

Addition of Restriction Fragment Length Polymorphism Markers to the Genetic Linkage Map of *Brassica rapa* L. (syn. *campestris*)

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Genetic linkage analysis of 151 restriction fragment length polymorphism (RFLP) loci, that included eight new loci, detected by the six probes in the present study, and four trait loci including seed colour, leaf pubescence, resistance to white rust caused by *Albugo candida* race-2 (AC-2) and race-7 (AC-7) employing the MAPMAKER/EXP 3.0 programme led to the development of 10 linkage groups (LGs) spanning over 44.4 centiMorgan (cM) to 130.4 cM containing 9 to 22 loci and two short LGs with two or three marker loci in *Brassica rapa*. The enriched map covers 993.1 cM of *B. rapa* genome with an average marker interval of 6.41. Eight new RFLP loci occupied new map positions on five linkage groups, LG 2, 3, 6, 8 and 9. Addition of these RFLP loci led to appreciable changes in the corresponding linkage groups and resulted in an increase of the total map length by 102.8 cM and of the marker interval by 0.35 cM. Interval mapping by using the computer programme MAPMAKER/QTL 1.1 for scanning the genetic map led to the detection of one major quantitative trait locus (QTL) in LG 4 and one minor QTL in LG 8 governing resistance to AC-7. Both QTLs contributed 7.89 to the interaction phenotype (IP) score with 96.3% genetic variation. The multi-locus model suggested additive gene action with 96.8% genetic variation.

Key words: *Brassica rapa*, RFLP, QTL, Linkage Map