Molecular markers for yield components in *Brassica juncea* – do these assist in breeding for high seed yield?

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**Summary**

A population of 112 F₁-derived doubled haploid lines was produced from a reciprocal cross of *Brassica juncea*. The parents differed for seed quality, seed color and many agronomic traits. A detailed RFLP linkage map of this population, comprising 316 loci, had been constructed, and was used to map quantitative trait loci (QTL) for seed yield and yield components, viz. siliqua length, number of seeds per siliqua, number of siliques per main raceme and 1000-seed weight. Stable and significant QTLs were identified for all these yield components except seed yield. For yield components, a selection index based on combined phenotypic and molecular data (QTL effects) could double up the efficiency of selection compared to the expected genetic advance by phenotypic selection. Selection indices for high seed yield, based on the phenotypic data of yield and yield components, could only improve the efficiency of selection by 4% of the genetic advance that can be expected from direct phenotypic selection for yield alone. Inclusion of molecular data together with the phenotypic data of yield components in the selection indices did not improve the efficiency of selection for higher seed yield. This is probably due to often negative relationships among the yield components. Most of the QTLs for yield components were compensating each other, probably due to linkage, pleiotropy or developmentally induced relationships among them. The breeding strategy for *B. juncea* and challenges to marker assisted selection are discussed.

**Abbreviations:** MAS, marker assisted selection; PS, phenotypic selection; QTL, quantitative trait loci.

**Introduction**

*Brassica napus* and *B. rapa* are traditionally grown canola species (low erucic acid, low glucosinolate) in North America. *Brassica juncea*, a non-canola type, is the most important oilseed crop in Indian subcontinent. Superior Agronomic traits of *B. juncea*, e.g. heat resistance, drought tolerance, blackleg resistance, shattering resistance, etc. have attracted plant breeders for its conversion into Canola type (Downey, 1990; Woods et al., 1991). With the development of canola quality *B. juncea*, the potential of this crop is increasing in other parts of the world, specifically North America and Australia (Rakow, 2003; Burton et al., 2003).

Genomic maps have been constructed in various crops to study genome evolution (Slocum et al., 1990), utilize genetic diversity (Thormann et al., 1994), tag qualitative and quantitative traits (Thormann et al., 1996; Butruille et al., 1999) and analyse the stability of detected quantitative trait loci (QTL) across different environments (Hittalmani et al., 2002). Stable and consistent QTLs provide an excellent opportunity to improve the efficiency of selection in crop improvement, especially for traits controlled by multigens and highly influenced by the environment (Dudley, 1993).
The efficiency of marker assisted selection (MAS) is dependent on a number of factors such as the distance between the QTLs and the marker loci (Dudley, 1993), the proportion of the total additive genetic variance explained by the QTLs (Lande & Thompson, 1990), the population size (Hospital et al., 1997; Moreau et al., 1998) and the earlier generation under selection due to genetic disequilibrium (Lee, 1995).

Reports on the efficiency of MAS for quantitative traits are scarce. For highly heritable traits like flowering time, MAS and phenotypic selection (PS) were found to be equally effective in Arabidopsis thaliana (Van Berloo & Stam, 1999). Similarly, both MAS and PS were effective for early generation testing in maize (Zea mays) (Stromberg et al., 1994). In case of low heritable traits like seed yield, Zhu et al. (1999) were successful in accumulating favorable QTLs in barley DH lines but the actual gain was not as high as expected. MAS can be more effective than phenotypic selection if the proportion of the total additive variance explained by QTLs is higher than heritability of the trait (Lande & Thompson, 1990). Yousef and Juvik (2001) found MAS superior to PS for traits such as seedling emergence, kernel sucrose concentration, kernel tenderness and hedonic date in composite populations of maize. Lande and Thompson (1990) reported that selections based on phenotypic and genotypic data, however, could be more efficient than phenotypic selection (PS) alone. In maize, selection indices based on phenotypic and marker data were successful in selecting high yielding lines for high yielding environments (Eathington et al., 1997). To our knowledge, no study has yet been done to investigate the prospect of application of MAS together with phenotypic selection in the breeding of Brassica oilseed crops for increased yield.

Yield, arguably the most important trait, is polygenic in nature, difficult to measure and improve, and highly influenced by the environment. In the Brassicas, like other crops, indirect selection for yield by selecting yield components could be more efficient than direct selection for yield (Thurling, 1974). According to Richards and Thurling (1979), inclusion of a single yield component, e.g. number of siliques or 1000-seed weight, in selection index with yield may result in a significant increase in the efficiency of selection for yield. However, it is very often that selection for yield through yield components is limited by negative correlations among yield components i.e. yield compensation (Adams, 1967). QTLs associated with yield components have been reported for many crops like rice (Oryza sativa) (Li et al., 1997; Hittalmani et al., 2002), maize (Zea mays) (Frova et al., 1999), wheat (Triticum aestivum) (Kato et al., 2000), barley (Hordeum vulgare) (Bazant et al., 1997), sugarcane (Saccharum spp.) (Hoarau et al., 2002), and beans (Tar’an et al., 2002). However, in most cases, potential use of the QTLs in breeding for improved cultivars has not been investigated. In this study, we report the effectiveness of inclusion of the yield components in the selection indices, both at phenotypic and genotypic (QTLs) levels, in selection for high seed yield in Brassica oilseed crops using B. juncea as a model.

Materials and methods

Plant material

The materials of B. juncea used in this experiment includes a black seeded, high yielding non-canola Indian cultivar RLM-514 (designated as HEP), a yellow seeded, low yielding canola breeding line (designated as LEP), and 112 recombinant DH lines from the reciprocal cross between these two parents (Thiagarajah & Stringam, 1993; Mahmood et al., 2003). Self-pollinated seeds of the parental and DH lines were sown in a field trial at the Edmonton Research Station in 1999, and the seed harvested from this trial was sown in 2000 at three locations, the Edmonton Research Station, Ellerslie and Kelsey, in Alberta, Canada.

Experimental design

A randomized complete block design with three replications was used at each site. To address the large size of the field experiments, each replication was randomly divided into four sets as described by Mahmood et al. (2003). The initial plot size was 6 m × 1.2 m of four rows with 0.3 m between rows. For each line, seed rate was adjusted according to its 1000-seed weight to ensure a uniform plant population. Seed was treated with Furadan 5G (with carbofuran as active ingredient) prior to sowing to protect the crop from flea beetle. Hand weeding was practiced throughout the growing season. To exclude border effects, the plot length was reduced to 5 m by removing 0.5 m from the ends of each plot after seed set was complete. The data were analyzed according to the following model:

\[ Y_{ijn} = \mu + E_i + R(E)_{i(j)} + S_j + L(S)_{j(k)} + E \times L(S)_{i(k)(j)} + \epsilon_{ijn} \]  

(1)