

Multomics studies of barley genotypes varied in brassinosteroid signal transduction under optimal and drought conditions

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Brassinosteroids (BRs) are a class of steroid hormones regulating a wide range of physiological processes in plants. Recent years have witnessed a significant advance in the elucidation of the molecular mechanisms underlying BRs signaling. It has been reported that some of the components of BRs signaling pathway act as multifunctional proteins involved in other signaling networks controlling diverse physiological processes. Regulation of some of these processes is mediated through a crosstalk between BRs signalosome and the signaling cascades of other phytohormones. These aspects of BRs metabolism have been extensively studied in *A. thaliana* and are, however, much less investigated in monocots, including barley. Semidwarf barley mutants with defects in BRs signaling or biosynthesis are a valuable tool to study the role of these hormones in response to different abiotic stresses, including drought and have been suggested as alternative resources for barley improvement in breeding programs. However, there are inconsistent reports about BRs positive/negative role in regulating plant development in various environmental conditions. Hence, the aim of the study was to perform a multomics characterization of two barley genotypes with different BRs signal transduction pathways under different water regimes. The experiment revealed differences between cv. Bowman (wild type) and its near isogenic line (NIL) BW885 (BR-insensitive) in the genetic background, which is manifested on phenotype level as a consequence. Also, the genotype-specific effects of both, drought and day of stress, were notable in all the measured parameters. The presented results are part of the project aimed to explain hormonal crosstalk and its role in shaping plant architecture in barley.

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