

Genetic and cytological studies on some triticale hybrids

Makhlouf Mohamed Mahmoud Bakheet

SUMMARY The present investigation was carried out through five successive seasons of 1986, 1987, 1988, 1989 and 1990. The data were obtained on two back-crosses (BC₃) i.e. «Giza 157 x Petka» x Giza 157) and «Sakha 8 x Petka» x Sakha 8). The recorded data were taken on the individual plant basis in case of agronomic characters within each of the four replicates of a given genotype. The proteins were identified through using electrophoresis analysis for the subunits of glutamine, ω-glucosyl, γ-glutamine, γ-glutamine and α-glutamine. The cytological studies were carried out on the meiotic and mitotic cells of the individual plants of each genotype. Accordingly, data will be classified into three parts. In the first part, some of the agronomic characters were evaluated. In the second part, proteins of the individual plants of the two back-crosses were identified. In the third part, cytological studies were carried out on the meiotic and mitotic cells of the individual plants for parents, F₁'s and both of the two back-crosses. The obtained results could be summarized as follows. 1. Genetic evaluation of characters. Some of the agronomic characters were studied. The characters included, plant height, spike length, peduncle length, number of tillers, stem waxiness, number of kernels per spike. Number of spikelets per ear (spike). 100-kernel weight per plant, number of kernels per spikelets and grain yield per spike. Means, S.E. and coefficient of variation were estimated for these characters for wheat parental Giza 157, Sakha 8 and for rye parent, Petka. Moreover, the characters were also evaluated in the two F₁'s, Giza 157 x Petka and Sakha 8 x Petka besides the two back-crosses plants. The results could be summarized as follows: 1. For plant height character, the two F₁'s were taller than the wheat parents and most of the back-cross plants were taller than the wheat parents. 2. For spike length character, the two F₁'s plants showed longer spikes than that of the wheat parents which showed correlation between the length of spike and the height of plant. Some plants of the two F₁'s were found to carry more than one spike on the main stem (3 - 14 spikes) which may be due to the presence of rye chromosomes in the genome of the F₁ plants. 3. For peduncle length character, the plants of the two F₁'s tend to be shorter similar to the wheat parent and most of the plants of the two back-crosses showed a shorter peduncle length than that of the rye parent. 4. For tillering ability character, the plants of the two F₁'s showed less number of tillers than that of the wheat and rye parents. Most of the two back-cross plants revealed less number of tillers than that of the parents. It was found that, the lower grain yield per plant was highly affected by the lower number of tillers. For stem waxiness character, a waxy layer was found in stem of the two F₁'s plants and most of the two back-crosses plants. This character was found only in rye plants and it may indicate the presence of rye chromosome in the hybrids. 6. For the number of kernels per spike character, it was found that lower number of grains per spike in the two F₁'s and the majority of plants of the two back-crosses may result from the effect of the barriers between the two species. 7. For the number of spikelets per spike character, it was found that number of spikelets per spike was low in the two F₁'s as compared to the wheat and rye parents. Most of the plants of the two back-crosses showed high number of spikelets per spike as compared to the wheat parent. 8. For the number of kernels per spikelets, it was shown that the number of kernels per spike was lower in the two F₁'s and the two back-crosses plants than that of the wheat parent. The low seed-setting in the two F₁'s and the two back-crosses plants reveals a strong reduction of fertility in these plants. 9. For 100-kernel weight per plant character, it was

noticed that there was a reduction in 1000-grain weight per plant in the two F₁'s and most of the two back-crosses compared to the wheat parents. 10. For the grain yield per plant character, lower yield per plant was recorded in the two F₁'s plants as well as in the two back-crosses plants which may be attributed to the greater instability of the hybrids containing rye chromosomes as compared to the wheat parents. The lower grain yield per plant was highly affected by the lower number of grains per spike, lower number of spikelets and the lower 1000-kernel weight per plant and lower tillering ability. 2. Protein identification by electrophoresis analysis: The SDS-PAGE analysis has shown that higher variability between the electrophoretic bands in the plants of the two back-crosses as compared to the wheat parent, Giza 157, Sakha 8 and rye parent, Petka. The obtained results could be summarized as follows: 1. S₁ plants of the two back-crosses showed deficiency in the principal α -gliadin and L₁-N glutenin subunits which are controlled by genes on the short arm of chromosome 1B. It is possible that the plants contain wheat-rye chromosome translocation. 2. S₂ plants of the two back-crosses showed deficiency in some bands of the HMW α -glutenin as compared to the wheat parents which may be due to the presence of rye chromosomes. 3. Two back-cross plants of (Sakha 8 X Petka) x Sakha 8 showed more bands in HMW and LMW glutenin subunits as compared to the wheat parents. 4. S₃ other plants of the two back-crosses showed different bands in the HMW glutenin, α -gliadin, LMW glutenin and γ -gliadin as compared to the wheat parent. 5. The rest of the two back-cross plants showed in addition to the bands of the wheat parent. 6. It was found that there is no difference between the parents and the two back-crosses plants in the α -gliadin. 3. Cytological behaviour of chromosomes: The cytological behaviour of chromosomes was studied at prophase I (diakinesis stage), metaphase I, anaphase I and tetrad for the parents, F₁' and the two back-cross plants. The results of such study could be summarized as follows: 1. At diakinesis stage, the PMC's of the parent showed that the univalent were lower than that of the two F₁'s. The unfused bivalents were not observed in the parent, Petka. The univalent appeared as dispersed in the extended loop of the two back-cross plants. In Petka, the average of univalents was 1.5 than 1 while in other plants it was more than 7 univalents. 2. At diakinesis stage, the PMC's of the parents showed ring and rod bivalents in a range less than that of the two F₁'s. In the case of the rye parent, Petka, univalents could be 7 or rod bivalents. The bivalent ranged from 1 to 2 to more than 8 in the PMC's of the two back-cross plants. Multivalent were detected in some plants of the two back-crosses. 3. At metaphase I, the α -IC's of the parents showed in a similar number of univalent. Meanwhile, in Ale's of the two F₁'s showed high degree of lagging univalent. The lagging univalent were found high in S₀-8 plant and low in the others of the two back-crosses (BCJ). 4. At anaphase I, the FMC's of the parents showed in a similar lagging chromosome. Meanwhile, the FMC's of the two F₁'s showed high percentage of lagging chromosome. Lagging chromosomes were also observed in 80% plant of the two back-crosses. The chromatid bridges were detected in anaphase I for the FMC's of the two F₁'s and some of the two back-cross plants. 5. At anaphase II, lagging chromosome were detected in the α -IC's of the two F₁'s with high percentage compared to the parents. The FMC's of some plants of the back-crosses showed high percentage of lagging chromosome. 6. At tetrad, micronuclei were found in the irregular FMC's of the two F₁'s. Some plant of the two back-crosses showed micronuclei in their FMC's with higher percentage than that of the F₁'s plants. S₃ other plants showed normal distribution of the nuclei. 7. The high degree of mitotic irregularities which is testified in the occurrence of multivalents, lagging chromosomes at anaphase I and II, and the higher number of tetrads with micronuclei, all suggest the presence of rye chromosomes in the wheat genomes. b. C-banding: The C-banding karyogram of Petka variety of rye was carried on. Every chromosome pair is characterized by a specific banding pattern. Chromosomes are suggested to be designated by 1R to 7R. The results could be summarized as follows: 1. Chromosome 2 showed a small band near the centromere position in the long arm. 2. Chromosome 3R showed a band on the short arm that is close to the centromere than in 2R. 3. Chromosome 6R characterized by the subterminal centromere position showed band in the long arm near the centromere. 4. The unband chromosome. a. The mitotic cells of the 41 b.c.k.; c.i.r.or (l-c) plants showed that 14 plants were found to contain 4n chromosomes. The number of plants which showed 43 and 44 chromosomes in their mitotic cells was one plant. 8 plants showed differences in their chromosome number as it

ranged from 35 to 41. One plant showed 28 chromosomes. Some mitotic cells of the two back-crosses showed micronuclei beside the main nucleus. These micronuclei were found in different stages of division (interphase, late prophase).