishiki	3.0467	0						
Giza 172	3.5005	4.3553	0					
Sakha 101	3.6921	5.9882	3.5712	0				
IR83526-38-3-3-1	4.1354	3.9803	4.6297	6.9952	0			
Sakha 105	1.4408	3.1133	4.6908	4.365	4.9064	0		



heading date and plant height traits. The results of general combining ability GCA effects among parents for short duration character showed that the rice genotypes Toride1, Fuknishiki and Sakha105 were the best combiners for duration rice varieties. The varieties Toride1, Sakha101 and Sakha105 were the best combiners for plant height or short stature. While, the positive value was desirable for yield trait and the best combiners were Toride1, Sakha101 and Giza172. SCA revealed that the crosses such as (IR 83526-38-3-3-1 x Sakha105), (Giza172 x Fuknishiki), (IR 83526-38-3-3-1 x Toride1) and (IR 83526-38-3-3-1 x Fuknishiki) these crosses could be utilized in rice breeding programs to develop new early duration rice varieties. Finally, best genotypes which showed desirable SCA effects could be obtained from crossing good by good, good by low and low by low general combiners. Similar conclusion was drawn by Abd El-Aty et al, Salgotra, - El-Malky et al., Asfaliza et al., Surek et al. and Hassan et al. [4,6,11,19,21,22]. The negative value for heterosis is desirable for the heading date and plant height characters it is useful for developing new early mature rice varieties and short stature which is suitable for mechanical harvesting. However, in this investigation, there were some different results which may be that due to genetic diversity among rice genotypes under this study. Heritability estimates at both broad and narrow senses in F_1 were found to be high for all characters. While, heritability in narrow sense were found to be lower than those of broad sense, indicating the importance of non-additive genetic variance in the inheritance of these characters. Therefore, it could be concluded from Hayman et al. [16] analysis and combining ability analysis that selection procedures which are known to be effective in shifting gene frequency when both additive and non-additive genetic variation are involved would be successful in improving the most traits

under examination. These results agreed with those obtained by Asfaliza, EL-Abd, Rather, El-Hissewy and Main [19,26,31,32,33]. The phenotypic correlation coefficients among all possible pairs of grain yield component traits. The grain yield trait was positively and strongly correlated with each of No. of tillers/plant, Panicle length (cm), No. of panicles/plant, 1000-grain weight, Panicle weight (g), and number of filled grains/panicles. This result indicated that these traits were found to be the principle yield components. This positive correlation might indicate the presence of loci, controlling these traits, on the same linkage group and consequently it might be used for early marker assisted selection [11].

Conclusion

The best cross combinations for earliness were (IR 83526-38-3-3-1 x Sakha105), (Giza172 x Fuknishiki), (IR 83526-38-3-3-1 x Toride1) and (IR 83526-38-3-3-1 x Fuknishiki), which indicated that one of these combinations could be useful for selecting early maturing lines and (Sakha101 x Fuknishiki) for grain yield per plant, it could be used in breeding program. Heritability in narrow sense was found to be lower than those of broad sense, indicating the importance of non-additive genetic variance in the inheritance of these characters. The phenotypic correlation coefficient for grain yield was positively and strongly correlated with each of 1000-grain weight number of panicles/plant, 1000-grain weight and number of filled grains/panicles. This result indicated that these traits were found to be the principle yield components and it could be on the same chromosome. Clustering varieties, based on similarity of quantitative characters, produced two large groups. The first one included IR83526-38-3-3-1 alone in one branch due to the highest value in plant height, number of field grains per panicle and this variety belonged to Indica-Japonica types, while the second group includes all the Japonica varieties.

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