

„Localization of QTL regions associated with powdery mildew (*Blumeria graminis*)
resistance / tolerance in triticale (*xTriticosecale* Wittm.)”

Triticale, a synthetic hybrid obtained by a man by a crossing between rye and wheat, is a young species with unstable genome, commercialized in the late 60s. It is a cereal of high economic importance however, with the increase of cultivation this cereal in Poland is increasingly infested by a fungal pathogen *Blumeria graminis* (DC.) Speer caused powdery mildew disease. The development of molecular biology methods, in particular techniques based on molecular markers of DNA, has become a tool used in modern plant breeding to monitor the introgression and accumulation of desired genes in breeding materials and also molecular markers can be used in the selection process assisted by a molecular markers (MAS).

The main aim of this study was to localize QTL (*Quantitative Trait Loci*) regions of triticale (*xTriticosecale* Wittm.) based on phenotypic data, associated with powdery mildew (*Blumeria graminis* (DC.) Speer) and indication of potential allele markers of this resistance. To localize QTL, high-density genetic map was constructed for 168 DH lines of population ‘Grenado’ x ‘Zorro’. Additionally, the previously described genetic map of 89 DH lines of population ‘Hewo’ x ‘Magnat’ has been used. QTLs for evaluated traits were identified by a single-marker analysis (SMA) and composite interval mapping (CIM) using Windows QTLCartographer version 2.5 software.

Observations of the degree of infection for both mapping populations were conducted in field conditions in three localizations belonging to DANKO Plant Breeders Ltd. - Choryń, Laski and Modzurów during three growing seasons - 2012/2013, 2013/2014 and 2014/2015. The evaluation of the degree of infection was based on a 9-point scale, where 9 means a completely healthy plant and 1, completely infected. Phenotypic data were used to localize QTL regions associated with triticale resistance / tolerance to powdery mildew infection.

Based on the mapping of DH ‘Grenado’ x ‘Zorro’ population genotyping, composed of 168 lines, the genetic map was developed with total length 7527,1 cM, consisting 1891 markers (including 326 DArT, 1443 DArTseq and 122 SNP). As a result, 40 QTL regions (11 QTLs on A group chromosomes, 15 on B group and 14 on R group) were identified and

explained 1.1 - 23.7% of phenotypic variation for DH 'Grenado' x 'Zorro' population. Furthermore, for DH 'Hewo' x 'Magnat' population, 25 QTL regions were identified (eight QTLs on A group chromosomes, seven on B group and ten on R group) common for observations from three different locations carried out in three growing seasons which explained 2.3 - 30.1% of phenotypic variation. Among that regions, nine *loci* common for both mapping populations were identified on chromosomes 1A, 5A, 1B, 3B, 4B, 3R and 5R, which explained 1.16 - 22.60% of phenotypic variation. In these regions, the presence of previously described and characterized powdery mildew resistance genes: *Pm3a*, *Pm4b*, *Pm5*, *Pm6* and *Pm41* from wheat and *Pm3* and *Pm4* from rye were very likely indicated. Additionally, 57 molecular markers were selected and those markers can be used in triticale breeding programs to select powdery mildew resistance plants.