

Towards understanding the barley response to abiotic stress using omics approaches

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Plants as sessile organisms have developed sophisticated mechanisms to survive in a changing environment. Recent advances in omics approaches have facilitated the exploration of plant genomes; however, the molecular mechanisms underlying the responses of barley and other cereals to multiple abiotic stresses remain largely unclear. Barley is one of the first domesticated cereal grains over ten thousand years ago, originating from Fertile Crescent. The barley genome has been unlocked in 2012 and it is one of the biggest diploid genomes sequenced to date; recently, it has become a model plant for cereals.

In this lecture, I will summarize my original studies aimed to elucidate the spring barley behavior under abiotic stress conditions. This was achieved by an integrative approach including: (i) high-throughput phenotyping and genotyping enabling identification of quantitative trait loci, (ii) lipids and sterols quantification, (iii) large-scale transcriptomics, and (iv) global proteomic profiling. The effect of single and combined drought and heat stress on reprogramming of genes expression and on proteins abundance in barley flag leaf will be broadly discussed. Last but not least, the molecular characterization of crown will be presented for the gibberellin-deficient and the brassinosteroid-insensitive barley plants exposed to heat and drought, respectively.

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