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

Jogeswar Panigrahia, Anjana Patnaik, Phullara Kole, and Chitta ranjan Kole

Laboratory of Plant Biotechnology, School of Life Sciences, Sambalpur University, Sambalpur-768019, Orissa, India. Fax: +91-6632430158.
E-mail: drjogeswar_panigrahi@ymail.com; jogesh_ckus@rediffmail.com

Department of Genetics and Plant Breeding, Allahabad Agriculture Institute, Deemed University, Allahabad-211007, U. P., India

Present address: Department of Genetics & Biochemistry, Clemson University, Clemson, SC 29634, USA

* Author for correspondence and reprint requests

Z. Naturforsch. 64c, 882 – 890 (2009); received June 8/July 13, 2009

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