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A Case of Genome Partition in Polyploid Oats

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Summary. At the second generation of the interspecific cross between the cultivated hexaploid (2n = 42) oat *A. sativa* and the wild tetraploid (2n = 28) *A. murphyi*, a plant having hexaploid and diploid (2n = 14) sectors was selected. Meiosis was highly regular in the diploid sector but the tillers failed to proceed beyond the boot stage and no seeds were produced. It is suggested that this diploid sector represents an entire genome of one of the diploid progenitors of the hexaploid oat.

Key words: Hybridization - Haploid - Meiosis - Mitosis - Chromosome Segregation

Reversible polyploidy is meaningful in autopolyploidy where a viable and fertile haploid can be formed either by parthenogenesis or as a result of hybridziation between an autotetraploid and its diploid parent. Such haploid derivatives contain the 2X chromosome number, similar to that of the diploid prgenitor and are often completely normal and fertile. It is obvious, however, that the fate of haploids of an allopolyploid plant is completely different. Such haploids also contain 2X chromosome number but are expected to be as sterile as the interspecific diploid F_1 hybrid. Theoretically extraction of a viable diploid from an allopolyploid is possible only if one genome of the polyploid will be isolated in double dose. The present note reports such a case in oats.

The common oat *Avena sativa* L. is a hexaploid (2n = 42) plant. The allopolyploid origin of this oat is indicated by the formation of 21 bivalents in meiosis and disomic inheritance of many traits. The diploid and the tetraploid parents of *A. sativa* have not yet been definitely identified. Recently two tetraploid (2n = 28) wild oats *A. magna* and *A. murphyi* were discovered. Both are related morphologically and cytogenetically to the hexaploid oats (Murphy et al. 1968, Rajhathy and Sadasivaiah 1969, Ladizinsky 1971). The F_1 hybrids between these two tetraploids and the hexaploid oats are fully sterile but produce some seeds when pollinated by viable pollen of their parental species.

The resultant BC generation is characterized by conspicuous variation in the chromosome number of different plants (Ladizinsky and Fainstein 1977). One particular plant resulted from backcrossing to *A. murphyi* had 2n = 37. Chromosome pairing in meiosis was not examined but the proportion of viable seeds was 32 %. Six plants grown from these seeds were examined cytologically. Three different chromosome numbers were found, 2n = 40, 2n = 42 and 2n = 43. One of the plant having 2n = 42 appeared to be peculiar. Among the four tillers examined in meiosis two had 2n = 42 and most of the chromosomes were arranged in 21 bivalents. The chromosome number in the other two tillers was 2n = 14 and the pairing was highly regular. Of altogether 45 cells examined in these tillers, seven bivalents were formed regularly in 32 cells, in 7 cells five bivalents a trivalent + univalent were observed and the rest of the cells showed six bivalents + two univalents (Fig. 1). At maturity two groups of tillers were observed in this plant, one group of tillers developed normally produced seeds and all were hexaploids. Another group did not proceed beyond the boot stage legt green for a relatively long time and no seeds were produced. These tillers are of special interest and we assume that they were of 2n = 14.

Change in the expected chromosome number following hybridization was reported in several plants. It is, however, interesting to note that in most cases the number of the missing chromosomes was very close to the basic X number of the complement. In polyploid tomato, asymmetric genomic reduction had occurred following irregular spindle formation at meiosis. Consequently, gametes having n = X chromosomes num-

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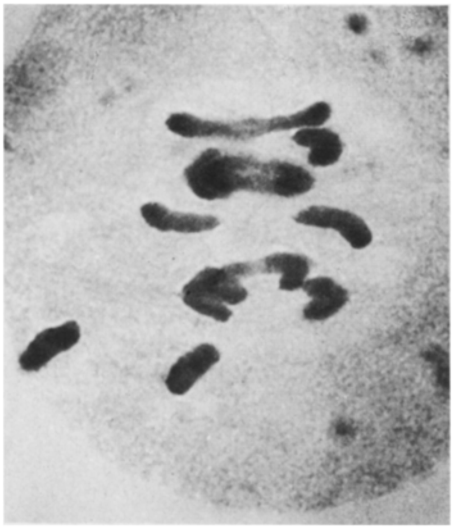

Fig. 1. Six bivalents and two univalents in p.m.c. of a diploid sector developed on a hexaploid plant

ber (instead of n = 2X) were formed (Gottschalk, 1971).

The diploid sector obtained in our case is unique not only because the diploid state has been obtained but also the chromosomes there were composed of rather seven pairs. Principally this could be formed in two different ways: 1) Seven out of the forty two chromosomes underwent non disjunction in mitosis and formed restitution nucleous. 2) Due to spontaneous multipolar spindle formation seven pairs of homologous or almost homologous chromosomes were congregated in a separate nucleus. The occurrence of meiotic cells with 6II + 21 or 5II + II + I indicate that the latter possibility was apparently the case. If this is indeed so, one might conclude that in polyploids chromosomes belonging to the same genome behave as a unit rather than individual during cell division. At least this accords well with the recent report on spatial relationships of chromosome during mitosis in wheat (Feldman and Avivi, 1974).

Genome partition of allopolyploids might be of major interest for evolutionary study since it might give us some idea about the diploid progenitor and also the rate of genetic change which occurred since the time of the polyploidy event. Extraction of specific genomes from polyploids was made in wheat where the tetraploid genome was obtained from the hexaploid wheat (Kerber, 1964). Oats, however, are much older than the hexaploid wheat and it is quite certain that the various geomes there have been change to that extent by gene and chromosome mutations so that they can no longer function as a separate unit. The diploid sector obtained in our study apparently could survive at the vegetative phase but could not proceed to the reproductive stage and failed to set seeds.

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