

DEVELOPMENT OF B-GENOME CHROMOSOMES INTROGRESSION LINES FROM INTERSPECIFIC HYBRIDS OF *BRASSICA NAPUS* x *B. CARINATA*

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Introduction

The Brassica family includes a large variety of different species and products from those species. Transfer of genes from distance relatives such as *Brassica carinata* (BBCC) which has a number of B-genome derived traits into *Brassica napus* (AACC) can increase the allelic diversity for plant breeders. There are two lineages suggested for the diploid Brassica genomes, the AC and B lineages. There is strong colinearity between the A and C genomes, however the B genome is significantly different.

Objectives

To identify and introgress traits of agronomic interest from the *B. carinata* genome, two inter-specific populations were developed in this project, using the advanced backcrossing approach to introgress traits into advanced germplasm. We used molecular markers and cytogenetic techniques to address the following objectives:

- 1) Track B genome chromosome segments in inter-specific backcross lines
- 2) Study the inheritance of different chromosomes from a close relative
- 3) Map agronomically interesting traits

Materials and Methods

Plant material: The development of the plant material and pedigree of the lines is demonstrated in Figure 1.

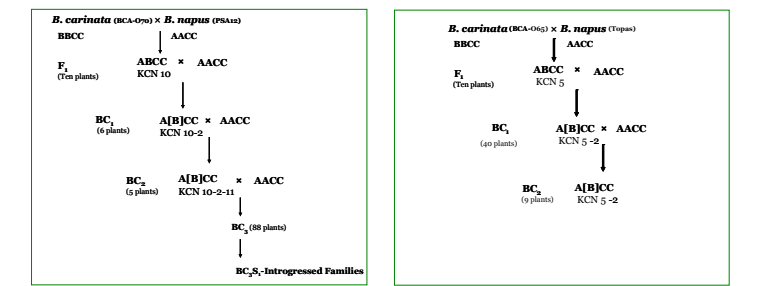


Figure 1. Pedigree and crosses used in the development of the KCN-10 (left) and KCN-5 populations.

Phenotyping: Morphological traits were measured using the IBPGR Brassica descriptor. (IBPGR 1990).

Microsatellite analysis: Amplification and resolution of microsatellite alleles by PCR and capillary electrophoresis was performed as described in Navabi et al (2010).

GISH analysis: Fluorescent in situ hybridization was performed as described in Navabi et al. (2010).



Figure 2. Segregation of the morphological traits in the BC3 backcross populations.

Results and Discussion

We mapped the B and C genomes of *B. carinata* from the KCN-10 population and observed their introgression into *B. napus* through an advanced set of backcrosses, using SSR markers, GISH assays and chromosome counts to study the inheritance of the B-genome chromosome(s) (Figure 3 and Table 1).

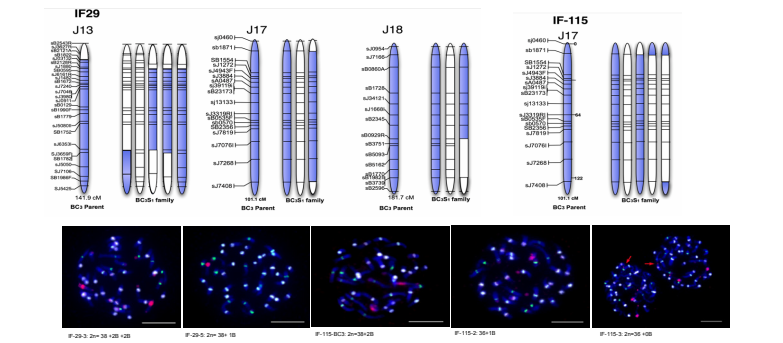


Figure 3. Physical representation chromosomes and their painting using *B. nigra* genomic DNA.

Table 1A. Summary of B chromosomes in individual BC2 plants from the KCN-5 population.

BC2 PLANT	Expected B Chromosome	Chromosomes with terminal deletions	Comments
5-2-1	J16/J17	J18	
5-2-2	J11/ J14/ J17	J18	Tip of J15
5-2-3	J14/ J15/ J17	J16/ J18	
5-2-4	J11/J16/J17		
5-2-5	J13/ J14/ J15	J12/ J17/ J18	
5-2-6	J13/ J15	J17/ J18	
5-2-7	J14/ J16/ J17	J12	
5-2-8	J15	J12/ J17/ J18	
5-2-9	J13	J17/ J18	
Westlar	None		
Carinata	All		

Table 1B. Summary of B chromosomes for individual plants from the KCN-10 population of five selected BC3S1 families.

BC3S1 PLANT	Expected B Chromosome	Number of Red Signal	Total Chromosome Count
IF-29-2,3,5	J13/J17/J18	1,2,1	38,40,39
IF-30-2,3,5	J16	1,0,0	39,40,40
IF-42-1	J13/tip of J17	3	42
IF-42-2	J13/ tip of J17	Fragments	36
IF-103-1,2	J17	1	37
IF-115-1	J13/J17	2	40
IF-115-2,3	J17	1	37
IF-174-3,5	J18	0	36, 37, 38
Westlar	None	0	38
Carinata	All	8	34

Conclusions

The material developed as part of this backcrossing program includes lines with one or several of the B-genome chromosomes, such as addition deletion and substitution lines. All of these lines are publicly available by contacting the senior author. Further characterization of this material will be presented in Navabi et al. (submitted).

References

IBPGR, 1990 Descriptors for *Brassica* and *Raphanus*. IBPGR, Rome.
 Navabi, Z. K. et al. Genome **53**: 619-629.

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