Yellow-seeded *Brassica napus* from interspecific crosses

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ABSTRACT

In *Brassica*, yellow seed naturally exists in *B. rapa* (AA), *B. juncea* (AABB) and *B. carinata* (BBCC). Cytogenetical studies by different authors have demonstrated a close homology between the chromosomes of the *Brassica* A and C genomes. This suggests that intergenomic transfer of genes between these two genomes is possible. In this light, interspecific crosses between yellow-seeded *B. rapa* var. 'yellow sarson', yellow-seeded *B. carinata*, black-seeded *B. alboglabra* (CC) and black-seeded *B. napus* (AACC) were done. These crosses were designed to introgress the yellow seed colour genes from the A genome of 'yellow sarson' into the *Brassica* C genome, and thus to develop *B. napus* carrying the yellow seed colour genes of 'yellow sarson' in its both AA and CC genomes. These interspecific crosses yielded yellow-seeded *B. napus* plants suggesting that introgression of the gene(s) into the C genome had been accomplished. In contrast, interspecific crosses that were designed to assemble the yellow seed colour genes of *B. carinata* and 'yellow sarson' into *B. napus* failed to produce yellow seed. This is probably due to interaction between the seed colour genes of these two species. Yellow-seeded *B. napus* of double low quality was developed by crossing the yellow-seeded *B. napus* lines with conventional *B. napus* followed by doubled haploid and pedigree breeding. The yellow seeds had higher oil and protein and lower fibre content than black seeds.

Key words: *Brassica napus* – interspecific cross – yellow seed – quality

INTRODUCTION

Yellow-seeded *Brassica* oilseed is desirable due to its higher oil and protein and lower fibre content. This form is naturally available in *B. rapa* (AA), *B. carinata* (BBCC) and *B. juncea* (AABB). Different authors attempted to introgress the yellow seed colour genes from these species into *B. napus* (AACC). To date, yellow-seeded *B. napus* developed from interspecific crosses was not stable under a wide range of environmental conditions (see Rahman 2001a).

Cytogenetical studies by different authors indicate that, of the three *Brassica* genomes, A, B and C, the A and C genome chromosomes are most closely related. Attia and Röbbelen (1986) observed up to 8.7 II and 14.0 chiasmata (Mean = 7.3 II, 12.3 chiasmata) in AC amphihaploid derived from interspecific crossing. This suggests the possibility of transferring genes from the A to the C genome. The pairing behaviour of the A and C genome chromosomes is not disturbed by the presence of B genome chromosomes (Busso et al. 1987).

The aim of the present study was to develop a stable yellow-seeded *B. napus*, carrying the yellow seed colour genes of *B. rapa* var. 'yellow sarson' into its both AA and CC genomes, through introgression of gene(s) from the A to the C genome. Furthermore, it was also aimed to develop a yellow-seeded *B. napus* through assembling the yellow seed colour genes of *B. carinata* and 'yellow sarson' into *B. napus*.

MATERIALS AND METHODS

The species used in the study were yellow-seeded *B. rapa* var. 'yellow sarson' (AA) and *B. carinata* (BBCC), and black-seeded *B. alboglabra* (CC) and *B. napus* (AACC).

Crosses between *B. alboglabra* and *B. carinata* were done to resynthesize *B. alboglabra* carrying the yellow seed colour gene(s) of *B. carinata*. The resynthesized *B. alboglabra* was crossed with *B. rapa* var. 'yellow sarson' to resynthesize *B. napus*, and thus to assemble the yellow seed colour genes of *B. carinata* and 'yellow sarson' into *B. napus* (Fig. 1).

Brassica alboglabra x 'yellow sarson' crosses were done to resynthesize *B. napus* (line No. 01) carrying the yellow seed colour genes of 'yellow sarson' in its AA genome.

Brassica carinata x 'yellow sarson' crosses were done with two aims. (i) To introgress the yellow seed colour genes from the A genome to the C genome and thus to develop *B. napus*

carrying the yellow seed colour genes of 'yellow sarson' in its CC genome. For this purpose, the F_1's (ABC) were crossed with conventional *B. napus* and the 3-way hybrids were selfed up to F_7 generation with selection for yellow seed. (ii) To assemble the yellow seed colour genes of 'yellow sarson' and *B. carinata* into *B. napus*. For this purpose, the ABC hybrids were chromosome doubled and the trigenomic amphidiploids (AABBCC) were crossed with the resynthesized *B. napus* line No. 01. The AABCC hybrids were selfed to eliminate its B-genome chromosomes and thus to develop yellow-seeded *B. napus* (Fig. 1).

From the above-mentioned 3-way cross, (*B. carinata* x 'yellow sarson') x *B. napus*, a yellowish-brown-seeded *B. napus* line (No. 06) was resynthesized. This line was further crossed with the resynthesized *B. napus* line No. 01. The F_1's were selfed and selection for yellow seed was applied up to F_7 generation. Two yellow-seeded *B. napus* lines developed from this cross were crossed with two conventional *B. napus* of double low ('00') quality, and doubled haploid (DH) and pedigree breeding was followed to develop yellow-seeded *B. napus* of '00' quality.

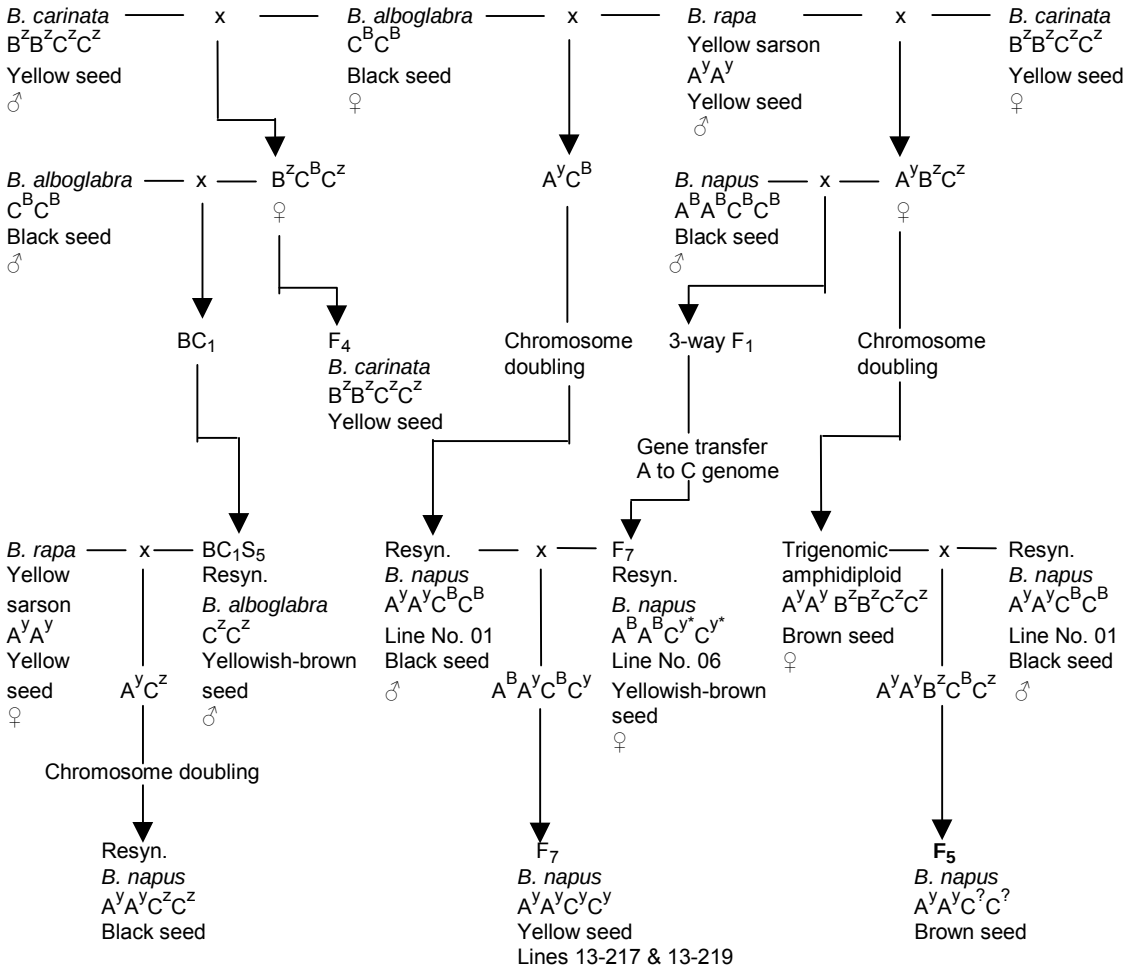

Fig. 1: Schematic diagram showing *Brassica* interspecific crosses done for development of the yellow-seeded *B. napus*. The capital letters A, B and C indicate the three *Brassica* genomes. The superscripted letter B indicates the black seed colour genes of conventional *B. napus*. The superscripted letter y indicates the yellow seed colour gene(s) of 'yellow sarson' (*B. rapa*). The superscripted letter z indicates the yellow seed colour gene(s) of yellow-seeded *B. carinata* which are in different genomes, relative to the yellow seed colour gene(s) of 'yellow sarson'. The symbol * indicates the transfer, through allosyndesis, of the yellow seed colour genes from the A to the C genome.

RESULTS

The F_2 population of *B. alboglabra* x *B. carinata* resembled *B. carinata* phenotype, from where yellow-seeded plants were obtained in F_3 generation. However, progenies of these plants

stabilized into *B. carinata* (BBCC) phenotype. In contrast, the BC_1 population of (*B. alboglabra* x *B. carinata*) x *B. alboglabra* resembled *B. alboglabra* phenotype. A yellowish-brown-seeded *B. alboglabra* line was obtained in BC_1S_5 generation. *Brassica napus* plants resynthesized from 'yellow sarson' x yellowish-brown *B. alboglabra* produced only black seeds (Fig. 1).

The *B. napus* line No. 01 (2n=38), resynthesized from *B. alboglabra* x 'yellow sarson' cross had black seeds. Selfing of the 3-way interspecific hybrids of (*B. carinata* x 'yellow sarson') x *B. napus* yielded a yellowish-brown-seeded *B. napus* line No. 06 (2n=38) in F_7 generation. Cross between these two resynthesized *B. napus* lines, No. 06 x No. 01, yielded a nearly yellow-seeded *B. napus* plant in F_3 generation. Further selection in the progeny of this plant yielded two bright-yellow-seeded lines 13-217 and 13-219 in F_7 generation (Fig. 1).

Seed colour of the trigenomic amphidiploid (AABBCC) was brown, in contrast to yellow seed colour of its parents *B. carinata* and 'yellow sarson'. Selfing of the hybrids of AABBCC x No. 01 (AACC), i.e. AABCC, up to F_5 generation failed to produce any yellow seed (Fig. 1).

The yellow-seeded *B. napus* lines, 13-217 and 13-219, contained 27% erucic fatty acid in seed oil and a high level of glucosinolate (GLS)(>40 μmol/g seed) in seed meal and had white petal like *B. alboglabra*. From 287 DH lines, produced from the crosses of yellow-seeded *B. napus* x '00' *B. napus*, a zero erucic acid, yellow-seeded and yellow-flowered *B. napus* line was obtained. This line was further crossed with '00' *B. napus* and pedigree breeding was followed. Yellow-seeded *B. napus* plants of '00' quality were obtained in F_4 generation. Oil + protein content in seeds of yellow-seeded *B. napus* was 3% higher and the fibre content was 55% lower compared to its black-seeded counterpart (Rahman et al. 2001).

DISCUSSION

The above-mentioned two crosses, 'yellow sarson' x yellowish-brown *B. alboglabra* and AABBCC x resynthesized *B. napus* line No. 01, failed to produce any yellow seed. The yellow seeds in *B. rapa* var. 'yellow sarson' is due to presence of recessive alleles of the seed colour genes in the two loci in homozygous state (Rahman 2001b), while in *B. carinata* it is due to presence of a dominant repressor gene (Getinet and Rakow 1997). Thus, two different genetic systems are involved in determination of yellow seed colour in these two species. The failure to obtain yellow seeds from these two crosses is probably due to interaction between seed colour genes of these two species. This is also evident from the brown coloured seeds in the AABBCC plants produced from yellow-seeded *B. carinata* x 'yellow sarson' crosses. However, bright yellow-seeded *B. napus* plants were obtained by crossing the two resynthesized *B. napus* lines, No. 06 and No. 01. The line No. 01 carried the yellow seed colour genes only in its AA genome. Generation of yellow-seeded *B. napus* from No. 06 x No. 01 cross would only be possible if the line No. 06 carries the yellow seed colour gene(s) of 'yellow sarson' in its CC genome. Introgression of the yellow seed colour gene(s) from the A to the C genome apparently has occurred through homeologous pairing of chromosomes of these two genomes.

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