Streszczenie w języku angielskim

Strigolactones (SL) are plant hormones with a broad spectrum of activity, playing a key role in the regulation of plant architecture and responses to environmental stresses. Despite increasing knowledge of their biosynthesis and perception pathways, the molecular mechanisms of SL action remain unclear. The aim of this doctoral dissertation was to deepen our understanding of the role of SL in the regulation of growth and development of barley (*Hordeum vulgare*), with particular emphasis on SL interactions with other hormones and their function in drought stress responses. To this end, studies were conducted to identify SL-dependent transcription factors.

Two barley mutants were used in this work: *hvd14.d*, carrying a mutation in the SL receptor gene (*DWARF14*), and *hvd53a.f*, identified within the scope of this dissertation, carrying a mutation in the SL repressor gene (*DWARF53*). Comprehensive phenotyping of these lines was performed under control and drought stress conditions, analyzing, among other traits, tillering, root system development, growth dynamics, chlorophyll content, photosynthetic activity, and reactive oxygen species (ROS) levels. Clear differences were observed between the mutants – *hvd14.d* exhibited reduced drought tolerance and highly branched shoots, whereas *hvd53a.f* displayed a contrasting phenotype characterized by a limited number of tillers and increased adaptation to drought stress.

To identify the molecular mechanisms responsible for the observed differences, transcriptomic and proteomic analyses were conducted, considering different developmental stages and growth conditions of barley. The results revealed numerous differentially expressed genes (DEG) and differentially accumulated proteins (DAP) associated with hormonal signaling, redox metabolism, and water management. It was shown that *hvd53a.f* activates pathways related to oxylipin and glutathione metabolism as well as DEHYDRIN family proteins, which may underlie the increased drought tolerance of this line.

Furthermore, using *in silico* approaches, an analysis of *cis*-regulatory motifs in the promoters of SL-dependent genes and their homologs in *Arabidopsis thaliana* was performed, which allowed the proposal of potential transcription factors not previously associated with SLs. These included transcription factors crucial for the regulation of the circadian cycle.

Under drought stress conditions, clearly different adaptive strategies were observed between the analyzed genotypes. The *hvd14.d* mutant, lacking a functional SL receptor, exhibited intensified drought stress symptoms, including stronger ROS accumulation, reduced

chlorophyll content, and decreased photosynthetic performance. In contrast, *hvd53a.f* plants maintained stable photosynthetic activity, more efficient water management, and increased antioxidant activity, suggesting a higher adaptive potential of this mutant.

The obtained results provide new evidence for the involvement of SLs in coordinating growth, development, and drought stress responses in barley. This work represents a significant contribution to understanding SL function in crop plants and opens new perspectives for applying this knowledge in breeding varieties better adapted to climate change.