Broadening of genetic diversity in spring canola *Brassica napus* L. by the use of the C-genome of *Brassica oleracea* L.

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Introduction

Rapeseed canola (*Brassica napus* L., AACC, 2*n* = 38) is one of the important vegetable oilseed crops in the world due to its premium oil quality (Fig 1).

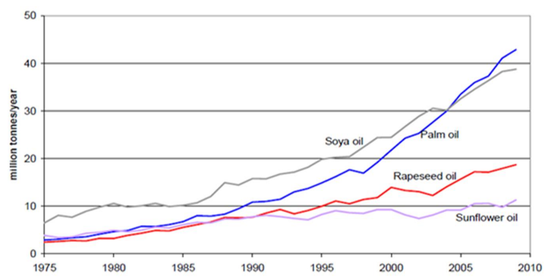


Fig 1. Major vegetable oil production worldwide from 1975 to 2010
(Source: www.fas.usda.gov/psdonline)

Presence of genetic variability is pre-requisite to develop new cultivars with improved yield to meet the demand of ever growing population in the world. However, there has been a decline in genetic diversity of spring canola *B. napus* over last few decades. Therefore, breeding efforts must be taken towards broadening of genetic diversity in spring canola *B. napus* (Cowling 2007, Rahman et al. 2011). This can be accomplished by introgressing genetic diversity from diploid progenitor species *Brassica rapa* L. (AA, 2*n* = 20), *Brassica oleracea* L. (CC, 2*n* = 18) and/or other allied species of the family Brassicaceae.

Research Objectives

- To assess the feasibility of developing spring canola *B. napus* recombinant inbred lines by crossing *B. oleracea* with *B. napus*.
- To compare the efficiency of filial and backcross breeding method in developing spring canola *B. napus*.
- To study the genetic diversity in interspecific *B. napus* inbred lines through SSR markers.

Materials and Methods

Parental material used in this study consisted of;

B. napus double haploid line A04-73NA

B. oleracea var. *italica*, broccoli cv. Premium Crop

B. oleracea var. *capitata*, cabbage cv. Balbro (Fig 2)

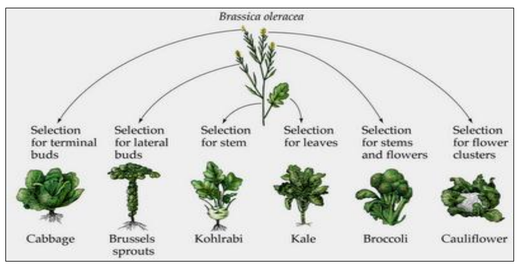


Fig 2. Parental germplasm of *Brassica oleracea* cultivars
(Source: www.feralbigten.wordpress.com/2012/02/13/wild-food)

Two types of population were developed according to scheme as shown in Fig 3 which were subjected to evaluation for following traits:

Agronomic traits like days to flowering, silique length (mm), seed number per silique, seed weight (g).

Seed quality traits like fatty acid, oil, protein and glucosinolate contents (µ mol g^{-1}seed).

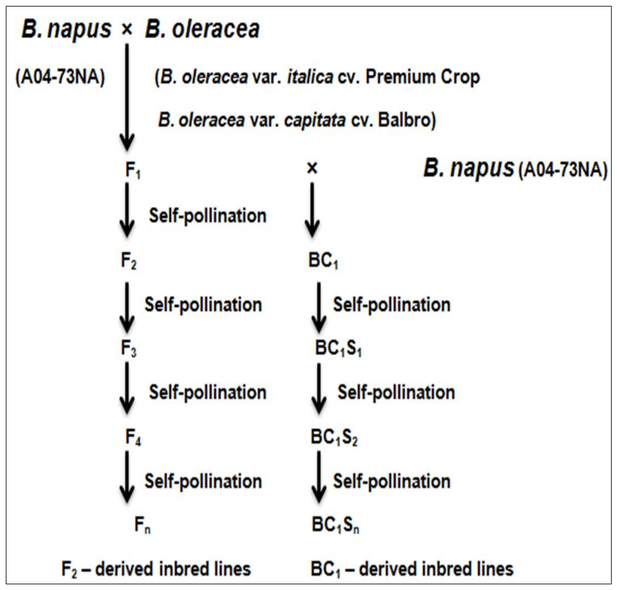
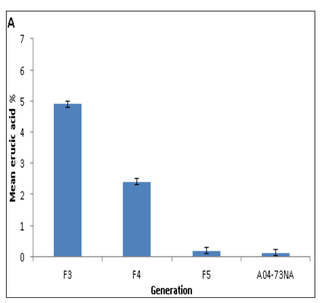


Fig 3. Crossing scheme for interspecific inbred line development

Results

- F_5 and BC_1S_3 generation had mean erucic acid 0.18 ± 0.02 SE and 0.27 ± 0.02 SE, respectively which were not significantly different from *B. napus* check parent A04-73NA.
- Mean glucosinolate content in F_6 and BC_1S_4 generations were less than 20 µ mol g^{-1}seed.
- Most of inbred lines in F_6 and BC_1S_4 had partec value in the range of *B. napus* check parent A04-73NA.



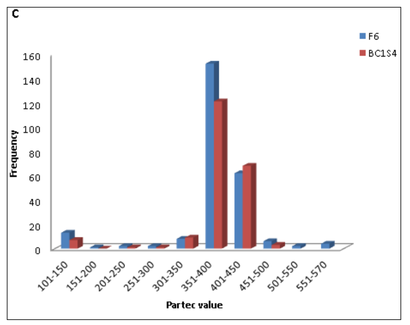


Fig 4. (A) Inheritance of erucic acid in F_2 derived generation;
(B) comparison of glucosinolate in F_6 and BC_1S_4 generation;
(C) Flow cytometry analysis.
Note: A04-73NA is check *B. napus* parent.

Conclusion

Several spring canola interspecific *B. napus* inbred lines are developed by crossing *B. napus* with *B. oleracea* which can be used in other breeding programs as well as to develop canola hybrid cultivars.

References

Cowling, W. A. 2007. Genetic diversity in Australian canola and implications for crop breeding for changing future environments. Field Crops Res. 104: 103111.

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