

Identification of molecular markers and genome mapping in *Brassica napus* L.

(Received: 10.11. 2000)

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ABSTRACT

Molecular markers provide an efficient method for estimating genetic relationships among genotypes of any organism. Moreover, they constitute an excellent source of landmarks for genome mapping. In the present investigation three *B. napus* varieties, i.e., A112, Furax and D353 were selected to identify RFLP and RAPD markers to establish a molecular marker-based linkage map of *B. napus*. These varieties were considered to be polymorphic based on a preliminary study, in addition to other criteria including variations in leaf shape, erucic acid content and isozyme analysis. The selected varieties were screened for RFLP markers using probes derived from a PstI genomic library and labeled with the non-radioactive digoxigenin labeling and detection system. The number of RFLP markers identified between the two varieties A112 and Furax was 136, while 98 RFLP markers were recognized between D353 and Furax. The mean number of markers/probe enzyme combination was 2.03 and 1.70 for A112/Furax and D353/Furax, respectively. The number of RAPD markers detected between the varieties A112 and Furax was 87, while 130 RAPD markers were realized between the varieties D353 and Furax. The mean number of markers/primer detected in both cases A112/Furax and D353/Furax was 3.62 and 3.71, respectively. Segregation analysis of the RAPD loci in the F₂ populations of A112/Furax and D353/Furax permitted the construction of two linkage maps covering a map distance of 2675.4 and 3004.4 cM, respectively. Eight markers (GPI-2 and seven RAPD markers) were common in the two populations and were used to combine the two maps.

Key words: RFLPs, RAPDs, molecular markers, genome mapping, *Brassica napus*.

INTRODUCTION

The development of molecular markers holds many promises to plant breeders and geneticists in different areas, such as varietal identification or fingerprinting, estimation of relatedness between different genotypes, discernment of evolutionary relationships and introgression of Mendelian traits into a population (Mayes *et al.*, 1996, Castagna *et al.*, 1997, Iqbal *et al.*, 1997, Lanza

et al., 1997, Garcia-Mas *et al.*, 2000 and Khan *et al.*, 2000). Moreover, genetic maps based on molecular markers allow analysis of genomes at a level of precision not previously possible. These maps enable scientists to locate quantitative trait loci (QTL's) controlling important complex agronomic characters.

Accumulation of this kind of information can be used to develop better breeding strategies for a crop. However, marker-based selection is the area where molecular markers