Identification of the SWI/SNF chromatin remodeling complex as a regulator of shoot branching in Arabidopsis and barley

The number and distribution of lateral shoots are among the main factors determining the yield of cultivated plants; however, the molecular mechanisms responsible for regulating this trait are relatively poorly understood. According to current knowledge, plant architecture is shaped by both developmental programs driven by different transcription regulators and plant hormones, among which strigolactones are thought to play a particularly important role. Our preliminary results, along with literature data, suggest that the BRM protein, a known transcriptional regulator, is involved in controlling the formation of lateral shoots. BRM is the central subunit of the SWI/SNF protein complex found in the cell nucleus. This complex, composed of several proteins, is evolutionarily conserved in eukaryotic organisms. It is known to influence the activity of many genes through its ability to remodel chromatin structures. Previous studies have demonstrated the importance of SWI/SNF complexes in regulating various developmental programs and plant responses to stresses and hormones. **The goal of this project is to investigate the role of the SWI/SNF complex associated with the BRM protein in regulating lateral shoot formation in the model plant *Arabidopsis thaliana* (thale cress) and the crop species *Hordeum vulgare* (barley).** Given that the known functions of SWI/SNF complexes often involve direct interactions with transcription factors and components of hormonal signaling pathways, we speculate that BRM and its complex may serve as integrator of gene regulatory networks related to shoot branching. Several research tasks are planned within the project, aiming to achieve the following outcomes: identification of SWI/SNF-dependent genes that are critical for the initiation of lateral shoots in *Arabidopsis*; verification of the hypothesis regarding the functional relationship between the SWI/SNF complex and the strigolactone signaling pathway; generation and characterization of mutants in *BRM* gene in barley, with an emphasis on changes in plant architecture; understanding the mechanisms by which BRM-associated SWI/SNF complex regulates expression of key genes associated with shoot branching in *Arabidopsis* and barley.

To achieve the project objectives, we will use a wide range of research tools, including mutant and transgenic lines analyses, transcriptome profiling and reporter assays, and protein-protein interaction tests. The results of this research project are expected to significantly expand our knowledge of the molecular mechanisms shaping plant architecture and their conservation between dicotyledonous and monocotyledonous plants. Moreover, the obtained barley mutants will serve as valuable tools for further studies on the function of the BRM protein in crops.