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Evaluation of Advance Mutant Genotypes and Interrelationship Analysis of Yield and Yield Associated Traits in Bread Wheat Genotypes

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Abstract: The current experiment was carried out to evaluate the advance mutant genotypes for yield and yield associated traits in bread wheat (*TriticumaestvumL.*) genotypes and also to analysis the interrelationship between the quantitative traits. In this regard, M_4 mutant lines fromMarvi and Sassui varieties were sown along with two check varieties viz. NIA-Amber and NIA-Saarangat Nuclear Institute of Agriculture, Tandojam during the rabi season 2014-15. The analysis of variance showed that all the genotypes performed significantly different for all the studied traits except biological yield plot^{-1}, signifying that studied materials possess useful genetic variability for traits studied thus can comprehensively be exploited for forthcoming breeding programs. On the basis of mean performance, the Marvi-mutant demonstrated better performance for a range of characters hence can be exploited as a parental line for future breeding programs. The results demonstrated significantly ($P \leq 0.05$) positive association between various traits, such as days to 75% heading made positive and significant correlation with days to maturity (0.93**). The character spike length demonstrated positive and significant association with grain yield plot^{-1} (0.852*). The trait spikelets spike^{-1}exhibitedsignificantly positive correlation with grain yield plot^{-1} (0.872*), whereas grains spike^{-1} also made positive and significant correlations with grain yield plot^{-1}(0.825*) and grains weight spike^{-1} (0.902*). The trait main spike weight developed significantly positive association with grains spike^{-1} (0.896*), spikelets spike^{-1} (0.849*), seed index (0.855*) and grains weight spike^{-1} (0.961*). The trait seed index also established positive and significant correlations with grains weight spike^{-1} (0.820*) and grain yield plot^{-1} (0.888*). Moreover, there was also a positive and significant correlation (0.947**) between harvest index and grain yield plot^{-1}.The characters spike length, spikelets spike^{-1}, grains spike^{-1} and main spike weight showed significant and positive associations with grain yield plot^{-1}, demonstrating a comprehensive selection for these traits will ultimately improve seed yield in bread wheat genotypes

Keywords: Bread wheat, correlation, mutants, agronomic traits

1. INTRODUCTION

Bread wheat is the essential diet of human population in Pakistan and occupies a central position in agriculture. Wheat is widely adapted to a great range of climatic conditions. A variety of food, which include chapaties, bread, noodles, crackers, cakes, breakfast food, cookies biscuits, and a number of confectionary items are being prepared from wheat (Laghari *et al.,* 2012).To obtain superior yield with potential resistance against biotic and biotic stresses in Pakistani wheat cultivars, many breeding efforts had been done in the recent past; consequently, due to its bidirectional breeding approaches a number of promising cultivars with better adaptability have also been released. Wheat has a unique position among cereal crops, mostly attributable to the reason that grains retain protein with exceptionally good chemical and physical properties (Ali *et al.,* 2013). For the improvements of wheat crops, the assessment and isolation of promising breeding materials from introduced crop materials is the primarily step. Nonetheless, an efficient hybridization program may be a reasonable approach. The success of such breeding programs primarily depends on the assessment of the important characters and pattern of genetic variability of the existing germplasm (Sanghera *et al.,* 2014).

Induced mutation, become an enormous tool in plant breeding to improve genotypes in particular traits. Large number of improved varieties of many crop species has been released, revealing the economic value of the technology (Micke *et al.,* 1990). Therefore, the current experiment was designed to assess the performance of advanced mutant lines and also to know the interrelationship between grain yield and its associated traits.

2. MATERIALS AND METHODS

The current experiment was carried out to evaluate the advance mutant genotypes for various quantitative traits in bread wheat genotypes. In this regard, M_4 mutant lines fromMarvi and Sassui varieties were sown along with two their parental lines and check varieties viz. NIA-Amber and NIA-Saarang on 14-11-2014 to investigate the advance mutant genotypes for different quantitative tratis.For producing the mutant genotypes, a single dose of 300 Gy was applied. The experiment was carried out in randomized complete block design (RCBD) with three replications at Nuclear Institute of Agriculture, Tandojam during the rabi season 2014-15. Analysis of variancewas applied to the data according to the method as suggested by Gomez and Gomez (1984)and the means were compared using least significant differences (LSD).

3. RESULTS AND DISCUSSION

Analysis of variances: The analysis of variance was carried out for thirteen studied parameters recorded

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from mutants, mother and check varieties of bread wheat. Results showed highly significant (P≤0.01) differences among the genotypes for all studied traits, with the exception of biological yield plot^{-1}. It indicates that evaluated genetic materials harbor significant genetic variations which could be utilized for further breeding programs in turn to evolve new bread wheat genotypes. Our results are in close agreement with Baloch *et al.* (2014) and Bhatti (2015), who also reported significant variations for variety of agronomical traits in bread wheat genotypes.

Mean performance: Mean values of the characters measured in six wheat genotypes are given in Table-2. Early maturity is a key character because early flowering varieties require less resources and vacant field earlier for other crops to be grown on time. For the trait of days to heading, the mutant wheat variety (sassui-mutant) took maximum (90.00) days, whereas the minimum days for heading were recorded in Marvi-parent (71.00), thus this genotype may be preferred for breeding early maturing genotypes in wheat breeding programs. While for the trait of plant height, the maximum height was recorded in NIA-Saarang (93.00cm) and the short height was recorded in Marvi-parent (84.00 cm), it is well established fact that dwarf wheat varieties are the choice breeding materials in turn to achieve maximum grain yield, consequently Marvi-parent may be chosen for breeding the dwarf stature wheat genotypes. The highest number of tillers plant^{-1} (11.67) was observed in NIA-Amber, however, the minimum number of tillers plant^{-1}were recorded in Marvi-mutant and Marvi-parent (6.67). The longer spike was recorded in Marvi-mutant (14.67 cm), whereas shorter spike was recorded in NIA-Amber (11.33 cm). Maximum number of spikelets spike^{-1} were recorded in Marvi-mutant (25.00), whereas minimum number of spikelets spike^{-1} were counted in NIA-Amber(19.00). Similar findings were reported by Singh and Baylan (2009) who also reported higher mean values for number of tillers plant^{-1} and number of spikelets spike^{-1} under the high irradiation doses. The results during present study revealed that maximum spike weight was recorded for Marvi-mutant (5.46 g) and lowest spike weight was recorded in NIA-Amber (3.16 g). While, the highest number of grains spike^{-1} were counted in Marvi-mutant (73.73); however, the lowest number of grains spike^{-1} were recorded in Sassui-mutant (59.60). Present results are in contrast with those ofSingh and Baylan (2009), who reported reduced number of grains spike^{-1} upon higher doses of radiations.

For the trait grain weight spike^{-1}, it was observed that Marvi-mutant showed the higher weight of grains spike^{-1} (3.58 g) and the lowest weight of single spike grains was observed in the NIA-Amber (2.39 g). From the productive trait seed index, the maximum weight of 1000- grains was gained by the Marvi-mutant (49.17 g), while the lowest weight 1000-grains weight was recorded in NIA-Amber (37.67 g). Similarly, the higher biological yield plot^{-1} was observed in the Marvi-mutant (2.77kg), while the lowest biological yield plot^{-1} was observed in Marvi-parent (2.47kg). Our findings found in close agreement with Rahimi and Bahrani (2011)who also reported that higher doses of gamma irradiation results in the increased biological yield and grain weight as compared to the control crop. Maximum grain yield plot^{-1}wasobserved in Marvi-mutant and Sassui-mutant (1.20 kg), whereas the minimum grainyield plot^{-1} was recorded in Sassui-parent (0.83 kg) along with NIA-Amber.Majed(2014)also reported that mutant genotypes produced maximum grain yield than their parental materials. Similarly, the higher harvest index was recorded in Sassui-mutant (46.64%), while the lower harvest index was recorded in NIA-Amber (32.42%). Based on mean performance, the genotype Marvi-mutant showed outstanding performance for variety of traits, thus can extensively be used as parental materials in upcoming breeding programs.

Correlation analysis: The current research demonstrated significant (P≤0.05) and positive correlation among various traits such days to 75% heading made significantly positive correlation with days to maturity (r= 0.930**). The character spike length demonstrated significantly positive correlation with grain yield plot^{-1} (r= 0.852*). The trait spikelets spike^{-1}indicated positive and significant correlation with grain yield plot^{-1} (r= 0.872*), whereas grains spike^{-1} also made positive and significant correlations with grain yield plot^{-1}(r= 0.825*) and grains weight spike^{-1} (r= 0.902*).The trait main spike weight developed positive and significant association with grains spike^{-1} (r= 0.896*), spikelets spike^{-1} (r= 0.849*), seed index (r= 0.855*) and grains weight spike^{-1} (r= 0.961*). The trait seed index also established positive and significant correlations with grains weight spike^{-1} (r= 0.820*) and grain yield plot^{-1} (r= 0.888*). Moreover, there was also a positive and significant correlation (r= 0.947**) between harvest index and grain yield plot^{-1}. This discloses a comprehensive selection ofthese identified characters will make a desirable improvement for seed yield in wheat,since these ten yield contributing characters are allied among themselves; consequently selection ofany these trait will indirectly show an improvement of the other traits.Overall, an intensive selection forspike length, spikelets spike^{-1}, grains spike^{-1} and seed index will ultimately improve seed yield in wheat.Fellahi*et al.* (2013), who worked on correlations in 29 bread wheat cultivars and reported that spike length and tillers plant^{-1}showed positive significant correlation with grain yield. Baloch *et al.*(2014) also studied 20 advance bread wheat genotypes and reported that different traits established positive and significant correlations with grain yield plant^{-1}. Nevertheless, significant negative relations were also noted between days to 75% heading and grains spike^{-1} (r= -0.867*), days to 75% heading and grains weight spike^{-1}(r= -0.858*), spike length and tillers plant^{-1} (r= -0.849*) and between tillers plant^{-1} and main spike weight (r=-0.821*). Similar to our results, Nukasani *et al* .(2013) also reported negative and significant correlation between tillers and spike length, while Gelalcha and Hanchinal (2013) also confirmed the negative and significant correlation between days to flowering and grains spike^{-1}.

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Table 1. Mean squares of various quantitative traits of advanced bread wheat genotypes.

Source of variance	DF	Day to 75% heading	Day to 75% maturity	Plant height	Tillers plant^{-1}	Spike length	Main spike weight	Spikelets Spike^{-1}	Grains Spike^{-1}	Grain Weight Spike^{-1}	Seed index	Biological yield plot^{-1}	Grain yield plot^{-1}	Harvest index
Replications	2	12.167	7.389	2.000	1.167	1.056	0.082	0.722	9.367	0.151	0.891	18.4039	0.04847	14.889
Genotypes	5	213.067**	290.456**	29.567**	12.133**	4.989**	1.770**	11.956**	90.823**	0.536**	43.019**	22.008^{NS}	0.082*	127.156**
Error	10	`2.233	3.256	3.267	2.900	0.389	0.045	0.456	11.673	0.016	0.765	0.24433	0.02331	0.016

**, * indicate significant at 1 and 5% of probability level and NS indicates non-significant

Table 2. Mean performance of advance wheat mutants along with mother and check varieties for various quantitative traits.

Genotypes	Day to 75% heading	Day to 75% maturity	Plant height (cm)	Tillers plant^{-1}	Spike length (cm)	Main spike weight (gm)	Spikelets spike^{-1}	Grains spike^{-1}	Grain weight spike^{-1}	Seed index(1000 grain weight gm)	Biological yield plot^{-1} (kg)	Grain yield plot^{-1} (kg)	Harvest index %
Marvi-mutant	76.00	125.00	85.33	6.66	14.67	5.46	25.00	73.73	3.58	49.17	2.77	1.20	43.32
Marvi-parent	71.00	123.00	84.00	6.66	13.33	4.46	20.00	68.97	3.35	44.83	2.47	0.86	35.00
Sassui-mutant	90.00	140.00	89.30	7.66	13.67	3.86	20.67	59.60	2.81	45.43	2.53	1.18	46.64
Sassui-parent	89.00	143.00	86.00	9.33	13.67	3.93	21.00	61.23	2.85	45.90	2.50	0.83	33.20
NIA-Amber	90.00	142.00	88.00	11.67	11.33	3.16	19.33	61.00	2.39	37.67	2.56	0.83	32.42
NIA – Saarang	80.00	123.00	93.00	10.00	11.67	4.00	20.67	64.63	3.03	45.23	2.77	0.90	33.49
LSD (5%)	2.71	3.28	3.28	3.09	1.13	0.38	1.22	6.21	0.23	1.59	0.89	0.27	8.47

Table 3. Correlation of coefficient among various quantitative traits in bread wheat genotyp

Characters	Day to heading	Day to maturity	Plant height	Spike length	Tillers plant^{-1}	Main spike weight	Grains spike^{-1}	Spikelets spike^{-1}	Seed index	Biological yield plot^{-1}	Grains yield plot^{-1}	Harvest index
Day to heading	**1**											
Day to maturity	**0.933****	**1**										
Plant height	**0.349^{NS}**	**0.008^{NS}**	**1**									
Spike length	**-0.313^{NS}**	**-0.142^{NS}**	**-0.620^{NS}**	**1**								
Tillers plant^{-1}	**0.637^{NS}**	**0.511^{NS}**	**0.474^{NS}**	**-0.849***	**1**							
Main spike weight	**-0.722^{NS}**	**0.682^{NS}**	**0.401^{NS}**	**0.772^{NS}**	**-0.821***	**1**						
Grains spike^{-1}	**-0.867***	**-0.811^{NS}**	**-0.454^{NS}**	**0.495^{NS}**	**-0.624^{NS}**	**0.896***	**1**					
Spikelets spike^{-1}	**-0309^{NS}**	**-0.339^{NS}**	**-0.252^{NS}**	**0.685^{NS}**	**-0.509^{NS}**	**0.849***	**0.701^{NS}**	**1**				
Seed index	**-0.461^{NS}**	**-0.480^{NS}**	**-0.141^{NS}**	**0.802^{NS}**	**-0.781^{NS}**	**0.855***	**0.568^{NS}**	**0.744^{NS}**	**1**			
Biological yield plot^{-1}	**-0.251^{NS}**	**-0.528^{NS}**	**0.478^{NS}**	**-0.102^{NS}**	**0.050^{NS}**	**0.432^{NS}**	**0.470^{NS}**	**0.604$_{NS}$**	**0.352^{NS}**	**1**		
Grains yield plot^{-1}	**-0.051^{NS}**	**0.143^{NS}**	**0.041^{NS}**	**0.852***	**0.582^{NS}**	**0.589^{NS}**	**0.825***	**0.872***	**0.888***	**0.383^{NS}**	**1**	
Harvest index	**0.089^{NS}**	**0.057^{NS}**	**-0.030^{NS}**	**0.601^{NS}**	**-0.597^{NS}**	**0.426^{NS}**	**0.110^{NS}**	**0.501^{NS}**	**0.486^{NS}**	**0.081^{NS}**	**0.947****	**1**
Grains weight spike^{-1}	**-0.858***	**-0.858^{NS}**	**-0.435^{NS}**	**0.716^{NS}**	**-0.849***	**0.961***	**0.902***	**0.680^{NS}**	**0.820***	**0.313^{NS}**	**0400^{NS}**	**0.260 NS**

*, **=significant at 5 and 1%, respectively; NS=Non-significant

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