Cytological and genetical evaluation of some promising wheat x rye lines

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The present study was carried out at the research station and cytological lab. in the departement of agricultural botany in Faculty of agriculture at Moshtohor and cytological lab. in Faculty of Agriculture at Alexandria through three successive seasons; 1994/1995, 1995/1996 and 1996/1997. Primary screening was carried out for all the 10 promising lines which obtained from previous studies and originated from back-cross seven of the hybrid (Sakha 8 of hexaploid wheat x Petka of diploid rye) x hexaploid wheat inaddition to their original parents.These studies were classified into three main catogories as the following:-Morphological studies on some main econocharacters of these promising lines and their original parents.Cytological studies on the chromosomal abnormalities during meiosis division and addition or substitution of rye chromosome or chromosomes and/or translocations to wheat genomes, chromosomal number in mitotic cells through using C- banding technique and DNAcontent during GI, S and G2 phases.Protein identification of the 10 promising lines in addition to theoriginal parents.1. Morphological studies:-Data were obtained on some economic characters for the 10 promising lines in addition to the two original parents; the wheat parent, Sakha 8 and for rye parent, Petka. The evaluatedcharacters were as the following:-Plant height,.Spike length of themain stem..,Number of tillers per plant,.Number of spikelets per spike of the main stem. ,1000-kernel weight per plant,. Number of grains per spike of the main stem., Grain yield of spike of the main stern.Data revealed that the plant height means in the promising lines were ranged from long (143.8-141.6 for line 7) to short (105.4 -103.8 for line 8 compared to the hexaploid wheat parent, 102.2-102.4) at the two successive seasons respectively.Concerning the spike length of the main stem, data showed that the spike length-in the promising lines ranged from 12.6 in line 9 to 15.0 in lines 3 while it was 13.2 in the wheat parent and 13.4 in the rye parent.It was found that the spike length was excceeded the two original parents in lines number 7, 6, 5, 4, 3 and 10 in thetwo seasons.Concerning the tillering ability, it was found that number of tillers per plants in parents was 13.3 and 19.4 lor hexaploid wheat (Sakha 8) at the two successive seasons and 13 and 12.2 for diploid rye (Petka). There was a non-significant increase in the number of tillers in line number 4 (20.2 and 18.0) at the two successive seasons. While lines number 6, 9, 5, 3 and 2 revealed significant decrease compared to the wheat parent (12.0 - 12,2, 14.4 - 14.6, 15.4 - 15.6 and 13.4 - 13.6, respectively). Lines number 1, 7, 8 and 10 showed non-significant decrease as compared to the wheat parent.For the number of spikelets per spike of the main stein, it was29.8 and 28.6 for wheat (Sakha 8) and 25.8 and 28.6 for rye (Petka), respectively. Number of spikelets per spike was non-significant lower in lines number 1, 2, 3, 4, 5, 6 and 10 with means (27.4 and 26.2, 27.3 and, 25.8, 28.4 and 28.6, 29.2 and 31.8, 29.2 and 29.2, 29.0 and 31.6 and 28.0 and 30.0, respectively) compaing to the original parent, Sakha 8. At the same time, lines number 7, 8 and 9 revealed significant decrease compared to the wheat parent (26.8 and 28.4, 26.8 and 28.4 and 25.8 and 25.4 in the two seasons, respectively).Concerning the 1000-kernel weight in parents were 57.00 and 53.40 gm for (Sakha 8) and 47.00 and 40.00gm for ryei 1.respectively. The 1000-kernel weight ranged from 47.64 gm in line 6 to 57.80 in the line 5 in the first season, while it showed highly significant increase in the second season as it ranged from 55.10 gm in the line 1 to 78.20 in line 9. Lines number 3, 4, 5, 6, 7, 8, 9 and 10 revealed high significant increase in 1000-kernel weight as compared to the parents (53.40 in wheat and 40,0 in rye) in second season. Lines number 1 and 2

showed to be nearly like wheat parent with non-significant increase (55.10 and 56.10).For the number of grains per spike in parents was 78.40 and 89.80 in (Saka 8) in the two seasons, respectively while it was 61.20 and 57.80 in rye. In the first season, the number of grains was decreased in the investigating lines significantly as compared to the wheat parent and ranged from 58.56 in line number 4 to 70.98 in line 8. In the second season, all lines revealed significant decrease as compared to wheat.In metaphase I, the occurrence of lagging chromosomes and chromatid bridge was absent in the Sakha 8 and rye, while it was somewhat little in wheat-including rye chromosome or chromosomes. The frequencies of PMC’s having lagging chromosomes in the examined lines were ranged from 1 in line number 3 to 34 in line number 1. The frequencies of PMC’s having chromatid bridge were ranged from 2 in line number 2 to23 in line number 1.Mixed metaphase 11 was also examined. It has been observed that the frequency of the mixed metaphase II was low in the rye (1) and not detected in wheat PMC’s. The frequencies of PMC’shaving mixed metaphase II were ranged from 2 in line number 4 to 13 line number 1.Tetrad stage was also examined, it has been observed that the frequencies of abnormal tetrad (tetrads showed micronuclei in different numbers) were very low in the PMC’s of parents, 2.0 for Sakha 8 and 1.0 for Petka. The frequencies of PMC’s having micronuclei in tetrad were ranged from 3 in lines number 8 and 2 to 19 in line number 1.Fragments were also examined. It has been observed that the frequency of the fragments was low in the rye parent (1) and (2) in wheat PMC’s. The frequencies of PMC’s having fragments were ranged from 2 in line number 8 to 10 in line number 6. b. Chromosomel number of mitosis through using C-banding technique:-Somatic chromosomes were counted on seed samples from the10 promising lines and the two parents. It was revealed that different chromosomel number in these lines was detected. The C-banding karyogram of the diploid rye showed that every chromosome pair is characterized by a specific banding pattern. 1R, 2R, 3R, 4R, 5R, 6R and 7R are the 7 pairs of the genome R of rye parent. Each chromosome had its identity as it differ from the other chromosomes in distribution of bands, position of centrromere and the length of the two arms.It was found that lines number 2 and 8 veuealed the same number of chromosomes of wheat but substitution may oceared in one chromosome due to the diffeneces in the morphological characters, and electrophoreticbands of protein.Lines number 3,4 and 5 were found to contain one rye chromosome (additional lines).Lines number 6 and 7 were found to contain two ryechromosomes. Lines number 1,9 and 10 were found to contain three rye chromosomes. DNA content in mitotic cells during GI, S and G2 phases:DNA content were quantitatively evaluted in mitotic cells during interphase stage. It showed that 7.357 % of the cells contained 1 c DNA in (Sakha 8) while 6.254 % of the cells contained lc DNA in rye. The majority of the cells contained 2c DNA (26.235 5) in the hexaploid wheat (Sakha 8) and 23.155 %) in diploid rye (Petka). lower number of cells were found to contain 4 c DNA in the two parents (6.510 % and 4.254 %,of wheat and rye, respectively).Line number 1:-The quantity of the DNA in the mitotic cells during the interphase stage was 6.254 % in the lc DNA of the examined cells (the same as Petka parent and less than. Sakha parent) , while the 2c DNA was detected in 15.458 % of the cells (less than the two original parents). On the other hand, the 4c DNA was found in 4.265 % of the cells (the same as Petka parent and less than Sakha parent).Line number 2:-It showed that the quantity of the DNA in the mitotic cells during the interphase stage was 7.254 % in the lc DNA of the examined cells (more than the Petka and less than Sakha) , while the 2c DNA was detected in 12.985 % of the cells (less than the two original parents). On the other hand, the 4c DNA was found in 3.254 % of the cells (less than the Petka and Sakha parents). Line number 3:-The quantity of the DNA in the mitotic cells during the interphase stage was in 7.245 % in the lc DNA of the examined cells (more than the Petka and less than Sakha) , while the 2c DNA was detected in 20.965 % of the cells (less than the two parents). On the other hand, the 4c DNA was found in 8.245 % of the cells (more than the two parents).Line number 4:-The quantity of the DNA in the mitotic cells during the interphase stage was 5.478 % in lc DNA of the examined cells (less than the two parents) , while the 2c DNA was detected in16.954 % of the cells (less than the two parents). On the other hand, the 4c DNA was found in 1.248 % of the cells (the same asPetka parent and less than Sakha parent).Line number 5:-The quantity of the DNA in the mitotic cells during theinterphase stage was 5.648 % in the 1c DNA of the examined cells (less than the two parents) , while the 2c DNA was detected in16.548 % of the cells (less than the two parents). On the other hand, the 4c DNA was found in 2.854 % of the cells (the same as Petka parent and less than Sakha parent).Line number 6:-The quantity of the DNA in the mitotic cells during theinterphase stage was found in 4.265 % in the lc DNA of the examined cells (the same as Petka parent and less than Sakha parent) , while the 2c DNA was detected in 26.848 % of the cells(less than the two original parents). On the other hand, the 4c DNA was found in 3.245 % of the cells (the same as Petka parentand less than Sakha parent).Line number 7:-Quantity of the DNA in the mitotic cells during the interphasestage was in 6.254 % in the lc DNA of the examined cells (the sameas Petka and less than Sakha parent) , while the 2c DNA was detected in 23.154 % of the cells (less than the two original parents). On the other hand, the 4c DNA was found in 6.245 % of the cells (the same as Petka parent and less than Sakha parent).Line number 8:-It revealed the quantity of the DNA in the mitotic cells during the interphase stage was found in 6.254 % in the lc DNA of the examined cells (the same as Petka parent and less than Sakha parent) , while the 2c DNA was detected in 14.965 % of the cells (less than the two parents). On the other hand, the 4c DNA was found in 2.965 % of the cells (the same as Petka parent and less than Sakha parent). Line number 9:-It revealed the quantity of the DNA in the mitotic cells during the interphase stage was 8.652 % in the lc DNA of the examined cells (the same as Petka and less than Sakha parent) , while the 2c DNA was detected in 13.654 % of the cells (less than the two original parents). The 4c DNA was found in 4.254 % of the cells (the same as Petka parent and less than Saklia8).Line number 10:-It showed the quantity of the DNA in the mitotic cells during the interphase stage was 4.658 % in the lc DNA of the examined cells (the same as Petka and less than Sakha8) , while the 2c DNA was detected in 27.254 % of the cells (less than the two parents).The 4c DNA was found in 3.568 % of the cells (the same as Petka parent and less than Sakha parent).3. Protein identification by electrophoresis analysis:-Gliadin and glutenin, two storage protein groups, have been recognized in the endosperm. Gliadin and glutenin are synthesized on the endoplasmic reteculum in the developing endosperm. The analysis revealed that higher variability between the electrophoreticbands in the 10 promising lines as compared to the two original parents; wheat (Sakha 8) and rye (Petka),It was found that lines number(1,2,3,8) and(10) showed deficiency in the principle w-gliadin and LMW glutenin components controlled by genes on the short arm of chromosome I B (MS). So, it is possible that these lines contain wheat - rye chromosomes translocation. Promising lines number(4,5,6) and(9) showed deficiency bands of the HMW glutenin subunits as compared to the wheat (Sakha 8). Lines number revealed different bands in the HMW, glutenin, w-glidin, LMW glutenin and y-gliadin as compared to the wheat parent. Line number showed non-significant differences from the bands of the wheat.