A WILD BRASSICEAE MATERIAL FROM CHINA: GENOMIC CONSTITUTION AND A NEW SOURCE OF THE GENE FOR LOW ERUCIC ACID CONTENT

B.Y. CHEN, B.F. CHENG, W.K. HENEEN

Dept. of Plant Breeding Research, The Swedish University of Agricultural Sciences, S-268 31 Svalöv, Sweden

A. JONSSON

Hilleshög AB, Box 302, S-261 23 Landskrona, Sweden

ABSTRACT

The Xinjiang wild *Brassiceae* material, collected from the northwestern part of China, was the subject of this study. On the basis of overall morphology, crossability, pollen fertility and meiotic pairing of the hybrids, it is concluded that the Xinjiang wild *Brassiceae* material belongs to the same cytodeme as *Sinapis arvensis* (genomes: SS, 2n=18). Zeroerucic seeds were found in the wild *Brassiceae* material, which could be of potential use for breeding and genetic studies in *Brassiceae*.

INTRODUCTION

Wild species are important sources of alien genetic variation for the improvement of cultivated crops. To exploit such alien genetic variation, one usually has to carry out interspecific or intergeneric hybridization. In this regard, knowledge of the genomic constitution of wild species and their relationship to cultivated crops is of crucial relevance.

Wild *Brassiceae* material, collected from Xinjiang Autonomous Region, northwestern China, was referred to as "the Xinjiang wild rape" by Wang *et al.* (1991). The genomic constitution of this wild *Brassiceae* material remains unkown although its chromosome number has been determined as 2n=18 (Chen *et al.*, 1985; Wang *et al.*, 1991). The aim of the present study is to ascertain the genomic constitution of this wild *Brassiceae* material. Since it had the same chromosome number as and was morphologically similar to *Sinapis arvensis* (SS, 2n=18), we decided to investigate whether they belonged to the same cytodeme. In addition, we report on the occurrence of zero-erucic seeds (less than 1%) in the wild material.

MATERIALS AND METHODS

Seeds of the wild *Brassiceae* material were provided by Xinjiang Academy of Agricultural Sciences, China. Reciprocal crosses were made between the Xinjiang wild *Brassiceae* material and *S. arvensis* accession No.7007 to study the crossability. Pollen fertility and chromosome pairing at meiosis in the parents and hybrids were recorded. For meiotic analyses, 50 pollen mother cells were examined from each parental accession and the hybrids. The cytogenetic techniques used were described in Chen *et al.* (1992). Fatty acid composition was assayed by the half-seed technique.

RESULTS

Crosses, pollen fertility and meiosis in parents and hybrids

Under the greenhouse condition, the overall morphology of the Xinjiang wild *Brassiceae* material and *S. arvensis* was similar. However, two morphological variants were observed in the wild material regarding the growth pattern of the siliques on the main inflorescence. The siliques could grow at an angle of about 45° toward the stem on most plants, or at a close parallel to the stem on some plants. These two morphological variants were otherwise morphologically similar and had the same chromosome number of 2n=18.

The reciprocal crossability between the Xinjiang wild *Brassiceae* material and *S. arvensis* No.7007 was good. The hybrid seed set (about 7 seeds /silique) in the crosses and the pollen fertility of the hybrids (96%) were as high as in the parents. The hybrids exhibited normal meiosis, i.e. 9 bivalents at metaphase I and 9/9 segregation at anaphase I as observed in the parents.

Inheritance of erucic acid content in the Xinjiang wild Brassiceae material

While 19 seeds were revealed to contain a high content of erucic acid (about 22%), the remaining 5 seeds contained only half that much (10-11%) among the 24 seeds analysed. These 5 seeds were assumed to be heterozygotes for the erucic locus since previous studies indicated an additive mode of inheritance of erucic acid content in some *Brassiceae* species (Dorrell and Downey, 1964). Self-pollination was therefore conducted on one plant derived from a seed containing 11% erucic acid for a progeny test. 25 seeds from this plant were determined for erucic acid content. The segregation pattern of erucic acid content fitted well with the expected Mendelian monogenic additive mode of inheritance, i.e. 1/4 EE (18-22%): 2/4 Ee (9-14%): 1/4 ee (<1%).

DISCUSSION

On the basis of overall morphology, crossability, pollen fertility and meiotic chromosome behavior of hybrids, we come to the conclusion that the Xinjiang wild *Brassiceae* material belongs to the same cytodeme as *Sinapis arvensis* (genomes: SS, 2n=18). The present results also revealed the occurrence of a zero-erucic allele at the erucic locus in the S genome of *Brassiceae*. The erucic acid content in the Xinjiang wild material (i.e. *S. arvensis*) was governed by one additive gene and was under the control of embryonic genotype, thereby being similar to the inheritance mode of this fatty acid in other *Brassiceae* diploid species such as *B. campestris* (Dorrell and Downey, 1964).

Now that the Xinjiang wild *Brassiceae* material endemic to northwestern part of China has been ascertained to be *S. arvensis*, one interesting question emerges whether there exist some other closely related *Brassiceae* diploid species in this region. Since *S. arvensis* is phylogenetically closely related to *B. nigra* (BB, 2n=16) (Song *et al.*, 1988), the endemic nature of *S. arvensis* to northwestern part of China may imply the occurrence of *B. nigra* in that region. This should arouse interests in future expeditions to that region.

REFERENCES

- Chen, Q., Z. Wang, W. Sun, W. Du and Y. Wang (1985). Preliminary studies of the Xinjiang wild rapeseed. <u>Chinese J. of Oil Crops 4</u>: 6-10. (in Chinese).
- Chen, B.Y., V. Simonsen, C. Lannér-Herrera and W.K. Heneen (1992). A *Brassica campestris-alboglabra* addition line and its use for gene mapping, interspecific gene transfer and generation of trisomics. <u>Theor. Appl. Genet. 84</u>: 592-599.
- Dorrell, D.G. and R.K. Downey (1964). The inheritance of erucic acid content in rapeseed (*Brassica campestris*). Can J. Plant Sci. 44: 499-504.
- Song, K., T.C. Osborn and P.H. Williams (1988). *Brassica* taxonomy based on nuclear restriction fragment length polymorphisms (RFLPs): 1. Genome evolution of diploid and amphidiploid species. Theor. Appl. Genet. 75: 784-794.
- Wang, Z., Q. Jiao and L. Yi (1991). Xinjiang wild rape. <u>Proc. of the 8th Intern.</u>
 <u>Rapeseed Congress Vol. 6</u>: 1840-1843. Saskatoon, Canada.