2019 Vol.3 No.1

## Plant Science 2018: Resistance to powdery mildew (*Blumeria graminis* f. sp. hordei) in winter barley, Poland- Jerzy H Czembor, Aleksandra Pietrusinska and Kinga Smolinska-Plant Breeding and Acclimatization Institute – National Research Institute

## Jerzy H Czembor, Aleksandra Pietrusinska and Kinga Smolinska

Plant Breeding and Acclimatization Institute – National Research Institute, Poland

Powdery mildew (Blumeria graminis f. sp. hordei) is the most ecomically important barley pathogen. This wind borne fungus causes foliar disease and yield loses rich up to 20-30%. Resistance for powdery mildew is the aim of numerous breeding programmes. The transfer of the MLO gene for resistance to powdery mildew into winter barley cultivars using Marker-Assisted Selection (MAS) strategy is presented. These cultivars are characterized by high and stable yield under polish conditions. Field testing of the obtained lines with MLO resistance for their agricultural value was conducted. Four cultivars (Souleyka, Titus, SU Vireni and Metaxa) as high yielding parents were used. In addition, existing resistance genes to powdery mildew in these cultivars were preserved. Two lines (BKH 735 and line 42) as parents with MLO resistance were used. Line BKH 735 was obtained in IHAR-PIB Radzikw in 2002-2011. Selection for presence of the MLO gene was conducted in backcross populations by phenotyping in the field (natural infection) and under greenhouse conditions (differential barley lines for resistance genes for powdery mildew and differential fungus isolates). In addition, to confirm the presence of the MLO gene in back cross populations MAS strategy was applied using SSR markers HvMLO1 and HvMLO3. Field trials with back crossed lines were conducted during 2017/18 in three locations in Central and Western Poland (Radzikw) (Szelejewo, Wiatrowo). The parental lines were used as control. The aim of these trials was to obtain information on agricultural value of obtained lines. Our results demonstrate the practical use by the introduction of MLO resistance into background of winter barley germplasm with valuable economical characteristics in polish agricultural conditions. This work was conducted in the project: Interaction between powdery mildew resistance determined by MLO gene and economical value characteristics in winter barley.

Barley powdery mildew is brought about by Blumeria graminis f. sp. hordei (Bgh) is one of the most damaging foliar maladies of grain. This growth is the main types of the family Blumeria however it has recently been treated as a types of Erysiphe. As per Braun (1987), it varies from all types of Erysiphe since its anamorph has special highlights, for instance, digitate haustoria, auxiliary mycelium with bristle-like hyphae and bulbous swellings of the conidiophores, and as a result of the structure of the ascocarps. Braun (1987) thinks about that, in view of these distinctions, there ought to be a detachment at conventional level. Sub-atomic arrangement examinations demonstrated the different situation of the fine mold on Poaceae and indicated that Blumeria takes a basal situation in the phylogenetic trees of the Erysiphales. Consequently, Blumeria is just remotely identified with Erysiphe and every different sort of the fine buildup organisms (Saenz and Taylor, 1999; Mori et al., 2000).

As a biotrophic parasite, B. graminis has developed to practice on specific poaceous has. Generally, eight unique structures or formae speciales of B. graminis were distinguished. They were ff. spp. tritici (Triticum and Aegilops spp.), hordei (Hordeum), avenae (Avena sativa), secalis (Secale cereale), agropyri (Agropyron and Elymus), bromi (Bromus spp.), poae (Poa spp.) and dactylidis (Dactylis spp.). The adjustment of B. graminis to explicit oat has includes both pathogenrelated atomic example activated insusceptibility (PTI) and effector-activated invulnerability (ETI) and has been named 'non-adjusted opposition' (Troch et al., 2014). This adjustment is sufficient that B. graminis f.sp. tritici doesn't parasitize tamed grain, and B. graminis f.sp. hordei doesn't taint wheat.

Taxonomic Tree

- Domain: Eukaryota
- Kingdom: Fungi

- Phylum: Ascomycota
- Subphylum: Pezizomycotina
- Class: Leotiomycetes
- Order: Erysiphales
- Family: Erysiphaceae
- Genus: Blumeria
- Species: Blumeria graminis

B. graminis continues to evolve, and new formae speciales can arise. For example, starting in 2001 in France, B. graminis was found on triticale (X Triticosecale), a wheat-rye hybrid (Walker et al., 2011). The new strains were themselves a hybrid of B. graminis ff. spp. tritici and secalis, and have been called f.sp. triticale (Menardo et al., 2016), which makes nine ff.spp. In the Middle Eastern centre of origin of the pathogen, B. graminis f.sp. tritici is significantly differentiated into populations primarily infecting tetraploid wild emmer or hexaploid domesticated wheat; however, it is unclear that the evidence supports the existence of a tenth forma specialis specialized on tetraploid wheats (Ben-David et al., 2016).

## References

Ben-David, R., Parks, R., Dinoor, A., Kosman, E., Wicker, T., Keller, B., Cowger, C., 2016. Differentiation among Blumeria graminis f. sp. tritici isolates originating from wild versus domesticated Triticum species in Israel. Phytopathology, 106(8), 861-870. doi: 10.1094/PHYTO-07-15-0177-R

Menardo, F., Praz, C. R., Wyder, S., Ben-David, R., Bourras, S., Matsumae, H., McNally, K. E., Parlange, F., Riba, A., Roffler, S., Schaefer, L. K., Shimizu, K. K., Valenti, L., Zbinden, H., Wicker, T., Keller, B., 2016. Hybridization of powdery mildew strains gives rise to pathogens on novel agricultural crop species. Nature Genetics, 48(2), 201-205. doi: 10.1038/ng.3485

Walker, A. S., Bouguennec, A., Confais, J., Morgant, G., Leroux, P., 2011. Evidence of host-range expansion from new powdery mildew (Blumeria graminis) infections of triticale (× Triticosecale) in France. Plant Pathology, 60(2), 207-220. doi: 10.1111/j.1365-3059.2010.02379.x

Troch, V., Audenaert, K., Bekaert, B., Höfte, M., Haesaert, G., 2012. Phylogeography and virulence structure of the powdery mildew population on its 'new' host triticale. BMC Evolutionary Biology, 12(76), (1 June 2012).

Saenz GS, Taylor JW, 1999. Phylogeny of the Erysiphales (powdery mildews) inferred from internal transcribed spacer ribosomal DNA sequences. Canadian Journal of Botany, 77(1):150-168; 50.