Marker assisted selection in *Brassica oleracea*

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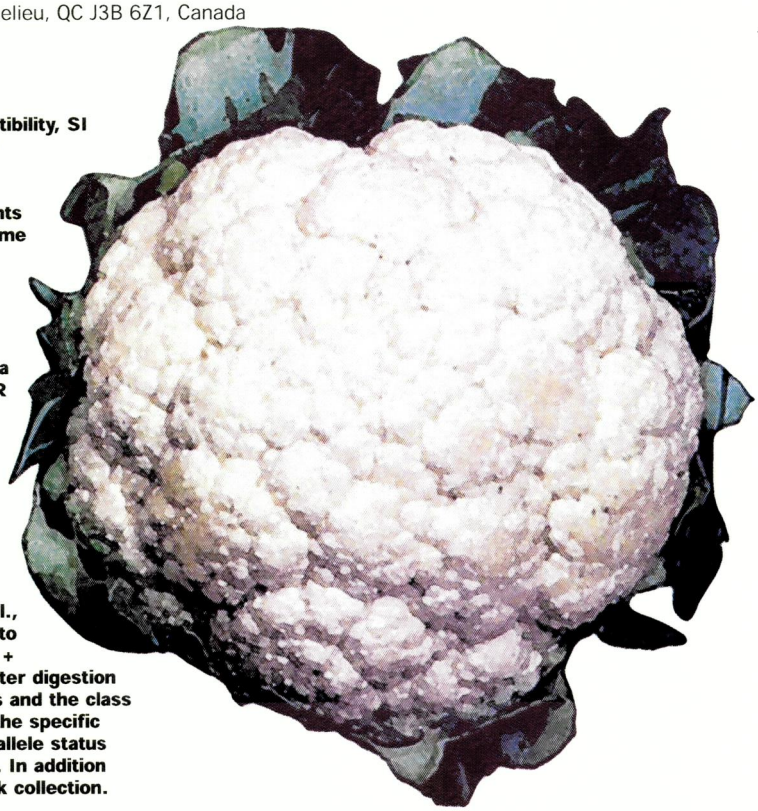

F_1 hybrids of *B.oleracea* are produced by the using self-incompatibility, SI system. A single multiallelic gene, the S locus glycoprotein SLG plays an important role in the cell - cell recognition event when pollen comes into contact with the stigma surface.
Traditionally, S-allele identification is carried out by crossing plants against tester lines with known S-haplotype. The pollination is time consuming and needs flowers as testing material. Alternatively, DNA markers based on the sequenced S locus can be used to characterise plants at the molecular level. A DNA test can be performed at any developmental stage of the plant.

The purpose of this study was to evaluate the reproducibility of a PCR based method as an alternative to pollination. We used PCR markers from Nishio et al. (1994) to:
a) characterise breeding lines of cauliflower and white cabbage at the S locus using *B. oleracea* of known S-types from HRI, Wellesbourne, UK as references.
b) to assess the purity of F_1 hybrid seeds of cabbage and cauliflower for variety multiplication and marketing.

Twenty-nine cauliflower and eighteen white cabbage lines could be grouped into SLG class I and SLG class II using two sets of primers, PS5 + PS15 and PS3 + PS21 respectively (Nishio et al., 1996). One white cabbage line failed to amplify and is believed to represent a SLG class I subclass because the primer pair PS18 + PS15 specific for this subclass did not amplify in our survey. After digestion with restriction enzyme *Mbo*I the class I 1.3 Kb DNA fragments and the class II 1 Kb fragments revealed banding profiles charactereistic for the specific S-alleles. Comparing DNA profiles with *B. oleracea* of known S-allele status from the gene-bank identified the S-alleles in the breeding lines. In addition four new alleles were detected not represented in the gene-bank collection.

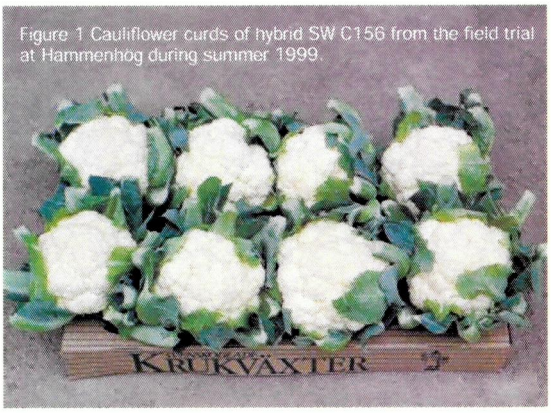

Figure 1 Cauliflower curds of hybrid SW C156 from the field trial at Hammenhög during summer 1999.

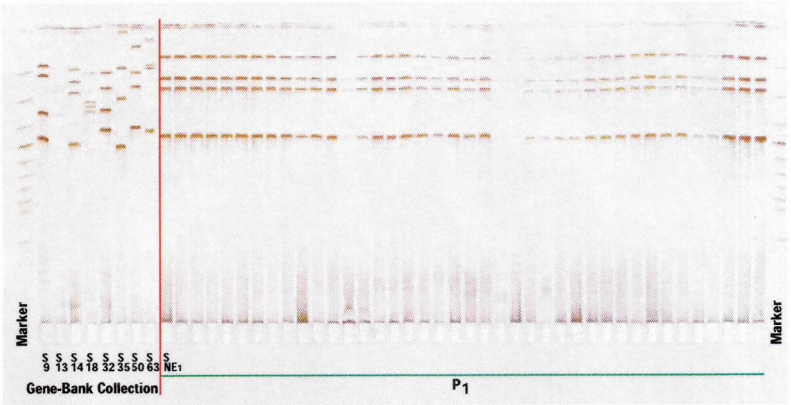

Figure 2 Purity testing of a cauliflower mother line belonging to SLG class I prior to hybridity check of the corresponding F_1. *Mbo*I-digested amplification products of primer pair PS5/15. P_1 has an S-allele mot identified in the gene-bank collection.

Conclusion

The PCR based methods from Nishio et al. (1996) proved to be robust, simple to use and highly reproducible for S-allele characterisation and hybrid purity testing in white cabbage and cauliflower.

Based on the SLG class and S-allele status of the parental lines, the purity of two cauliflowers and three white cabbage hybrids were determined (Table 1). The hybridity of the two cauliflowers SW C130 and SW C156 and one white cabbage SW 25161 were 100%. White cabbage SW 25144 and SW 25163 showed 98% and 85% hybridity respectively. These findings together with the results of three years field trial of the hybrids in Canada make them well suited to hit the Canadian market.

Table 1. Assessment of the purity of F_1 hybrid seeds of white cabbage and cauliflower.

	Purity P_1	Purity P_2 [1]	Hybridity F_1	Diagnostic primers
Cauliflower SW C130	100%	88%	100%	PS5/15
Cauliflower SW C156	100%	96%	100%	PS5/15
White cabbage SW 25144	100%	100% [2]	98%	UBC #890 [3]
White cabbage SW 25161	100%	94%	100%	PS3/21
White cabbage SW 25163	100%	97%	85%	PS3/21

[1] The cauliflower P_2's are open pollinated lines and purity is expected to be less than 100%.
[2] The hybridity is calculated based on the observed number of hybrids and the frequency of diagnostic bands in the father line.
[3] The P_2 belongs to a SLG group that did not amplify. ISSR markers (Zietkiewicz et al., 1994) were used for hybridity test. Primer #890 from University of British Columbia.

Acknowledgements

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References

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