Proceedings of the 50th Italian Society of Agricultural Genetics Annual Congress
Ischia, Italy – 10/14 September, 2006
ISBN **88-900622-7-4**

Poster Abstract – D.21

FUNCTIONAL CHARACTERIZATION OF THE RICE *WRKY* TRANSCRIPTION FACTOR GENE FAMILY

G. BRUSCHI*, S. BERRI**, P. ABBRUSCATO*, O. FAIVRE-RAMPANT*,
E. GUIDERDONI***, M.E. PÈ**, P. PIFFANELLI*

*) Genomics Platform, CERSA - AgBiotech Research Centre, Parco Tecnologico Padano – PTP, Via Einstein, 26900 Lodi, Italy
**) University of Milan, Dept. of Biomolecular Sciences and Biotechnology, Via Celoria 26, 20133 Milan, Italy
***) Centre de Coopération Internationale en Recherche Agronomique pour le Developpement (CIRAD), UMR 1096, Avenue Agropolis, TA40/03, 34398, Montpellier, Cedex 5, France

transcription factor, WRKY, Gene famil, microarray

WRKY genes encode for a family of transcription factors characterized by having one or two ~60 aa consensus sequence characterized by a very highly conserved WRKYGQK motif together with a zinc-finger domain that provides binding properties to DNA. All proteins so far analyzed have shown binding specificity to the W-box motif (T)(T)TGAC(C/T). Initially believed to be plant-specific, a single copy of a two-motif WRKY gene has been subsequently found in some unicellular non-photosynthetic Eukaryota. In the plant kingdom an extended duplication and diversification of this ancient WRKY gene has occurred. In Rice, indeed, 112 WRKY genes have been identified distributed across all 12 chromosomes.

WRKY genes have been shown to be involved in the regulation of several cellular processes such as control of metabolic pathways, drought and heat shock, senescence, development and hormone signaling pathways.

However, the most studied role of this gene family appears to be in response to biotic and abiotic stress stimuli.

Aim of this work is to perform a whole rice WRKY gene family transcription analysis upon application of biotic and abiotic stress conditions to identify WRKY genes involved in signal transduction pathways leading to resistance to external stimuli. Our objective is to investigate the existence of "key transcriptional regulators" to biotic and/or abiotic type of stress in plants. To achieve this goal our transcriptome data were integrated with microarray results obtained by NIAS in Japan using a rice genome-wide microarray.

Bioinformatic analysis of set of data from both our WKRY thematic array and from the NIAS Agilent 22K array points to the existence of co-regulated WRKY genes.

In an effort to test the involvement of *WRKY* genes of rice in plant response to pathogens, we screened 15 lines containing a T-DNA insertion in *WRKY* genes, inoculated with host and non-host strains of *Magnaporthe grisea* (isolates BR29, BR32 and FR13). No phenotype was detected in such lines but a T-DNA insertion event in the promoter of *OsWRKY55* showed a tissue-specific Gus expression in roots, vascular tissues and in the cotyledon of a 10-days old seedling. According to our phylogenetic analysis, this gene belongs to a subgroup of Monocot specific *WRKY* genes. A more detailed analysis is currently ongoing to characterize the expression pattern of the *WRKY55* gene and possibly to identify a phenotype correlating with the insertion.