

5th World Congress on Biotechnology

June 25-27, 2014 Valencia Conference Centre, Valencia, Spain

RAPD and ISSR molecular markers in analysis of barley DH lines with different level of susceptibility to *Fusarium culmorum* infection

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Genetic diversity among 32 spring barley (*Hordeum vulgare* L.) genotypes: 2 parental genotypes (breeding lines 1N86 and R63/1), and 30 doubled haploid (DH) lines derived from F1 hybrids (15 hulled and 15 hullless) was analyzed. Leaves of examined DH lines were used to isolate the genomic DNA utilizing the Plant Mini AX kit (A and A Biotechnology). The analyses were conducted with ISSR-PCR and RAPD-PCR. PCR was carried out using a Gene Amp 2400 thermal cycler (Perkin Elmer). PCR products were separated in a 1% agarose gel in TBE buffer. A DNA marker of 100 to 1000 bp (Fermentas) was used to determine the length of the PCR fragments. The gels were imaged using ImageMaster VDS gel reader (Amersham - Pharmacia Biotech). Gel analysis was performed using GelScan ver. 1.45 (Kucharczyk - Electrophoretic Techniques). The study was also aimed to explore the DNA markers linked with resistance to *Fusarium culmorum* in the set of barley DH lines. Earlier the plant material had been evaluated according to its susceptibility to *Fusarium culmorum* infection. The most interesting products for further investigation linked to *F. culmorum* resistance are 750, 720, 670 bp amplified by RAPD primer OPB 18, present in the most resistant lines. Also important for further evaluation could be PCR fragments: 320 bp amplified by primer ISSR 01 and 210 bp generated by primer ISSR 06 which were found in the least affected by the pathogen lines: R63N/9 and R63N/1.

Acknowledgement: The research was financially supported by National Science Centre Poland (Project No. NN310 725740)

Biography

Tomasz Warzecha has completed his PhD in 2001 from University of Agriculture in Kraków, Poland. He has participated at the International Postgraduate Course on Biotechnology in Agriculture, Plants and Microorganisms at the Hebrew University of Jerusalem. Additionally he completed the Pedagogical Studium, majored in Biology and Chemistry at Jagiellonian University Krakow, Poland. He has worked in a project focused to examine natural variation in the recombination pathways in maize at the Department of Plant Breeding and Genetics at Cornell University, Ithaca, USA. At present he is Research Associate at the Department of Plant Breeding and Seed Science in Krakow.

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