

QTL analysis of phytosterols in *Brassica napus* L.

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Phytosterols are natural plant oil constituents known since more than 50 years for their LDL-cholesterol-lowering properties. In rapeseed, one of the richest natural sources of phytosterols, four major phytosterols were identified: sitosterol, campesterol, brassicasterol and avenasterol. However, a further increase of the phytosterol content could give a higher added value to rapeseed oil and oil-derived products. The objective of this study was to identify QTL for individual and total phytosterol content in a winter rapeseed doubled haploid (DH) population.

The plant material consisted of 148 DH lines derived from a cross between two DH lines obtained from the French cultivar 'Samourai' (low in erucic acid and glucosinolates) and the old Dutch cultivar 'Mansholt's Hamburger Raps' (high in erucic acid and glucosinolates).

The DH lines were grown in a field trial carried out with two replications during two years at two locations each near Göttingen. Seeds from 3 open pollinated plants were harvested and bulked for the analysis.

A high throughput gas chromatographic method for the analysis of phytosterol content and composition in seeds was developed. Near Infrared Reflectance Spectroscopy (NIRS) was applied to assess the oil, protein and fatty acids content. Means for phytosterol phenotypic data over all environments were used for composite interval mapping performed with the PLABQTL program. The framework map used for the QTL mapping includes 185 evenly distributed markers.

It was extracted from a primary map, which consists of 580 markers covering 1739 cM (Kosambi) in 20 linkage groups (based on the RFLP linkage map by UZUNOVA et al. 1995). The DH population showed a large genetic variation for total phytosterol content, ranging from 2570 g to 4104 mg/kg seeds. The analysis of variance revealed a highly significant genetic variation for phytosterol content with overall high heritabilities. Total phytosterol content was negatively correlated to erucic acid and oil content. QTL analysis resulted in the detection of 3 QTL localized on different linkage groups explaining 60% of

the genetic variance. Two of the QTL, located on linkage groups 6 and 12 showed the highest additive effects and were located at the similar position as the QTL detected for all individual phytosterols. This could indicate the presence of few QTL affecting the content of all phytosterols. However, at the same time the QTL on the linkage groups 6 and 12 were mapped within the confidence intervals for the two erucic acid genes - which in this population have a main positive effect on oil content. This is in accordance with the observed negative correlations between oil, erucic acid and phytosterols content, respectively. It seems likely that the erucic acid genes express a negative pleiotropic effect on phytosterol content. This effect may be explained by the competitive use of the cytoplasmic acetyl-CoA, the common precursor in both biosynthetic pathways.

Reference

UZUNOVA, M., W. ECKE, K. WEISSLEDER and G. RÖBBELEN, 1995: Mapping the genome of rapeseed (*Brassica napus* L.). I. Construction of an RFLP linkage map and localization of QTLs for seed glucosinolate content. *Theor Appl Genet* **90**: 194-204.

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