



Figure 1. Inter connected PMCs at telophase I and II showing cytomixis and chromatin elimination.

most probable reason for the observed anomalies might be either gene mutation or chromosomal or genetic imbalance due to genomic dissimilarity between *A. hypogaea* and *A. chacoense* involved in the interspecific hybridization (figure 1).

Though chromosome elimination was observed in a few allohexaploids of groundnut⁶, the reasons for it were not fully known. As observed in this case, cytomixis seems to be one of the reasons for such chromosomal stabilization in the interspecific hybrids of the genus *Arachis*. Both cytomixis and chromosome elimination indicate immense selection pressure exerted by nature on the hybrid genotype. Pollen stainability of the plants showing these anomalies ranged from 24.7 to 52.7%. These interspecific triploids did give a few viable seeds thereby indicating that cytomixis and chromosome elimination observed in this case have some evolutionary significance. As cytomixis is known to produce hypo-aneuploids and lead to reduction in basic chromosome number in *Lilium* species⁷, it would be interesting to test this assumption by determining the chromosome numbers of the progenies of these triploids.

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A CHROMOSOMAL RANGE IN THE INTERSPECIFIC HYBRIDS AND THE HYBRID DERIVATIVES OF *COIX* L (POACEAE)

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WHEN two species varying in chromosome number hybridize, the hybrids usually carry an odd number of chromosomes in their constitution. If such interspecific hybrids happen to be semi-fertile, they provide in the subsequent generations a great variability, at times even showing up entirely new phenotypes through random and novel recombinations. Such variability in the interspecific hybrid derivatives has been reported earlier¹⁻³. Chromosomal screening of one such open-pollinated population of hybrid progeny is reported in this communication.

Three species of *Coix* L of the tribe Maydeae of family Poaceae are reported to grow wild all over India⁴. Spontaneous interspecific hybrids with $2n = 14$, $2n = 15$ and $2n = 16$ chromosomes were isolated when aneuploids of *C. gigantea* ($2n = 18-24$)⁵ and *C. aquatica* ($2n = 10$) were grown in close association⁶. In the following year, these semisterile hybrids were planted along with their parents and allowed to open-pollinate. The progeny was raised and the young male racemes from individual plants were fixed in acetic-alcohol (1:3). Anthers were squashed in acetocarmine (1%) and the chromosome numbers were tabulated in a total of 256 plants.

Since the two parents, *C. gigantea* ($2n = 20$) and *C. aquatica* ($2n = 10$) differed in chromosome number, the interspecific hybrids carried 15 chromosomes in their somatic complement, the 10 and 5 chromosomes being contributed by the *gigantea* and the *aquatica* parents, respectively. Further variability in the hybrid constitution was due to aneuploidy in the *C. gigantea* parent that produced male and female gametes with variable number of chromosomes^{7,8}, especially $n = 9$ ($n - 1$) and $n = 11$ ($n + 1$) in large quantities. Also,

nullisomics of *C. gigantea* ($2n = 18$) occurred in exceptionally high frequency in the population⁹ contributing $n = 9$ gametes, in greater number than even the normal gametes ($n = 10$). However, the *C. aquatica* parent constantly contributed gametes with $n = 5$ chromosomes. The two genomes could be easily identified in the hybrid constitution because of the notable difference in the size of the chromosomes; *aquatica* has larger chromosomes than *gigantea*. The two genomes are partially homologous and although the hybrids have shown regular pairing between the parental chromosomes giving heteromorphic bivalents and some multivalents⁶; segregational irregularities have led to unequal chromosomes at anaphase-I mainly due to the variable number of univalent laggards. Whatever the chromosomal pairing in the hybrids, the distribution of univalent chromosomes at anaphase-I, both in regard to the number and kind, has led to the formation of some functional female gametes that usually carried five or more chromosomes from *gigantea* and *aquatica* parents. This is evident from the fact that when these hybrids were grown in close association with *C. gigantea* (especially nullisomics, $2n = 18$) and *C. aquatica* ($2n = 10$) and allowed to open-pollinate, it resulted in a progeny of plants showing a wide range of chromosomal numbers from $2n = 10$ to $2n = 21$ (table 1). Among these, plants with $2n = 10$ and $2n = 18$ resembled the *aquatica* and the nullisomic *gigantea* parents, morphologically and cytologically (unpublished data). Such a parental recovery from hybrids through a single spontaneous back-cross is unusual, although types close to original parents have

been isolated from the F-2 generation by Anderson¹⁰ and from the F-2 and F-3 generations of hybrids involving New World X Asiatic species of cotton¹¹. The male meiosis of the present interspecific hybrids shows some tendency towards genomic segregation at anaphase-I, and a similar segregation is likely in some of the megaspore mother cells producing parental gametes. This is explained on the basis of non-random assortment of chromosomes mediated by genotypic affinity among the centromeres contributed to the hybrid by each parent¹².

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Table 1 Number of plants isolated in each of the chromosomal types from $2n = 10$ to $2n = 21$ among the hybrids and hybrid-derivatives of *Coix*.

Chromosome number in hybrid derivatives ($2n$)	No. of plants
10	56
11	14
12	4
13	3
14	101
15	22
16	21
17	5
18	24
19	4
20	1
21	1
Total no of plants screened	256

ANTIPODAL HAUSTORIUM IN *BRIZA MINOR* LINN

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EMBRYOLOGICALLY the family Poaceae (Gramineae) has been worked out significantly because of its high economic potential. A perusal of the literature indicates that the antipodals in the family are characteristic and exhibit variation in respect of their number,