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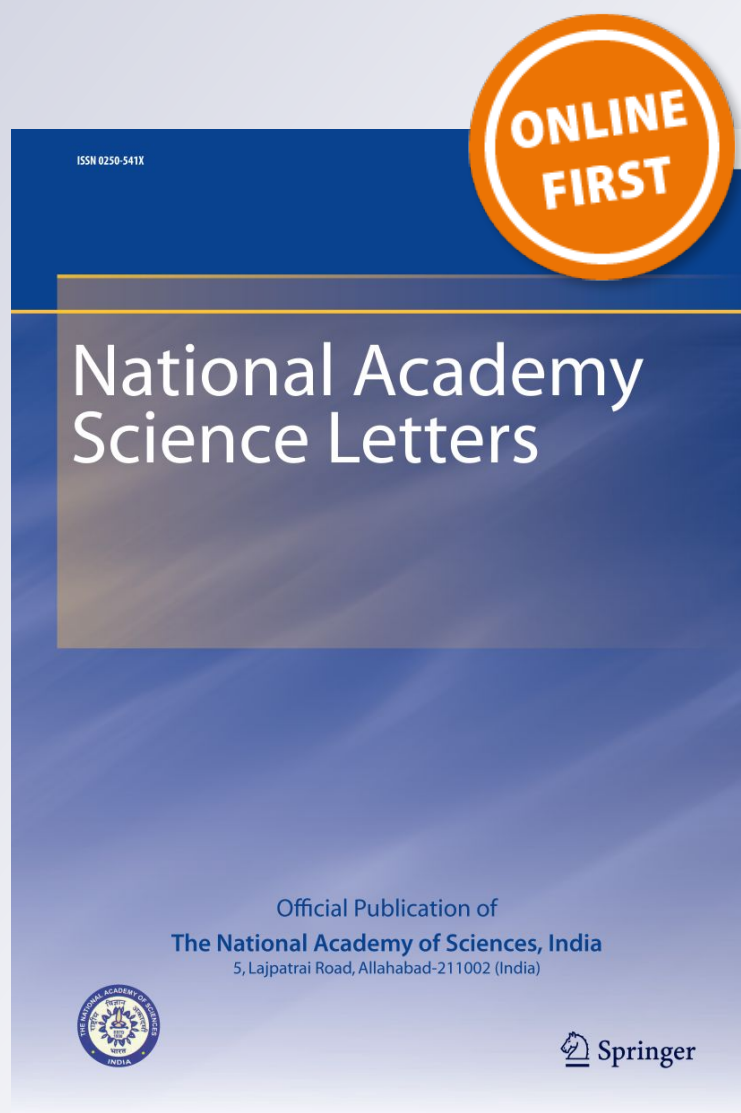
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# Identification of Superior Recombinant Inbred Lines for Seed Yield and Related Traits in Indian Mustard (*Brassica juncea* L.) from a Population Derived from Rohini × PBR-97

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**Abstract** In the present study, a set of 230 recombinant inbred lines (RILs) was developed through a cross between high yielding commercially released Indian mustard cultivars Rohini and PBR-97. These RILs were evaluated in F<sub>6:7</sub> generation during the *rabi* season of 2012–2013 for quantitative and qualitative traits. High genetic advance in conjunction with high heritability for seed yield/plant (43.81, 80.89%), biological yield (39.34, 88.77%), fruiting zone length (9.36, 70.21%), fibre (28.35, 72.63%) and glucosinolates content (68.75, 97.56%) indicated the effectiveness of selection for these traits. Plant height (0.207), number of seeds/siliquea (0.169), biological yield (0.615) and 1000-seed weight (0.160) were positively associated with seed yield. On the basis of seed yield/plant, 25 RILs were identified as highly promising and some of these lines may be considered for multi-location testing for varietal release or used as parents for breeding high yielding Indian mustard varieties. Moreover, the recombinant inbred population developed in the study may be used for molecular dissection of yield and yield related traits in Indian mustard.

**Keywords** *Brassica juncea* · Recombinant inbred line · Seed yield · Component traits

*Brassica juncea* L. commonly known as “Indian mustard” accounts for nearly 85% of the total rapeseed-mustard acreage [1]. Seed yield is a complex trait that includes

various components and finally results in a highly plastic yield structure [2]. Improvement in seed yield therefore can be more effectively achieved by constantly creating new combinations of best traits from different genotypes and identify superior genotypes on the basis of highly heritable yield related traits. It is known that the improvement of the genetic architecture of yield must be based on a more intensive study of individual yield components [3]. Hence, in the context of yield improvement, assessment of the nature and degree of variability existing within a breeding population is pertinent while selecting desirable genotypes. Moreover, it is also crucial to understand the interrelationship between each yield component and seed yield [4]. Keeping this in view, the present study was undertaken with two main objectives: (i) to develop a recombinant inbred line (RIL) population through cross between two high yielding commercially released cultivars Rohini and PBR-97, and (ii) to determine the extent of genetic variability, heritability, genetic advance and genotypic and phenotypic correlations for determining the degree to which various yield contributing characters are associated, and identify some of the superior lines for seed yield and related traits.

The two parental Indian mustard cultivars Rohini and PBR-97, obtained from ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur, were crossed and propagated until F<sub>6</sub> generation and 230 RILs were generated using single-seed-descent approach. The RILs were evaluated during *rabi* 2012–2013 under rain-fed condition in augmented block design where each block had 10 RILs along with four checks (RB-50, RH-819, PBR-97 and Rohini). Five plants were randomly selected from each RIL to record data. Oil, glucosinolates, fiber and phenol contents were estimated using FT-NIR spectroscopy. Analysis of variance (ANOVA) was performed as per the method

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suggested by Federer [5]. The estimation of magnitude of variability (variance and coefficient of variation), heritability, genetic advance and correlation coefficients were done using the standard statistical procedures.

A significant amount of variability was revealed among the RILs through ANOVA for seed yield and component traits. The results strongly suggested that selection may be expected for seed yield and related component traits in these RILs. The estimates of mean and range for different characters indicated that seed yield/plant ranged from 11.04 to 33.63 g while glucosinolates content among the RILs varied from 66.90 to 121.66  $\mu\text{M/g}$  defatted seed meal. Estimates of GCV and PCV for different characters revealed that the phenotypic variances were significantly higher than the genotypic variances reflecting the role of environmental factors on character expression as reported earlier in *B. juncea* [6]. In the present study, a narrow difference was observed between the phenotypic and genotypic variances as expected in augmented designs. The estimates of mean, range, genotypic and phenotypic coefficient of variation (GCV and PCV), heritability in broad sense, and genetic advance for different traits are indicated in Table 1. The maximum PCV was observed for glucosinolates (34.21%) followed by seed yield/plant (26.30%), biological yield (21.51%), fibre content (18.98%) and 1000-seed weight (13.86%). The PCV varied from 2.56% (oil content) to 34.21% (glucosinolates). Similarly, the maximum GCV was observed for glucosinolates (33.79%) followed by seed yield/plant (23.65%) and biological yield (20.27%). These are very similar to the results obtained earlier in oilseed Brassicas [6–10].

It is reported that high heritability assisted with high genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone [11]. In the present study, the heritability estimates were more than 50% for all the characters. High heritability values in conjunction with high genetic advance were observed for glucosinolates (97.56, 68.75%), seed yield/plant (80.89, 43.81%), biological yield (88.77, 39.34%), fibre content (72.63, 28.35%) and 1000-seed weight (58.18, 16.64%). Similar levels of heritability and genetic advance for different characters have already been reported earlier in Brassicas [12, 13].

Seed yield is a complex trait that encompasses the interactions between different yield contributing traits. Therefore, selection should be on the basis of the desirable traits and their correlation with seed yield [14]. The seed yield/plant showed positive and significant correlation coefficient with plant height (0.207), number of seeds/silique (0.169), biological yield (0.615) and 1000-seed weight (0.160). Significant and positive correlations of yield with these characters have also been reported by earlier workers [15, 16]. Significant positive correlations of main shoot length were observed with plant height, length of fruiting zone and biological yield. Hence, selection for the higher values of these traits would be desirable for increasing the seed yield. This is in conformant of a number of earlier reports on Brassicas [6, 15, 16].

In the present study, a total of 25 promising RILs were identified, primarily on the basis of seed yield/plant. Seed yield/plant among the selected lines varied from 25.63 to 34.63 g; 1000-seed weight from 4.11 to 7.29 g; oil content from 39.32 to 42.99% and harvest index from 26.13 to

**Table 1** Overall mean value of RILs, their range, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance

Characters	Mean	Range	GCV	PCV	h <sup>2</sup>	GA
Plant height (cm)	189.28	168.21–209.67	3.44	4.32	63.15	5.63
Main shoot length (cm)	82.94	65.52–102.07	5.77	7.59	57.68	9.02
Fruiting zone length (cm)	88.75	66.95–104.99	5.43	6.47	70.21	9.36
Silique length (cm)	4.58	3.42–5.81	*	*	*	*
Seeds/silique	12.75	9.39–16.89	*	*	*	*
Biological yield/plant (g)	63.80	40.83–99.58	20.27	21.51	88.77	39.34
1000-seed weight (g)	5.35	3.32–7.69	10.57	13.86	58.18	16.64
Harvest index (%)	29.59	17.48–46.33	*	*	*	*
Seed yield/plant (g)	18.67	11.04–33.63	23.65	26.30	80.89	43.81
Oil content (%)	40.93	38.53–43.40	2.04	2.56	63.64	3.35
Glucosinolates	58.43	66.90–121.66	33.79	34.21	97.56	68.75
Fiber	8.89	2.78–11.99	16.18	18.98	72.63	28.35
Phenol	2.11	1.22–2.89	*	*	*	*

\* Genetic parameters could not be calculated because of non-significant progeny mean squares

56.17%. However, among all the 230 RILs evaluated, 34 RILs had seed yield/plant >25 g, 22 RILs had >42% oil content, 50 RILs had >6 g 1000-seed weight, 20 RILs had <70 µM/g glucosinolate content, 24 had <6% fibre content and 16 RILs had >40% harvest index. Some of these lines may be considered for multi-location testing for varietal release or used as parents for breeding high yielding Indian mustard varieties. Moreover, the RIL population developed in this study may serve as a useful genetic resource for mapping genes/QTLs for seed yield or other related traits. Since, the parental cultivars Rohini and PBR-97 used for developing RILs are known to vary considerably for drought tolerance in addition to morphological and physiological aspects, these RILs may also be used for identification of superior drought tolerant lines and also for the genetic dissection of drought related traits through mapping and analysis of major genes and/or QTLs.

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