Poster Communication Abstract – 7.23

EXPRESSION PROFILING OF THE WRKY MONOCOT-SPECIFIC CLADE IN RICE

ABBRUSCATO P.*, NEPUSZ T.**, MIZZI L.***, DEL CORVO M.*, MORANDINI P.****, FUMASONI I.*, MICHEL C.****, PACCANARO A.**, GUIDERDONI E.*****, SCHAFFRATH U.*****, MOREL J.B.****, PIFFANELLI P.*, FAIVRE-RAMPANT O.*,****

*) Rice Genomics Unit, Parco Tecnologico Padano, Via Einstein, 26900 Lodi (Italy)
**) Centre for Systems and Synthetic Biology, Department of Computer Science, Royal Holloway, University of London, Egham Hill, Egham, Surrey, TW20 0EX (United Kingdom)
***) Department of Biomolecular Sciences and Biotechnology, University of Milan, Via Celoria 26, 20133 Milan (Italy)
****) Department of Biology, University of Milan and CNR Institut of Biophysics (Milan Section), Via Celoria 26, 20133 Milan (Italy)

*****) UMR BGPI, Campus International de Baillarguet, 34398 Montpellier Cedex 5 (France) *****) CIRAD, UMR AGAP, Avenue Agropolis, 34398 Montpellier Cedex 5 (France) ******) Institute for Biology III (Plant Physiology), RWTH Aachen, 52056 Aachen (Germany)

WRKY genes, rice, monocotyledons, Magnaporthe oryzae

WRKY proteins constitute a large family of plant transcriptional factors which have been shown to be involved in a range of biological processes. They are usually classified in three main groups. In this study, we showed the existence of a monocot-specific (MCS) clade within group 3 in rice WRKY family, composed of 19 genes. Fourteen out of these 19 MCS *WRKYs* fell into three segmental duplicated blocks on chromosomes 1, 11 and 12. Several residues and/or motifs are conserved within these 19 MCS proteins.

Expression analysis indicated that some MCS OsWRKY genes are developmentally regulated in rice while others are not. In addition they are differentially regulated in response to several abiotic stress conditions, pathogens or parasites. In particular, the MCS *OsWRKY* genes were transcriptionally regulated upon rice blast fungus infection. Duplicated MCS OsWRKY genes have divergent expression profiles, likely reflecting a diversity of rice responses to environmental constraints. The MCS *WRKYs* are also poorly co-regulated among them as showed by co-regulation analysis. To conclude, we defined the existence of a monocot-specific *OsWRKY* clade with diverse transcriptional profiles supporting their role in rice specific regulatory pathways.