Functional Analysis and Utilization of Rice Genes
Related to Disease Resistance and Abiotic Stress Tolerance

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Rice diseases and abiotic stresses such as sheath blight, blast, low temperature and salinity cause significant losses in rice yield and quality each year in Arkansas. Identification and functional characterization of rice genes related to disease resistance and abiotic stress tolerance will greatly enhance our understanding of host defense mechanisms and facilitate the development of novel strategies for reducing biotic and abiotic stresses. The new knowledge and technology resulting from the research project will help improving rice varieties and cultural practices and eventually benefiting Arkansas rice growers.

Whole genome analysis has been conducted to identify and characterize all members of the mitogen-activated protein kinases (MAPKs) gene family in rice. More than a half of the rice MAPK genes were induced by pathogen infection or environmental stresses. Two of them, OsMPK5 and OsMPK7, were functionally characterized in detail via transgenic analysis and shown to be important for abiotic stress tolerance and disease resistance, respectively. In addition, members of the Myb gene family were also examined for their role in disease resistance and abiotic stress tolerance.

Salicylic acid (SA), jasmonic acid (JA), ethylene (ET) and abscisic acid (ABA) signal pathways have been individually examined in relation to disease resistance and abiotic stress tolerance. SA is not an effective signal molecule in rice but functions as a constitutive antioxidant to modulate redox balance and protect rice plants from oxidative damage caused by abiotic and abiotic stress. By contrast, JA appears to act as an important defense signal in rice. Inducible overproduction of JA in transgenic rice carrying allene oxide synthase transgene activates defense gene expression as well as enhanced resistance to the blast fungus. ET is also critical for signaling disease resistance response in rice. Following the infection by the rice blast fungus, ET-insensitive transgenic rice lines exhibit reduced levels of defense gene expression and increased levels of disease susceptibility. Interestingly, ABA suppresses ET production in rice and enhances disease susceptibility to the blast fungus. Taken together, our studies demonstrate a complex network of defense pathways and signal interactions in rice that eventually determine the disease resistance and abiotic stress tolerance.

Extramural research grants have been obtained to further study rice functional genomics related to disease resistance and abiotic stress. These include a grant award from the International Rice Research Institute to study drought-related rice genes and a major USDA/NRI Rice Coordinated Agricultural Project grant to study rice genes related to sheath blight resistance.

Postscript: This project did not receive continued funding beyond this year of study.