

Mapping of QTL for fibre and tannin compounds associated with meal quality in yellow-seeded oilseed rape

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Rapeseed meal is an important product for animal nutrition and is also a potential source of vegetable protein for human nutrition. The meal possesses around 40% protein with a favorable composition of amino acids and high contents of the essential amino acids methionin and cystein. However, due to the high proportion of crude fibre and antinutritive components the utilisation of rapeseed meal/protein in animal and human nutrition is limited. Breeding of yellow-seeded oilseed rape varieties is of high interest with regard to reduction of antinutritive phenolic compounds, in particular lignin and tannins.

Yellow-seeded genotypes often possess a thin seed coat that is associated with a considerable reduction in the size of endothelium cells; this leads to a spatial re-

duction of condensed tannins and simultaneously reduces the seed fibre content.

Because seed colour is very environmentally sensitive we are trying to generate alternative selection tools, including the development of gene-linked markers via mapping of major QTL and relevant candidate genes for major fibre and tannin compounds. A doubled haploid (DH) population segregating for seed colour is being used to localise QTL for major fibre and tannin compounds and compare these to map positions of relevant genes for phenolic compounds, including structural and regulatory *transparent testa (TT)* genes from *Arabidopsis thaliana*. Analysis of neutral detergent fibre (NDF), acid detergent fibre (ADF) and acid detergent lignin (ADL) enables esti-

mation of cellulose, hemicellulose and lignin contents in the seed meal.

The contents of lignin and hemicellulose, which are involved in secondary cell wall thickening, are considerably different in yellow and black seeded genotypes. Because these compounds derive from different biochemical pathways they are presumably influenced by different genes. Dissection of QTL for fibre content into these constituent components may therefore help to simplify the location of the major genes. Similarly, QTL for individual flavonoid compounds measured by HPLC could help identify further genes contributing to the accumulation of antinutritive condensed tannins (proanthocyanidins) in dark-seeded oilseed rape genotypes.

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