Streszczenie w języku angielskim

Leaf rust caused by the fungus *Puccinia triticina* Eriks (*Pt*) is one of the most damaging diseases causing significant losses in common wheat crops. In *Pt*-resistant adult plants, an APR-type resistance is observed, which protects the plant against multiple pathogen races and is notable by its persistence under production conditions. A more comprehensive understanding of the molecular mechanisms underlying the function of APR genes will enable the development of new strategies for resistance breeding in wheat. Currently, mainly APR genes, such as *Lr34*, *Lr46* and *Lr67*, are widely used in resistance breeding, as they confer durable resistance to many fungal races occurring under different climatic and environmental conditions. In the case of the *Lr46* locus, the gene determining APR resistance has still not been identified. However, several candidate genes have been proposed in the literature and characterisation of these genes was undertaken in the present study. The aim of presented dissertation was a multi-level analysis of the molecular mechanisms of resistance in common wheat in response to leaf rust inoculation. The research undertaken was aimed at analysing the identification of APR type genes, expression profiles of *Lr34*, *Lr67* and candidate genes for the *Lr46* gene, following inoculation with *Pt* fungal spores. Additionally, the influence of small RNA molecules (miRNA) on the expression of these genes was determined. The plant material consisted of resistant cultivars from the gene bank and the F1, F2 and BC1F1 generations, obtained by crossing the above-mentioned genotypes with economically important Polish wheat varieties. Biotic stress was induced in adult plants by inoculation with Pt fungal spores under controlled conditions. The study used RT-qPCR to analyse the expression profiles of the genes studied at five time points (0, 6, 12, 24 and 48 hpi). In addition, the expression profiles of miRNA molecules complementary to the *Lr34* gene (tae-miR9653b, tae-miR9773 and tae-miR9677b) and candidate genes for *Lr46* (tae-miR5384-3p, tae-miR9780, tae-miR9775 and tae-miR164) were analysed. Of the candidate genes tested (*Lr46-Glu1*, *Lr46-Glu2*, *Lr46-Glu3*, *Lr46-RLK1*, *Lr46-RLK2*, *Lr46-RLK3*, *Lr46-RLK4*, *Lr46-Snex* and *Lr46-WRKY*), the highest expression occurred in only one candidate gene (*Lr46-Glu2*), indicating that it may be a contributing factor in the response to infection caused by *Pt*.

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