

## Summary

Abscisic acid (ABA) acts as a seed germination inhibitor, but the molecular mechanism of this process, especially in crops, is still not fully understood. The aim of this doctoral dissertation was to investigate the role of ABA in the regulation of seed germination of barley (*Hordeum vulgare* L.), with particular emphasis on the nuclear mRNA Cap-Binding Complex (CBC), composed of the CBP20 (Cap-Binding Protein 20) and CBP80 subunits. We used grains and embryos of four barley genotypes: the double mutant *hvcbp20.ab/hvcbp80.b*, the single mutant *hvcbp20.ab* and *hvcbp80.b*, and their parent variety 'Sebastian'. An integrated research approach was applied, including physiological, transcriptomic and metabolomic analyses. Mutation of both CBC subunits was shown to abolish the inhibitory effect of ABA on germination of *hvcbp20.ab/hvcbp80.b*, suggesting a compensatory mechanism between *HvCBP20* and *HvCBP80*, as single mutants are sensitive to ABA. The double mutant *hvcbp20.ab/hvcbp80.b* phenotype was associated with significant changes in the transcriptome of germinating embryos in response to ABA, including increased numbers of differentially expressed genes and transcripts, enhanced alternative splicing, and interactions between ABA signaling and brassinosteroid signaling and metabolism. *In silico* protein-protein interactions between CBC subunits and components of the splicing machinery were also identified. In addition, a barley genotype-specific reference transcriptomic dataset for germinating embryos was elaborated. In the second part of the work, the effect of ABA on 'Sebastian' embryos at an early stage of germination was analyzed in detail. Transcriptomic, metabolomic and Visium spatial transcriptomic data were combined. ABA revealed a repressive effect on the expression of genes related to metabolism and growth, while simultaneously activating stress processes and phytohormonal pathways. A high correlation between the transcriptome and the metabolome changes indicates a coordinated regulation of gene expression and metabolic processes in germinating embryos after ABA treatment. It was revealed that the response to ABA is tissue-specific, with dominant transcriptional activity in the coleoptile. Together, the obtained results make a significant contribution to the research on the molecular and spatial control of the crop germination process.