(24-26 % in cultivated var.) and resistance to lodging and pod shattering. Morphologically, the new plant type closely resembled with B. juncea. It was named as selection 165-93, and when tested for yield under normal plant density(20 plants per M^2), yielded 20 quintals as compared to best B. juncea var.,19q/Ha. Its performance in trials with increasedplant densities(40 plants/ M^2 or more) in pure and intercropping with matching height companion crops, is being tested. The new plant type is of great importance as in addition to the abovesaid desirable traits, it escapes the critical period of insects and diseases attack, requires less inputs and offer higher yield per unit area and time, fits under the specific situations where moisture is available for shorter period or where crop season is shorter.

(2) Disease resistant genotype:

Alternaria black spot(A. brassicae), downy mildew (Peronospora parasitica) and white rust(Albugo candida) are 3 major diseases in India, inflicting heavy losses(up to 30%) to seed and oil yield and quality. Almost all present var. of B. juncea are succeptible to abovesaid diseases and natural inoculum present in the field is enough to damage the crop during pathogen favouring season. Therefore, a B. carinata (Braun) line, showing good degree resistance to abovesaid diseases, was crossed to B. juncea to combine the resistance in B. juncea.Segregating generations were screened for the resistance in the field during the years of natural disease spread, and carried forward as mass during the years of low or no incidence. In F_7 generation a selection showing stable and good degreeof resistance to Alternaria and white rust was isolated. This genotype is tall(195 cm), late maturing(150 d), possesses thicker-dark green and shining leaves. Very small lesions develop on leaves nearing completion of fruiting in this genotype as compared to large lesions with higher frequencies at flowering time in existing B. juncea var.Morphologically, the new genotype has greater resemblance with B. juncea but change in thickness, colour and serration of leaves and seed colour indicates its recombinant nature.

Besides its late maturity, the seed size is smaller and yield is lower than the existing B. juncea varieties. These defects are being rectified by crossing the resistant genotype with high-yielding and early maturing varieties.

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RFLP Mapping in Indian Mustard (*Brassica juncea*)

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RFLP linkage maps are useful for studying genome organization and tagging genes of agronomic importance. In the genus *Brassica*, linkage maps have been constructed in *B. oleracea* (1, 2), *B. campestris* (3, 4) and in *B. napus* (5). We have initiated molecular mapping in Indian mustard (*B. juncea*), considering its importance as an edible oil source in India. Construction of a partial linkage map of this crop is presently reported.

Materials and Methods

An intervarietal cross of *B. juncea* was generated using cv. Varuna as female and exotic collection BEC 144 as male. By selfing a single F_1 plant the F_2 population was obtained. A total of 48 random F_2 plants were genotyped. DNA was extracted as described by Mohapatra *et al* (6) and restricted with either *Eco* RI, *Hin* dIII or *Eco* RV. Southern blotting, hybridization and washing were carried out as described by Sharma *et al* (7). Thirty four random genomic DNA clones from *Pst* I subgenomic library of mustard cv. Varuna (6) were used as probes. Besides, *cab* 3C cDNA of tomato (8) was also used. Linkage relationship among markers was established at recombination frequency $\leq 50\%$ and log likelyhood of odds (LOD) of 3.0 using the computer package, MAPMAKER/EXP. 3.0 (9).

Results and Discussion

All the thirty five probes used to genotype F_2 plants, hybridized to multiple restriction fragments indicating high degree of sequence duplication in the *B. juncea* genome. Due to occurrence of duplicate loci, these probes generated a total of 65 markers. The probe BJG 357 was hyper-polymorphic and revealed eight polymorphic bands in combination with *Hin* dIII. Similarly, *cab* 3C hybridized to more than twenty *Hin* dIII fragments and yielded six polymorphic loci. Thirty six (55-3%) markers were characterized by presence-absence polymorphism and the rest by band to band polymorphism. Predominance of presence-absence polymorphism suggested that differential chromosomal rearrangements, particularly, insertion/deletion events had contributed to genetic differentiation of the parents.

Segregation analysis revealed significant deviation from the expected 1:2:1 or 3:1 ratio for 21% of the markers. This is comparable to that observed in *B. napus* (5). Based on linkage analysis 45 RFLP markers and one seed coat colour marker (designated by the symbol r_1) could be arranged on 14 linkage groups, covering 407.9 cM of the genome (Fig. 1). Cosegregation of markers BJG 472a and 472b suggested tandem duplication of the sequence. There were another five linked pairs of duplicate loci on linkage groups 1, 2, 4, 6 and 7. Presence of linked duplicate loci is known in other *Brassica* spp. Addition of more markers to the map is in progress. A total of 500 genomic DNA clones are available with us in *Pst* I subgenomic library of mustard. Use of these probes will generate a fairly saturated RFLP linkage map that will facilitate characterization of important traits in mustard.

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