

Original article

Genetic Variability, Heritability and Genetic Advance for Yield and Associated Traits in F₂ Rice Population

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Article citation: Hefena AG, Sultan MS, Abdel-Moneam MA, Hammoud SA, Barutçular C, EL-Sabagh AE. **Genetic Variability, Heritability and Genetic Advance for Yield and Associated Traits in F₂ Rice Population.** *Journal of*

Agricultural Biotechnology 2016; 01(02):49-58. DOI: <https://doi.org/10.20936/JAB/160202>

ABSTRACT: This study was conducted at Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt in 2010, 2011 and 2012 growing seasons to estimate genetic variances, genotypic coefficients of variability, heritability (in broad sense) and the expected genetic advance upon selection of all studied characters of F₂ hybrid populations. The four characteristics viz. number of days to heading, plant height; number of tillers plant⁻¹ and flag leaf area had a wide range of variability. The mean square variances were highly significant for all studied traits among this population. Heritability percentage (H²b %) was detected higher for all traits, indicated that the dominance and additive genetic variance play an important role in the inheritance of these traits. The rice genotypes showed a wide range of variation for grain yield plant⁻¹, number of panicles plant⁻¹, 1000-grain weight, number of filled grains panicle⁻¹ and panicle weight. The mean squares for all traits were highly significant. Thus, selection for these traits among these genotypes would be effective in all cases.

KEYWORDS F₂ Population, Genotypic Phenotypic Variability, Heritability, Genetic variation, Genetic advance, Rice.

INTRODUCTION

Rice is the world's most important food crop. Rice (*Oryza sativa* L.) is the staple food for 65% of the global population and forms the cheapest source of food, energy and protein (Padmaja et al. 2008). Worldwide, it is grown on an area of 166.1 million hectares with yield of 745.2 million tonnes (Anon., 2013). Rice crop plays a significant role in Egypt, as strategic crop for sustaining the food self-sufficiency and for increasing the export, the total rice production in Egypt reached 7.1 million tons with a national average of 9.9 tonnes/hectare in 2012 growing season. This average ranked the first

among the rice producing countries in the world (RRTC, 2013).

Genetic variability is important for breeding and in selecting desirable traits. Thus, character association of component traits with yield and among themselves is very important. The relationship between rice yield and yield component traits has been studied widely at a phenotypic level (Ogunbayo et al. 2014). Genetic variability existence for various desirable maturity and yield related traits in segregating generations is of utmost importance in crop breeding programs

to develop desirable recombinant inbred lines and cultivars (Shinwari et al. 2013). Estimation of Heritability for the desired traits takes into account the extent of transmission of the traits from the parents to progeny and serves as a analytical role in crop breeding programs (Khan & Naqvi, 2011).

The development of high yielding cultivars with wide adaptability is the ultimate aim of plant breeders. Therefore, by exploiting the good adaptation and stability of yield and its components in rice genotypes, it would be possible to develop/identify high yielding and well adapted varieties (Ogunbayo, 2011). A systematic evaluation and characterization of germplasm a line not only helps in identification of superior and genetically divergent germplasm lines but also provides information on the utility of the genetic resources. Characterization of accessions provides the information on morphological and agronomic aspects of the material that is essential for the gene bank management (Padmaja et al. 2008). Estimates of genotypic coefficient of variation (GCV, phenotypic coefficient of variation (PCV), heritability and genetic advance will play an important role in exploiting future research projections of rice improvement (Paikhomba et al. 2014). The present study was, therefore, carried out to estimates of genetic variances, genotypic coefficients of variability, heritability (in broad sense) and the expected genetic advance upon selection of all studied characters of F₂ hybrid populations.

MATERIALS AND METHODS

This study was conducted at the Research Farm, Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt during the three successive rice growing seasons in 2010, 2011 and 2012. The study was involved six rice genotypes viz. two commercial varieties (Giza 178 and Sakha 103) as lines and four American/Egyptian bold grains genotypes as testers (Table 1). The six genotypes were sown in the summer growing season (2010) in three sowing dates. A line × tester design was conducted among the six parents to produce eight crosses. The hybridization technique of Jodon (1938) and modified by Butany (1961), was utilized. The parental varieties and the resulting crosses were evaluated in a Randomized Complete Block Design (RCBD) with three replications in 2011 growing season. Each replication had 25 individual plants from each genotype.

In 2012 growing season, eight F₂ generations were evaluated to estimate the phenotypic and genotypic variance (PV and GV), genetic coefficient of variability (GCV %), phenotypic coefficient of

variability (PCV %), heritability in broad sense (H²b %) and genetic advance under selection at 5% plant (GS %) according to the formula suggested by Burton (1952). All agronomic practices such as fertilization, irrigation, and weed and pests control were done as per recommendation with rice crop during the both seasons. The data on number of days to heading, plant height (cm), number of tillers plant⁻¹, flag leaf area (cm²), grain yield plant⁻¹ (g), number of panicles plant⁻¹, 1000-grain weight (g), number of filled grains panicle⁻¹, panicle weight (g), spikelets fertility (%), panicle length (cm), number of primary branches panicle⁻¹, and panicle density were recorded as per schedule.

RESULTS AND DISCUSSION

Mean performance and genetic parameters in the F₂ generation

Estimates of mean performance, phenotypic, genotypic coefficients of variability, heritability in broad sense and the genetic advance for two main parts i.e. earliness and vegetative characters, yield and its components are presented in Tables 1 to 13.

Earliness and vegetative characters

Number of days to heading showed a wide range of variation among eight crosses (Table 1). The phenotypic coefficients variability (PCV %) were higher than genotypic coefficients of variability (GCV%) indicated that the more effective environmental inheritance this trait. The highest GCV (%) was found (5.44 and 5.72%) at the crosses, No. 3 and 5, respectively. These results indicated that the genetic variance played an important role in the inheritance for these crosses. On the other hand, the lowest GCV (%) was found (3.29%) at cross, No. 6. The cross No. 5 showed high heritability (98.83%) in broad sense. Burton (1952) suggested that genotypic coefficient of variation together with heritability estimates give a clear picture about that extent of genetic advance to be expected from selection. For this trait, high genetic gain associated with high heritability estimates was found for the cross No. 5. Consequently, selection for these cross should be effective and satisfactory for successful breeding purposes. The highest and moderate estimates of heritability were obtained from most of the crosses, the heritability percentage values ranged between 96.35 (for cross No. 6) to 98.83% (for cross No. 5). While the genetic advance percentages were over 100, except for the cross No. 6 (67.82%) and 8 (71.29%). Selection for this trait in these populations will be effective, but probably of less success than in the former previously other crosses. Low genetic gain was associated with low heritability values for reminds

crosses. Similar results were obtained by Keshava al.(2016) and Anis et al. (2016 b,c). et al. (2011); Sharma et al. (2014), Gautam et

Table 1. Number of days to heading for all the studied crosses in the F₂ generation.

No	Crosses	No. of days to heading (day)							
		Mean	V F ₂	VE	GCV (%)	PCV (%)	h ² _b (%)	Gs	Gs (%)
1	Giza178xSKC23819-189-1-1-1-3-1-2-4-2	96.4	24.24	0.60	5.05	5.11	97.53	100.2	103.95
2	Giza178xSKC23819-192-2-1-2-2-4-2-1-2	96.9	23.69	0.63	4.96	5.02	97.36	98.94	102.13
3	Giza178xSKC23819-192-2-1-2-3-1-1-1-2	100.0	30.29	0.70	5.44	5.51	97.70	102.1	112.11
4	Giza178xSKC23819-192-2-1-2-4-5-3-2-1	97.0	24.21	0.63	5.00	5.07	97.42	100.0	103.09
5	Sakha103xSKC23819-189-1-1-1-3-1-2-4-2	99.4	32.75	0.38	5.72	5.76	98.83	100.2	117.90
6	Sakha103xSKC23819-192-2-1-2-2-4-2-1-2	100.0	11.25	0.41	3.29	3.35	96.35	67.82	67.82
7	Sakha103xSKC23819-192-2-1-2-3-1-1-1-2	96.9	22.99	0.48	4.90	4.95	97.90	97.74	100.84
8	Sakha103xSKC23819-192-2-1-2-4-5-3-2-1	96.0	11.46	0.41	3.46	3.52	96.42	68.47	71.29

VE: Environmental variance; **PCV%:** Phenotypic coefficient of variability; **GCV%:** Genetic coefficient of variability; **H²_b:** Broad sense heritability; **Gs:** the expected genetic advance and **Gs%:** the expected genetic advance percentage.

Yield contributing traits

For plant height, the highest GCV (%) was found in the crosses No. 7 and 6 with values of 4.67 and 5.06%, respectively, while, the lowest value (3.65%) was gn the cross No. 4 (Table 2). However, the PCV (%) was higher than the GCV (%) in all crosses but, the most portion of PCV was contributed more by the genotypic component than by environmental one. Heritability in broad sense and genetic advance under selection were compacted and the obtained results are illustrated in Table 2. High heritability estimates were detected for all the studied crosses and highest values (93.78 and 93.90%) from the cross No. 5 and No. 8, respectively. Genetic advance under

selection showed the possible gene from selection as present increase in the F₃ over F₂ generation when the most desirable (5%) of the F₂ plants are selected for all crosses. The crosses, No. 2 and 1 gave the highest values (111.97% and 115.69%), respectively. Similar results were found by Fahliani et al. (2010); Vanisree et al. (2013), Thirumala et al. (2014) and Anis et al. (2016b).

Concerning to number of tillers plant⁻¹, all the eight crosses showed a wide range of variation (Table 3). The values of PCV was more than the GCV (%), indicated that PCV was more affected by environmental effects. The cross No. 1 and 2 gave the highest values for GCV% with the values of 29.90 and 34.82%, respectively (Table 3).

Table 2. Plant height for all the studied crosses in the F₂ generation.

No	Crosses	Plant height (cm)							
		Mean	V F ₂	VE	GCV (%)	PCV (%)	h ² _b (%)	Gs	Gs (%)
1	Giza178xSKC23819-189-1-1-1-3-1-2-4-2	120.03	30.79	0.73	4.57	4.62	92.43	96.38	115.69
2	Giza178xSKC23819-192-2-1-2-2-4-2-1-2	124.53	28.91	0.62	4.27	4.32	92.18	89.91	111.97
3	Giza178xSKC23819-192-2-1-2-3-1-1-1-2	122.90	28.75	0.67	4.31	4.36	92.37	90.93	111.76
4	Giza178xSKC23819-192-2-1-2-4-5-3-2-1	123.80	21.13	0.73	3.65	3.71	93.60	77.85	96.38
5	Sakha103xSKC23819-189-1-1-1-3-1-2-4-2	106.23	21.98	0.80	4.33	4.41	93.78	92.61	98.38

6	Sakha103xSKC23819-192-2-1-2-2-4-2-1-2	92.60	22.66	0.68	5.06	5.14	93.11	107.54	99.58
7	Sakha103xSKC23819-192-2-1-2-3-1-1-1-2	106.07	25.24	0.73	4.67	4.74	92.99	99.02	105.02
8	Sakha103xSKC23819-192-2-1-2-4-5-3-2-1	100.23	21.32	0.80	4.52	4.61	93.90	96.74	96.96

The heritability and genetic advance under selection were compacted. High heritability estimates were found for all crosses and the values ranged between 92.07% for cross No. 2 and 95.95% for cross No. 4. Genetic advance under selection (GS %) was found high for most studied crosses and ranged from 71.10 (for cross, No. 4) to

110.89% (for cross, No. 6). The differences of both heritability and genetic advance were found for all crosses as contained the presence of both additive and non-additive genetic variance for the inheritance of this trait. This result is in agreement with Essa et al. (2011), Mirarab et al.(2011) and Aniset al. (2016a,b).

Table 3. Number of tiller plant⁻¹ for all the studied crosses in the F₂ generation.

No	Crosses	No. of tillers plant ⁻¹							
		Mean	V F ₂	VE	GCV %	PCV %	h ² _b %	Gs	Gs %
1	Giza178xSKC23819-189-1-1-1-3-1-2-4-2	15.53	22.26	0.68	29.90	30.37	93.17	16.08	103.49
2	Giza178xSKC23819-192-2-1-2-2-4-2-1-2	17.87	39.50	0.80	34.82	35.18	92.07	15.00	83.96
3	Giza178xSKC23819-192-2-1-2-3-1-1-1-2	17.17	24.14	0.68	28.22	28.62	92.91	13.92	81.09
4	Giza178xSKC23819-192-2-1-2-4-5-3-2-1	17.60	14.25	0.80	20.84	21.45	95.95	12.51	71.10
5	Sakha103xSKC23819-189-1-1-1-3-1-2-4-2	16.93	15.65	0.57	22.94	23.36	93.76	16.93	99.95
6	Sakha103xSKC23819-192-2-1-2-2-4-2-1-2	16.93	16.00	0.68	23.11	23.62	94.46	18.78	110.89
7	Sakha103xSKC23819-192-2-1-2-3-1-1-1-2	16.13	15.84	0.57	24.23	24.67	93.71	13.87	85.96
8	Sakha103xSKC23819-192-2-1-2-4-5-3-2-1	17.60	15.01	0.68	21.50	22.01	94.77	15.01	85.30

Eight crosses showed a wide range of variation in flag leaf area (cm²), and mean squares for all studied crosses in F₂ generation were highly significant (Table 4). The GCV ranged from 2.06% for the cross No. 8 to 6.22% for the cross No. 3. High heritability estimates were detected in all crosses under study, which ranged from 34.09% for the cross No. 8 to 89.03% for the cross, No. 3, indicated that the presence of both additive and

non-additive genetic variance in the inheritance of most crosses. Genetic advance under selection (GS %) was found high for most studied crosses and ranged from 42.49 (cross, No. 8) to 108.04% (cross, No. 3). Similar results were previously obtained by Kiran et al. (2012),Gautam et al. (2016) and Anis et al. (2016a).

Table 4. Flag leaf area for all the studied crosses in the F₂ generation.

Crosses	Flag leaf area (cm ²)								
	Mean	V F ₂	VE	GCV%	PCV %	h ² _b %	Gs	Gs %	
1	Giza178xSKC23819-189-1-1-1-3-1-2-4-2	44.66	4.18	0.80	4.11	4.58	80.77	37.83	84.71
2	Giza178xSKC23819-192-2-1-2-2-4-2-1-2	41.27	3.35	0.52	4.08	4.43	84.59	34.68	84.02
3	Giza178xSKC23819-192-2-1-2-3-1-1-1-2	36.35	5.73	0.63	6.22	6.59	89.03	46.53	108.04
4	Giza178xSKC23819-192-2-1-2-4-5-3-2-1	35.72	1.49	0.50	2.79	3.42	66.37	20.51	57.42

5	Sakha103xSKC23819-189-1-1-1-3-1-2-4-2	29.79	2.59	0.83	4.44	5.40	67.74	27.26	91.52
6	Sakha103xSKC23819-192-2-1-2-2-4-2-1-2	30.10	2.31	0.55	4.41	5.05	76.27	27.32	90.78
7	Sakha103xSKC23819-192-2-1-2-3-1-1-1-2	28.52	1.50	0.66	3.21	4.29	56.00	18.87	66.17
8	Sakha103xSKC23819-192-2-1-2-4-5-3-2-1	25.46	0.81	0.53	2.06	3.53	34.09	10.82	42.49

The mean square of number of panicles plant⁻¹ was highly different for all crosses indicating over all differences among these populations (Table 5). The GCV for the eight studied crosses ranged from 21.30% (cross, No. 4) to 29.86% (cross, No. 2). The highest values (25.28 and 27.70%) were recorded from the cross No. 7 and 3, respectively. However, the phenotypic coefficients of variability (PCV) was higher than the genotypic one (GCV %) in all the studied crosses, but the most portion of

PCV was attributed by the genetic components. The highest heritability (95.80%) was observed at cross, No. 7 and the lowest (92.40%) at cross No. 2. The high estimated values of heritability indicated the presence of both additive and non-additive genetic variance. The GS (%) was found high and varied from 91.53% (cross, No. 2) to 107.91% (cross, No. 5). This phenomenon is in agreement with other researchers in rice (Vanisree et al., 2013 and Thirumala et al., 2014).

Table 5. Number of panicle plant⁻¹ for all the studied crosses in the F₂ generation.

No	Crosses	No. of panicles plant ⁻¹							
		Mean	V F ₂	VE	GCV%	PCV%	h ² _b %	Gs	Gs %
1	Giza178xSKC23819-189-1-1-1-3-1-2-4-2	16.07	15.77	0.57	24.72	25.16	93.59	15.41	95.91
2	Giza178xSKC23819-192-2-1-2-2-4-2-1-2	17.87	28.47	0.68	29.86	30.22	92.40	16.35	91.53
3	Giza178xSKC23819-192-2-1-2-3-1-1-1-2	16.77	21.58	0.82	27.70	28.22	93.79	16.78	100.07
4	Giza178xSKC23819-192-2-1-2-4-5-3-2-1	16.93	13.01	0.57	21.30	21.76	94.35	16.05	94.77
5	Sakha103xSKC23819-189-1-1-1-3-1-2-4-2	16.43	15.23	0.68	23.74	24.27	94.49	17.73	107.91
6	Sakha103xSKC23819-192-2-1-2-2-4-2-1-2	16.57	14.76	0.80	23.19	23.81	95.42	15.89	95.91
7	Sakha103xSKC23819-192-2-1-2-3-1-1-1-2	15.87	16.08	0.93	25.28	26.00	95.80	16.63	104.82
8	Sakha103xSKC23819-192-2-1-2-4-5-3-2-1	17.17	14.91	0.68	22.49	23.00	94.58	16.21	94.42

A wide range of variation for 1000-grain weight (g) was recorded for all the crosses and the highest mean values (34.73 and 35.91g) were for cross No. 7 and 8, respectively; while the lowest was at cross No. 4 with value of 28.86 g (Table 6). High heritability estimates were detected more than 60% for most of the crosses. The cross No. 1, 6 and 2 recorded the highest values (90.92, 90.96 and

94.62%), respectively, while the lowest value was 62.15% for cross, No. 7. On the other hand, genetic advance under selection gave the highest values for most crosses, and the values ranged between 57.99% for cross No. 8 and 113.23% for cross, No. 5. Similar results were previously reported by Keshava et al. (2011), Sharma et al. (2014) and Gautam et al. (2016).

Table 6. 1000-grain weight for all the studied crosses in the F₂ generation.

No	Crosses	1000-grain weight (g)							
		Mean	V F ₂	VE	GCV%	PCV%	h ² _b %	Gs	Gs %
1	Giza178xSKC23819-189-1-1-1-3-1-2-4-2	30.79	2.76	0.25	5.15	5.40	90.92	32.66	96.07
2	Giza178xSKC23819-192-2-1-2-2-4-2-1-2	30.53	3.56	0.19	6.01	6.18	94.62	37.79	103.77
3	Giza178xSKC23819-192-2-1-2-3-1-1-1-2	31.26	1.83	0.52	3.67	4.33	71.85	23.63	75.61
4	Giza178xSKC23819-192-2-1-2-4-5-3-2-1	28.86	2.67	0.37	5.24	5.66	85.95	31.18	98.02
5	Sakha103xSKC23819-189-1-1-1-3-1-2-4-2	30.34	4.13	0.39	6.37	6.70	90.49	39.82	113.23

6	Sakha103xSKC23819-192-2-1-2-2-4-2-1-2	32.50	3.69	0.33	5.64	5.91	90.96	37.73	96.11
7	Sakha103xSKC23819-192-2-1-2-3-1-1-1-2	34.73	1.74	0.66	2.99	3.80	62.15	21.41	61.64
8	Sakha103xSKC23819-192-2-1-2-4-5-3-2-1	35.91	1.54	0.52	2.81	3.45	66.43	20.82	57.99

Number of filled grains panicle⁻¹ showed a wide variation of mean squares for all crosses studied (Table 7). The PCV was higher than the GCV (%) and the GCV values ranged from 2.90% for the cross, No. 4 to 3.99% in the cross, No. 5. The h²b (%) were more than 96% for all crosses which

signified the importance of additive and non-additive genetic variance in the inheritance. The genetic advance under selection was varied from 98.50% (cross No. 1) to 107.91% (cross No. 4). These results are in agreement with Fahliani et al. (2010) and Vanisree et al. (2013).

Table 7. Number of filled grains panicle⁻¹ for all the studied crosses in the F₂ generation.

No	Crosses	No. of filled grains panicle ⁻¹							
		Mean	V F ₂	VE	GCV%	PCV%	h ² _b %	Gs	Gs %
1	Giza178xSKC23819-189-1-1-1-3-1-2-4-2	149.55	34.03	0.80	3.55	3.60	97.25	79.24	98.50
2	Giza178xSKC23819-192-2-1-2-2-4-2-1-2	149.75	35.83	0.68	3.67	3.71	97.79	81.43	102.94
3	Giza178xSKC23819-192-2-1-2-3-1-1-1-2	134.95	39.10	0.88	3.94	4.00	96.97	94.00	106.85
4	Giza178xSKC23819-192-2-1-2-4-5-3-2-1	17dx2.35	39.61	0.68	2.90	2.94	97.34	74.22	107.91
5	Sakha103xSKC23819-189-1-1-1-3-1-2-4-2	132.05	38.42	0.63	3.99	4.04	97.78	95.62	106.26
6	Sakha103xSKC23819-192-2-1-2-2-4-2-1-2	134.70	37.48	0.51	3.86	3.89	98.13	92.75	104.94
7	Sakha103xSKC23819-192-2-1-2-3-1-1-1-2	144.75	35.72	0.71	3.39	3.44	97.12	83.83	101.34
8	Sakha103xSKC23819-192-2-1-2-4-5-3-2-1	144.50	35.63	0.51	3.47	3.50	98.00	84.24	101.73

The maximum mean values of panicle weight (g) were obtained from the cross No. 8, 1, 4 and 7 with values of 5.25, 5.24, 5.17 and 5.17 g, respectively (Table 8). On the other hand, cross No. 5 exhibited the lowest mean value of 4.72 g. With reference to GCV%, the values were ranged from 4.80% (cross No. 8) to 6.41% (cross, No. 5). The highest h²b% value was 92.45% at cross, No. 3 and the lowest was 59.52% at the cross, No. 8. In case of GS% the values ranged from 98.85 to 112.04%

at 8 and 5, respectively. The highest hybrids which had relatively high, and moderate to high GCV (%) and h²b (%) showed the highest values of most genetic studied parameters, indicating the ability of selecting plants with narrow panicle weight for their F₂ and later segregating populations. This result is similar to Essa et al. (2011); Kiranet al. (2012), Lingaiah et al. (2014) and Anis et al. (2016b).

Table 8. Panicle weight (g) for all the studied crosses in the F₂ generation

No	Crosses	Panicle weight (g)							
		Mean	V F ₂	VE	GCV%	PCV%	h ² _b %	Gs	Gs %
1	Giza178xSKC23819-189-1-1-1-3-1-2-4-2	5.24	0.12	0.01	6.27	6.53	91.95	6.76	109.07
2	Giza178xSKC23819-192-2-1-2-2-4-2-1-2	4.94	0.10	0.01	6.22	6.55	90.10	6.33	108.12
3	Giza178xSKC23819-192-2-1-2-3-1-1-1-2	4.84	0.10	0.01	6.28	6.53	92.45	6.39	111.93
4	Giza178xSKC23819-192-2-1-2-4-5-3-2-1	5.17	0.11	0.03	5.37	6.36	71.50	5.72	100.71
5	Sakha103xSKC23819-189-1-1-1-3-1-2-4-2	4.72	0.11	0.02	6.41	7.14	80.66	6.23	112.04
6	Sakha103xSKC23819-192-2-1-2-2-4-2-1-2	4.78	0.11	0.02	6.26	7.01	79.62	6.16	108.94

7	Sakha103xSKC23819-192-2-1-2-3-1-1-1-2	5.17	0.11	0.02	5.85	6.46	82.02	6.23	100.55
8	Sakha103xSKC23819-192-2-1-2-4-5-3-2-1	5.25	0.11	0.04	4.80	6.22	59.52	5.19	98.85

Regarding to spikelets fertility (%), the GCV (%) values ranged between 4.42% for cross No.8 and 5.78% for cross No. 1 (Table 9). The heritability estimates for spikelets fertility (%) were more than 95% for all crosses thus, the selection procedures deprecated on the additive and non-additive genetic variance in the inheritance of this trait for all crosses. The lowest value of heritability (95.14%) was recorded in cross No. 3, while the highest value (97.63%) was in cross No. 5. The genetic advance under selection for spikelet's fertility showed that the possible gain from selection as percent in the crosses of F₃ generation over the F₂ mean when the most desirable 5% of the F₂ plants are studied. The genetic advance under selection for this trait ranged from 91.13% for cross No. 8 to 109.05% for cross No. 1. Same

heritability and genetic advance were also calculated by Essa et al. (2011), Hammoud et al. (2012) and Venkanna et al. (2014). For panicle length, the highest values of PCV% were found for all crosses under investigation more than the GCV%, indicating PCV was more affected by environmental factors (Table 10). The GCV ranged from 4.27% (cross, No. 6) to 5.53% (cross, No. 2). The cross combination No. 6 recorded the lowest value for genetic advance (87.99%) and No. 2 recorded the highest value (105.95%). The lowest value of heritability estimate (59.11%) was found in the cross, No. 5, but the heights (80.46%) was for the cross No. 4. This result was in agreement with Keshava et al. (2011), Lingaiah et al. (2014) and Aniset al. (2016a).

Table 9. Spikelets fertility % for all the studied crosses in the F₂ generation.

No	Crosses	Spikelets fertility %							
		Mean	V F ₂	VE	GCV%	PCV%	h ² _b %	Gs	Gs %
1	Giza178xSKC23819-189-1-1-1-3-1-2-4-2	78.70	21.29	0.60	5.78	5.86	97.17	93.69	109.05
2	Giza178xSKC23819-192-2-1-2-2-4-2-1-2	79.32	21.31	0.65	5.73	5.82	96.96	93.64	108.05
3	Giza178xSKC23819-192-2-1-2-3-1-1-1-2	76.97	19.93	0.97	5.66	5.80	95.14	89.71	106.55
4	Giza178xSKC23819-192-2-1-2-4-5-3-2-1	88.05	20.59	0.81	5.05	5.15	96.09	91.62	100.07
5	Sakha103xSKC23819-189-1-1-1-3-1-2-4-2	91.14	20.67	0.49	4.93	4.99	97.63	92.53	101.53
6	Sakha103xSKC23819-192-2-1-2-2-4-2-1-2	89.15	18.60	0.54	4.77	4.84	97.11	87.55	98.21
7	Sakha103xSKC23819-192-2-1-2-3-1-1-1-2	91.14	19.17	0.86	4.70	4.80	95.53	88.16	96.73
8	Sakha103xSKC23819-192-2-1-2-4-5-3-2-1	87.13	15.55	0.69	4.42	4.53	95.53	79.39	91.13

Table 10. Panicle length for all the studied crosses in the F₂ generation.

No	Crosses	Panicle length (cm)							
		Mean	V F ₂	VE	GCV%	PCV%	h ² _b %	Gs	Gs %
1	Giza178xSKC23819-189-1-1-1-3-1-2-4-2	23.14	2.21	0.73	5.26	6.43	67.00	25.07	100.37
2	Giza178xSKC23819-192-2-1-2-2-4-2-1-2	25.28	2.46	0.50	5.53	6.20	79.53	28.80	105.95
3	Giza178xSKC23819-192-2-1-2-3-1-1-1-2	23.71	2.21	0.68	5.21	6.27	69.07	25.45	99.36
4	Giza178xSKC23819-192-2-1-2-4-5-3-2-1	24.25	2.01	0.39	5.24	5.85	80.46	26.20	100.03
5	Sakha103xSKC23819-189-1-1-1-3-1-2-4-2	20.03	1.48	0.61	4.68	6.08	59.11	19.29	96.31
6	Sakha103xSKC23819-192-2-1-2-2-4-2-1-2	21.67	1.24	0.38	4.27	5.13	69.27	19.06	87.99

7	Sakha103xSKC23819-192-2-1-2-3-1-1-1-2	21.60	1.90	0.56	5.36	6.38	70.49	23.83	102.34
8	Sakha103xSKC23819-192-2-1-2-4-5-3-2-1	22.05	1.20	0.27	4.37	4.97	77.52	19.86	90.09

The genetic parameters i.e. phenotypic and genotypic coefficients of variability, heritability and genetic advance on number of primary branches panicle⁻¹ are presented in Table 11. The highest value of GCV (6.66%) was found in cross No. 5 followed by cross No. 6 (5.52%). On the other hand, the lowest (3.48%) was found in the cross, No. 7. The crosses No. 6 gave the highest values for

genetic advance 103.76% followed by 1 (97.69%) and 5 (95.03%), while for the lowest value was 71.73% for the crosses No. 7. The highest heritability (42.12%) was recorded at cross No. 5. This phenomenon was in agreement with that of Mirarab et al. (2011), Hammoud et al. (2012) and Anis et al. (2016a,b).

Table 11. Number of primary branches panicle⁻¹ for all the studied crosses in the F₂ generation.

No	Crosses	No. of primary branches panicle ⁻¹							
		Mean	V F ₂	VE	GCV%	PCV%	h ² _b %	Gs	Gs %
1	Giza178 SKC23819-189-1-1-1-3-1-2-4-2	11.90	1.00	0.62	5.23	8.42	38.56	12.82	107.69
2	Giza178xSKC 23819-192-2-1-2-4-2-1-2	11.70	0.73	0.47	4.40	7.31	36.21	10.60	90.62
3	Giza178xSKC23819-192-2-1-2-3-1-1-1-2	12.15	0.77	0.53	3.97	7.20	30.36	9.93	81.75
4	Giza178xSKC23819-192-2-1-2-4-5-3-2-1	11.45	0.80	0.53	4.53	7.82	33.51	10.68	93.27
5	Sakha103xSKC23819-189-1-1-1-3-1-2-4-2	12.60	0.98	0.97	6.66	10.26	42.12	13.23	105.03
6	Sakha103xSKC23819-192-2-1-2-4-2-1-2	13.15	1.34	0.82	5.52	8.82	39.24	14.96	113.76
7	Sakha103xSKC23819-192-2-1-2-3-1-1-1-2	12.70	1.08	0.88	3.48	8.18	18.13	9.11	71.73
8	Sakha103xSKC23819-192-2-1-2-4-5-3-2-1	12.70	1.09	0.88	3.57	8.22	18.92	9.35	73.64

Concerning to panicle density, the maximum mean values were obtained for the two cross combinations No. 1 and 4 with values of 8.37 and 7.97, respectively; contrary, the cross No. 6 exhibited the lowest mean value of 6.96 (Table 12). The estimates of GCV were ranged from 3.19% for the cross, No. 2 to 19.18% for the cross No. 8. For

h²_b%, the lowest value was 18.92% for the cross, No. 2, and the highest value was 83.78% for the cross, No. 8. In the case of GS %, the values ranged from 65.64% for the cross, No. 2 to 105.27% for the cross, No. 5. This result is in agreement with Vanisree et al. (2013), Venkanna et al. (2014) and Anis et al. (2016a).

Table 12. Panicle density for all the studied crosses in the F₂ generation.

No	Crosses	Panicle density							
		Mean	V F ₂	VE	GCV%	PCV%	h ² _b %	Gs	Gs %
1	Giza178xSKC23819-189-1-1-1-3-1-2-4-2	8.37	0.23	0.25	9.06	10.88	69.31	8.22	98.28
2	Giza178xSKC23819-192-2-1-2-4-2-1-2	7.54	0.31	0.25	3.19	7.33	18.92	4.95	65.64
3	Giza178xSKC23819-192-2-1-2-3-1-1-1-2	7.00	0.33	0.44	8.72	12.84	46.10	8.03	114.82
4	Giza178xSKC23819-192-2-1-2-4-5-3-2-1	7.97	0.27	0.17	4.00	6.52	37.53	6.56	82.31
5	Sakha103xSKC23819-189-1-1-1-3-1-2-4-2	7.25	0.44	0.50	8.59	12.97	43.87	9.08	125.27
6	Sakha103xSKC23819-192-2-1-2-4-2-1-2	6.96	0.22	0.49	11.15	15.02	55.15	7.18	103.16

7	Sakha103xSKC23819-192-2-1-2-3-1-1-1-2	7.36	0.23	0.68	12.38	16.68	55.06	7.33	99.66
8	Sakha103xSKC23819-192-2-1-2-4-5-3-2-1	7.59	0.24	0.41	19.18	20.96	83.78	9.24	121.66

Yield

Grain yield plant⁻¹ showed the values of GCV (%) for eight crosses ranged from 4.38% (cross, No. 6) to 6.24% (cross, No. 2) (Table 13). Estimates of heritability in broad sense were high (>90%) for all crosses. The additive and non-additive genetic variance were more important for improvement this trait. On the other hand, heritability was found high (ranged between 91.54% for cross No. 6 and 95.16% for cross No. 1) in all crosses which can be used for effective and successful breeding

purposes. The genetic advance under selection which varied from 90.21% in the cross, No. 6 to 108.56% in the cross, No. 2 was the possible gain from selection for the crosses in the F₃ generation over the F₂ generation when the most desirable 5% of the F₂ plants were studied. Similar results were obtained for heritability and genetic advance by Fahliani et al. (2010) and Vanisree et al. (2013), Thirumala et al. (2014) and Anis et al. (2016b).

Table 13. Grain yield plant⁻¹ for all the studied crosses in the F₂ generation.

No	Crosses	Grain yield plant ⁻¹ (g)								
		Mean	V F ₂	VE	GCV%	PCV%	h ² _b %	Gs	Gs %	
1	Giza178xSKC23819-189-1-1-1-3-1-2-4-2	87.04	21.66	1.05	5.22	5.35	95.16	93.52	107.45	
2	Giza178xSKC23819-192-2-1-2-2-4-2-1-2	74.40	22.86	1.30	6.24	6.43	94.31	95.65	108.56	
3	Giza178xSKC23819-192-2-1-2-3-1-1-1-2	69.30	16.38	1.03	5.65	5.84	93.73	80.72	106.48	
4	Giza178xSKC23819-192-2-1-2-4-5-3-2-1	82.86	15.00	1.19	4.49	4.67	92.09	76.56	92.40	
5	Sakha103xSKC23819-189-1-1-1-3-1-2-4-2	73.33	13.57	0.93	4.85	5.02	93.12	73.23	99.86	
6	Sakha103xSKC23819-192-2-1-2-2-4-2-1-2	81.75	14.00	1.19	4.38	4.58	91.54	73.74	90.21	
7	Sakha103xSKC23819-192-2-1-2-3-1-1-1-2	67.60	10.87	0.91	4.67	4.88	91.60	64.99	96.14	
8	Sakha103xSKC23819-192-2-1-2-4-5-3-2-1	72.55	13.27	1.07	4.81	5.02	91.92	71.95	99.18	

CONCLUSION

The results in this experiment propose that some good characteristics are existing in the local cultivars. Phenotypic and genotypic coefficients of variability, heritability and genetic advance revealed that days to heading, plant height, number of tillers plant⁻¹, number of panicles plant⁻¹, grain yield plant⁻¹, 1000-grain weight, number of filled grains panicle⁻¹, panicle length, panicle weight, spikelets fertility (%), and panicle density were improved by proper selection. The desirable characteristics may be transfer in the modern varieties by using suitable breeding techniques for developing superior varieties of rice and play an important role in meeting the global demand.

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Source of funding: None.

Statement of originality of work: The manuscript has been read and approved by all the authors, the requirements for authorship have been met, and that each author believes that the manuscript represents honest and original work.

Competing interest / Conflict of interest: The author(s) have no competing interests for financial support, publication of this research, patents and royalties through this collaborative research. All authors were equally involved in discussed research work. There is no financial conflict with the subject matter discussed in the manuscript.

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