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RNA INTERFERENCE OF THE STRESS RELATED OSMADS26 TRANSCRIPTION FACTOR IN RICE INCREASES RESISTANCE TO VARIOUS PATHOGENS AND REDUCES PLANT DEVELOPMENT

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Several transcription factors have been involved in rice response against biotic and abiotic stresses (Khong et al., 2008). In A. thaliana, the MADS box transcription factor AGL12 control cell division in root meristem and is involved in flowering transition (Tapia-Lopez et al., 2008). When over expressed in Catharanthus roseus cell suspension AGL12 promotes tissue like organization and alkaloid biosynthesis (Montiel et al., 2007). OsMADS26, the rice orthologous of AGL12 in A. thaliana was recently over expressed under the control of a DEX inducible promoter and described as a stress related gene Lee et al., 2008). Nevertheless its precise function remains unknown. QPCR analysis revealed that this gene is expressed both in leaves and roots and is upregulated in response to osmotic stress. In order to precise the function of OsMAD26 in stress response or in development, and in absence of insertion mutant, we had generated rice lines RNA interfered for this gene. Interfered lines were obtained with two GST tagging the 5' or the 3' end of the mRNA. Interfered lines were affected in their development (root, tillering, height, dry weight) and were delayed for their flowering time in comparison to control. Roots of interfered lines present a reduced geotropism. Interfered lines were not affected in comparison to control line in their availability to resist to drought stress. But interestingly, interfered lines present an increased resistance against Magnaeporthae grisea, Xanthomonas oryzae and the Rice Yellow Mottle Virus. This suggests that OsMADS26 is a negative regulator of biotic stress response and acts as a general activator of development. In order to identify the genes and the biological pathways regulated by OsMADS26 we have proceeded to a transcriptome comparative analysis of genes expressed in WT and RNA interfered lines. Data analysis is in progress.