

F-68 *GzGRR1* encoding a putative F-box protein is involved in pathogenesis and sexual development by *Gibberella zeae*. You-Kyoung Han¹, Sung-Hwan Yun², and Yin-Won Lee¹ ¹School of Agricultural Biotechnology and Center for Agricultural Biomaterials, Seoul National University, Seoul 151-921; ²Division of Life Sciences, Soonchunhyang University, Asan, 336-745, Korea

Gibberella zeae is an important pathogen of cereal crops in many areas of the world, causing head blight of small grains including corn, wheat, barley, and rice. In addition, this fungus produces mycotoxins such as trichothecenes and zearalenone on diseased crops and has been a potential threat to human and animal health. To identify pathogenesis-related genes, we selected several *G. zeae* mutants defective for the traits involved in disease development. The mutant ZH436, generated by restriction enzyme-mediated integration, showed significantly reduced virulence toward host plants along with other pleiotropic phenotypes such as reduced hyphal growth on nutrient rich conditions and no sexual development. In addition, this mutant produced incomplete tetrads with aberrant morphology when outcrossed to a *mat1-2* deletion strain. Molecular characterization revealed that vector insertion point was located within the ORF, designated *GzGRR1* showing a high similarity to *GRR1*, a regulator for glucose repression in *Sacharomyces cerevisiae*; the translation product of *GzGRR1* carries both a putative F-box and a leucine-rich repeats (LRR) domain. Northern blot analysis showed that *GzGRR1* was constitutively expressed but the transcript was highly produced during the perithecial stage. These results suggest that *GzGRR1*, as other F-box proteins, may be involved in degradation of proteins by ubiquitination, specifically those required for virulence or sexual development in *G. zeae*.

F-69 Molecular characterization of genomic regions associated with pathogenesis of *Xanthomonas oryzae* pv. *oryzae* str. KACC10331. H.W.Jang¹, J.K.Kim² ¹Graduate School of Biotechnology and Information Technology, Hankyong National University, Ansong 456-749, Korea; ²National Institute of Agricultural Biotechnology, Rural Development Administration, Suwon 441-707, Korea

The nucleotide sequence that comprised 4,941,439 bp was determined for *Xanthomonas oryzae* pathovar *oryzae* str. KACC10331, a bacterial blight pathogen of rice. The genes likely to be associated with pathogenesis include eight novel avirulence (avr) genes, a set of hrp genes, gum operons for exopolysaccharide productions and extracellular plant cell wall-degrading enzymes including cellulase, proteases, polygalacturonase, pectin degrading enzymes, xylanases, xylosidases and