

## MORPHOCYTOGENETICS OF *BRASSICA NAPUS* L. X *SINAPIS ALBA* L. SEXUAL HYBRIDS

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### ABSTRACT

Meiotic analysis of *B. napus* x *S. alba* sexual hybrids at MI showed a mean chromosome pairing ratio of 16.5 I, 6.97 II (rings + rods), 0.47 III and 0.13 IV per meiocyte. Partial fertility of the F<sub>1</sub> hybrids and the ease of obtaining BC<sub>1</sub> seeds when crossed to *B. napus* suggest the possibility of transferring useful gene(s) to the cultivars of *B. napus*.

**Key words:** *Brassica napus*, *Sinapis alba*, sexual hybrids.

Yellow or white mustard (*Sinapis alba* L. 2n=2x=24, Sal Sal) is highly resistant to nematodes [1], black spot, white rust and powdery mildew. It is well adapted to drought conditions and sufficiently rich in erucic acid [2, 3] which finds considerable use as a lubricant, plasticizer, slipping and antiblocking material, antifoam agent and in perfume-, aroma- and pharmaceutical industries [4]. This species is also a potential source of proteins in human diet [5]. Thus, genetic traits of *S. alba* could be valuable for *B. napus* (2n=4x=38, AACC) improvement.

Interspecific hybrids between *B. napus* and *S. alba* have been obtained both through protoplast fusion [6] and by sexual crossing via embryo rescue [7]. However, sexual hybridization between the two species by conventional breeding methods has not been accomplished so far. Here we report the morphocytogenetics of the first conventional hybrids of *B. napus* with *S. alba*.

### MATERIALS AND METHODS

Buds of *B. napus* were pollinated with freshly collected pollen of *S. alba*. Pollinated flowers were bagged and left on the mother plant(s) until fruit maturity. Neither pre- or post-pollination hormone treatment nor embryo rescue was necessary.

Carnoy's fixative and acetocarmine squash method were used to study meiotic chromosomes in pollen mother cells (PMCs).

### RESULTS AND DISCUSSION

Of the 35 crosses made between *B. napus* and *S. alba* seven seeds were obtained at maturity. Of these 5 germinated and produced the normal plants. All but one were confirmed to be true hybrids. *S. alba* x *B. napus* sexual hybrids via embryo rescue were obtained only when *S. alba* was used as the female parent and the resultant hybrid was completely male sterile [7]. In the present study, *B. napus* x *S. alba* sexual hybrids have been obtained using *B. napus* as the female parent. The phenotype of *B. napus* x *S. alba* hybrid plants was similar to *B. napus* but the siliquae were remarkably smaller than those of the female parent, *B. napus* (Fig. 1). Average stainability of the pollen from the F<sub>1</sub> hybrids was 40%. Crossing the F<sub>1</sub> hybrids back to *B. napus* gave good seed setting (32.5%), however, the recovery of BC<sub>1</sub> seeds with *S. alba* as male was relatively difficult (< 2.0% seed set). Over 50 pollinations of the F<sub>1</sub> hybrids with *S. alba* could produce only one BC<sub>1</sub> seed.

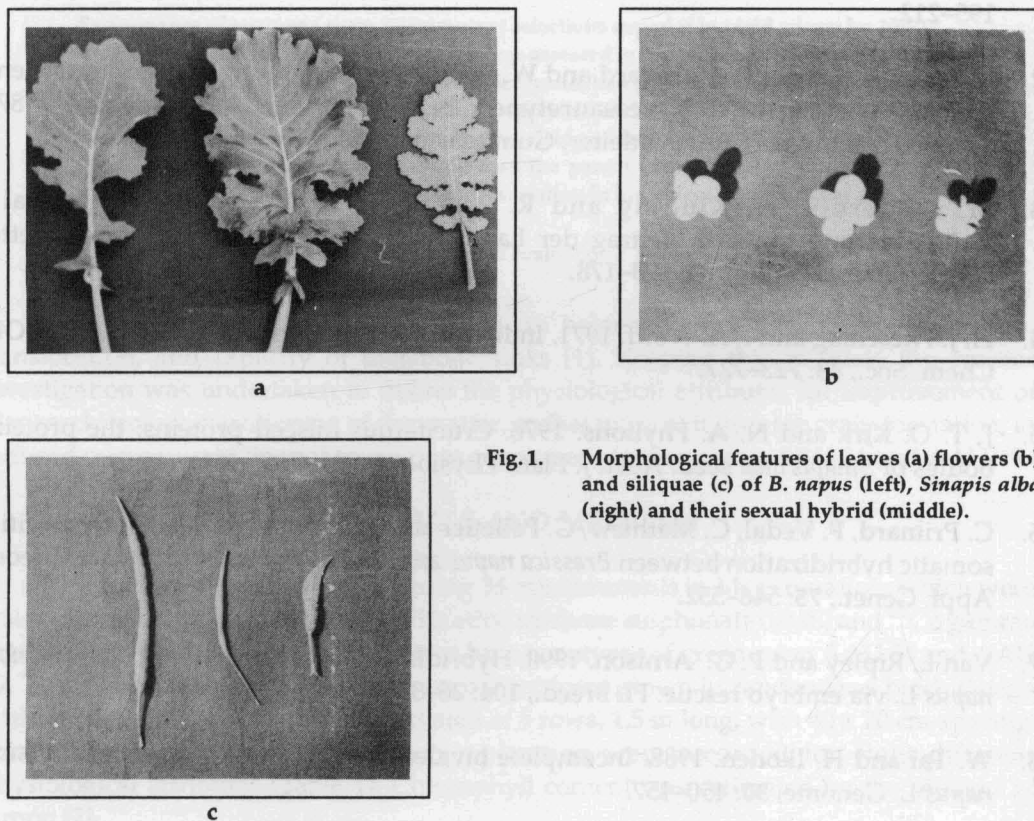


Fig. 1. Morphological features of leaves (a) flowers (b) and siliquae (c) of *B. napus* (left), *Sinapis alba* (right) and their sexual hybrid (middle).

Meiotic analysis of 30 PMCs of the 31-chromosome trigonomic hybrids (10A+9C+12Sal) at metaphase I showed the mean chromosome pairing ratio of 16.5 I, 6.97 II (rings + rods), 0.47 III and 0.13 IV per meiocyte. The extent of chromosome pairing was almost similar to that observed in *S. alba* × *B. napus* hybrid (6 II + III + 2 IV) [7]. The presence of 6.97 II (rods + rings) does not necessarily indicate homology between *B. napus* and *S. alba* because intergenomic pairing between A and C genomes in dihaploids of *B. napus* has been reported to be 7.73 II [8]. However, a maximum of 8 to 10 ring bivalents in some of the cells coupled with the presence of multivalents (trivalents and quadrivalents) in 26.6% of the meiocytes analysed indicates some nonhomologous recombination between A, C and Sal genomes.

Partial fertility of *B. napus* × *S. alba* hybrids and the ease of obtaining BC<sub>1</sub> seeds with *B. napus* indicates the possibility of transferring useful genes to the target genotypes of *B. napus*.

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