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Evaluation of Selected Wheat Mutants for Grain Yield Contributed By Yield Constituents

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Abstract: To evaluate the performance of M_3 Mutant wheat genotypes for grain yield and its related characters, an experiment was initiated at Nuclear Institute of Agriculture (NIA) Tandojam. The experimental material consisted of wheat mutant lines and approved varieties i.e., MASR-09, MASR-11, MASR-13, MASR-23, MASR-64, T.J-83 and Khirman sown under R.C.B.D. Replications were 03, plantation of entries was done as four rows of every entry in individual replication, while row and plant spaces were of 15 and 30 cm, respectively. Among all genotypes the highly significant results were observed for height of plants (cm), days to 75% maturity, number of spikelets spike per spike, weight of 1000 grains in grams, while the parameters number of grains per spike, yield of main spike (g) showed significant results. However, the non-significant results were obtained for number of tillers per plant, length of spike (cm) and grain yield of each plant (g).The outstanding performance of mutant MASR-64 was observed for traits such as number of grains spike per spike, main spike yield, 1000-grain weight and grain yield per plant over check varieties and other mutants. The constant and better performance of the mutant MASR-64 was noted for the remaining traits such as height of plants, maturity as per 75 in percent, number of tillers produced by individual plant, length of spike, number of spikelets present in an individual spike, hence MASR-64 showed the vigor and promising features for the upcoming variety.

Keywords: Mutation Breeding, Wheat mutants, Grain yield, Evaluation of mutants, Selection of mutants.

1. INTRODUCTION

On global scale wheat is important food grain for humans, stands second cereal crop behind maize in overall production (Zeb *et al.,* 2009). One-third of the world population receives above than half of calories and protein requirements from wheat (Dhanda *et al.,* 2004). It is a Rabi season crop of Pakistan, sown in late October and early November, harvested in late April and early May (Ali *et al.,* 2009). Food security is a major task related with enhanced yields. There are certain regulatory restrictions on the production of genetically modified organisms but, mutagenesis is exempted. It is a tool to improve crops. This is a forward genetic approach that facilitates highlighting of phenotypes which are new and improved, the same could further be evaluated in primitive breeding planes.

To detect induced point mutations in populations that are mutagen zed, potential genetic tactics are required to serve several chief tasks including awareness on linking sequence information supplemented with the functions of genes of biological nature, detection of novel variation that could be included in breeding of crop plants etc. The challenge against these is climate change folding higher temperatures and unpredicted rainfall, consequently crop production is most often disturbed (Parry *et al.,* 2005). Therefore, a swift need for developing crop varieties with higher yields always lie (Parry *et al.,* 2007), (Reynolds *et al.,* 2009) suggest development of crop varieties with improved nutrients (Lea and Azevedo, 2006), simultaneously water use efficiency is advocated by Richards, 2000.

Mutation breeding aims at increased mutation rate in a short span of time so as to create new varieties of crop plants, it is easy and important way to induce variation via mutations. Mutation breeding is an efficient tool by which variation is induced. Traditional physical mutagenes are gamma radiation, chemicals include ethyl methane sulfonate. Mutations are successful in both the seed and vegetatively propagated crops (Jain, 2010). Rice mutants have been created, (Singh *et al.,* 1998; Suzuki *et al.,* 2008), *Triticum durum* (Sakin and Yildirim, 2004), maize mutants have been developed (Till *et al.,* 2004), sorghum mutants have been successfully produced (Xin *et al.,* 2008), barley mutants are released (Caldwell *et al.,* 2004; Talamè *et al.,* 2008 and mutants of hexaploid bread wheat have also been developed (Slade *et al.,* 2005).

2. MATERIALS AND METHOD

M_3 Mutant wheat genotypes were evaluated under R.C.B.D having 03 replications for yield of grains and interrelated traits. Experiment was done at NIA, Tandojam during 2011-12. The experimental material consisted of wheat mutants and approved varieties *i.e.*, MASR-09, MASR-11, MASR-13, MASR-23, MASR-64, T.J-83 and Khirman. Every entry had four rows in individual replication. Plants as per rows and within rows were 15 and 30 cm, respectively apart from each other. The traits studied were:

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Table-1a: Analysis of variance (mean square) for important agronomic characters of wheat genotype.
*** Significant at 5% level of probability ** significant at 1% *** highly significant at 5%**

Source of variation	D.F	Mean Square (M.S)					
		Plant height (cm)	Days to 75 % maturity	Number of tillers plant $^{-1}$	Spike length (cm)	Number of spikelets spike^{-1}	Number of grains spike^{-1}
Replication	2	26.7	1.85	1.6	0.52	0.32	127.5
Genotype	6	574.5***	48.4***	1.60 n.s	0.95 n.s	12.3***	98.6*
Error	12	15.1	2.69	0.82	0.37	1.84	27.1
Total	20	-	-	-	-	-	-

Table-1b: Analysis of variance (mean square) for important agronomic and physiological characters of wheat genotype.
*** Significant at 5% level of probability ** significant at 1% *** highly significant at 5%**

Source of variation	D.F	Mean Square (M.S)					
		Main spike yield (g)	1000-grain weight (g)	Grain yield plant^{-1} (g)	Leaf area (cm^2)	Chlorophyll content (%)	Relative Water Content (%)
Replication	2	0.4	0.22	9.27	130.7	8.26	8.49
Genotype	6	0.41*	33.1***	4.63 n.s	271.4***	12.7 n.s	45.6 n.s
Error	12	0.10	0.44	2.73	34.9	7.39	62.6
Total	20	-	-	-	-	-	-

1. Plant height (cm) 2. Spike length (cm) 3. Number of spikelets spike^{-1} 4. Number of grains spike^{-1} 5. Main spike yield (g)
6. 1000-grains weight (g) 7. Number of tillers plant^{-1} 8. Grain yield plant^{-1} (g)
Analysis of variance was done while means were compared using DMRT**.**

3. RESULTS

Plant height (cm):

The analysis of variance and DMRT for plant height as given in **(Table-1A)** show that genotypes were statistically highly significant ($p \leq 0.05$) and the mutant MASR-09 has shown significantly minimum plant height of 70.4 cm

Days to 75% Maturity:

The analysis of variance for the character days to 75% maturity is given in **(Table-1A)**, the mean performance for the same is presented in **(Table-2)**. The minimum days were taken by the check variety Khirman (134.0) to mature.

Table-2: Mean performance and DMRT of mutant wheat lines and two local checks for plant height (cm), days to 75 % maturity and number of tillers plant $^{-1}$.

Genotype	Plant height (cm)	Days to 75 % maturity	Number of tillers plant $^{-1}$
MASR-09	70.4 d	137.0 cde	5.66 ab
MASR-11	98.4 b	146.0 a	4.20 b
MASR-13	104.9 b	142.0 b	4.60 ab
MASR-23	100.7 b	139.0 bcd	6.20 a
MASR-64	89.4 c	136.0 de	4.53 ab
T.J-83	90.0 c	140.0 bc	5.40 ab
Khirman	113.6 a	134.0 e	4.60 ab
Mean	95.3	133.7	5.03
Lsd at 0.05	6.915	2.918	1.612

Number of tillers plant^{-1}:

The analysis of variance as given in **(Table 1-A)** indicates non- significant difference at $P \leq 0.05$ among the genotypes. The mean performance of genotypes in this regard is given in **(Table-2)**. The mutant MASR-23 produced maximum number tillers plant per plant (6.2).

Spike length (cm):

The results regarding mean square for spike length is presented in **(Table-1A)**. which indicates non-significant differences among the genotypes. The mean performance of genotypes for spike length is depicted The check variety T.J-83 produced longest spikes (12.2 cm).

Number of spikelets spike^{-1}:

The F-value (6.68) indicating significant difference among the genotypes for the character number of spikelets spike^{-1}. The mean values of the genotypes for number of spikelets spike^{-1} ranged between18.50-23.77. The check variety Khirman produced maximum number of spikelets spike^{-1} (23.77).

Number of grains spike^{-1}:

The data regarding analysis of variance for the character number of grains spike^{-1} is summarized in Table-1a. Mean squares indicate significant difference

Table-3: Mean performance and DMRT of mutant wheat lines and two local checks for spike length (cm), number of spikelets spike^{-1} and number of grains spike^{-1}.

Genotype	Spike length (cm)	Number of spikelets spike^{-1}	Number of grains spike^{-1}
MASR-09	10.9 bc	18.6 c	47.4 bc
MASR-11	11.5 abc	20.5 bc	51.6 abc
MASR-13	10.9 bc	18.5 c	44.8 c
MASR-23	10.7 c	20.6 bc	52.5 abc
MASR-64	12 ab	23.1 ab	60.8 a
T.J-83	12.2 a	21.5 ab	57.4 ab
Khirman	11.5 abc	23.7 a	57.0 ab
Mean	11.4	20.9	53.0
Lsd at 0.05	1.088	2.414	9.266

among the genotypes. The mean performance of M_3 mutant and check varieties for the trait number of grains spike^{-1} is shown in **(Table-3)**. The mutant MASR-64 (60.87) produced maximum number of grains spike^{-1}.

Main spike yield (g):

The analysis of variance for main spike yield (g) is presented in **(Table-1A)**. Among genotypes significant differences were observed. The mean performance of genotypes for main spike yield (g) is depicted in **(Table-4)**. The mutant MASR-64 produced highest spike yield (3.03g).

Table-4: Mean performance and DMRT of mutant wheat lines and two local checks for main spike yield (g), 1000-grains weight (g) and grain yield plant $^{-1}$ (g) characters.

Genotype	Main spike yield (g)	1000-grains weight (g)	Grain yield plant $^{-1}$ (g)
MASR-09	2.26 bc	46.9 c	10.9 ab
MASR-11	2.26 bc	45.1 d	10.1 ab
MASR-13	2.00 c	45 d	8.60 b
MASR-23	2.03 c	42.9e	10.5 ab
MASR-64	3.03 a	50.5 a	12.5 a
T.J-83	2.30 bc	40.6 f	11.7 ab
Khirman	2.70 ab	48.5 b	11.0 ab
Mean	2.41	45.6	10.7
Lsd at 0.05	0.5819	1.184	2.939

1000- Grains weight (g):

The analysis of variance for the character 1000-grains weight is presented in **(Table-1A)**. The mean values in **(Table-4)** revealed that the genotypes were highly significantly different from each other. The mutant MASR-64 produced the highest 1000-grian weight.

Grain yield plant^{-1} (g):

The analysis of variance **(Table-1A)** for the character grain yield plant^{-1} revealed non-significant differences at ($P \leq 0.05$) among the genotypes. The mean value of genotypes **(Table-4)** revealed that the genotypes were non- significantly different from each other. The mutant MASR-64 (12.53g) produced maximum grain yield plant^{-1}. The mutant MASR-13 (8.6g) produced the lowest grains plant^{-1}.

4. DISCUSSION

The results are discussed here with reference to mean values of genotypes and analysis of variance for main morphological characters. The analysis of variance revealed great genotypic difference among the genotypes for the characters *viz* plant height (cm), days to 75 % maturity, number of spikelets spike^{-1} , number of grains spike^{-1}, main spike yield (g), 1000-grains weight (g), leaf area (cm^2) reflecting utilization of such genetic variability for the improvement of crop as well as for the trait concerned. Results regarding mean performance for each of the character presented in various tables from (2-5) are discussed character wise:

Plant height (cm):

Medium plant height with short stem is important with breeding point of view in order to avoid lodging and contribution to biomass. Most of the plant breeders are of the view that plant height is governed by several gene pairs, while some have reported as degenic and yet some of workers have the view that it is inherited mono genetically. The data regarding mean performance presented in **(Table-2)** showed highly significant differences among genotypes. Khirman (113.6 cm) produced maximum plant height. Among all the mutants and check varieties the mutant MASR-09 (70.4 cm) produced reduced heighted plants, such significant differences were also observed by Morad *et al*. (2011), Sial *et al*. (2010), Ram din *et al*. (2003).

Days to 75 % maturity:

The highly significant differences among genotypes were observed for this trait. The mean square analysis of variance is mentioned in **(Table-1A)**. The mutant MASR-11 (146.0 days) was late maturing, followed by MASR-13 (142.0 days). The check variety Khirman (134.0 days) matured earlier than the other check variety and the contesting mutants, similar results have been shared by Laghari *et al*. (2010).

Number of tillers plant $^{-1}$:

Shoot architecture in wheat is determined by the extent of branching which is significant among morphological traits. Number of spikes to be produced by a plant depends upon its ability to tiller, moreover, number of tillers likely to be produced by a plant is the chief element for enhanced grain yield and biomass (Vasu *et al.,* 2007). The data regarding number of tillers plant^{-1} of wheat genotypes is depicted in **(Table-2)**. The mean square analysis of variance is represented in **(Table-1A)**. In present study, the genotypes were non- significantly different. Maximum tillers were produced by MASR-23 (6.2). The mutant MASR-11 (4.2) produced minimum tillers as compared to both check varieties and other competing mutants, the same was observed by Sial *et al*. (2010).

Spike length (cm):

The importance of this trait lies on the close relationship with grain yield in the genotypes. Better performance of a genotype can be judged on the basis of spike length. Larger spikes having dense spikelets are desirable for maximization of ultimate yield (Shahid *et al.,* 2002; Usman *et al.,* 2006). The results represented in **(Table-3)** revealed non-significant differences among genotypes for the trait spike length (cm). According to the results the check variety T.J-83 (12.2 cm) produced longest spikes as compared to the other check variety and the mutants. The shortest spikes were produced by MASR-23 (10.7 cm). Kusaksiz and Dere (2010), Laghari *et al*. (2010) also confirm these findings.

Number of spikelets spike^{-1}:

Number of spikelets spike per spike has significant and positive correlation with grain yield in wheat (Usman *et al.,* 2006). Therefore, wheat breeders often desire to develop genotypes with relatively longer spikes with greater number of spikelets for grain yield maximization. The pooled analysis of variance is represented in **(Table-1A)** indicating significant differences among genotypes. The higher number of spikelets in a spike were produced by Khirman (23.77). However, number of spikelets were lesser in spikes produced by MASR-13 (18.5).

Number of grains spike^{-1}:

Grains per spike is the important yield component and has direct correlation with the increased grain yield in wheat. The data regarding mean square of analysis of variance in **(Table-1A)** showed significant difference at P≤0.05 among genotypes regarding the trait grains spike per spike. The mean performance of all genotypes revealed that MASR-64 (60.87) gave maximum number of grains on one spike basis followed by the check varieties T.J-83 and Khirman (57.40 & 57.07) respectively. Whereas, the minimum grains on individual spike basis were recorded in MASR-13 (44.87) as compared to the other genotypes. Identical results were obtained by Kusaksiz and Dere. (2010), Sial *et al*. (2010), Jamil and Khan (2002).

Main spike yield (g):

The pooled analysis of variance for the trait main spike yield is depicted in **(Table-1A)** showing significant differences among all genotypes. The mean performance of all genotypes is represented in **(Table-4)**. According to the results the highest spike yield produced by MASR-64 (3.03 g). The lowest main spike yield was produced by MASR-13 (2.0 g). Laghari *et al*. (2010) and Sakin *et al*. (2004) have shared matching findings

1000-grain weight (g):

1000-grain weight (g) or seed index is important yield contributing trait. The data regarding the analysis of variance for the trait 1000-grain weight is depicted in **(Table-1A)** and the mean performance of all genotypes is represented in **(Table-4)**, this revealed that all genotypes are highly significant. The mutant MASR-64 (50.5 g) produced greater 1000-grain weight as compared to the check varieties and other contesting mutants. The lowest 1000-grain weight was observed in T.J-83 (40.67 g). Rahimi and Bahrani. (2011), Jamil and Khan (2002) and Amri *et al*. (2000) also obtained same results.

Grain yield plant $^{-1}$ (g):

Grain yield is a complex trait that is influenced by many traits both in positive and negative direction. Grain yield being polygenic and is highly influenced by cultivar, environment and cultivar × environment interactions. The mean squares of genotypes were non-significant at P≤0.05. Jamil and Khan (2002) also found non- significant results for the trait grain yield plant^{-1}. The average performance of grain yield plant^{-1} of all genotypes is depicted in **(Table-4)**. Results regarding to the trait revealed that the higher yield plant per plant was observed in MASR-64 (12.53 g) while MASR-13 (8.6 g) produced lowest grain yield per plant as compared to the other genotypes, our results are in confirmation with those of Morad *et al*. (2011).

5. CONCLUSION

The mutant MASR-64 out yielded among all genotypes and stood first as compared to other mutants and check varieties in yield associated traits *viz* number of grains spike^{-1}, main spike yield (g), 1000-grains weight (g), grain yield plant^{-1} (g) and relative water content (%). The check variety Khirman remarkably performed better among all genotypes in these traits *viz* days to 75 % maturity, number of spikelets per spike and leaf area (cm^2), however, mutant MASR-64 followed the check variety Khirman and performed better than others after it. The mutant MASR-09 produced dwarf plants and showed higher chlorophyll content (%) among all genotypes and mutant MASR-64 also performed better for these traits. The mutant MASR-23 and the check variety T.J-83 produced maximum number of tiller plant^{-1} and spike length (cm) respectively as compared to the other genotypes. It is concluded from this study that desirable mutation variability in wheat can be created through gamma rays and various traits can be improved in various genotypes. On the basis of results and conclusion it is further suggested that the mutant MASR-64 may play a vital role to produce high yielding genotype, therefore, should be included in further breeding programs for exploitation of its genetic potential in new cross combinations.

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