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Czech J. Genet. Plant Breed.

**L., Świącicki W.,
Krajewski P.:**

**Variability in the
oligosaccharide
concentration in seeds
of the mapping
population of pea
(*Pisum sativum* L.)**

Czech J. Genet. Plant Breed., 50 (2014):
157-162

Anti-nutritional compounds are among the obstacles to the use of pea seeds as a protein source in both feed and food. These compounds are poorly digested by both monogastric animals and humans. There are three main oligosaccharides in pea: raffinose, stachyose and verbascose (raffinose family oligosaccharides – RFOs). The concentration of oligosaccharides in dry seeds, the oligosaccharide percent to the total content of soluble sugars and quantitative trait loci (QTLs) were analysed in the

mapping population Wt10245 × Wt11238. The composition and concentration of soluble carbohydrates in seeds harvested from two field experiments (2002 and 2004) were analysed by the high resolution gas chromatography method. The Wt10245 × Wt11238 population was chosen because of the greater difference in the concentration of RFOs in seeds between parental lines (56.48 mg/g seed in Wt10245 and 99.1 mg/g seed in Wt11238). The average levels of oligosaccharides (mg/g seed) from both field experiments in the mapping population were: *myo*-inositol 1.5, sucrose 33.3, galactinol 0.8, raffinose 9.6, stachyose 30.1, verbascose 37.1. The total oligosaccharide concentration was 76.8 mg/g seed. This comprised an average of 68% soluble sugars, with the range from 59% to 75%. There was no interaction between lines and years of experiments (significance of lines × year interaction, *F* statistic > 0.01). One main quantitative trait locus was found for both experiments in LG VA (the *tl-r* interval) and three additional: in LG I (five traits 2002 and 2004 near *afp1k*), LG II (two

traits 2004 and 2002 near *afp4i* and *M16*). The main QTL was responsible for the level of RFOs and the total soluble sugar concentration in seeds. The results are in agreement with the knowledge of RFO biosynthesis. This makes selection for changes in the proportion of the particular oligosaccharides difficult, like in *Phaseolus*. However, it is possible to decrease the RFO content in pea seeds. The linkage between QTL and the gene *r* is interesting. The *rugosus* (*r*) locus changes the morphology and distribution of starch grains, decreases the total starch accumulation, produces a higher ratio of amylose to amylopectin and higher sugar and water content during development along with changes in cell size and lipid content.

Keywords:

genetic map; molecular markers; QTL; *rugosus* (*r*) locus; seed oligosaccharide

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