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ROLE OF LRR-RLKS IN STRESS RESPONSE AND DEVELOPMENTAL PROCESSES THROUGH SYSTEMATIC K.O. ANALYSIS IN RICE

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The function of a small number of Leucine-Rich Repeat Receptor-Like Kinase (LRR-RLK) genes has been studied, mostly in *Arabidopsis thaliana*. They are involved in several important biological processes, including development, resistance/defence and adaptation to biotic and abiotic stresses. We are interested in deciphering the function of these genes in rice. In this aim, we decided to take advantage of the availability of T-DNA and Tos17 insertion mutant libraries of rice cv. Nipponbare to start a systematic screen of knock-out mutants of these genes. The rice genome contains ~320 LRR-RLK genes. Our search in international collections of insertion mutant lines which are catalogued by Flanking Sequence Tag (FST) information from most of the rice insertional mutagenesis projects around the world revealed that 238 insertional mutant lines are available for the 323 genes. Phenotypical evaluation of homozygous mutants is performed under various biotic and abiotic stresses and mutant plants are observed for phenotypes at several stages of growth, from seedlings in Petri dishes to flowering and grain development stages in the greenhouse. Thus, with this project, we aim first to decipher and explore new genes involved in defence and developmental responses to stresses. Second, our analysis will be of great benefit to provide potential targets for cereal improvement, notably in the breeding of drought-tolerant and pathogen-resistant crops. This project is supported by grant #ANR-08-GENM-021 from Agence Nationale de la recherche (ANR), France.