Barley, wheat and other cereal crops are agronomically important plants. However, significant yield loses every year are related with drought and pathogenic diseases. Cereals exposed to fusarium crown rot (FCR) infection caused by mycotoxinogenic *Fusarium pseudograminearum* is very urgent problem world-wide. Climate changes observed nowadays with frequent drought periods intensify severity of FCR leading to serious yields reduction. Nevertheless, the molecular basis of the plant-drought-pathogen interaction remains largely unknown. Evidences suggest that under co-occurred drought and pathogen infection plants display a sophisticated pattern of gene expression that could not have been observed by studying individual stress. Multiomic platform will be ideal for objective of proposed project: describing complexity of this mechanism as well as cross-talk in phytohormonal regulatory pathway. RNA-Seq based transcriptomic will indicate on functional genes and the pathways involved in plant response to concurrent stresses. In addition, advanced metabolomics, lipidomic and bottom-up proteomic will serve for illustration of dynamic in metabolic networks. Moreover, multiple phytohormone profiling unravel signaling network during multiple stress. Advanced mass spectrometry with liquid chromatography (LC-MS and nanoLC-MS) approaches is perfect tool for all four mentioned omic task. Antioxidative state of plant and level of pathogen infestation will be also measured for holistic picture of plant-pathogen-drought interaction. Close attention will be put on creation of integrative framework by bioinformatics and statistical analysis. Multifactorial statistical approaches followed by innovative clustering and precise correlation methods will be created for handling high-throughput data sets. Integration of different omics level will facilitate description how crop plant cope with concurrent stress. The significantly changed proteins and genes will be annotated to available databases. Two cultivars of agronomically important crop barley (*Hordeum vulgare*) with different susceptibilities to drought will serve for molecular markers of susceptibilities to combined stress. The illustration of the dynamics of change in metabolome, proteome and transcriptome during combined stress will be a new, important contribution to knowledge about the molecular background into family Poaceae.

Studies on interactions of plant with environment are undoubtedly one of the most interdisciplinary projects of plant biology. Combining data from chemistry, plant physiology, mycology, metabolomics, transcriptomics, mathematics and statistics will allow us to explain and illustrate metabolic changes in plants during combined stress. To our knowledge, such detailed and comprehensive studies in this field have not yet been conducted. In addition, multivariate statistics and correlation network for the first time will provide a holistic view of the regulatory trade-off in cooccurred stresses. The plants - fungal pathogen relationships during drought are interesting also from the point of view of the creation an ideal model for the development and standardization of high throughput multiomic research. Comprehensive knowledge describing plant response to combined stress offer tremendous potential for modern plant breeding struggling with changes in environment. As final output of proposed project will be essential data for the development of food crops better equipped for extreme environmental conditions.