Proceedings of the LXII SIGA Annual Congress
Verona, Italy – 25/28 September, 2018
ISBN **978-88-904570-8-1**

Oral Communication Abstract – 5.06

TRANSCRIPTOME PROFILING OF SHORT TERM RESPONSE TO CHILLING STRESS IN TOLERANT AND SENSITIVE RICE SEEDLINGS

BUTI M.*, PASQUARIELLO M.**, RONGA D.*, MILC J.A.*,***, PECCHIONI N.***,****, VIET THE HO*****,******, PUCCIARIELLO C.*****, PERATA P.*****, FRANCIA E.*,***

*) BIOGEST-SITEIA, University of Modena and Reggio Emilia, Reggio Emilia (Italy)
**) Department of Crop Genetics, John Innes Centre, Norwich (UK)
***) Department of Life Sciences, University of Modena and Reggio Emilia, Reggio Emilia (Italy)
****) Cereal Research Centre, Council for Agricultural Research and Economics, Foggia (Italy)
*****) PlantLab, Scuola Superiore Sant'Anna, Pisa (Italy)
******) Present address: Ho Chi Minh City University of Food Industry, HoChi Minh (Vietnam)

Oryza sativa, chilling tolerance, short-term response, RNA-Seq, differentially expressed genes

Low temperature is a major factor limiting rice growth and yield, and seedling is one of the developmental stages at which sensitivity to chilling stress is higher. Tolerance to chilling is a complex quantitative trait, so one of the most effective approaches to identify genes and pathways involved is to compare the stress-induced expression changes between tolerant and sensitive genotypes. Phenotypic responses to chilling of 13 *Oryza sativa* ssp. *Japonica* cultivars were evaluated, and Thaibonnet and Volano were selected as sensitive and tolerant genotypes, respectively.

To thoroughly profile their short-term response to chilling, RNA-Seq was performed on Thaibonnet and Volano seedlings after 0 (not stressed), 2 and 10 hours at 10°C. Differential expression analysis revealed that the ICE-DREB1/CBF pathway plays a primary role in chilling tolerance, mainly due to some important transcription factors involved (some of which had never been reported before). Moreover, the density of differentially expressed genes along rice genome was compared to the position of known QTLs, and remarkable co-locations were detected, delivering an overview of genomic regions determinant for low temperature response at seedling stage.

Overall, a deep reconfiguration of the transcriptome in both genotypes succeeding the chilling stress was observed, and a great number of molecular mechanisms and signal transduction pathways resulted involved in these alterations. However, some important evidences could provide an explanation for the differences between the contrasting genotypes: a stronger up-regulation of several OsDREB1 genes in the tolerant genotype, a slower activation of some transcription factors in susceptible one, and an overlapping between known chilling tolerance-related QTLs and genomic regions where the density of cultivar-specific DEGs sensibly diverge.

Our study contributes to a better understanding of the molecular mechanisms underlying rice response to chilling, and provides a solid background for development of low temperatures tolerant germplasm.