

IDENTIFICATION OF NEW HIGH YIELDING INDICA-JAPONICA AND EFFECTIVE RESTORER VARIETY FOR DIFFERENT CYTOPLASMIC MALE STERILE (CMS) SOURCES IN RICE

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ABSTRACT: The development and use of hybrid rice technology on a commercial scale may be an innovation to reduce the gap between rice production and demand to feed more than half of the world's population. Hybrid rice production is based on a combination of the cytoplasmic male sterile line (CMS) and the restored line through cross-pollination, thus identification of effective and strong restorer is an important part in this process. In the present study, the promising line GZ10848-1-2-2-1 (Giza 183) was screened using three different CMS sources (Wild Abortive, Gambiaca and Kalinga) to study the fertility restoration ability through a test-cross nursery. The results identified that GZ10848 behaved as a suitable and complete restorer variety in synchronization and some other traits for all the four CMS lines. Four strongly heterotic F₁ hybrid combinations along with the check variety were evaluated to yield and its component characters. The analysis of variance of hybrid crosses revealed that highly significant differences for all studied traits. The hybrid combinations IR69625A/GZ10848 and E2021A/GZ10848 were superior for most studied traits and have high yield advantage than check commercial hybrid. All crosses demonstrated highly significant and positive standard heterosis for grain yield with values ranged from 15.58% to 20.42%. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all studied traits. Broad-sense heritability estimates for studied characters ranged from 31.23 to 99.04%. Highly significant positive correlations coefficient observed between grain yield and each of grain thickness and grain width. According to findings, hybrid combinations produced from this R line showed better performance relative to check variety EHR1. These results demonstrate that GZ10848 line including five fertility restorer genes *Rf3*, *Rf4*, *Rf5*, *Rf6* and *Rf1* in addition high yielding and desirable traits. Identification of like this high yield restorer line can be used in hybrid and inbred rice breeding programs to develop new hybrid rice varieties on a commercial scale.

Keywords: Cytoplasmic male sterile (CMS) line; restorer line; hybrids; high-yielding.

INTRODUCTION

As a strategic and staple crop, rice is the staple food and most widely cultivated cereal crop in the world (Liesack *et al.*, 2000). Today rice is a source that provides 50-80% of the daily calories for more than third world countries (Wynn, 2009). The World Food Program (WFP 2016) reports indicate that global warming is making rice fields less productive and on average, rice production per hectare is growing more slowly than that of the world's population, and this would likely lead to a food crisis (Masipa, 2017). Therefore, it is necessary to

increase rice productivity to meet the needs of growing population. Hybrid rice, as one of the most successful crops exploiting heterosis, has greatly contributed to global food security. The exploitation of hybrid rice technology has enabled the commercialization of heterosis in rice, with a significant increase yield and total production of this major staple food crop (Huang *et al.*, 2014).

Hybrid rice cultivation is a new technology should be popularized among farmers in rice growing areas. The increase in yield of hybrid rice varieties is about 20-25% than the existing

inbred high-yielding varieties (Julfiqar, 2009). The hybrid rice variety is produced either through the three-line system or the two-line system (Huang *et al.*, 2014; Kim and Zhang, 2018). Three-line hybrid rice technology, which is also known as the first generation of hybrid rice, consists of three types of parental lines; a cytoplasmic male sterile (CMS) line, a maintainer line and a restorer line (Zhu, 2016; Chen and Liu, 2014). Rice hybrid seeds are produced between the cytoplasmic male sterile (CMS) line and a fertility restorer line of different genotypes. Several CMS systems with different cytoplasm and nucleus sources have been generated through backcross breeding program. According to the previous studies, a total of 13 types of cytoplasmic male sterile (CMS) lines have been used in developing hybrid rice varieties (Huang *et al.*, 2014).

The pollen fertility of CMS lines can be restored in the presence of nuclear fertility restorer (*Rf*) genes and some of them are distinguished by molecular biology studies (Itabashi *et al.*, 2010). For instance, Wild Abortive-CMS line requires two major fertility restoration genes, *Rf3* and *Rf4*, for recovery of pollen fertility and these major genes (*Rf3* and *Rf4*) have been mapped on chromosomes 1 and 10, respectively (Zhang *et al.*, 1997; Ahmadikhah and Karlov, 2006). Gambiaca-CMS lines are restored by two fertility restorer genes *Rf5* and *Rf6*, which has been located on chromosome 10 (Liu *et al.*, 2004). The *Rf* gene responsible for restoration ability of Kalinga-CMS lines, *Rf1* is mapped to chromosome 10 (Shinjyo, 1975). Development of parental lines is the main reason of continuous success of the hybrid rice breeding program. Therefore, a need to develop and improve new parental lines such as maintainer and restorer lines with high yielding and good floral traits is necessary (Anis, 2019).

There are many advanced lines derived from diverse crosses and bred by Rice Research and training center (RRTC). These lines were also included in the breeding program in preliminary

yield trials (PYT) for targets different. Annually, most of Indica and Indica-Japonica advanced lines are selected based on good phenotypic acceptability for testcross nursery with different CMS lines to identify restorer and maintainer lines. The best of locally adaptable parental lines (restorers and maintainers) are nominated in the hybrid source nursery. One of these nominated lines namely GZ10848; was selected as an effective restorer line for further studies. GZ10848 combines the complementary advantages of its two parents and shows the wide adaptability, superior grain quality and agronomic traits including yield and resistance. Fortunately, this promising line GZ10848-1-2-2-1 was released with the new variety "Giza 183" by Rice Research and Training Center (RRTC) in 2023. The study aimed to: utilize potential restorer variety to further enhance the restorer line gene pool of hybrid breeding program. In addition to perform phenotype screening and discrimination of a new variety of rice in terms of floral and morphological traits and genetic variability as well as screening of the distinctive fertility restoration genes with different cytoplasmic male sterile (CMS) sources in rice.

MATERIALS AND METHODS

Genetic materials and field experiment

The new promising line GZ10848-1-2-2-1 (Giza 183) is an effective indica-japonica rice restorer line for different cytoplasmic male sterile (CMS) sources according to the previous testcross nursery (unpublished). In the study, this line was selected as a male parent to cross with four CMS lines of rice obtained from different sterile sources of Wild Abortive (WA), Gambiaca (GA) and Kalinga using three lines system of hybrid rice technology for conformation the resultant (Table 1). The used cytoplasmic male sterile (CMS) included two exotic lines (IR69625A is an IRRI-bred CMS and G46A was provided by China) and two new locally adapted lines E2015A and E2021A (unpublished).

Table 1. Background information of the seven rice genotypes evaluated in the study

Genotypes	Cytoplasmic source	Parentage	Origin	Remarks
IR69625A	Wild Abortive (WA)	----	IRRI	Commercial line
G46A	Gambiaca	----	China	Commercial line
E2015A	Kalinga	Large stigma A/advanced line-23 ^a	Egypt	New CMS line
E2021A	Wild Abortive (WA)	IR69625A/ advanced line-106 ^b	Egypt	New CMS line
GZ10848	----	Giza 178/ SKC23819	Egypt	Promising inbred lines
Giza 178 (ck)	----	Giza 175/Milyang 49	Egypt	Cultivar
EHR1 ^c (ck)	----	IR69625A/Giza 178	Egypt	Cultivar

^a and ^b; Advanced lines 23 and 106 derived from a cross between G46B and Large stigma B. ^c EHR1: Egyptian Hybrid Rice 1. ck; Check cultivar

The investigation was conducted at the experimental farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt, during two growing successful seasons 2022 and 2023. To study the genetic fertility restoration ability among the restorer line GZ10848 and three CMS sources, single crosses were made using A-lines and R-line. In 2022 growing season, the parental lines were planted with two sowing dates at fifteen days intervals to overcome the differences in flowering date. Sets plants of CMS lines were transferred to pots previously filled with water for facilitating of hybridization at flowering stage. The CMS panicles were clipped in the evening and hand pollination was done in the following morning by dusting pollen from the selected effective restorer rice genotype GZ10848. The crossed panicles were tagged and bagged properly with white papers to avoid unwanted pollination. The sufficient spikelets of four crosses were collected from panicles after 25 days and properly packed for sowing in the following season. In 2023, four F₁s hybrids along with their parents, Giza 178 (ck) and standard check EHR1 (Egyptian Hybrid Rice 1) were grown in the nursery. After 30 days of sowing, the seedlings were transplanted in 7 rows with 5m long and 20 x 20 cm spacing. The experiment was laid out in Randomized Complete Block Design (RCBD) involving seven rice genotypes (4 hybrids, R-line, two check cultivars) with three replicates was followed. The agronomic practices such as irrigation, fertilizers application, herbicides and pests control were done as recommended with rice crop during both

seasons of the study as recommended by RRTC (2020).

Data collection

The following attributes were gathered: duration (day), plant height (cm), panicles plant⁻¹, panicle length (cm), panicle weight (g), primary branches panicle⁻¹, 1000-grain weight (g), spikelet fertility %, grain yield (t/f), grain length (mm), grain width (mm) and grain thickness (mm) were measured according to the description for rice (IRRI, 1996).

Spikelets fertility (%) =

$$\frac{\text{Number of filled spikelets/panicle}}{\text{Total number of spikelets/panicle}} \times 100$$

The stamen floral traits were measured for GZ10848 and Giza 178 with a micrometer under a stereo-microscope. Ten florets (plants/panicles) per each variety were used for measurement of anther length (mm), anther width (mm), pollen fertility (%), number of pollen grains/anther and filament elongation (mm) for pollen parent compared with Giza 178.

Statistical Analysis

Differences between rice genotypes for the studied traits were tested for significance by the Analysis of Variance (ANOVA) using MSTAT software. Based on mean data, standard heterosis was calculated for the four hybrid combinations over the check variety EHR1, according to Mather and Jinks (1982) using the following formula:

Standard heterosis (%) =

$$\frac{\bar{F}_1 - \text{check variety}}{\text{check variety}} \times 100$$

Genotypic and phenotypic coefficients of variation were estimated as per Singh and Chaudhary (1985). The broad sense heritability in percent of mean was calculated as suggested by Jonson *et al.* (1955). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were assessed according to Burton (1952)

Where \bar{x} = grand mean of character under study.

$$\sigma^2_g = (\text{MSG} - \text{MSE})/r$$

$$\sigma^2_p = (\text{GV} + \text{MSE})$$

$$\text{PCV} (\%) = (\sqrt{\sigma^2_p / \bar{x}}) \times 100$$

$$\text{GCV} (\%) = (\sqrt{\sigma^2_g / \bar{x}}) \times 100$$

$$H^2 = (\sigma^2_g / \sigma^2_p) \times 100$$

Where: MSG is the mean square of accessions, MSE is mean square of error, and r is number of replications. Normal Pearson's correlation was calculated using SPSS 10.0 software.

RESULTS AND DISCUSSION

Characterization of GZ10848 compared with Giza 178 as restorer varieties

Giza 178 is the inbred commercial variety derived from the female parent Giza 175, and the male parent Milyang 49 as shown in (Table 1). Giza 178 is cultivated in large areas inside Egypt, especially in the lands affected by salinity. At the same time, it is the only commercial restorer line of rice in the Egyptian rice breeding program and is used in the production of Egyptian hybrid rice 1 (EHR1). Despite the distinction of Giza 178 in most of the characteristics as a restorer line, there are some defects such as the plant height and some other floral traits which lead to the lowest outcrossing in the field of seed production. Giza 178 also has a small size of grain and therefore low weight for a thousand grains (Awad-Allah *et al.*, 2022). So, the new restorer line GZ10848 was derived by hybridizing between Giza 178 and SKC23819. This line featured many characteristics, such as high (tallest) plant height, high grain size, high pollen fertility %, long anther length, anther width and filament elongation compared with the local restorer line

Giza178 (Figure 1). According to the results, the respective restorer line, which is GZ10848, was superior by having a longer anther length (1.80 mm), wider anther width (0.49 mm), longer filament length (0.69 mm) and much more spikelet fertility % (98.07 %) compared with Giza 178 and showed the best values and stability over two seasons (Figure 1d,e,f,g). Therefore, it is expected that the out-crossing rate of the new restorer lines GZ10848 with CMS lines might be better than Giza 178. Information on flowering behaviors such as anther length, anther width and filament elongation of parental lines may be beneficial to the breeders in hybrid rice seed production fields (Anis *et al.*, 2019; Hashim *et al.*, 2021).

GZ10848 synchronization and compatibility with various CMS lines

Flowering synchronization of male and female plants is basic to obtaining a high yielding because this depends on the amount of pollen provided from the male parent during flowering period (Mondo *et al.*, 2016). To achieve the optimum synchronization of flowering to obtain a good outcrossing, the CMS line should flower 1-2 days earlier than the restorer line (Sindhu and Kumar, 2002). Days to heading was expressed differentially between CMS and restorer lines. Data in Table 2 showed the restorer line GZ10848-1-2-2-1 was earlier than the four studied CMS lines, but this difference is insignificant and can be overcome by planting date. Also plant height of parental lines plays a significant role in determining the extent of seed set in the hybrid rice seed production (Vishwakarma *et al.*, 2016). The ideal and quality of seed production requires that the pollinator be longer than the female parent. According to the results, the restorer line GZ10848 showed the tallest plant height (104 cm) as compared to studied CMS lines IR69625A(98 cm), G46A (95 cm), E2015A (89 cm) and E2021A(92 cm). Our results identified that GZ10848 behaved as a suitable and complete restorer variety for all the four CMS lines and it could be utilized in the heterosis breeding. Previous studies reported many restorer lines.

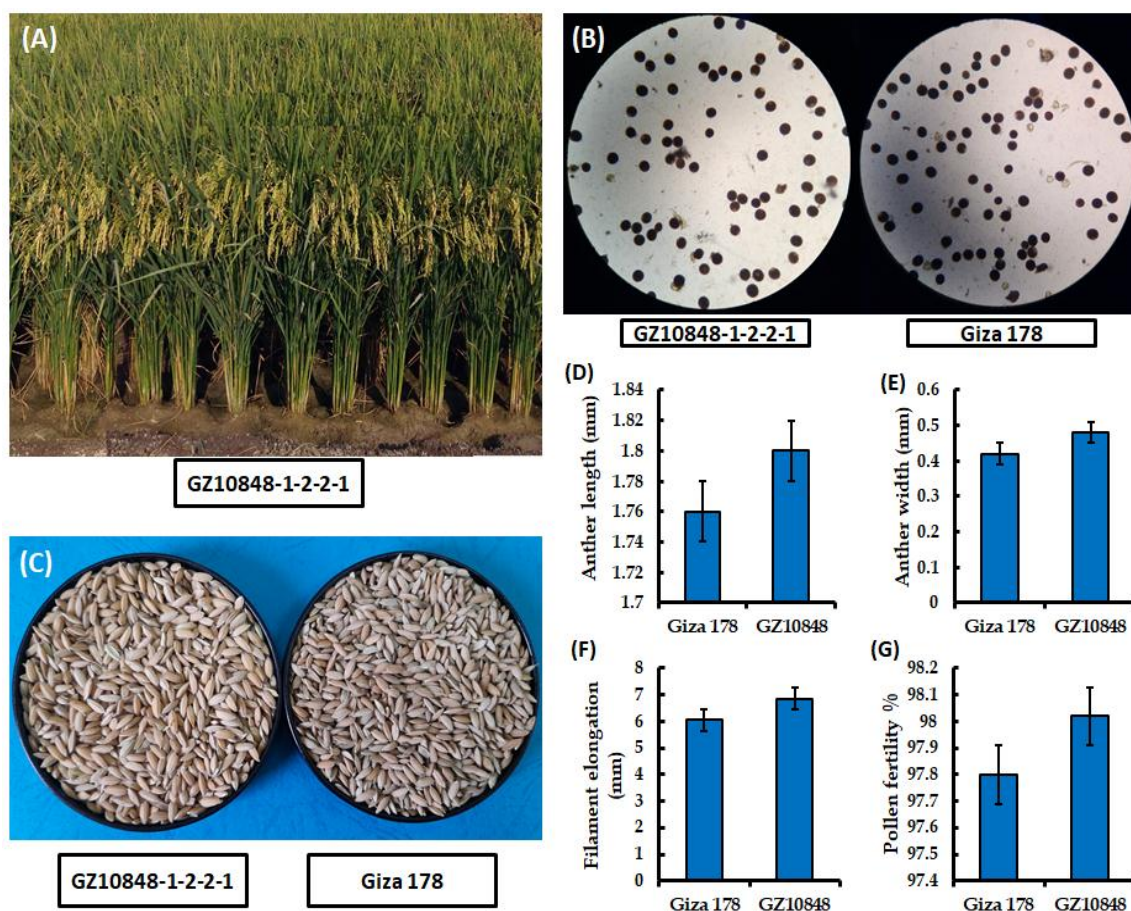


Figure (1). Characterization of GZ10848 compared with Giza 178 for morphological and cytological traits.

Table (2). Flowering period of different cytoplasmic male sterile (CMS) line sources and their suitability with the new restorer line GZ10848.

Genotypes	Start flowering	End flowering	Days to		Flowering period (day)	Plant height (cm)	Compatibility with GZ10848
			Start	End			
IR69625A	5 August	11 August	98	104	7	98	G
G46A	24 July	2 August	86	95	10	95	VG
E2015A	9 July	17 July	71	79	8	89	EX
E2021A	21 July	29 July	83	91	9	92	EX
GZ10848	21 July	27 July	83	89	6	104	----

G: Good; VG: Very good; EX: Excellent.

The performance of agronomic traits for new hybrid combinations

To test whether the phenotypic traits of four new hybrids combinations derived from a cross

between GZ10848 and different CMS lines, we examined nine agro-morphological traits and three rice dimension traits of Egyptian hybrid rice 1 (EHR1 as check variety) and four hybrids

combinations (Table 3 and 4). Based on days to maturing (duration), the hybrid combinations matured in 125-132 days from sowing date while the check variety EHR1 matured in 135 days. These indicating that the four developed hybrid combinations IR69625A/GZ10848 (125), G46A/GZ10848 (132), E2015A/GZ10848 (126) and E2021A/GZ10848 (126) were earlier than the check variety. Moreover, the plant height trait of the four developed hybrid combinations was higher than that of EHR1. Plant height ranged from 109 cm for hybrid combination IR69625A/GZ10848 to 115 cm for hybrid combination E2021A/GZ10848, while the check variety EHR1 was 108 cm.

Results concluded that three hybrid combinations G46A/GZ10848 (114 cm), E2015A/GZ10848 (113 cm) and E2021A/GZ10848 (115 cm) recorded significant values compared with the check EHR1 (108 cm). For panicles plant-1, the EHR1 showed high mean value (23.10 panicles) compared with the other hybrid combinations that ranged from 15.67 to 20.40 for E2015A/GZ10848 and E2021A/GZ10848, respectively. The hybrid combinations IR69625A/GZ10848 and G46A/GZ10848 recorded longer panicle length (24.50 cm) and (28.87cm), respectively compared with the check variety EHR1 (26.20 cm). In the contrary, hybrid combinations E2015A/GZ10848 and E2021A/GZ10848 were

lower than EHR1 in panicle length with values 26.17 and 24.33, respectively. For panicle weight, all hybrid combinations were higher than the check variety EHR1 with values ranged from 4.96 g (IR69625A/GZ10848) to 7.29 g (G46A/GZ10848) while the EHR1 recorded 4.25 g for panicle weight. Regarding number of primary branches panicle-1, the top performers being hybrid combinations IR69625A/GZ10848, G46A/GZ10848 and E2015A/GZ10848 with values ranged from 11.33 to 12.33 branches. Based on the 1000-grain weight, rice hybrid E2015A/GZ10848 had the highest value of 31.50 g compared with EHR1 (25.03 g), while the hybrid combination IR69625A/GZ10848 had the lowest value of 25.83 g. Spikelet fertility % reached to 95.03 % for hybrid combination IR69625A/ GZ10848 compared with the check variety EHR1 87.52%. The rest of hybrid combinations were lower spikelet fertility % than EHR1. All of the hybrids gave higher yield than EHR1 as a check. The hybrid combination E2021A/GZ10848 produced the highest grain yield (5.72 t/f) followed by IR69625A/GZ10848 with value of 5.61 t/f. Several scientists reported that the hybrid rice combinations produced heavy panicle, higher number of branches/panicle and heavy grain weight also showed higher grain yield (Bhuiyan *et al.*, 2014 and Sarkar *et al.*, 2016 and Hassan *et al.*, 2017).

Table (3). Mean performance values of hybrid combinations for agro-morphological characters.

Hybrid combinations	Duration (day)	Plant height (cm)	Panicles plant ⁻¹	Panicle length (cm)	Panicle weight (g)	Primary branches panicle ⁻¹
IR69625A/ GZ10848	125.33	109.00	20.00	24.50	4.96	11.33
G46A/ GZ10848	132.00	114.00	17.33	28.87	7.29	12.33
E2015A/ GZ10848	126.67	113.00	15.67	26.17	6.08	12.00
E2021A/ GZ10848	126.33	115.67	20.40	24.33	5.25	10.33
EHR1 (ck)	135.00	108.33	23.10	26.20	4.25	10.67
Grand mean	129.07	112.00	19.30	26.01	5.57	11.33
SE	0.54	1.16	0.99	0.84	0.19	0.42

Table (4). Mean performance values of hybrid combinations for yield characters.

Hybrid combinations	1000-grain weight (g)	Spikelet fertility %	Grain yield (t/f)	Grain length (mm)	Grain width (mm)	Grain thickness (mm)
IR69625A/GZ10848	25.83	95.03	5.61	8.10	2.95	2.07
G46A/GZ10848	27.83	85.59	5.53	7.98	3.21	2.15
E2015A/GZ10848	31.50	83.21	5.49	8.32	3.24	2.16
E2021A/GZ10848	31.00	86.26	5.72	8.14	3.16	2.12
EHR1 (ck)	25.03	87.52	4.75	8.04	2.74	1.98
Grand mean	28.24	87.52	5.42	8.12	3.06	2.10
SE	0.23	2.13	0.12	0.04	0.06	0.07

The results in Table 4 revealed that all new promising hybrids had high values for grain length with values ranged from 7.98 mm to 8.32 mm compared with the check variety EHR1 (8.04 mm). The new hybrid combination E2015A/GZ10848 had the highest grain width (3.24 mm) while IR69625A/GZ10848 had the lowest value (2.95 mm). The results for grain thickness revealed that, all the hybrid combinations have best values of grain thickness

compared with EHR1 (Figure 2). Finally it can be concluded that the hybrid combinations IR69625A/GZ10848 and E2021A/GZ10848 were superior for most studied traits and have high yield advantage than check and commercial hybrid. Thus, these two promising hybrids will promote for evaluation in multi-locations yield trails. Abd El-Hadi *et al.*, (2013) and Anis (2013) found similar results during evaluating several new hybrid combinations.

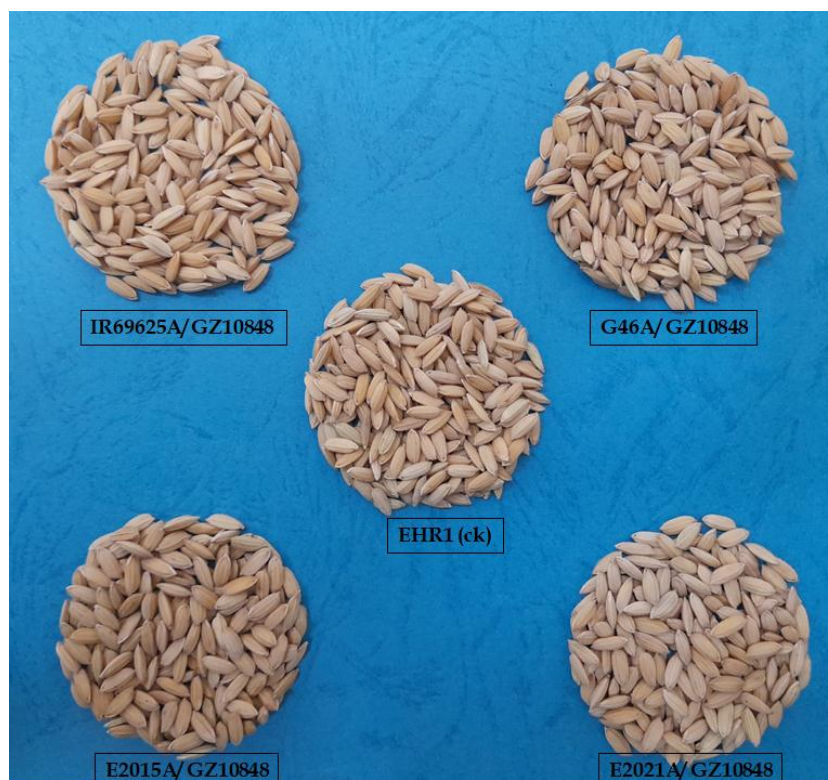


Figure (2). Comparison view between commercial hybrid rice (EHR1) and the new promising hybrids derived from GZ10848.

Analysis of variance

The analyses of variance for four developed hybrid combinations as well as the check variety (EHR1) in terms of twelve agronomical traits are shown in (Table 5). Analysis of variance for augmented design showed highly significant differences among the genotypes for all studied

traits except grain thickness, this result indicating the existence of wide variation among the genotypes for different studied traits. Previous studies in rice also found significant variation for these traits (Jayasudha and Sharma, 2009; Rahimi *et al.*, 2010, Latha *et al.*, 2013, Anis *et al.*, 2016 and ElShamey *et al.*, 2022).

Table (5). Analysis of variance for five hybrid rice combinations based on agro-morphological and yield traits in rice

S.O.V	d.f.	Duration (day)	Plant height (cm)	Panicles plant ⁻¹	Panicle length (cm)	Panicle weight (g)	Primary branches panicle ⁻¹
Replications	2	1.27	0.20	1.69	0.34	0.09	0.27
Genotypes	4	53.23**	30.67**	24.91**	9.98**	4.07**	2.17**
Error	8	0.43	1.87	1.48	1.05	0.05	0.27
S.O.V	d.f.	1000-grain weight (g)	Spikelet fertility %	Grain yield (t/f)	Grain length (mm)	Grain width (mm)	Grain thickness (mm)
Replications	2	0.01	3.44	0.01	0.01	0.00	0.00
Genotypes	4	25.86**	60.26**	0.44**	0.05**	0.14**	0.02 ^{ns}
Error	8	0.08	6.81	0.02	0.01	0.01	0.01

Estimation of standard heterosis

Heterosis for yield and yield component traits was calculated over check variety. The magnitude of heterosis varied from trait to trait, and cross to cross (Table 6). The hybrid combinations demonstrated highly significant negative (desirable) heterosis over the check variety EHR1 for duration. While the hybrids G46A/GZ10848, E2015A/GZ10848 and E2021A/GZ10848 showed significant and positive heterotic effects for plant height. For panicles plant⁻¹, all hybrids showed highly significant negative estimates and these results undesirable for rice breeder. Regarding panicle length (cm), the hybrid combinations IR69625A/GZ10848 and E2021A/GZ10848 showed significant negative estimate value while the hybrid G46A/GZ10848 gave highly significant positive estimate value at the same time the hybrid E2015A/GZ10848 gave insignificant value. For panicle weight, 1000-grain weight, grain yield and grain width all crosses demonstrated highly significant and positive desirable estimates. The two hybrids

G46A/GZ10848 and E2015A/GZ10848 recorded highly significant positive estimate value and the other two hybrids gave insignificant estimate value for primary branches panicle-1 trait. For spikelet fertility %, the hybrid IR69625A/GZ10848 recorded highly significant positive estimate value, also the hybrid E2015A/GZ10848 gave significant negative estimate value and the hybrids G46A/GZ10848 and E2021A/GZ10848 gave insignificant estimate value. For grain length, the two hybrids E2015A/GZ10848 and E2021A/GZ10848 showed significant and highly significant positive estimates, while the hybrids IR69625A/GZ10848 and G46A/GZ10848 showed insignificant estimate value. Regarding grain thickness, all hybrids gave significant positive estimate value except the hybrid IR69625A/GZ10848 showed insignificant estimate value (Figure 3). Similar results were proved by (Jelodar and Bagheri, 2010; Rahimi *et al.*, 2010, Hussain and Sanghera, 2012, Latha *et al.*, 2013 and Gaballah *et al.*, 2022).

Table (6). Estimation of standard heterosis over commercial hybrid rice variety (EHR1).

Traits	Crosses	H ₁	H ₂	H ₃	H ₄	LSD	
						0.05%	0.01%
Duration (day)		-7.16**	-2.22**	-6.17**	-6.42**	0.99	1.55
Plant height (cm)		0.62 ^{ns}	5.23**	4.31**	6.77**	2.07	3.23
Panicles plant ⁻¹		-13.42**	-24.96**	-32.18**	-11.69*	1.84	2.87
Panicle length (cm)		-6.49*	10.18**	-0.13 ^{ns}	-7.12*	1.55	2.42
Panicle weight (g)		16.54**	71.39**	42.95**	23.35**	0.35	0.54
Primary branches panicle ⁻¹		6.25 ^{ns}	15.63**	12.50**	-3.12 ^{ns}	0.78	1.22
1000-grain weight (g)		3.20**	11.19**	25.83**	23.83**	0.44	0.68
Spikelet fertility %		8.59**	-2.20 ^{ns}	-4.93*	-1.43 ^{ns}	3.96	6.17
Grain yield (t/f)		18.11**	16.42**	15.58**	20.42**	0.23	0.34
Grain length (mm)		0.76 ^{ns}	-0.79 ^{ns}	3.48**	1.24*	0.08	0.13
Grain width (mm)		7.66**	17.27**	18.25**	15.33**	0.13	0.20
Grain thickness (mm)		4.49 ^{ns}	8.75*	9.09*	7.24*	0.12	0.19

Abbreviations: H₁: IR69625A/ GZ10848; H₂: G46A/ GZ10848; H₃: E2015A/ GZ10848 and H₄: E2021A/ GZ10848.

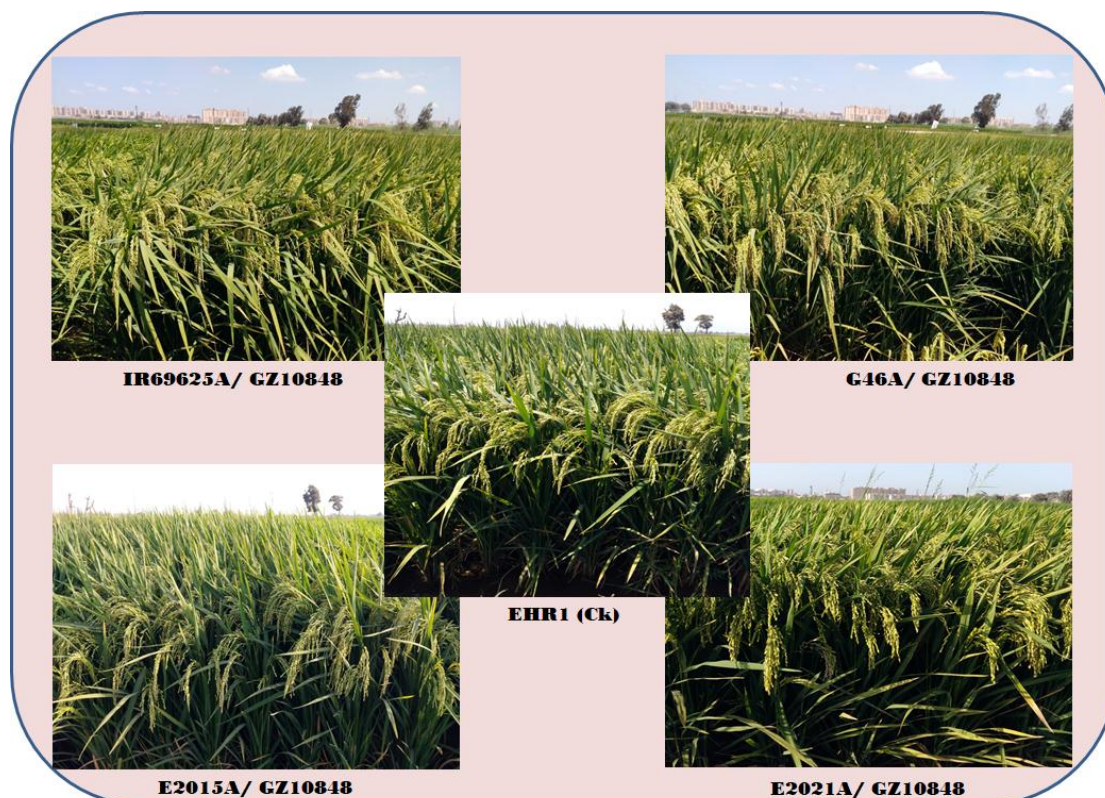


Figure (3). Field view between commercial hybrid rice (EHR1) and the new promising hybrids derived from GZ10848.

Estimation of genetic variability and heritability

In general, the phenotypic coefficient of variation was higher than the genotypic coefficient of variation. Variance and Heritability presented in Table 7 showed that the phenotypic variance exhibited higher than genetic variance for most studied trait except grain length, grain width and grain thickness were equal. The phenotypic coefficient of variation (PCV) was close to the genotypic coefficient of variation (GCV) for all characteristics. Panicle weight and panicles plant-1 exhibited the highest estimates of GCV and PCV, followed by 1000 grain weight, panicle length, grain yield and grain

width. The lowest estimates of PCV were for grain length. Broad-sense heritability estimates for all studied traits ranged from 31.23 to 99.04%. Most of the traits showed relatively high heritability values (>80%) except for panicle length (73.94%), primary branches panicle-1 (70.37%), spikelet fertility % (72.34%) and grain thickness (31.23%). The present results demonstrated a relatively influence of environmental factors on the expression of the studied traits. These results agreed well with those of earlier researchers (Sabri *et al.*, 2020; Esther *et al.*, 2021; Faysal *et al.*, 2022; El-Malky and Al-Daej 2023; Rezk *et al.*, 2024)

Table (7). Genetic parameters of variability for yield and yield attributing characters in rice

Characteristics	Genotypic variance	Phenotypic variance	Genotypic coefficient of variability (GCV)	Phenotypic coefficient of variability (PCV)	Broad sense heritability (%)
Duration (day)	17.60	18.03	3.25	3.29	97.60
Plant height (cm)	9.60	11.47	2.77	3.02	83.72
Panicles plant ⁻¹	7.81	9.29	14.48	15.79	84.07
Panicle length (cm)	2.98	4.03	6.63	7.72	73.94
Panicle weight (g)	1.34	1.39	20.81	21.21	96.26
Primary branches panicle ⁻¹	0.63	0.90	7.02	8.37	70.37
1000-grain weight (g)	8.59	8.68	10.38	10.43	99.04
Spikelet fertility %	17.82	24.63	4.82	5.67	72.34
Grain yield (t/f)	0.14	0.16	6.93	7.42	87.27
Grain length (mm)	0.01597	0.01877	1.56	1.69	85.09
Grain width (mm)	0.04281	0.04969	6.76	7.28	86.16
Grain thickness (mm)	0.00322	0.01030	2.70	4.84	31.23

Estimation of correlation coefficient

Correlation coefficients analysis among twelve agro-morphological traits is shown in Figure 4. Results revealed that duration possessed significant positive correlation with panicle length and significant negative correlation with grain yield and grain length. Also, plant height was positive significant with grain width, 1000-grain weight, grain thickness and panicle weight with values of ($r = 0.87$, 0.84 , 0.81 and 0.63 , respectively). Correlation results

revealed significant and highly significant negative values between panicles plant-1 and each of panicle weight ($r = 0.82$), primary branches panicle⁻¹ ($r = 0.82$), 1000 grain weight ($r = 0.65$), grain width ($r = 0.87$) and grain thickness ($r = 0.91$). Results indicated that panicle length was positive correlation and highly significant with panicle weight ($r = 0.73$) and primary branches panicle-1 ($r = 0.73$) this indicated that increasing the panicle length will increase the panicle weight and number of

branches per panicle. On the other hand, highly significant and positive correlation was found between panicle weight and each of primary branches panicle⁻¹ (r = 0.82), grain width (r = 0.82) and grain thickness (r = 0.83). Also, 1000 grain weight recorded highly significant positive correlation with grain thickness, grain width and grain length and significant correlation with grain yield at the same time observed negative correlation with spikelet fertility %. Highly significant positive correlation observed between grain yield and grain thickness and width. This means increasing the grain thickness and width traits will increase the grain yield. Also, observed highly correlated between grain width and grain thickness. In terms of grain form, grain width was recorded highly significant and positive strong correlation with grain thickness and the value was (r = 0.99). These results agree with the findings of Kumar *et al.* (2017), Bhutta *et al.* (2019), Panda *et al.* (2019) and Saleh *et al.* (2020).

Expected *Rf* genes in GZ10848 line

Based on the previous reported, Wild Abortive-CMS line requires two major fertility restoration genes, *Rf3* and *Rf4*, for recover fertility and these major genes (*Rf3* and *Rf4*) have been mapped on chromosomes 1 and 10, respectively (Zhang *et al.*, 1997; Ahmadikhah and Karlov, 2006; Ngangkham *et al.*, 2010; Suresh *et al.*, 2012), Gambiaca-CMS lines are restored by two fertility restorer genes *Rf5* and *Rf6*, which has been located on chromosome 10 (Liu *et al.*, 2004) and Kalinga-CMS lines are restored by *Rf1* which mapped to chromosome 10 (Shinjyo, 1975). We can confirm that, GZ10848 is restorer and including five fertility restorer genes *Rf3* and *Rf4*, *Rf5*, *Rf6* and *Rf1* (Figure 5). In addition, this superior line performed high yielding and desirable traits. Identification of like this high-yielding restorer line could be effectively utilized in inbred and hybrid rice breeding programs to develop new hybrid rice varieties.

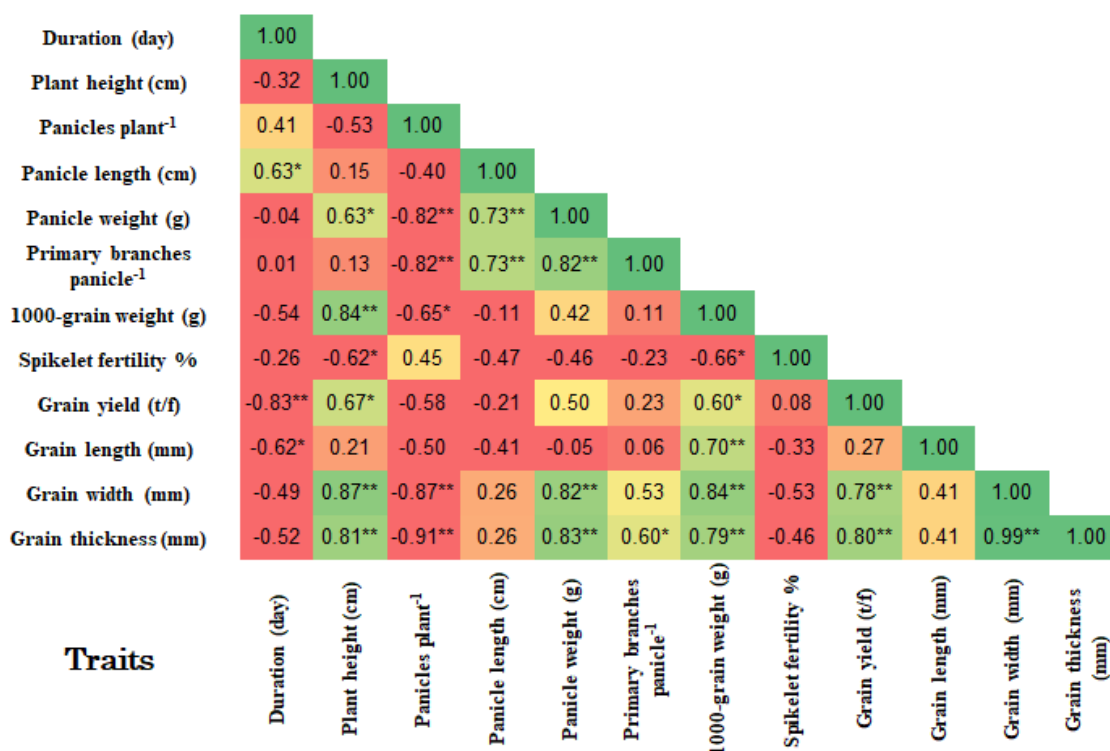


Figure (4). Phenotypic correlation coefficients among 12 different characters in studied rice genotypes.

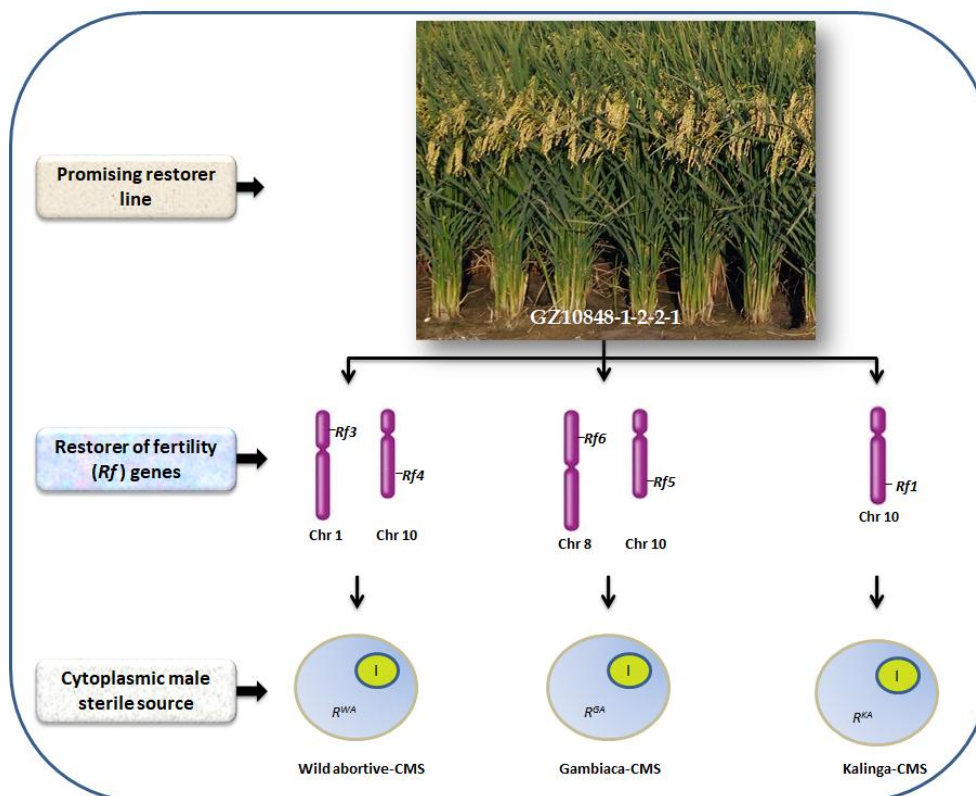


Figure (5). Schematic presentation of the restorer fertility (*Rf*) genes involved in the promising restorer line GZ10848 as well as cytoplasmic sources of CMS types.

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تحديد صنف أرز جديد هندي- ياباني عالى المحصول ومعيد للخصوبة لمصادر مختلفة من العقم الذكري السيتوبلازمي فى الأرز

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المخلص العربى

إستخدام وتطوير تكنولوجيا الأرز الهجين على نطاق تجاري بمثابة نهج وراثي مبتكر لتقليص الفجوة بين إنتاج الأرز والطلب عليه لإطعام العدد الزائد من السكان في بلدان العالم الثالث. يعتمد الأرز الهجين على التهجين بين سلالات العقم الذكري السيتوبلازمي والأب المعيد للخصوبة من خلال التلقيح، وبالتالي فإن تحديد السلالة المعيدة للخصوبة الفعالة والقوية يعد جزءاً مهماً في هذه العملية. في هذه الدراسة تم فحص السلالة المبشرة GZ10848 (جيزة 183) باستخدام ثلاثة مصادر مختلفة للعقم وهى (Wild Abortive ، Gambiaca و Kalinga) لدراسة القدرة على استعادة الخصوبة من خلال التهجين الاختباري. حددت النتائج أن GZ10848 هى سلالة معيدة للخصوبة بشكل جيد وان هناك تزامن في التزهير وبعض الصفات الاخرى بينها وبين سلالات العقم الذكري السيتوبلازمي CMS الأربعة. تم تقييم أربع تراكيب هجينية مع الصنف المقارن من ناحية المحصول ومكوناته. أظهر تحليل التباين لجميع التراكيب الهجينة وجود فروق عالية المعنوية لجميع الصفات المدروسة. كانت التراكيب الهجينية IR69625A/GZ10848 و E2021A/GZ10848 متفوقة في معظم الصفات المدروسة ولها ميزة إنتاجية عالية مقارنة بالهجين التجاري. أظهرت جميع الهجن معنوية عالية وموجبة لصفة المحصول بقيم تراوحت بين 15.08% إلى 20.42%. وكان معامل التباين المظهري قريباً من معامل التباين الوراثي لجميع الصفات. تراوحت تقديرات درجة التوريث بالمعنى الواسع لجميع الصفات المدروسة من 23.31 إلى 99.04%. لوحظ وجود معامل ارتباط موجب عالي المعنوية بين محصول الحبوب وكل من سمك الحبة و عرض الحبة. وفقاً للنتائج، أظهرت التراكيب الهجينية المنتجة من تلك السلالة المعيدة للخصوبة أداء أفضل مقارنة بالهجين التجاري. وتوضح هذه النتائج أن السلالة GZ10848 قد تحتوى على خمسة جينات معيدة للخصوبة Rf3 و Rf4 و Rf5 و Rf6 و Rf1 بالإضافة إلى صفات عالية الإنتاجية ومرغوبة. تحديد مثل هذا السلالة المعيدة للخصوبة والعالية الإنتاجية يمكن استخدامها بشكل فعال في برامج تربية الأرز الهجين لاستنباط هجن جديدة من الأرز.