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The mutants of winter rapeseed (*Brassica napus* L. var *oleifera*), having increased amount of oleic acid in seeds, have been included in the various breeding programs. The mutations found in the $\Delta 12$ oleate desaturase gene from *B. napus* genome A (M10453 – HOR3 type and M10464 – HOR4 type) (Spasibonek 2006) seem to have the great contribution to that changed character. However, it is known, that the environmental factor can also be an important component of such variability. Thus, it is of great importance to assess the influence of the particular mutated allele on the final phenotype.

Based on the sequence of the BnaA.FAD2 gene from *B. napus* genome A (Falentin et al. 2007a, 2007b, 2009), the allele-specific codominant CAPS marker has been designed and used in marker assisted selection (MAS). The marker is able to distinguish between two types of mutated and wild-type alleles. The additional value of this marker is the ability to distinguish between heterozygotes and homozygotes of both kinds (Falentin et al. 2007a, 2009, Matuszczak et al. 2013, Matuszczak and Tokarczuk 2014, Matuszczak et al. 2018). The sequences that served to develop that marker are patented (WO 2007/138444, Falentin et al. 2007a).

The marker can be used to precisely genotype the alleles in the BnaA.FAD2 locus of studied *B. napus* lines. The previous comparisons of both genotypes and phenotypes have led to the conclusion that there is an evident correlation between the allele in the BnaA.FAD2 locus and the level of oleic acid in seeds. The more detailed analysis of such interdependence will further improve the results of the marker assisted selection of new high oleic varieties of *B. napus*. The use of the allele-specific CAPS marker for that purpose gives the chance to monitor the presence of functional and non-functional alleles in the studied material and thus will facilitate the assessment of the GxE interaction for that trait.

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