



Condensed tannins in *Brassica napus*: QTL mapping, candidate genes and associations with quality traits

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Condensed tannins (syn. proanthocyanidins, PAs) from rapeseed meal can potentially have a negative impact on non-ruminant livestock and human nutrition, particularly because of their ability to form indigestible, astringent or bitter-tasting complexes with proteins. One option to overcome this problem is the breeding of yellow-seeded rapeseed with reduced condensed tannins in the seed coat. This might be achievable via selection of genotypes with smaller endothelium cells and consequently a spatial reduction in condensed tannin accumulation (seed coat structural cell mutants), or alternatively by selection of genotypes with reduced biosynthesis of condensed tannins (flavonoid biosynthesis mutants). Both types of transparent testa (tt) mutants are well-characterised in *Arabidopsis*; however the genetic basis of the yellow-seed trait in the polyploid genome of rapeseed is still not completely understood. As plant material 166 DH lines derived from a cross between an inbred line of the black-seeded German winter oilseed rape cultivar 'Express' and the true-breeding, yellow-seeded line '1012/98', both with 00-seed quality were used. The genetical map was constructed using AFLP and SSR markers. The QTL were mapped using the software PLABQTL based on seed analyses of DH lines grown on field trials in Rauischholzhausen and Gross-Gerau (Germany). Quality traits were measured quantitatively based on digital reflectance values. Total PAs content was via Vanillin assay quantified. Individual PAs and total flavonoid content were quantified via HPLC (High Performance Liquid Chromatography) using internal standards for quantification. By localising quantitative trait loci (QTL) for condensed tannin content, seed colour and other quality traits in *B. napus* seeds and comparing these to the positions of promising candidate tt-genes, we hope to develop closely-linked molecular markers for selection regarding important genes involved in the accumulation of antinutritive compounds in rapeseed meal.