

In the nature, variation of plant traits within species is usually observed. This phenomenon is caused by various mechanisms functioning at the molecular level, including action and interaction of plant hormones (phytohormones) that are important for plant physiology and regulation of growth, and affect the plant architecture. Up to date, this complex regulatory network remains unravelled and there are some indications for the existence of a master agent, which can manage these processes. The ideal candidate for such molecule is melatonin, which the functional roles in plants can be associated with crosstalk with plant hormones. The multiple changes in gene expression caused by melatonin point to its role as a multiregulatory molecule capable of coordinating many aspects of plant development. This item, together with its role as an alleviating-stressor agent, suggests that melatonin is an excellent prospect for crop improvement. However, some aspects of melatonin in plants, including the metabolism and regulation pathway under stressful conditions, are still unclear. Research on interactions between signalosomes of phytohormones currently constitutes an important area of plant systems biology and is a source of information on molecular mechanisms of physiological processes. However, the understanding of these processes in monocot species, including barley, is far from complete. In spite of recent progress in elucidating the biological function of melatonin, only limited evidences of its functioning in barley has been demonstrated so far. The understanding of the molecular mechanisms of melatonin-mediated root growth and development is still at a beginning stage. The research hypotheses of the project assume that melatonin-mediated hormonal homeostasis is pivotal for drought tolerance and, moreover, melatonin acts to determine barley response to drought by regulating phytohormones-related genes in roots. Plant material will consist of cv. Bowman and its NILs BW091 and BW885. The regulation of hormone levels will be investigated by using state of the art NGS-based approaches to gene expression analysis. Observations will be done on barley roots growing in optimal and drought stress conditions, by classical phenotyping methods (modern field phenotyping), as well as by image phenotyping (high-throughput phenotyping platform). Project will provide new information about biology of crop plants, which are a subject of breeding processes aimed at improvement of economically important traits. Although the results of the project will not be directly valid for other cereal crops, the obtained knowledge will be very important for them, as barley is becoming the model plant, especially for plant architecture studies.