Broadening of genetic diversity in spring canola (*Brassica napus* L.) by use of the C genome of *Brassica oleracea* var. *alboglabra* and *B. oleracea* var. *botrytis*.

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Introduction

➢ *Brassica napus* L. (AACC genome, $2n = 38$) is an important oilseed crop in the world

➢ Canada is top canola producer in the world generating over \$19 billion each year.

➢ Genetic diversity (GD) in breeding germplasm of spring canola *B. napus* needs to increase for continuous progress in this crop (Diers et al. 1996, Fu and Gugel, 2010, Bennett et al. 2012).

➢ Germplasm to broaden GD in spring canola *B. napus* ;

- **Primary gene pool**

  (Rutabaga, winter and semi-winter types *B. napus*)

- **Secondary gene pool**

  (*B. rapa*, *B. oleracea*, *B. junceae* etc)

Fig. Major vegetable oil production worldwide (www.fas.usda.gov/psdonline)

Study Objectives

➢To Investigate the feasibility of developing canola quality *B. napus* ($2n = 38$) inbred lines of spring growth habit from *B. napus* × *B. oleracea* and (*B. napus* × *B. oleracea*) × *B. napus* interspecific cross.

➢Estimate the allelic diversity introgressed from C genome of *B. oleracea* into *B. napus* by simple sequence repeat (SSR) markers.

Materials & Methods

Parental materials was comprised of one canola quality spring type *B. napus* (AACC, $2n = 38$) double haploid line A04-73NA and two types of *B. oleracea* var. *alboglabra* and var. *botrytis*.

Crossing scheme

The following two interspecific crosses were made using *B. napus* as female and *B. oleracea* as male parent to develop interspecific F_1 hybrids.

- A04-73NA × *B. oleracea* var. *alboglabra*
- A04-73NA × *B. oleracea* var. *botrytis*

F_1 plants were self-pollinated to produce F_2 seeds as well as backcrossed to the *B. napus* parent A04-73NA to develop backcross (BC_1) seeds.

- (A04-73NA × *B. oleracea* var. *alboglabra*) × A04-73NA
- (A04-73NA × *B. oleracea* var. *botrytis*) × A04-73NA

Materials and Methods (continued)

➢ Development of Recombinant inbred lines

F_2 and BC_1 derived interspecific inbred lines were developed according to scheme as shown below with evaluation for following agronomic and Seed quality traits in each generation population;

- Days to flower
- Plant fertility
- Fatty acid composition
- Glucosinolate contents

➢ Ploidy level

In F_6 and BC_1S_4 generation population.

➢ Genotyping

F_4 and BC_1S_3 families were genotyped by using polymorphic SSR markers.

Results

Table: Summary of plant fertility traits in F_2 and BC_1S_2 derived interspecific generation populations of *B. napus* × *B. oleracea* crosses.

Fig. Frequency distribution of erucic acid content in different generations of *B. napus* × *B. oleracea* cross with percent population falling in different groups indicated on top of each bar.

A comparison of glucosinolate (µmol/g seed) inheritance in F_2 and BC_1 derived generation populations.

Table: Summary of erucic acid (%) and glucosinolate (µmol/g seed) in different generation populations of *B. napus* × *B. oleracea* interspecific cross.

Distribution of particular in F_2 and BC_1S_3 generation.

Fig. Bar chromatic diagram of % and BC4 generation showing percentage of population in each group based in partex value.

Fig. Principal coordinate plots for 52 F_4 and 41 BC_1S_3 lines derived from interspecific *B. napus* × *B. oleracea* and (*B. napus* × *B. oleracea*) × *B. napus* cross, respectively based on polymorphic bands derived from 24 simple sequence repeat (SSR) markers.

Conclusion

➢ Despite the complex inheritance pattern of glucosinolate contents, this study demonstrated the feasibility of developing double low canola quality *B. napus* lines from *B. napus* × *B. oleracea* cross.

➢ Study on plant fertility traits showed the need of repeated cycle of selection to overcome sterility during *B. napus* × *B. oleracea* type interspecific crosses.

➢ Ploidy results showed that *B. napus* inbred lines with $2n = 38$ are achievable from *B. napus* × *B. oleracea* and (*B. napus* × *B. oleracea*) × *B. napus* cross.

➢ From molecular results it can be concluded that genetic diversity from *B. oleracea* types var. *alboglabra* and var. *botrytis* can be introgressed successfully into spring canola *B. napus*.

Future Perspective

Genetically diverse canola quality *B. napus* recombinant inbred lines can be developed through reconstitution of C genome of *B. napus* with *B. oleracea* and such genetically distinct interspecific cross derived inbred lines may have potential to develop commercial canola quality spring type hybrid cultivars.

Acknowledgments

References

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