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DETECTION OF SNPS ACCOMPANYING DIFFERENT RHIZOMANIA RESISTANCE SOURCES IN BREEDING MATERIALS OF SUGAR BEET

ABSTRACT

The aim of this study was to identify selected rhizomania resistance accompanying SNPs in breeding materials of sugar beet. The populations defined for the study were provided by Kutnowska Hodowla Buraka Cukrowego Ltd. In order to perform molecular characterization of the materials, the following methods were applied: 1) DNA isolation according to Davis *et al.* (1986), 2) HRM analysis in the Gene Scanning module (LightCycler 480) using Luminaris Color HRM Master Mix (Thermo Scientific), 3) PCR, 4) verification of sequential variants within several PCR products following restriction site design with RestrictionMapper version 3, 5) agarose gel electrophoresis of digestion products, documentation (Gel DocTM 2000, BIO-RAD; Quantity One, version 4.0.3), 6) real-time PCR analysis of BNYVV content (after RNA isolation and reverse transcription) in the Relative Quantification module as compared to actin gene (LightCycler 480) using SYBR Green I Master (Roche Applied Science). Among investigated SNPs three turned out to be polymorphic, thus allowing for unequivocal distinction between homozygous and heretozygous sugar beet materials and further selection. As shown in this study, HRM analysis may be supported/replaced by RFLP for several sequences. The presence of two different rhizomania resistance sources was confirmed for the sugar beet breeding materials under study. Within delivered populations genetic heterogeneity was found, which may also correspond to variable levels of BNYVV. The work was fulfilled as a part of the PBAI-NRI Multiyear Programme 2015-2020, task 2.4.