

Characterization of a seed meal quality locus on chromosome A09 of *Brassica napus*

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The development of oilseed rape or canola (*Brassica napus* L.) with reduced levels of antinutritive seed phenolic acid and fibre compounds would considerably improve the value of the seed meal that is used as an animal feed after oil extraction. This study describes a forward genetics approach to discover potential candidate genes for antinutritive components in seed meal from oilseed rape. Analysis of quantitative trait loci (QTL) in a doubled haploid (DH) population derived from a cross between the black-seeded winter oilseed rape inbred line 'Express 617' and the yellow-seeded line '1012-98' revealed a major QTL on chromosome A09 with strong effects on phenotypic variation for seed colour, neutral detergent fibre (NDF) and acid detergent lignin (ADL), respectively (Figure 1). Comparative mapping of markers from the QTL region in other rapeseed populations confirmed the importance of the detected locus.

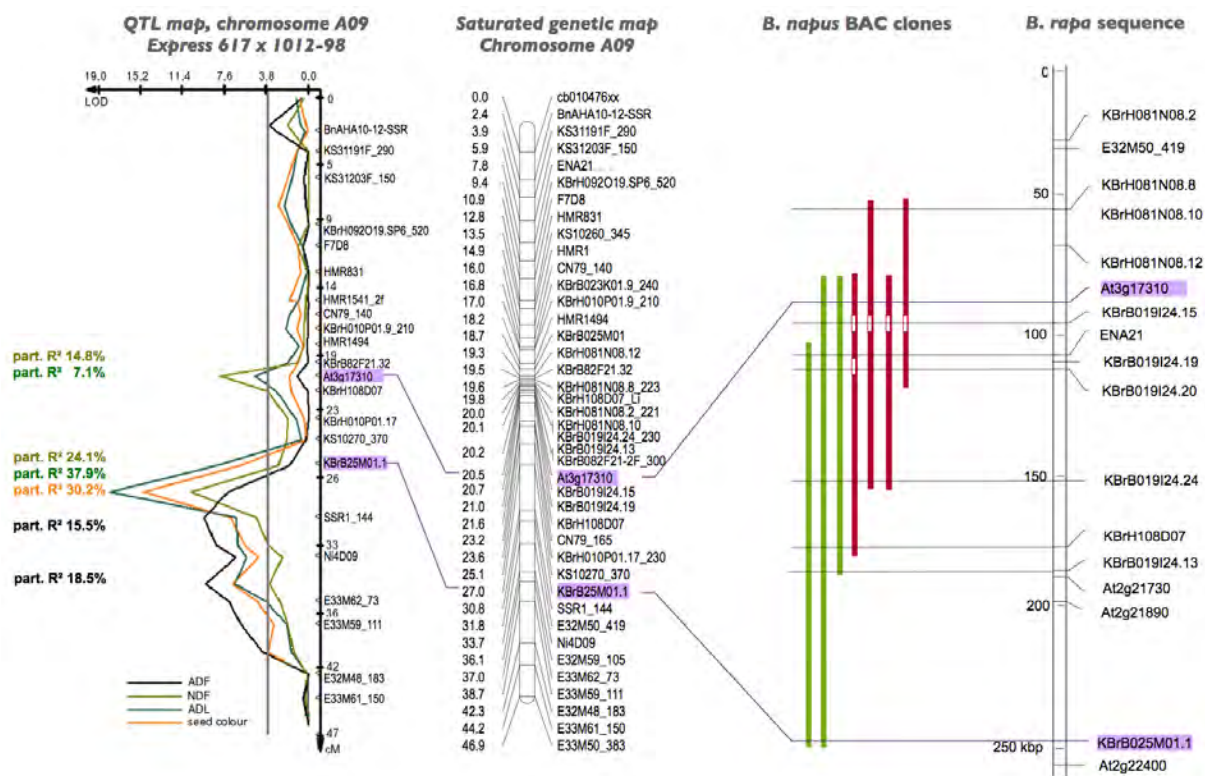


Figure 1. Comparison of a seed fibre QTL region on *B. napus* chromosome A09 with BAC clones from the QTL region and the corresponding sequence from the *B. rapa* physical map.

Saturation of the genetic map with molecular markers derived from the corresponding *B. rapa* genomic sequence region increased the average marker density to 1 marker per centimorgan. This allowed us to use selected markers for identification and characterisation of BAC clones spanning the QTL-region in the mapping parent 'Express 617'. Fingerprinting of all positive BACs identified by high-density filter hybridisation indicated the presence of at least three different homoeologous loci corresponding to the QTL region in Express 617. Representative BACs for each of the loci were subjected to 454-FLX shotgun sequencing for comparative analysis (Figure 2).

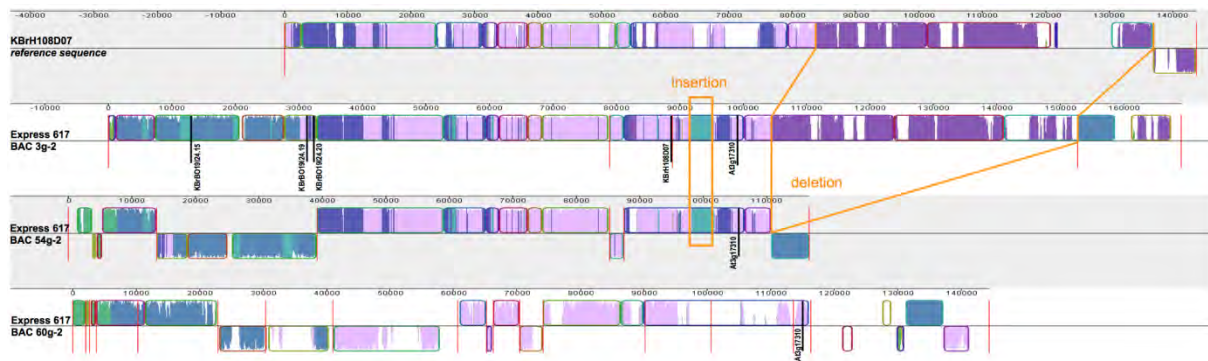


Figure 2. Sequence analysis of three BAC clones corresponding to homoeologous copies of the sequenced QTL region revealed structural differences among the different loci. In particular, one copy contained a large deletion in a region containing interesting candidate genes for seed coat lignin biosynthesis.

Two loci showed very high collinearity to the *B. rapa* reference sequence, thus representing highly similar A-genome homoeologues. Interestingly, a major deletion between these two loci contains interesting candidate genes for seed lignin and cell wall biosynthesis. The third BAC showed significant divergence from the other two and presumably represents a C-genome homoeologue. Detailed analysis of the corresponding regions in low-fibre, yellow-seeded *B. napus* lines may help to identify key genes controlling meal quality. This will open new possibilities for breeding of oilseed rape varieties with a more favorable composition of the meal, enhancing its potential use as an animal feed.

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