

## Physical and Physicochemical Properties for Selected Hybrid Rice Combinations Derived from Three Line System

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### ABSTRACT

Ten hybrid rice genotypes were evaluated during 2015 and 2016 rice growing seasons at the Experimental Farm of the Rice Research and Training Center (RRTC), Sakha, Kafrelshiekh, Egypt. The experiments were assessed to study Physical and physicochemical properties of rice hybrids grain and heritability with genetic advance which is more helpful in predicting the quality under selection than heritability estimates alone. Combined analysis was performed for data over the two years. Most of studied characters were significantly greater in 2015 than in 2016 season except the duration, grain yield and appearance quality of rice. Highly significant differences were observed among the genotypes for all studied traits. G46A/WTR1 genotype followed by G46A/LH1 produced the highest grain yield. All the hybrid combinations have medium grain shape ( $< 3.0$  ratio) except for G46A/IR04A132 (slender  $> 3.0$  ratio). The hybrid IR69625A/WAB6-125 recorded higher milling yield (70.5%). The hybrid G46A/IR43 showed less broken rice (6.8 %) followed by G46A/HHZ5-Y3-Y1-DT1 (8.1%). All hybrid combinations were intermediate for gelatinization temperature except for IR69625A/CT19021-3-4 was high. Amylose content % of all genotypes ranged from 21.6 to 25.7%. The interaction between genotypes and years had a non-significant effect except for 1000-grain weight and head rice recovery. The estimates of heritability were high for all traits except for gelatinization temperature and ranged from 71.05% to 99.95%. The presence of high heritability values indicates the effectiveness of selection on the basis of phenotypic performance. Grain L/W ratio (95.52% and 26.57%), head rice recovery (99.84% and 21.03%) and elongation ratio (71.05% and 34.09%) recorded high heritability and high genetic advance, respectively. Significant positive phenotypic correlation was found between grain yield and days to maturing (0.635), number of panicles per plant (0.655) and grain width (0.712). The trait grain length showed highly significant and positive correlation with grain L/W ratio ( $r = 0.927$ ) and significant negative with grain width ( $r = -0.700$ ). The trait brown rice recovery showed significant and positive correlation with milled rice recovery ( $r = 0.760$ ) and amylose content ( $r = 0.730$ ).

**Keywords:** Correlations, duration, grain quality, yield, head rice recovery.

### INTRODUCTION

Rice (*Oryza sativa*, L.) is a staple food for nearly one-fifth of the world's seven billion people (Padmaja *et al.*, 2008). The world population is expected to reach 8.5 billion in 2030 (Gampala *et al.*, 2015). Rice production must be increased by more than 50% for the mid-nineties levels to meet the overpopulation and growing demand by 2025 (Peng *et al.*, 2004). The extension in rice cultivated area will be restricted by the scarcity of water resources. Hybrid rice show 15-20 % higher yield than inbred varieties (Peraudeau *et al.*, 2015). The major limitation to the generalization of hybrid rice in Egypt is its poor grain quality. Genetic improvement of hybrid rice by breeding methods is also a key aim to develop a good quality of rice grain. The diversity in quality of rice depends mainly on the genetic and environmental factors (Patindol *et al.*, 2015). Rice marketing value depends on physical properties including milling ratio and grain shape (Nikam *et al.*, 2014). Variability between rice genotypes was mentioned in several studies, grain length, grain width and grain L/W ratio (Chukwuemeka *et al.*, 2016; Rafii *et al.*, 2014 and Singh *et al.*, 2005) and brown, milled and head rice recovery (Babu *et al.*, 2013 and Nazmy *et al.*, 2014). Physicochemical properties of rice were determined based on amylose content, elongation ratio and gelatinization temperature (Babu *et al.*, 2013 and Nazmy *et al.*, 2014). Cooking and eating qualities mostly depend on the physicochemical properties preferred by consumers.

In breeding program, the knowledge of genetic variability for evolving high grain quality is important. Genetic advance is more helpful in predicting the gain

under selection than heritability estimates alone (Anbanandan *et al.*, 2009; Fahliani *et al.*, 2011; Gampala *et al.*, 2015 and Padmaja *et al.*, 2008).

Therefore, this study was conducted to evaluate the diversity of rice grain quality of selected new promising hybrid rice combinations based on physical and physicochemical properties that will provide highly important information for future rice breeding programmes as well as for consumers.

### MATERIALS AND METHODS

Two field trials were conducted during 2015 and 2016 rice growing seasons at the Experimental Farm of the Rice Research and Training Center (RRTC), Sakha, Kafrelshiekh, Egypt. The experiments were conducted to compare yield, physical and physicochemical properties from new promising hybrid rice combinations. The experimental soil was clay in texture with a pH of 8.01 and organic matter 1.51 %. Total nitrogen, available phosphorus and potassium were 0.16%, 17.6 mg kg<sup>-1</sup> and 230 mg kg<sup>-1</sup>, respectively. Climatic data were recorded from an agrometeorological Sakha station of RRTC, as given in Table 1.

The experimental material consisted of ten hybrid rice combinations selected from 45 test cross nursery. Cytoplasmic male sterile lines and restorer lines used for hybrid production (Table 2).

Hybrid rice seeds were obtained from RRTC. The selection for these hybrids based on spikelet fertility % and high yielding during test cross 2015 and retest cross 2016. After 25 days from sowing in the nursery, single seedling/hills of each hybrid were transplanted into the permanent field. Each plot contains seven rows in 20 x 20 cm spacing and 5 m long rows.

Experiment was designed in a randomized complete block design (RCBD) with three replications. All agronomic practices of hybrid rice were done as recommended. Duration (days) from seed to maturity was recorded. At harvest, ten plants were taken randomly from five middle rows to count number of panicles/plant. Ten main panicles were collected randomly to estimate number of filled grains and 1000-grain weight (g). Grain yield was recorded as tons per feddan (fed). A composite sample was used to record grain quality characters. Brown rice recovery, milled rice recovery, head rice recovery, grain length, grain width, GL/GW ratio, Amylose content %, gelatinization temperature and elongation ratio were estimated according to Kush *et al.* (1979).

**Table 1. Monthly mean of maximum (Max) and minimum (Min) temperatures and relative humidity (RH, %) during the two winter growing seasons.**

Month	Temperature (°C)				Relative humidity (%)	
	2015		2016		2015	2016
	Max.	Min.	Max.	Min.		
April	27.2	11.1	30.0	18.6	63.1	61.7
May	28.9	12.7	30.0	22.	59.3	58.4
June	33.9	19.1	33.6	26.	63.1	61.1
July	33.3	20.4	33.7	26.1	65.9	69.7
August	34.7	19.1	33.6	26.0	66.9	70.3
September	32.8	19.1	32.6	24.3	62.1	67.4

**Table 2. Cytoplasmic male sterile lines and restorer lines used for hybrid rice.**

CMS Lines		
CMS	Cytoplasmic source	Origin
G46 A	Gambiaca	China
IR69625 A	Wild Abortive (WA)	IRRI
Restorer Lines		
Varieties	Pedigree	Origin
IR04A132	-----	IRRI
HHZ5-Y3-Y1-DT1	HUANG-HUA-ZHAN*2/OM 1723	IRRI
LH1	-----	China
HHZ12-SAL8-Y1-SAL1	HUANG-HUA-ZHAN*2/TE QING	IRRI
Weed tolerant rice 1 (WTR1)	-----	China
IR43	IR 305-3-17-1-3/IR 661-1-140-3	IRRI
WAB6-125	-----	WARDA
CT19021-3-4	BG 90-2*2/ORYZA RUFİPOGON//BG 90-2*2/ORYZA RUFİPOGON	CIAT

The obtained data were statistically analyzed for analysis of variance according to Gomez and Gomez (1984) by using computer statistical software of MSTAT-C. Treatment means were compared by Duncan's Multiple Range Test (DMRT) (Duncan, 1955). The combined analysis was computed over the two years. Before the calculations of the combined experiments, the error variance of the experiments was tested for the homogeneity of variance as described by Bartlett (1937).

The genetic parameters were computed according to formula suggested by Burton (1952) and Hanson *et al.* (1956), and the correlation coefficients between the traits were fixed using Pearson's correlation coefficients.

## RESULTS AND DISCUSSION

### 1. Yield and its attributes:

#### 1. a. Effect of season:

Combined analysis of variance for grain yield (ton/fed) and its components over the two years are presented in Table 3. Year's mean squares were not significant for all the studied traits except for No. of filled grains/panicle and 1000-grain weight (g). No. of filled grains/panicle and 1000-grain weight (g) were significantly greater in 2015 than in 2016 season (tables 4 and 5). These differences between the two seasons in No. of filled grains/panicle and 1000-grain

weight (g) were probably related to differences in weather conditions (table 1). Monthly mean of minimum air temperature tended to be higher in 2016 than 2015 season through growing season. In addition, monthly mean relative humidity percentage tended to be greater in 2016 than 2015 season during July, August and September.

Peng *et al.* (2004) reported that direct evidence of decreased rice yields from increased nighttime temperature associated with global warming. Peraudeau *et al.* (2015) stated that increasing night temperature increases night respiration and thus the increase in carbon losses over time.

**Table 3: Mean squares of ten rice genotypes for yield and its attributes in combined analysis across 2015 and 2016 seasons.**

S.O.V.	d.f.	Duration (days)	No. of Panicles/plant	No. of Filled grains/panicle	1000-Grain weight (g)	Grain Yield (t/fed)
Year	1	3.55	0.27	1092.27*	4.74*	0.58
Replication with Year	4	11.77	6.18	300.42	0.31	1.50
Genotypes	9	128.62**	19.60**	5274.14**	6.29**	0.66**
Genotypes x Year	9	0.01	4.08	873.60	8.91**	0.02
Error	36	1.52	3.81	212.56	0.07	0.04

\*significant at 5% probability level, \*\*significant at 1% probability level.

**1. b. Effect of genotypes:**

Table 3 shows that hybrid rice genotypes exhibited a significant difference in duration (day), No. of panicles/plant, No. of filled grains/panicle, 1000-grain weight (g) and grain yield (t/fed).

Data in table 4 indicate that the duration was substantially earlier in promising rice hybrids G46A/IR04A132 and G46A/IR43 than other genotypes. G46A/WTR1 and IR69625A/IR43 recorded the longest duration of 142.2 and 141.2 days, respectively.

Maximum No. of panicles/plant was exhibited by the G46A/HHZ5-Y3-Y1-DT1, G46A/LH1 and G46A/WTR1 hybrids while the minimum one was produced by G46A/IR43 (table 4). IR69625A/CT19021-3-4 was significantly superior overall other genotypes in No. of filled grains/panicle, while hybrid IR69625A/WTR1 was significantly lower than the other genotypes in this respect (table 4). Hybrids G46A/HHZ12-SAL8-Y1-SAL1 had the highest 1000- grains weight

followed by G46A/HHZ5-Y3-Y1-DT1, while the hybrid G46A/WTR1 had the lowest (table 5). G46A/WTR1 hybrid followed by G46A/WTR1 produced the highest grain yield. R69625A/WAB6-125 hybrid produced significantly the lowest grain yield compared with other genotypes without significant differences compared with G46A/IR04A132 (table 5).

The real genetic difference in yield and its components between genotypes are expected and found also by Anis *et al.* (2016b); Prasad *et al.* (2015) and Rai *et al.* (2015).

**1. c. Effect of interaction:**

The interaction between genotypes and years had a non-significant effect except for 1000-grain weight (Table 2). G46A/HHZ12-SAL8-Y1-SAL1 recorded the highest 1000-grain weight in the first and second year. The decrease in 1000-grain weight ranged from 24.9% to 28.6% in the 2016 season compared to 2015 season for all genotypes.

**Table 4: Duration (day), number of panicles/plant and number of filled grains/panicle of rice hybrids as affected by season, genotype and interaction in combined analysis across 2015 and 2016 seasons.**

No	Genotypes	Duration (days)			No. of panicles/plant			No. of filled grains/panicle		
		Y1	Y2	Com.	Y1	Y2	Com.	Y1	Y2	Com.
1	G46A/IR04A132	129.0a	129.5a	129.2 f	26.3a	28.7a	27.5 cde	206.7a	227.3a	217.0 c
2	G46A/HHZ5-Y3-Y1-DT1	132.3a	132.8a	132.6 e	31.0a	31.0a	31.0 a	206.7a	213.0a	209.8 cd
3	G46A/LH1	137.0a	137.5a	137.2 c	31.0a	30.0a	30.5 ab	245.3a	268.7a	257.0 b
4	G46A/HHZ12-SAL8-Y1-SAL1	139.0a	139.5a	139.2 b	28.0a	27.3a	27.7 cde	260.7a	225.7a	243.2 b
5	G46A/WTR1	142.0a	142.5a	142.2 a	28.7a	29.0a	28.8 abc	234.0a	193.7a	213.8 cd
6	G46A/IR43	129.3a	129.8a	129.6 f	25.0a	26.0a	25.5 e	200.3a	195.0a	197.7 d
7	IR69625A/WAB6-125	132.7a	133.2a	132.9 e	26.7a	26.7a	26.7 cde	266.0a	234.7a	250.3 b
8	IR69625A/CT19021-3-4	134.3a	134.8a	134.6 d	25.7a	26.0a	25.8 de	288.7a	263.7a	276.2 a
9	IR69625A/WTR1	138.0a	138.5a	138.2bc	27.0a	29.3a	28.2 bcd	171.7a	187.7a	179.7 e
10	IR69625A/IR43	141.0a	141.5a	141.2 a	29.0a	25.7a	27.3 cde	223.0a	208.3a	215.7 cd
	Mean	135.4a	135.9a	135.6	27.8a	27.9a	27.9	230.3a	221.7b	226.0
	S.E.	1.46	1.47	1.45	0.65	0.59	0.57	11.22	8.88	9.37
	CV %	3.42	3.40	3.39	7.48	6.70	6.48	15.41	12.66	13.11

Means of each factor designated by the same letter are not significantly different at 5% level using DMRT.

**Table 5. 1000-Grain weight (g), Grain yield (t/fed) of rice hybrids as affected by season, genotype and interaction in combined analysis across 2015 and 2016 seasons.**

No	Genotypes	1000-Grain weight (g)			Grain yield (t/fed)		
		Y1	Y2	Com.	Y1	Y2	Com.
1	G46A/IR04A132	27.2d	28.1bc	27.7c	4.9a	5.1a	5.0 de
2	G46A/HHZ5-Y3-Y1-DT1	28.5b	27.8c	28.2b	5.4a	5.6a	5.5 bc
3	G46A/LH1	26.2fg	27.2d	26.7d	5.6a	5.8a	5.7 ab
4	G46A/HHZ12-SAL8-Y1-SAL1	29.6a	28.2bc	28.9a	5.3a	5.5a	5.4 c
5	G46A/WTR1	24.6k	25.0jk	24.8g	5.7a	5.9a	5.8 a
6	G46A/IR43	25.4ij	26.1fg	25.8ef	5.3a	5.5a	5.4 c
7	IR69625A/WAB6-125	26.5ef	25.5hi	26.0e	4.7a	4.9a	4.8 e
8	IR69625A/CT19021-3-4	26.8de	26.4efg	26.6d	5.0a	5.2a	5.1 d
9	IR69625A/WTR1	26.8de	25.9gh	26.4d	5.3a	5.5a	5.4 c
10	IR69625A/IR43	25.9gh	25.1ij	25.5f	5.0a	5.2a	5.1 d
	Mean	26.75a	26.53b	26.66	5.22a	5.42a	5.32
	S.E.	0.45	0.38	0.40	0.10	0.09	0.10
	CV %	5.42	4.59	4.76	6.04	5.82	5.93

Means of each factor designated by the same letter are not significantly different at 5% level using DMRT.

2. Grain quality:

2.a. Effect of season:

Year's means were significant for milling and cooking quality in combined analysis across 2015 and 2016 seasons (table 6 and 7). Data in table 8, 9 and 10 showed that mean of first year was higher than mean of second year for brown rice recovery, milled rice

recovery, head rice recovery, elongation ratio and Amylose content % of hybrid rice genotypes. Gelatinization temperature was the lowest at first seasons.

Means of each factor designated by the same latter are not significantly different at 5% level using DMRT.

**Table 6: Mean squares of ten rice genotypes for appearance and milling quality in combined analysis across 2015 and 2016 seasons.**

S.O.V.	d.f.	Appearance			Milling		
		Grain Length (mm)	Grain width (mm)	Grain L/W ratio	Brown recovery	Milled recovery	Head recovery
Year	1	0.793	0.104	0.036	60.160**	112.477**	122.522**
Replication with Year	4	0.011	0.005	0.002	2.403	5.466	0.566
Genotypes	9	1.050**	0.187*	0.668**	29.520**	26.846**	173.036**
Genotypes x Year	9	0.010	0.012	0.004	0.662	0.700	8.393*
Error	36	0.010	0.007	0.005	0.003	0.058	0.046

\*significant at 5% probability level, \*\*significant at 1% probability level

**Table 7: Mean squares of ten rice genotypes for cooking and eating quality in combined analysis across 2015 and 2016 seasons.**

S.O.V.	d.f.	Cooking		
		Gelatinization temperature	Elongation ratio	Amylose content
Year	1	8.363**	33.361**	9.134**
Replication with Year	4	0.749	52.913	7.734
Genotypes	9	1.474**	265.323**	11.119**
Genotypes x Year	9	0.416	0.093	0.393
Error	36	0.728	16.869	0.106

\*significant at 5% probability level, \*\*significant at 1% probability level

Environmental temperature, especially nighttime temperature during grain development, plays an integral role in grain quality. When nighttime temperature increases from 18 to 30 °C, head rice yields, grain dimensions and the amylase content were decreased (Cooper *et al.*, 2008). High temperature causes interruption during the final stages of grain filling, resulting in excessive chalkiness. Likewise, high-temperature stress during ripening results in starch with a higher gelatinization temperature and higher amounts of broken grains (Krishnan *et al.*, 2011). Counce *et al.* (2005) indicated that high nighttime temperatures have also been suspected of reducing rice milling quality including head rice yields but there was no effect of temperature on grain length or thickness.

**Table 8: Grain length (mm), grain width (mm) and grain L/W ratio of rice hybrids as affected by season, genotype and interaction in combined analysis across 2015 and 2016 seasons.**

No	Genotypes	Grain length (mm)			Grain width (mm)			Grain L/W ratio		
		Y1	Y2	Com.	Y1	Y2	Com.	Y1	Y2	Com.
1	G46A/IR04A132	6.9a	6.6a	6.8a	2.2a	2.1a	2.2e	3.2a	3.3a	3.2a
2	G46A/HHZ5-Y3-Y1-DT1	6.4a	6.3a	6.4b	2.6a	2.4a	2.5d	2.5a	2.6a	2.6d
3	G46A/LH1	5.5a	5.2a	5.4g	2.8a	2.7a	2.8a	2.0a	2.1a	2.0h
4	G46A/HHZ12-SAL8-Y1-SAL1	6.1a	5.8a	5.9d	2.7a	2.6a	2.7b	2.2a	2.3a	2.3g
5	G46A/WTR1	5.8a	5.6a	5.7ef	2.6a	2.6a	2.6c	2.3a	2.2a	2.3g
6	G46A/IR43	6.2a	6.0a	6.1c	2.5a	2.3a	2.4d	2.5a	2.6a	2.5e
7	IR69625A/WAB6-125	6.0a	5.7a	5.8de	2.4a	2.3a	2.4d	2.5a	2.6a	2.5e
8	IR69625A/CT19021-3-4	6.2a	6.1a	6.2c	2.4a	2.4a	2.4d	2.6a	2.7a	2.7c
9	IR69625A/WTR1	5.7a	5.5a	5.6f	2.5a	2.3a	2.4d	2.3a	2.4a	2.4f
10	IR69625A/IR43	6.5a	6.3a	6.4b	2.3a	2.4a	2.4d	2.8a	2.7a	2.8b
	Mean	6.13a	5.91a	6.03	2.51a	2.41a	2.48	2.49a	2.55a	2.53
	S.E.	0.13	0.13	0.14	0.06	0.06	0.05	0.11	0.11	0.10
	CV %	6.72	7.24	7.11	7.63	7.45	7.04	13.46	13.22	12.90

Means of each factor designated by the same latter are not significantly different at 5% level using DMRT.

**Table 9: Brown rice recovery, milled rice recovery and head rice recovery ratio of rice hybrids as affected by season, genotype and interaction in combined analysis across 2015 and 2016 seasons**

No	Genotypes	Brown rice recovery			Milled rice recovery			Head rice recovery		
		Y1	Y2	Com.	Y1	Y2	Com.	Y1	Y2	Com.
1	G46A/IR04A132	82.0a	80.6a	81.3b	68.1a	65.4a	66.7d	49.4bc	47.1c	48.2g
2	G46A/HHZ5-Y3-Y1-DT1	77.0a	74.6a	75.8g	66.1a	63.4a	64.7f	57.3a	56.0a	56.6c
3	G46A/LH1	79.0a	76.6a	77.8e	67.1a	64.7a	65.9e	57.8a	55.4a	56.6c
4	G46A/HHZ12-SAL8-Y1-SAL1	78.0a	75.6a	76.8f	65.1a	62.4a	63.7h	56.3a	53ab	54.6e
5	G46A/WTR1	77.0a	74.6a	75.8g	67.1a	64.4a	65.7e	56.3a	58.0a	57.1b
6	G46A/IR43	78.0a	75.6a	76.8f	66.5a	61.9a	64.2g	58.3a	56.6a	57.4a
7	IR69625A/WAB6-125	81.0a	79.1a	80.1c	71.6a	69.4a	70.5a	45.3c	37.9d	41.6i
8	IR69625A/CT19021-3-4	80.4a	79.6a	80d	68.1a	65.4a	66.7d	57.1a	53.2ab	55.1d
9	IR69625A/WTR1	81.5a	78.7a	80.1c	69.1a	66.8a	67.9c	49.2bc	45.0c	47.1h
10	IR69625A/IR43	82.0a	80.8a	81.4a	70.1a	67.5a	68.8b	53.2ab	49.1bc	51.1f
Mean		79.5a	77.5b	78.59	67.8a	65.1b	66.48	54.02a	51.13b	52.54
S.E.		0.63	0.77	0.70	0.61	0.73	0.67	1.43	1.99	1.69
CV %		2.53	3.14	2.82	2.87	3.55	3.19	8.38	12.36	10.19

Means of each factor designated by the same letter are not significantly different at 5% level using DMRT

**Table 10: Gelatinization temperature, elongation ratio and Amylose content % of rice hybrids as affected by season, genotype and interaction in combined analysis across 2015 and 2016 seasons**

No	Genotypes	Gelatinization temperature			Elongation ratio			Amylose content %		
		Y1	Y2	Com.	Y1	Y2	Com.	Y1	Y2	Com.
1	G46A/IR04A132	4.0a	4.7a	4.3bc	0.34a	0.32a	0.33ab	25.5a	24.0a	24.8b
2	G46A/HHZ5-Y3-Y1-DT1	4.3a	5.0a	4.7abc	0.28a	0.26a	0.27ab	23.8a	23.2a	23.5c
3	G46A/LH1	4.0a	5.0a	4.5abc	0.29a	0.27a	0.28ab	22.1a	21.9a	22d
4	G46A/HHZ12-SAL8-Y1-SAL1	4.0a	5.0a	4.5abc	0.36a	0.34a	0.35ab	22.5a	21.8a	22.2d
5	G46A/WTR1	4.0a	5.7a	4.8ab	0.45a	0.43a	0.44a	22.8a	21.7a	22.2d
6	G46A/IR43	3.7a	4.7a	4.2bc	0.39a	0.37a	0.38ab	21.9a	21.3a	21.6e
7	IR69625A/WAB6-125	5.0a	4.7a	4.8ab	0.33a	0.32a	0.33ab	23.8a	23.5a	23.6c
8	IR69625A/CT19021-3-4	3.3a	3.8a	3.6c	0.22a	0.21a	0.21b	26.2a	25.2a	25.7a
9	IR69625A/WTR1	4.0a	5.0a	4.5abc	0.32a	0.30a	0.31ab	25.3a	23.7a	24.5b
10	IR69625A/IR43	5.3a	5.7a	5.5a	0.40a	0.38a	0.39a	24.0a	23.8a	23.9c
Mean		4.16b	4.93a	4.54	0.34a	0.32b	0.33	23.79a	23.01b	23.4
S.E.		0.18	0.17	0.15	0.02	0.02	0.02	0.47	0.47	0.43
CV %		14.11	10.98	10.75	19.61	20.09	20.13	5.51	6.28	5.84

Means of each factor designated by the same letter are not significantly different at 5% level using DMRT.

**2.b. Effect of genotypes:**

Combined analysis of variance exhibited highly significant difference for genotypes in all rice quality traits (tables 9 and 10). The results in table 5 revealed that all hybrids had medium grains with values ranged from 5.4 to 6.4 except for the combination G46A/IR04A132 which showed long grain (6.8) at pooled data. The promising hybrid G46A/LH1 had the highest grain width while G46A/IR04A132 had the lowest value. The proportion of length to width reveals the grain shape of rice. All the hybrid combinations have medium grain shape (< 3.0 ratio) except for G46A/IR04A132 (slender > 3.0 ratio). High grain length with low grain width could lead to long grain shape.

Brown rice recovery of all genotypes ranged from 75.8 to 81.4% (table 6). IR69625A/IR43 showed the highest brown rice recovery (81.4 %), whereas G46A/HHZ5-Y3-Y1-DT1 and G46A/WTR1 had the lowest brown rice recovery (75.8 %). All rice hybrids gave less than 70 % milled rice recovery except for the hybrid IR69625A/WAB6-125 recorded significantly

higher milling yield (70.5%) but it gave the lowest values for head rice recovery (41.6%). The hybrid G46A/IR43 showed less broken rice (6.8 %) followed by G46A/HHZ5-Y3-Y1-DT1 (8.1 %) and highest broken rice was noticed in IR69625A/WAB6-125 (28.9 %) (Fig. 1).

Gelatinization temperature ranged from 3.6 to 5.5 (table 7). All hybrid combinations were intermediate for gelatinization temperature except for IR69625A/CT19021-3-4 was high. The results revealed that the hybrid IR69625A/CT19021-3-4 showed gelatinization temperature of (3.6) and contrary, IR69625A/IR43 was the lowest gelatinization temperature (5.5). This indicates that the promising hybrids under investigation needed less time for cook and saved the energy.

For elongation ratio, the results indicated that all hybrid rice combinations showed medium grain elongation ratio (< 0.70). G46A/WTR1 followed by IR69625A/IR43 genotypes gave the highest grain elongation ratio (0.44 and 0.39), respectively. Amylose content % of all genotypes was ranged from 21.6 to 25.7%.

The combination of IR69625A/CT19021-3-4 had high amylose content at while the rest all hybrids had intermediate. This variation in the rice quality characteristics may due to genotypic differences of rice hybrids (Gampala *et al.*, 2015; Nazmy *et al.*, 2014 and Rafii *et al.*, 2014). The milling breakage in rice genotypes is an indicative of poor milling quality and the breakage may be due to either genetic characteristics or improper drying after harvest or may be due to grain length and presence of more of immature grains (Gangadharaiah *et al.*, 2015).

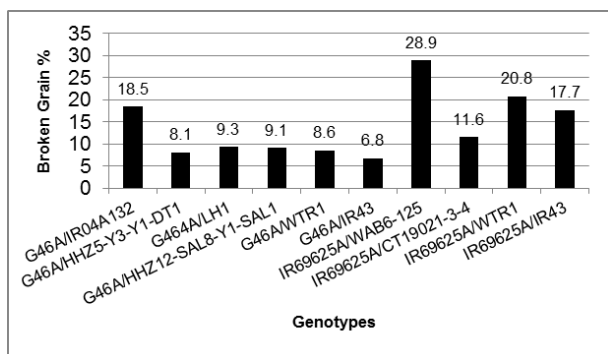


Fig 1. Broken grain (%) after milled rice recovery as affected by genotypes.

2.c. Effect of interaction:

The interaction between years x genotypes for head rice recovery was significant (Table 9). However, none of the other interactions had a significant effect in tables 9 and 10. The difference for head rice recovery at

the same genotype during the two seasons was not significant except for head rice recovery for IR69625A/WAB6-125 that decreased significantly by 16.3 % in the 2016 season as compared to 2015 season.

3. Genetic parameters

3. a. Analysis of variance

In the two growing seasons of 2015 and 2016, all hybrid combinations were evaluated to determine the magnitudes of genotypic variations which are presented among them. Data of ten hybrids were subjected to statistical analysis of variances for all studied traits for each year and over the two years and the results are shown in (Tables 8, 9 and 10). The results indicated that the mean squares of years were insignificant for grain length, grain width and grain L/W ratio. The results of the F-test indicated that the mean squares of the hybrids (genotypes) showed significant and highly significant values. This finding indicated the presence of large variations among them. The interaction of years with hybrids (genotypes) was found to be significant for head rice recovery and highly significant for 1000-grain weight. It could be concluded that best of potential hybrids could be necessarily conducting over a number of environmental conditions and that genetic diversity would not guarantee the expression.

3. b. Genetic variability

The estimates of genetic variance components including co-efficient of variation, heritability and genetic advance deserve attention in deciding selection criteria for improvement in the concerned traits (table 11).

Table 11: Grand mean, Variance components, estimates of phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability (h<sup>2</sup>b %) and genetic advance for yield and its attributes and grain quality traits in rice in combined analysis across 2015 and 2016 seasons.

Studied traits	Grand mean	Variance components			Coefficient of variation		Heritability (h <sup>2</sup> b %)	Genetic Advance	
		σ <sup>2</sup> g	σ <sup>2</sup> p	σ <sup>2</sup> e	GCV	PCV		G.S.	G.S. (%)
Duration (day)	135.71	21.18	22.71	1.52	3.39	3.51	93.30	9.16	6.75
No. of Panicles/plant	27.90	2.63	6.44	3.81	5.81	9.10	40.83	2.14	7.65
No. of Filled grains/panicle	226.03	843.60	1056.16	212.56	12.85	14.38	79.87	53.47	23.66
1000-Grain weight (g)	26.28	1.04	1.11	0.074	3.88	4.01	93.37	2.03	7.71
Grain Yield (t/fed)	5.32	0.10	0.14	0.04	6.06	7.08	73.33	0.57	10.70
Grain length (mm)	6.02	0.17	0.18	0.010	6.92	7.11	94.72	0.83	13.87
Grain width (mm)	2.46	0.03	0.04	0.007	7.05	7.81	81.37	0.32	13.09
Grain L/W ratio	2.52	0.11	0.12	0.005	13.20	13.50	95.52	0.67	26.57
Brown rice recovery	78.59	4.92	4.92	0.003	2.82	2.83	99.95	4.57	5.81
Milled rice recovery	66.48	4.46	4.52	0.058	3.18	3.20	98.71	4.32	6.50
Head rice recovery	52.55	28.83	28.88	0.046	10.22	10.23	99.84	11.05	21.03
Gelatinization temperature	4.54	0.12	0.85	0.728	7.76	20.32	14.57	0.28	6.10
Elongation ratio	32.78	41.41	58.28	16.86	19.63	23.29	71.05	11.17	34.09
Amylose content	23.39	1.84	1.94	0.106	5.79	5.96	94.53	2.71	11.60

σ<sup>2</sup>g= Genotypic variance, σ<sup>2</sup>p = Phenotypic variance, σ<sup>2</sup>e = Error variance, GCV = genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, h<sup>2</sup>b = heritability, G.S. = genetic advance and G.S. (%) = genetic advance as percent of mean

The estimates of genotypic coefficient of variation (GCV) were lower than the respective phenotypic coefficient of variation (PCV), indicating the influence of environmental factors on the expression of the traits studied which are in agreement with the

findings of Anis *et al.* (2016b). Phenotypic coefficient of variation (PCV) was found to be highest in grain elongation ratio (23.29) followed by gelatinization temperature (20.32) and grain L/W ratio (13.50) while brown rice recovery had the least PCV value (2.83).

Similarly, GCV was found to be highest in elongation ratio (19.63) followed by grain L/W ratio (13.20) and head rice recovery (10.22). But brown rice recovery had the least GCV value (2.82) which was significantly differed by milled rice recovery (3.18) and 1000-grain weight 3.88. Similar results were obtained by Anis *et al.* (2016b); Paikhomba *et al.* (2014) and Verma *et al.* (2013).

Heritability in broad sense includes both fixable (additive) and non-fixable (dominant and epistatic) variances and provides a good indication about the repeatability of the traits. The estimates of heritability for different traits were high for all traits except for gelatinization temperature and ranged from 71.05% to 99.95% (Table 11). Although, the presence of high heritability values indicate the effectiveness of selection on the basis of phenotypic performance, it does not show any indication to the amount of genetic progress for selecting the best individuals which is possible using the estimate of genetic advance.

Heritability estimates (above 60%) along with genetic advance (above 20%) would be helpful in predicting gain under selection than heritability estimates alone. In this study, grain L/W ratio (95.52% and 26.57%), head rice recovery (99.84% and 21.03%) and elongation ratio (71.05% and 34.09%) recorded high heritability as well as high genetic advance.

These observations corroborate well with those of

Nirmaladevi *et al.* (2015) and Veerabhadhira *et al.* (2009). The high estimates of heritability and lower estimates of genetic advance as percent of mean was recorded for the traits of brown rice recovery (99.95% and 5.81%), milled rice recovery (98.71% and 6.50%) and 1000-grain weight (93.37% and 7.71%). This is an indication of more environmental influence on these characters. (Das *et al.*, 2007) also observed similar results for brown rice recovery. These traits showing high heritability with low genetic advance indicated the presence of non-additive gene action. Hence, selection could be postponed for these traits. In other words, these traits could be improved by intermating of superior genotypes of segregating population from recombination breeding. The high estimates of heritability coupled with medium estimates of genetic advance were observed for grain length (94.72% and 13.87%), grain width (81.37% and 13.09%) and amylose content (94.53% and 11.60%). These were in accordance with the findings of Anis *et al.* (2016b) and Nayak and Reddy (2005). Thus, it is interpreted that the traits i.e. grain length, grain width and amylose content showed high heritability estimates and moderate genetic advance rendering them unsuitable for improvement through selection.

### 3. C. Correlation coefficient

Correlation coefficient analysis among grain yield and quality traits were computed (Table 12).

**Table 12: Correlation coefficients among fourteen agronomic and grain quality traits over the two years.**

Traits	DM	NPP	NFG	1000-GW	GY	GL	GW	L/W R	BRR	MRR	HRR	GT	ER	AC
DM	0.00													
NPP	0.264	0.00												
NFG	0.011	-0.114	0.00											
1000-GW	-0.296	0.287	-0.642*	0.00										
GY	0.635*	0.655*	0.539	0.164	0.00									
GL	-0.488	-0.239	-0.119	0.292	-0.505	0.00								
GW	0.543	0.544	0.327	0.131	0.712*	-0.700**	0.00							
L/W R	-0.474	-0.384	-0.147	0.121	-0.675*	0.927**	-0.882**	0.00						
BRR	-0.110	-0.433	0.099	-0.139	-0.775**	0.333	-0.638*	0.598	0.00					
MRR	0.081	-0.232	0.096	-0.456	-0.650*	-0.037	-0.431	0.252	0.760*	0.00				
HRR	0.158	0.274	0.050	0.065	0.750*	-0.052	0.524	-0.340	-0.715*	-0.833**	0.00			
GT	0.499	0.330	-0.344	-0.270	0.030	-0.028	0.114	-0.050	0.061	0.362	-0.231	0.00		
ER	0.365	-0.121	-0.493	-0.468	0.214	-0.061	0.027	-0.055	-0.193	-0.028	0.017	0.599	0.00	
AC	-0.178	-0.245	0.141	0.097	-0.620	0.469	-0.663*	0.664*	0.510	-0.471	-0.265	-0.552	0.00	

\*significant at 5% probability level, \*\*significant at 1% probability level. DM= days to maturing, NPP= number of panicles per plant, NFG= number of filled grains per panicle, 1000-GW= 1000-grain weight, GY= grain yield. GL=grain length, GW=grain width, L/W R=GL/GW ratio, BRR= Brown rice recovery, MRR=milled rice recovery, HRR= head rice recovery, GT= gelatinization temperature, ER= elongation ratio, AC= Amylose content % .

Correlation estimates showed the possibility of improvement of a trait through selection for other trait. Correlation analysis among the studies traits revealed that significant positive phenotypic correlation was found between grain yield and days to maturing (0.635), number of panicles per plant (0.655), grain width (0.712) and head rice recovery (0.750). It means increase of one character will cause increase in the correlated character also. On the other hand, significant and highly significant negative phenotypic correlation was found between grain yield and grain L/W ratio (-0.675) , brown rice recovery (-0.775) and milled rice recovery (-0.650). Only phenotypic correlation was found significant negative between number of filled grains per panicle and 1000-grain weight, indicating

that more number of filled grain effect on grain weight. Similar trend was found by Anis *et al.* (2016a). Genotypes with long slender grains are more prone to breakage than those possessing short bold grain. The trait grain length showed highly significant and positive correlation with grain L/W ratio ( $r = 0.927$ ) and showed highly significant negative with grain width ( $r = -0.700$ ) but non-significant correlations with the rest of studied traits. Grain width showed significant and highly significant negative correlation with grain L/W ratio, brown rice recovery and amylose content with ( $r = -0.882$ ,  $-0.638$  and  $-0.663$ ), respectively. These findings were in agreement with the findings reported earlier by Nirmaladevi *et al.* (2015) and Oladi *et al.* (2014).

Grain L/W ratio showed significant and positive correlation with amylose content ( $r = 0.664$ ) and recorded non-significant correlations with other traits. The trait brown rice recovery showed significant and positive correlation with milled rice recovery ( $r = 0.760$ ) and amylose content ( $r = 0.730$ ). In the present study the positive significant correlation of brown rice recovery with milled rice recovery indicated that the genotypes with higher hulling percent also showed higher estimates for milled rice. Similar results were reported by several researchers (Fazaa *et al.*, 2016 and Oladi *et al.*, 2014). Brown rice recovery (hulling %) and milled rice recovery (milling %) are important quality attributes for rice that enhances commercial success of a variety. Simultaneous improvement of these two quality traits can be made with the selection of a single trait is either hulling percent or milling percent. These findings were in agreement with the findings reported earlier by (Fazaa *et al.*, 2016).

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### الخصائص الطبيعية و الطبيعية-الكيميائية لتراكيب أرز هجينية منتخبة بنظام الثلاثة سلالات

جلال بكر أنيس<sup>1</sup> ، هانى صبحى غريب<sup>2</sup>

- 1- مركز البحوث والتدريب فى الأرز بسخا - معهد بحوث المحاصيل الحقلية - مركز البحوث الزراعية - كفر الشيخ - مصر.
- 2- قسم المحاصيل - كلية الزراعة - جامعة كفر الشيخ - مصر.

تم تقييم عشرة تراكيب وراثية من هجن الأرز بالمزرعة البحثية بمركز البحوث والتدريب بسخا - كفر الشيخ - مصر، فى موسم ٢٠١٥ و ٢٠١٦ لدراسة الاختلاف الوراثى و الارتباط البينى بالإضافة الى تحديد التراكيب الوراثية المرغوب فيها. أعطى موسم ٢٠١٥ أعلى المتوسطات بين معظم التراكيب الوراثية لجميع الصفات تحت الدراسة مقارنة بموسم الزراعة ٢٠١٦ ما عدا عدد الايام الى النضج ، محصول الحبوب (طن/فدان) و صفات شكل الحبة (طول ، عرض الحبة). وجدت اختلافات عالية المعنوية بين جميع التراكيب الوراثية لجميع الصفات تحت الدراسة. أعطى الهجين G46A/WTR1 يليه G46A/LH1 أعلى محصول حبوب . كانت حبوب كل التراكيب الوراثية لهجن الأرز ذات شكل حبوب متوسط (نسبة > ٣) ماعدا G46A/IR04A132 ذات شكل حبة اسطوانى (نسبة < ٣). سجل الهجين IR69625A/WAB6-125 أعلى نسبة تبيض (٧٠.٥%). أعطى الهجين G46A/IR43 أقل نسبة حبوب مكسورة (٦.٨%) يليه G46A/HHZ5-Y3-Y1-DT1 (٨.١%). كانت كل الهجن ذات درجة حرارة جلتنة متوسطة ما عدا الهجين IR69625A/CT19021-3-4 ذو درجة حرارة جلتنة عالية. تراوحت نسبة الاميلوز فى حبوب كل الهجن بين ٢١.٦% الى ٢٥.٧%. لا توجد فروق معنوية بين متوسطات مربعات التفاعل بين التراكيب الوراثية و السنوات لكل الصفات تحت الدراسة ما عدا صفة وزن ١٠٠٠- حبة و نسبة الحبوب السليمة. كانت قيم تقدير درجة التوريث عالية و تراوحت بين (٧١.٠٥% الى ٩٩.٩٥%) باستبعاد صفة درجة حرارة الجلتنة . وجدت اختلافات وراثية واسعة بين التراكيب الوراثية المستخدمه و التى يمكن ان تستخدم فى الانتخاب على اساس الشكل المظهري. كانت درجة التوريث و التحسين الوراثى عالية لكل من شكل الحبة (طول / عرض) (٩٥.٥٢ ، ٢٦.٥٧%) ، نسبة الحبوب السليمة (٩٩.٨٤% ، ٢١.٠٣%) و نسبة الاستطالة (٧١.٠٥% ، ٣٤.٠٩%) على التوالى. لوحظ أن هناك ارتباط معنوى موجب بين المحصول وكلا من عدد الايام حتى النضج (ر = ٠.٦٣٥) و عدد الداليات للذبات (ر = ٠.٦٥٥) و عرض الحبة (ر = ٠.٧١٢). كما لوحظ ان هناك ارتباط عالى المعنوية و موجب بين طول الحبة و شكل الحبة (طول/ عرض) (ر = ٠.٩٢٧) و وجد ارتباط معنوى سالب مع عرض الحبة (ر = -٠.٧٠). كان الارتباط بين نسبة التفتير و كل من نسبة التبيض (ر = ٠.٧٦٠) و نسبة الاميلوز (ر = ٠.٧٣٠) معنوى و موجب.