

The Use of Number of Kernels per Spike as Selection Criteria in Durum Wheat (*Triticum turgidum ssp.durum* Desf.) Breeding

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Abstract: Mutation breeding has been used for improving some quantitative characters in durum wheat. The aim of this study were to; (i) determine the variation on the number of kernels per spike with selection after mutagen treatment, and (ii) find out effects of selection on population parameters in the M_2 and M_3 generations. Durum wheat (*Triticum turgidum ssp.durum* Desf.) variety 'Gediz-75' seeds without presoaking treated with 0.1 %, 0.2 %, 0.3 % and 0.4 % EMS for 8 hours at 24 °C and were washed for 6 hours after treatment. Base populations were retained by randomly selecting normal appearing single plants and those with high number of kernels per spike. The selected plants were grown as the M_3 generation. The 0.1, 0.2 and 0.3 % progeny populations exhibited higher number of kernels per spike means as compared to control. High heritability estimates in the generations were an indication of response to selection and of induced variation maintained. Due to the high genetic advances of populations in M_4 , obtaining plants with a higher number of kernels per spike by selection might be possible. Mutations affecting quantitative characters such as the number of kernels per spike are expected to be used in durum wheat breeding.

Key words: durum wheat, genetic advance, heritability, selection, mutation breeding.

Makarnalık buğday (*Triticum turgidum ssp.durum* Desf.) İslahında Başakta Tane Sayısının Seçim Kriteri Olarak Kullanılması

Özet: Mutasyon ıslahı makarnalık buğdayda bazı kantitatif karakterlerin ıslahı için kullanılmaktadır. Bu çalışmanın amacı mutagen uygulamasından sonra seçimle başakta tane sayısı için elde edilen varyasyonu belirlemek ve M_2 ve M_3 kuşaklarında populasyon parametreleri üzerinde seçimin etkilerini ortaya koymaktır. Gediz-75 makarnalık buğday (*Triticum turgidum ssp.durum* Desf.) çeşidinin tohumlarına ön ıslatma yapılmaksızın % 0.1, % 0.2, % 0.3 ve % 0.4 EMS 8 saat süreyle 24 °C'de uygulanmıştır. Kaynak populasyonlar tesadüf olarak normal görünüşlü tek bitkilerin ve bunların yüksek başakta tane sayısına sahip olanlarının seçilmesiyle oluşturulmuştur. Seçilen bitkiler M_3 kuşağı olarak yetiştirilmiştir. % 0.1, % 0.2 ve % 0.3 döl populasyonları kontrolle karşılaştırıldığı zaman daha yüksek başakta tane sayısı ortalamaları göstermiştir. Kuşaklardaki yüksek kalıtım dereceleri seçime olan tepkinin ve devam eden varyasyonun bir kanıtıdır. M_4 kuşağındaki yüksek genetik kazançlar sebebiyle seçimle daha yüksek başakta tane sayısına sahip bitkilerin elde edilmesi mümkündür. Başakta tane sayısı gibi kantitatif karakterleri etkileyen mutasyonların makarnalık buğday ıslahında kullanılması beklenilmektedir.

Anahtar kelimeler: makarnalık buğday, genetik kazanç, kalıtım derecesi, seçim, mutasyon ıslahı

1.Introduction

Although durum wheat has great economic importance in Turkey, durum wheat cultivation is restricted to marginal lands. If high yielding durum varieties with good quality characteristics were selected, Turkey would be self sufficient in durum wheat production. It was possible to select mutant lines with increased agronomic value in durum wheat treated with mutagenic agents (Bozzini et al., 1973). Recently, 28 durum wheat varieties in the world have been released by using mutagens (IAEA, 2003).

The efficient selection of mutants can only begin in the M_2 generation by using the bulk selection technique (Konzak, 1987) and selection is maintained in the M_3 generation. Induced mutations have been used in wheat

breeding if strong selection was applied in the populations after treatment (Borojevic, 1991). The expected response to selection can be measured by determining the parameters such as mean, variation, standard deviation, heritability and genetic advance (Scossiroli, 1977). The genetic variability resulted from mutations allows breeding of quantitative characters (Borojevic, 1965). The segregating populations are being used to obtain mutants with good yielding properties. Variation of quantitative characters for a given generation can depend on the genotype, the characters investigated and the mutagen used (Rao and Siddiq, 1977).

In the M_2 generation, the mean values for some quantitative characters can be lower than

the control. Sarkar (1986) indicated that estimated variation of the quantitative characters was higher for the M_3 generation than that for the M_2 generation. On the contrary, the population means and variation of some characters have been found to be higher than control in the base (M_2) mutant populations in wheat (Yildirim, 1980). The mean values of the quantitative characters decreased in the M_2 , M_3 and M_4 generations in relation to the control, while variability increased more in later generations (Gaul, 1964). The decreases in the mean values in this case, can be moderated by selection.

Yield components such as the number of kernels per spike can be used effectively as selection criteria in durum wheat breeding. Between the number of kernels per spike and the weight of kernels per spike there is a high positive correlation ($r = 0.94$) (Borojevic, 1965). The number of kernels per spike showed typical polygenic variation after mutagenic treatment (Borojevic, 1991). The aim of this study were to; (i) determine the variation on the number of kernels per spike with selection after mutagen treatment, and (ii) find out effects of selection on population parameters in the M_2 and M_3 generations.

2. Material and Methods

This research was conducted during 1997 (spring) and 1997-1998 (autumn) growing seasons at the Kazova Plain in Tokat. The mutant and control populations of Gediz-75 (*Triticum turgidum ssp. durum* Desf.) were used as a plant material. Dry seeds were treated with 0.1 %, 0.2 %, 0.3 % and 0.4 % ethyl-methane-sulfonate (EMS) for 8 hours at 24 ° C and washed for 6 hours after treatment (Ciftci et al., 1988).

M_1 material grown in field was harvested as single spikes. Seeds of each M_1 spike were sown in field as spike to row progeny for the M_2 generation. A control or mother line was planted at every 10 row as a check. The M_2 plants different from the control were labeled, selected and further evaluated. The base control and mutant populations consisted of randomly selected 100 single plants. (Gaul et al., 1969). The populations were analyzed for mean values (X), the range and standard deviation (S_f) of the number of kernels per spike. The plants with 20 - 25 % higher number of kernels per spike were

selected and grown as M_3 generation. Based on plant progeny test, selected 40 - 50 % of M_3 plants with high number of kernels per spike were retained. They were grown in plots which 1 m long rows, 0.2 m between rows. Twenty seeds per row were planted. Both in M_2 and M_3 generations, rows planted were in a randomized complete block design with 3 replications.

Population means (X), range and standard deviation (S_f) were calculated from the mean values of replications. The data were subjected to analysis of variance (ANOVA) using the Statistical Software Package (MSTATC). Heritabilities (H) were estimated according to genotypic and phenotypic variances (Table 1) (Cagirgan, 1989).

Table 1. The estimation parameters for the analysis of variance table

Sources of variation	Degrees of freedom	Mean square	Expected mean square
Blocks (r)	r-1		
Genotype (t)	t-1	M_1	$\hat{\sigma}^2_e + r \hat{\sigma}^2_g$
Error	(r-1)(t-1)	M_2	$\hat{\sigma}^2_e$
General	(rt-1)		

$$\text{Genotypic variance} = \hat{\sigma}^2_g = (M_1 - M_2) / r$$

$$\text{Phenotypic variance} = \hat{\sigma}^2_p = \hat{\sigma}^2_g + \hat{\sigma}^2_e$$

$$\text{Heritability} = H = \hat{\sigma}^2_g / \hat{\sigma}^2_p$$

The difference between mean of selected plants and the base or progeny populations mean was used for selection. Expected genetic advance (G) was calculated separately for each treatment using the Yildirims' (1980) formula: $G = H * S_f * i$ (H = heritability, S_f = standard deviation, i = selection intensity). The deviation of selection intensity (i) was taken as suggested by Falconer (1981). The expected progeny population mean was obtained by adding expected genetic advance to population means (Yildirim, 1980).

3. Results and Discussion

3.1. Means

The number of kernels per spike of 0.3 % and 0.4 % populations in the M_2 was found lower as compared to control population, but 0.1 % population had a higher value than that of control (Table 2). Similar results were reported by other researchers (Gaul, 1964; El-Rassas, 1991). In the M_3 generation, the means of mutant populations were higher than that of control except for the 0.4 % population. The reason for this could be probably due to the selection of the

normal and best spikes of the M₂ as the parents for next generation. In addition, the increase in population mean of the M₃ was perhaps from the more favorable growing conditions from winter sowing. Variation observed at 0.4 % population accompanied with a reduction in the mean values (32.3 and 47.1) indicated that major part of the induced genetic variability was in negative direction (Borojevic, 1991).

Table 2. Variation in the number of kernels per spike in the M₂ and M₃ generations

Population	X ± S _x	Range	F test	H
M ₂ generation				
Control	38.7 ± 1.08	24 – 56	*	0.22
0.1 %	39.0 ± 0.57	28 – 52	**	0.12
0.2 %	38.7 ± 0.65	19 – 54	**	0.36
0.3 %	32.4 ± 1.05	10 – 53	**	0.82
0.4 %	32.3 ± 0.86	17 – 47	**	0.68
M ₃ generation				
Control	49.4 ± 1.63	17 – 75	NS	-0.05
0.1 %	53.8 ± 1.47	16 – 76	NS	0.03
0.2 %	57.6 ± 1.79	22 – 91	NS	0.13
0.3 %	52.3 ± 1.48	12 – 86	**	0.37
0.4 %	47.1 ± 1.58	8 – 81	**	0.43

* = 5 % level, ** = 1 % level significance, NS: not significant (X = mean, S_x = standard error, H = heritability)

3.2. Range, Variance

Mutant populations for the number of kernels per spike had a negative direction in the M₂. On the contrary, in the M₃, the mutant populations range showed that variability was increased in the both directions with the new plus and minus variants (Table 2). In the mutant populations, upper limits of the range exceeding the controls' indicated that the selection of individual plants with high number of kernels per spike was applicable. The populations showed a response to selection for the number of kernels per spike. The need for mutant selection in the M₃ was dictated in some experiments, especially with chemical mutagens. The number of mutations isolated exceeded the number of mutations recovered in the M₂ (Scarascia-Mugnozza et al., 1991). The ranges obtained in the M₃ generation were wider than those of M₂ generation. As mentioned by Rao and Siddiq (1977), the increase of variation of quantitative characters for a given generation can depend on the genotype, trait investigated, and the mutagen used.

The analysis of variance for the number of kernels showed that all mutant populations in the M₂ had significant variation (p < 0.01), but in the

M₃ generation among mutant lines, only the 0.3 and 0.4 progenies had significant differences (Table 2). Significant variances maintained in the M₃ generation demonstrated the increases of genetic variability. As a result, variation in these populations could be utilized for M₄ and M₅ generations.

3.3. Heritabilities

The heritability estimates of 0.2 %, 0.3 %, 0.4 % populations were higher than that of control in the M₂ generation (Table 2). The increase in heritability was an indication of effective selection. In the next generation, the heritabilities of all mutant progenies were higher than that of control and positive relationship between EMS doses and heritability estimates was observed. However, the heritability did not increase much. The heriability estimates were 0.37 and 0.43 at 0.3 % and 0.4 % progenies, respectively. The expected response of 0.3 % and 0.4 % populations to selection was greater than the others. Borojevic (1991) reported that heritability estimates for number of kernels were 0.20 in the M₂ and 0.25-0.40 in the M₃.

The heritability estimates in both generations indicated that a part of induced variability maintained in generations (Borojevic and Borojevic, 1969). For the prediction of response to selection, heritability must be expected to give more realistic estimates (Gaul et al., 1969). Significant advances can be achieved at the mutant populations with high number of kernels per spike and heritability.

3.4. The Effects of Selection

The means of plants selected for the number of kernels per spike varied with populations after selection applied with 20 - 25 % selection proportion in the M₂ generation. The highest means in the M₂ were obtained from 0.1 % and 0.2 % selected populations (Table 3). The other populations had lower means than that of control. After the second selection, number of kernels per spike of 0.1 %, 0.2 %, 0.3 % selected progenies had higher values (60.0, 66.2, 59.1 respectively) as compared to control in the M₃ generation.

Selection differentials of mutant populations in the M₂ and M₃ generation were higher than those of controls (Table 3).

Table 3. The selection values for number of kernels per spike in M₂ and M₃ generations

Population	Base or progeny population		Selected population		Selection differential (X ₂ - X ₁)	Proportion (P) (n ₂ / n ₁)	Selection intensity (i)	Standard deviation (S _f)
	n ₁	(X ₁)	n ₂	(X ₂)				
M ₂ generation								
Control	100	38.7	20	43.9	5.2	0.20	1.40	6.85
0.1 %	100	39.0	25	46.1	7.1	0.25	1.27	5.44
0.2 %	100	38.7	25	46.6	7.9	0.25	1.27	6.47
0.3 %	100	32.4	25	42.2	9.8	0.25	1.27	9.00
0.4 %	100	32.3	25	39.6	7.3	0.25	1.27	7.11
M ₃ generation								
Control	20	49.4	10	55.2	5.8	0.50	0.80	12.60
0.1 %	25	53.8	10	60.0	6.2	0.40	0.97	12.72
0.2 %	25	57.6	10	66.2	8.6	0.40	0.97	15.47
0.3 %	25	52.3	10	59.1	6.8	0.40	0.97	12.84
0.4 %	25	47.1	10	54.3	7.2	0.40	0.97	13.64

(n₁= number of plant in base or progeny population n₂= number of plant selected in base or progeny population, X₁= mean of base or progeny population, X₂= mean of plants selected in base or progeny population)

However, selection differential alone could not be enough to estimate of genetic advance gained by selection (Yildirim, 1980). Standard deviations of 0.3 % and 0.4 % populations in the M₂ generation had higher than those of other populations whereas these values of all mutant populations increased in the M₃ in relation to control (Table 3). High values were an indication of the positive measure of successful selection.

Expected genetic advances calculated from the M₂ data of mutant populations were higher than that of control except for the 0.1 % population (Table 4). Similarly, the realized genetic advances of mutant populations were higher. Expected genetic advances in the M₄ estimated from the M₃ generation were found higher in all mutant populations than that of control (Table 5). Expected genetic advances in the M₄ estimated from the M₃ generation were increased approximately 10.8 % as a percentage of advances. Genetic advances calculated from

mutant progenies also were higher than those of control in wheat (Yildirim, 1980). In addition, the 0.2 % and 0.3 % progenies with high means along with genetic advances indicated that a certain effect of selection in the populations and it might be possible to select the plants with higher number of kernels per spike. Scossiroli (1977) also reported that the genetic advances were obtained by using the variability of quantitative characters through selection.

Expected means of 0.2 and 0.3 % progenies in the M₃ were higher than that of control generation (Table 4). Realized means of these progenies also were higher in relation to control. Similarly, the expected and realized means of the 0.4 % progeny population were lower in the M₃ generation. This result enables the estimation of next generation means in advance. However, the expected means of 0.1 % progenies were not in agreement with expected ones.

Table 4. The expected means, realized means and genetic advance in the M₃ after selection in the M₂ for the number of kernels per spike.

Population	Base population	Expected genetic advance	Expected (M ₃) mean	Realized (M ₃) mean	Realized genetic advance
	(M ₂) mean	(G= H * S _f * i)	(M ₂ mean + G)		(M ₃ mean-M ₂ mean)
Control	38.7	2.1	40.8	49.4	10.7
0.1 %	39.0	0.8	39.8	53.8	14.8
0.2 %	38.7	3.6	42.3	57.6	18.9
0.3 %	32.4	9.4	41.8	52.3	19.9
0.4 %	32.3	6.1	38.4	47.1	14.8

(H= heritability, S_f= standard deviation, i= selection intensity)

The expected means in the M₄ generation were estimated higher in mutant populations than in that of control (Table 5). Populations showed a positive response to selection. The 0.2 % population had the highest value (59.6). The

expected means of the number of kernels per spike in mutant populations were determined 9 - 17 % higher than that of the control. Thus, the lines with high number of kernels per spike could be obtained after selection in durum wheat.

Table 5. The expected genetic advance and means in the M₄ generation after selection in the M₃ for the number of kernels per spike.

Population	Progeny population (M ₃) mean	Expected genetic advance (G= H * S _f * i)	Expected (M ₄) mean (M ₃ mean + G)	Advance (%) (M ₃ / M ₄ x 100)
Control	49.4	0.0	49.4	0.0
0.1 %	53.8	0.4	54.2	0.7
0.2 %	57.6	2.0	59.6	3.4
0.3 %	52.3	4.6	56.9	8.1
0.4 %	47.1	5.7	52.8	10.8

The negative heritability estimates were used as zero in the formula of genetic advance (H= heritability, S_f= standard deviation, i= selection intensity)

4. Conclusion

Means of the numbers of kernel per spike for 0.3 and 0.4 % populations in the M₂ generation were found lower than that of control. In the M₃, 0.1, 0.2 and 0.3 % progeny populations exhibited higher number of kernels per spike means as compared to control. Induced variation by selection could be utilized for further generations. The heritability estimates in the generations were an indication of response to selection and of induced

variation maintained. Due to the high genetic advances of populations in M₄, obtaining plants with a higher number of kernels per spike by selection might be possible. The 0.2 % and 0.3 % progeny populations with high means in the M₃ generation have also given the high values for expected means in the M₄ generation. Mutations affecting quantitative characters as the number of kernel per spike are expected to be used in durum wheat breeding.

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