

## METABOLIC AND MOLECULAR RESPONSES OF ITALIAN RICE CULTIVARS TO BTH TREATMENT

BALDONI E.\*, MATTANA M.\*, LOCATELLI F.\*, PICCHI V.\*, CAGLIANI L.R.\*\*,  
CONSONNI R.\*\*, GENGA A.\*

\*) Institute of Crop Biology and Biotechnology, IBBA-CNR, Via Bassini 15, 20133 Milan (Italy)

\*\*\*) Institute for the Study of Macromolecules, ISMAC-CNR, Via Bassini 15, 20133 Milan (Italy)

*Italian rice cultivars, BTH, Reactive Oxygen Species, Transcription factors, metabolomics*

Benzothiadiazole (BTH), a functional analog of Salicylic Acid (SA), is one of the so-called plant activators that protect various plants from infectious diseases. BTH treatments have been used by several authors to study disease plant response, since it is a potent inducer of both SAR and PR genes. It has been proposed that in rice the SA/BTH-signalling pathway branches in at least 2 subpathways downstream of SA (*OsWRKY45*-dependent and *OsNPR1*-dependent). Both *OsWRKY45* and *OsNPR1* play an essential role in BTH-induced blast resistance. Most of the current Italian varieties have intermediate to low resistance to blast in field conditions and the development of new rice varieties with a higher resistance to blast disease is of great interest, but precise molecular information on resistance genes present in Italian commercial varieties is still missing.

In this work, we provide a characterization of 10 Italian rice cultivars, selected on the basis of their resistance or susceptibility to blast disease, for metabolic content and gene expression after BTH treatment.

We performed a metabolic profiling of mock and BTH-treated plants through <sup>1</sup>H-NMR. Interestingly, statistical analysis of the obtained spectra showed a distribution of resistant cultivars separated from the susceptible ones. Resistant varieties were characterized by a higher content of sucrose, whereas susceptible ones presented a higher content of fructose, suggesting that a difference in metabolic response occurs between resistant and susceptible cultivars.

A qRT-PCR analysis showed that, after 24 hours from BTH treatment, *OsWRKY45* was induced in all the cultivars, whereas *OsNPR1* was induced only in three blast resistant cultivars. Besides, the transcription level of two *myb* and one *WRKY* genes increased in most of the resistant cultivars and decreased or did not change in the susceptible ones, thus suggesting a positive correlation between their expression level and the resistance phenotype of the rice cultivars. Moreover, we analysed some genes involved in the ROS signalling pathway (*SOD* and *CAT* encoding genes), belonging to the *OsNPR1* pathway. Whereas the *CAT* gene was not induced in any of the analysed cultivars, the *SOD* gene expression was up-regulated after BTH treatment in two of the resistant cultivars that showed an induction of *OsNPR1*, suggesting the occurrence of different levels of H<sub>2</sub>O<sub>2</sub> among cultivars.

These preliminary data suggest that in Italian cultivars the resistance to blast could be due to the activation of different pathways. Further analysis of the expression of TF genes and of other genes involved in ROS scavenging and signalling are needed to understand the role of these branches of the SA/BTH-signalling pathway in Italian cultivars.

This research was supported by the funding “Accordo Quadro CNR - Regione Lombardia” Project 2 “Risorse biologiche e tecnologie innovative per lo sviluppo sostenibile del sistema agro-alimentare”.