Proceedings of the XLIX Italian Society of Agricultural Genetics Annual Congress
Potenza, Italy – 12/15 September, 2005
ISBN **88-900622-6-6**

Poster Abstract - C.15

TOWARDS THE FUNCTIONAL CHARACTERIZATION OF A RICE *WRKY* TRANSCRIPTION FACTOR

S. BERRI*, P. PIFFANELLI**, E. GUIDERDONI**, M.E. PÈ*

*) 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, insertion mutant, GUS expression, gene family

WRKY genes belong to a heterogeneous family of transcription factors sharing a 60 aa conserved consensus sequence that provide DNA-binding properties to a target sequence (T)(T)TGAC(C/T). Although one copy of this gene is present in some unicellular organisms such as *Giardia lamblia, Trypanosoma brucei* and *Dictyostelium discoideum*, indicating their very ancient origin, they were apparently lost in fungi and animals, but underwent to extensive duplication events in the plant kingdom which produced 72 members in Arabidopsis and 107 members in rice. *WRKY* genes seem to be involved in several biological processes such as responses to the abiotic stresses of wounding, the combination of drought and heat and cold. It is also evident that some members of the family may play important regulatory roles in morphogenesis of trichomes, embryos, senescence, dormancy and metabolic pathways. Many *WRKY* genes are involved in response to biotic stresses. In an effort to verify the involvement of *WRKY* genes of rice in plant response to pathogens, we screened 15 lines containing 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 this *WRKY* gene and possibly to identify a phenotype correlating with the insertion.