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MACROMUTATIONAL VARIABILITY IN METRIC TRAITS OF BARLEY*

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SUMMARY

An applied macromutation study was planned to induce the variability of various metric traits in barley. In accord with this aim, seeds of "Kaya" variety were treated with the 15 and 30 krad of gamma rays. The M_2-bulk population of each doses were grown at two locations, Bornova and Tokat in 1985-1986. During the vegetation period all the viable mutants were selected at both locations. The selected potential mutants and the control plants were grown as the M_3 generation in 3 separate trials in Tokat. Heritability values in broad-sense based on variance components were estimated and the frequency poligons were plotted for 14 characters studied in each populations. The results obtained have clearly showed that there were the wide induced variability in all quantitative traits studied in the macromutant populations, which were generally on the left side of the control's. The frequency poligons for days to heading and number of kernels had multiple peaks in the mutant populations which clearly indicated that the induced variation were discrete and qualitative in nature. In spite of obtaining useful mutations in individual characters such as early heading, shorter plant height, higher thousand kernel weight etc. in this study, these mutant lines could not be used directly since no over yielding mutant lines were found as compared to the best control line. Considering the selection procedure applied in this study and the magnitude of the induced-changes obtained, it could be concluded that the increase of the variation was due to macromutations. Therefore these mutant lines have a potential of indirect use.

INTRODUCTION

Induced mutations have been effectively used as supplemental or complemental sources of natural variation in practical plant breeding programs. Now there are around 1300 cultivars derived from the induced mutations (1) as compared to 600 in 1987 (2) indicating a steady increase in this area.

In general, all the traits observed in the plants, qualitative or quantitative, could be genetically changed by means of artificial

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mutagenesis. Although the micromutations have been considered more suitable to a breeder than the macromutations (3), the released mutant varieties have been mostly based on the mutations detected visually in the M2 generation on the individual plant basis (4). Therefore macromutations appeared to be widely acceptable and easy to work with.

The aim of the present study was to evaluate the macromutational variability in terms of quantitative traits in barley. Preliminary report has been published (16).

MATERIALS AND METHODS

Seeds of barley (**Hordeum distichum** L.) cultivar, Kaya, were treated with the 15 and 30 krad of gamma rays. The M2-bulk populations of each dose were grown at two locations, Bornova and Tokat, in 1985-1986. During the vegetation period all visible mutants were selected at both locations.

A total of 100 potential mutants comprising 44 from the 15 krad and 56 from the 30 krad doses were obtained. The selected mutants and 50 plants from untreated seeds were grown as the M3 generation in 3 separate trials arranged in the Randomised Complete Blocks design with 2 replication under the Tokat's ecological conditions in the Spring, 1987. Each plot consisted of 1 row, 1m long and 30 cm apart. 20 seeds were hand sown in each plot.

The following traits were measured on the plot or on the plant basis: Grain yield, biological yield, harvest index, number of spikes, kernels per spike, kernels per spike, thousand kernel weight, days to heading, length and width of flag leaf, length of flag leaf sheath, plant height, spike length and protein content. Spike density was calculated according to Ibrahim and Sharaan (5).

Statistical analysis of the data were performed according to Steel and Torrie (6) and accord with the experimental design. Population mean, F-ratio were calculated and frequency poligons were plotted for all the traits except the protein content. In addition the broad-sense heritabilities based on variance components (7) were estimated for the traits. Mutant populations were compared with the control in terms of these estimates. Range and the direction of variation were found by using the frequency poligons.

RESULTS

The means and the heritability values for the traits studied in the macromutant and control populations are given in Table 1, Table 2 and Table 3. The frequency poligons are depicted in Figure 1 and Figure 2.

Grain Yield

The plot grain yields calculated for the 15 krad population (108.8 g) and for the 30 krad population (109.6 g) were apparently behind the mean of the control (131.6 g). The highest heritability value (0.45) was in the 30 krad population which has a among lines variance significant at the $p < 0.01$ probability level (Table 1). It can be seen from the frequency distributions that variability occurred in the mutant populations were negative in sign and there was no over-yielding lines (Figure 1).

Table 1. Mean and heritability values for yield and yield components in mutant and control populations grown as M3.

Characters	Control		15 Krad		30 Krad	
	Mean	Herit.	Mean	Herit.	Mean	Herit.
Grain yield/im	131.6ns	0.01	108.8ns	0.22	109.0**	0.45
Biological yield/im	375.1ns	0.11	291.0**	0.40	341.3*	0.31
Harvest index (%)	35.2ns	0.02	37.6ns	0.20	32.6**	0.42
Number of spikes/im	99.8ns	0.04	94.3*	0.31	90.9**	0.44
Kernels per spike	28.7ns	0.00	25.3**	0.73	26.8**	0.64
Thousand kernel weight	54.6ns	0.00	56.0**	0.83	54.4**	0.72
Number of lines	50		44		56	

ns : non-significant

* : significant at % 5 level

** : significant at % 1 level

Biological Yield

The biological yield of the control (375.1 g) was followed by the mean of the 30 krad population (341.3 g) and the lowest mean was in the 15 krad population (291.0 g). The among lines variation in the mutant populations was statistically significant and the heritability values were 0.40 and 0.31 for the 15 krad and the 30 krad populations respectively (Table 1). The widening variation in the mutant populations in the negative side of the control (Figure 1).

Harvest Index

The highest harvest index was in the 15 krad population (37.6 %). The among lines variation was statistically significant ($P < 0.01$) in the 30 krad population which had the lowest harvest index (32.6 %) but the highest heritability, 0.42, (Table 1). The variation appeared in the 15 krad population was in the positive side as compared to the control. Eventhough there was a negative side variation in the 30 krad population, there were some lines with higher harvest index exceeding the control distribution (Figure 1).

Number of Spikes

The 15 krad and 30 krad populations were low for mean of the number of spikes in 1m row compared to the control (94.3, 90.9 vs 99.8). The among lines variation in the mutant populations was significant and the heritability values were 0.31 and 0.44 for the 15 krad and 30 krad population, respectively (Table 1). The distribution of the mutant lines was at the left side of the control (Figure 1).

Kernels Per Spike

The mutant lines (15 krad: 25.3 and 30 krad: 26.8) had lower means for kernels per spike than the control (28.7). The variation among the lines in the mutant populations were statistically significant ($p < 0.01$). The heritabilities were 0.73 and 0.64, respectively (Table 1). The two distributions of the mutant populations were at the negative side exceeding the control. However frequency distribution of the 15 krad population had 2 peaks (Figure 1).

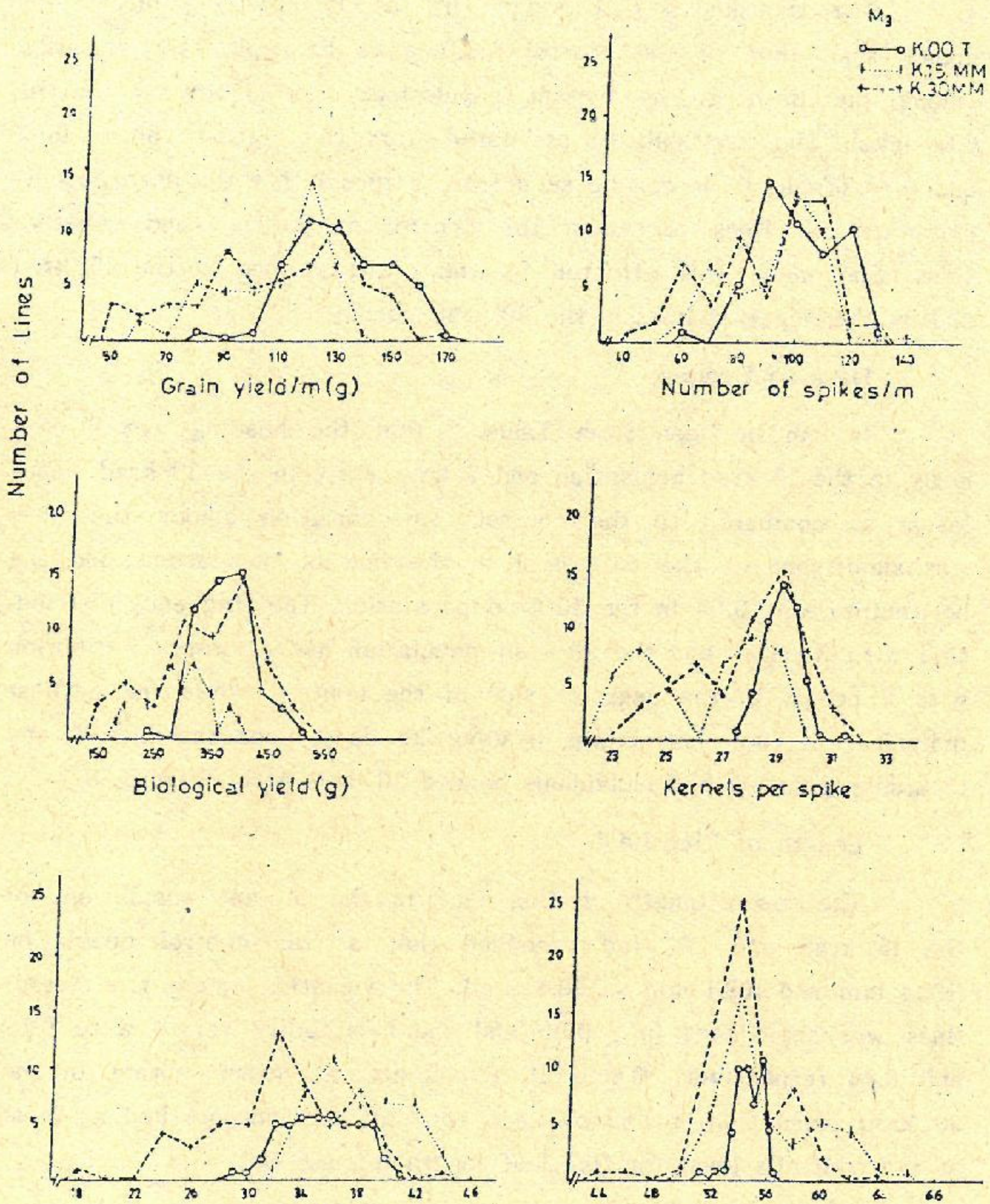

Fig 1. Frequeney poligons of mutant and control populations for yield and yield components in M_3 generation

Thousand Kernel Weight

The thousand kernel weight in the 15 krad population was higher than that of the control (56.0 g vs 54.6 g). The variation among the lines in the mutant populations was significant at the 0.01 level. The heritabilities estimated were the highest values, 0.83 and 0.72 (Table 1). It can be seen from Figure 1 that the both populations contain lines exceeding the control at positive and negative sides. The mean was affected by the positive lines in the 15 krad and by the negative lines in the 30 krad population.

Days to Heading

It can be seen from Table 2 that the heading was 9 days early in the 15 krad population and 7 days early in the 30 krad population as compared to the control. The variation among the lines was significant at the 0.01 level in the mutant populations and the heritability was 0.94 in the 30 krad population. The frequency distribution with 3 peaks and the 30 krad population had discrete distribution with 2 peaks, in the negative side of the control. While the earliest individual in the control was heading 39 days after the May 1, the 15 krad population had individuals headed 20 days early (Figure 2).

Length of Flag Leaf

The mean length of flag leaf in the mutant populations of the 15 krad and 30 krad exceeded that of the control population (112.4 mm and 108.1 mm vs 90.8 mm). The variation among the mutant lines was significant ($p < 0.01$) and the heritability values were 0.52 and 0.44 respectively (Table 2). Excluding one dwarf mutant in the 30 krad population it can be seen that all the mutants had at least at the control's level for flag leaf length (Figure 2).

Width of Flag Leaf

The mean of the flag leaf width was 5.4 mm in the control and the 15 krad and 30 krad population had 6.5 mm and 6.3 mm means respectively. There were significant variation in the mutant populations for this trait ($p < 0.01$). The heritability values were 0.61 and 0.55 respectively (Table 2). The distributions of the mutant populations were at the right side of the control (Figure 2).

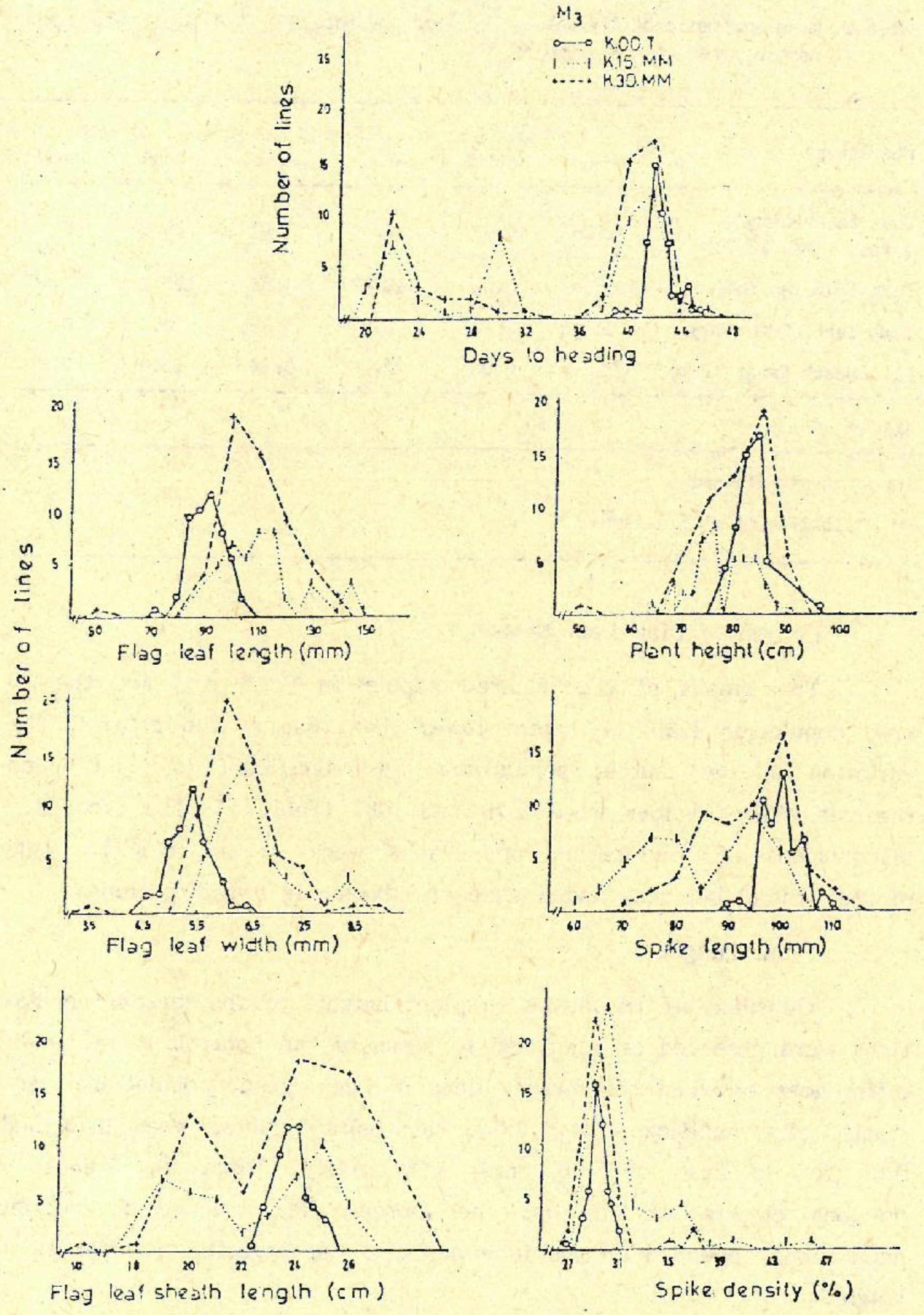

Fig. 2. Frequency poligons of mutant and control populations for some physiological and morphological characters in M_3 generation.

Table 2. Mean and heritability values for some physiological traits in mutant and control populations grown as M3.

Characters	Control		15 krad		30 krad	
	Mean	Herit.	Mean	Herit.	Mean	Herit.
Days to heading (after 1 May 1987)	42.5ns	0.02	33.3**	0.60	35.2**	0.94
Flag leaf length (mm)	90.8ns	0.00	112.4**	0.52	108.1**	0.44
Flag leaf width (mm)	5.4ns	0.20	6.5**	0.61	6.3**	0.55
F.L.sheath length (cm)	23.8ns	0.00	22.5**	0.79	23.0**	0.87
Number of lines	50		44		56	

ns : non-significant

** : significant at % 1 level

Length of Flag Leaf Sheath

The means of the 15 krad population (22.5 cm) and the 30 krad population (23.0 cm) were lower than that of the control. The variation in the mutant populations was significant ($p < 0.01$) and the heritability values were 0.79 and 0.87 (Table 2). The frequency distributions of the mutant populations were at the negative side of the control but they had a wide distribution in two directions.

Plant Height

Considerable reductions in plant heights of the mutant populations were observed as compared to mean of the control. Plant height differences between the mutant lines in two mutant populations were statistically significant ($p < 0.01$). Heritability values were 0.73 and 0.66 for 15 krad and 30 krad, respectively (Table 3). Frequency poligons clearly showed that the increase of variance in mutant populations depended on the individuals at the negative side for plant height.

Spike Length

An apparent decrease in the mean values for spike length was observed in the mutant populations as compared to the control. The unexpected result for this character was that the control has the variance which was statistically significant ($p < 0.05$), which is possibly due to a sampling error. However the variance among the mutant lines was more significant ($p < 0.01$) in both mutant populations and the heritabilities were higher (0.84 and 0.91) than in the control, 0.25, (Table 3). It was clearly understood from frequency poligons that widened variance in the mutants was only on the left side of the control (Figure 2).

Table 3. Mean and heritability values for some morphological traits and protein content in mutant and control populations grown as M3.

Characters	Control		15 krad		30 krad	
	Mean	Herit.	Mean	Herit.	Mean	Herit.
Plant height (cm)	82.5ns	0.18	77.7**	0.73	80.3**	0.66
Spike length (mm)	99.5*	0.25	84.3**	0.84	93.6**	0.71
Spike density (%)	29.3*	0.26	31.4**	0.93	29.6**	0.74
Protein content (%)	9.8ns	0.32	10.6*	0.34	10.8**	0.67
Number of lines	50		44		56	

ns : non-significant

* : significant at % 5 level

** : significant at % 1 level

Spike Density

An apparent increase of the mean values of the mutant populations, especially that of the 15 krad as compared to the control was observed. Variance between lines was also significant at 5 % level in the control, at 1 % level in the mutant population. Greater heritabilities, such as 0.93 and 0.74, were obtained in the mutant populations than that of the control, 0.26, (Table 3). Concerning the frequency poligons of the populations in the Figure 2, the sizable increase in spike density was evidently resulted from large number of dense-spike individuals which were eroctoid in both mutant populations or in the 15 krad, especially (Figure 2).

Protein Content

The slight increases in protein content of mutant populations as compared to the control mean were noticed. Both mutant population had the variance which was statistically significant at least at the 5 % level. The highest heritability for protein content was obtained in the 30 krad population. Since only twelve control lines were analysed for this trait, therefore the frequency poligons could not be plotted.

DISCUSSION

Present study clearly showed that there were the wide induced variability in all quantitative traits studied in the macromutant populations and the heritability values were between 0.20 and 0.94 indicating large genotypic variances for most of the quantitative characters.

Most of these mutant lines, regarding frequency polygons, were characterized by very extreme early heading as much as 20 days, although intense screening and selection have not been applied for this trait.

Concerning the behaviour of the other quantitative characters, it was evident that grain yield, biological yield, number of spikes, number of kernels, spike length, plant height, flag leaf sheath length were reduced in the mutant populations than those of in the control. However a clear increase in thousand kernel weight (in 15 krad), length and width of flag leaf, spike density, protein content and harvest index (in 15 krad) in the mutant populations over the control was obtained. The increase of thousand kernel weight by 10 g of certain mutant lines may be explained as a result of the extending grain filling period and decresing the number of kernels per spike.

In cereal crops, early varieties are suitable for short growing season, showing high adaptability particularly under hot and dry conditions. Among other mutations, earlytypes are certainly not all rare, since the earliness might often arise as a short of by-product in connection with other changes in morphological and physiological characters (5, 8, 9), as indicated also in this study. A number of mutants heading and/or maturing early were reported and early mutants in various crops were released as varieties (2, 4). Kawai (9) has reported that late mutants were obtained more often as compared to the early ones and Ibrahim and Sharaan (5) have reported the opposite of this conclusion. The discrepancies appeared in terms of earliness might result from the genetic background (10, 11).

The frequency poligons for days to heading and number of kernels had multiple peaks in the mutant populations which clearly indicated that the genotypic variation in these populations were discrete and qualitative in nature. Similar results were reported by Ukai and Yamashita (12) and Hussein (13).

In spite of obtaining useful mutations in individual characters such as early heading, shorter plant height, higher thousand kernel weight, longer and wider flag leaf in this study, these mutant lines could not be used directly for the practical breeding purposes under the normal environmental conditions since no over yielding mutant lines were found as compared to the best control line.

Considering the selection procedure applied in this study and the magnitude of the changes obtained, it can be concluded that the increase of the variation was due to macro mutations, according to Gaul's terminology (3). Even a single mutation results generally in a wide spectrum of phenotypic changes. Most of these pleiotropic effects or multiple mutations in an individual result in a reduction of vitality of the mutants. Hence, these additional effects on fitness characters generally prevent the direct use of a desirable mutant character which may have been produced (3, 14).

In this case, indirect use of mutants are of great importance. Therefore the mutant genes, practically desirable, should be placed in a new genetic background and the negative pleiotropic effects should be eliminated as well as purifying from deleterious independent mutations. The success of this type of attempts may depend on the suitable combining parents.

The second possibility of using the mutants other than hybrid breeding is to grow under different ecological conditions. Yıldırım and Çağırgan (15) reported that selection pressure applied for grain yield has eliminated the visually selected mutants under normal environmental conditions, but one early heading line had a good selection value under drought stress. So they concluded that such mutant selections should be tested in different environments before using them in crossing programs.

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ÖZET

ARPA MAKROMUTANT POPULASYONLARINDA KANTİTATİF KARAKTERLERİN VARYABİLİTESİ

Gama ışınlarının 15 ve 30 krad dozlarıyla muamele edilen Kaya arpa çeşidinin M_2 bulk populasyonlarından makromutasyon yöntemi uyarınca tek bitkiler seçilmiştir. Seçilen potansiyel mutantlar kontrol bitkileri ile birlikte M_3 generasyonu olarak 3 ayrı populasyon halinde 2 tekerrürlü tesadüf blokları deneme deseninde döl kontroluna alınmıştır (Tokat, 1986-87). Parsel değeri veya üç bitkinin ortalaması olarak 14 özellik ölçülmüştür. Her populasyon ve özellik için varyans analizi uygulanmış ve geniş anlamda kalıtım derecesi tahminleri elde edilerek frekans poligonları çizilmiştir. Elde edilen sonuçlar, makromutant populasyonlarında incelenen özelliklerde kontrol populasyonuna kıyasla geniş bir suni değişkenlik ortaya çıktığını açıkça göstermiştir. Varyans artışına paralel olarak mutant populasyonların ortalaması birçok özellik için düşük bulunmuştur. Başaklanma süresi ve dane sayısında görülen çok tepeli frekans eğrilerinden makromutant populasyonlarında belirlenen kalıtsal varyasyonun kesikli (kalitatif) bir yapıya sahip olduğu anlaşılmıştır. Bu çalışmada erkenci, kısa boylu, yüksek bin dane ağırlığına vb. olumlu özelliklere sahip mutant hatlar elde edilmesine rağmen, dane verimi bakımından en iyi kontrolu geçen mutant hat bulunmamıştır. Bu çalışmada uygulanan seleksiyon yöntemi ve değişkenliğin miktarı gözönüne alınarak mutant populasyonlardaki varyans artışının makromutasyonlardan kaynaklandığı kabul edilmiştir. Bu nedenle bu mutantların dolaylı kullanım potansiyeline sahip olduğu sonucuna varılmıştır.

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