

CLIMBER - CONFRONTING CLIMATE CHANGE IMPACTS IN BARLEY AND RICE

ROSSINI L.*, FERRARIO C.*, ARRIGHI M.*, ROSSI R.*, CORNARO L.***, BERETTA V.***, CASELLI F.***, ZANZANI V.***, MENDES M.***, CAVALLERI A.***, SHAAF S.*, BISWAS A.*, VAJANI A.*, JANIAK A.***, CHMIELEWSKA B.***, BATTAGLIA R.****, VON KORFF M.*****, HORNER D. S.***, GREGIS V.**

*) University of Milan – DiSAA, Via Celoria 2, 20133 Milan, Italy

**) University of Milan – DBS, Via Celoria 26, 20133 Milan, Italy

***) University of Silesia, Katowice, Poland

****) CREA-GB, Via San Protaso 302, Fiorenzuola d'Arda (PC), Italy

*****) University of Dusseldorf, Germany

Hordeum vulgare, Oryza sativa, phytohormones, inflorescence, abiotic stress

The CLIMBER project exploits rice and barley, important genetic models for the grass family and among the most significant crops worldwide to explore conserved and species-specific responses to abiotic stresses such as heat and drought which cause substantial crop loss worldwide threatening food security particularly in the context of climate change. We are generating and characterizing rice and barley plants expressing specific hormone biosensors to explore the role of auxin and cytokinin signaling and identify tissue domains in the developing inflorescence where hormone levels change under stress conditions.

In parallel, transcriptomic analyses of developing rice and barley inflorescences under control and heat-stress conditions are underway. The resulting data will be analyzed with innovative approaches to identify molecular mechanisms that are either shared, or distinct between the relatively distantly related species in question, and generate testable hypotheses regarding the role and mechanism of action of phytohormones in developmental responses to stress.

In addition to auxin and cytokinin, strigolactones have also emerged as players in abiotic stress responses in rice and other species, but the role of this pathway is largely unexplored in barley. To fill this gap, allelic variants of a barley strigolactone pathway gene were identified from screening the HorTILLUS TILLING population. Phenotypic analyses of different barley lines suggest a role for this gene in the determination of plant architecture and complementation of the corresponding Arabidopsis mutant is underway to test for functional conservation between the two species.

Acknowledgements

CLIMBER is funded by the University of Milan under the SEED 2019 call.