F-68 ***GzGRR1* encoding a putative F-box protein is involved in pathogenesis and sexual development by *Gibberella zeae*.** You-Kyoung Han[1], Sung-Hwan Yun[2], and Yin-Won Lee[1] [1]School of Agricultural Biotechnology and Center for Agricultural Biomaterials , Seoul National University, Seoul 151-921; [2]Division 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.Jang[1], J.K.Kim[2] [1]Graduate School of Biotechnology and Information Technology, Hankyong National University, Ansung 456-749, Korea; [2].National Institute of Agricultural Biotechnology, Rural Development Administration, Suwon 441-707, Korea

The nucreotide sequence that comprisidasesed of 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 , polygaracturonase, pectin degrading enzymes, xylanases, xylosidases and

1,4-β-cellobiowere were found in Xoo genome. Gene clusters (xps and rpf) associated with regulation of extracellular enzymes was distributed in the genome. In addition, the genes for two apparent RTX toxins, rtxA and rtxC, that can potentially function as virulence factor were identified in the Xoo-genome. Functional studies of these genomic regions allow us to further our understanding of the pathogenesis between this pathogen and rice host.

F-70 Sequence analysis of the genes expressed during conidial germination of pepper anthracnose pathogen, *Colletotrichum acutatum*. Woobong Choi[1], Seungyoun Yi[2], Yong-Hwan Lee[3], and Heung-Tae Kim[4]. [1]Department of Biotechnology and Bioengineering, Dongui University, Busan 614-714, Korea; [2]National Instrumentation Center for Environmental Management (NICEM), Seoul National University, Seoul, 151-921, Korea; [3]School of Agricultural Biotechnology, Seoul National University, Seoul 151-742, Korea; [4]Department of Agricultural Biology, Chungbuk National University, Cheongju 360–763, Korea.

Pepper anthracnose is one of the major limiting factors in pepper production. During last over 15 years, *Colletotrichum gloeosporioides* has been known as the most prevalent species among five *Colletotrichum* spp. involved as anthracnose causing agents. Recently, however, a change of a major species causing pepper anthracnose has been proposed. A number of approaches have identified the major pepper anthracnose pathogen collected in recent years as *C. acutatum* not *C. gloeosporioides*. To understand the molecular mechanisms involved in the infection process of *C. acutatum*, the genes expressed during initial conidial germination were explored by analyzing expressed sequence tags (ESTs). A cDNA library was constructed with total RNA extracted from *C. acutatum* conidia germinated. A total of 980 randomly chosen cDNA clones were sequenced in a single pass. Based on the quality of bases sequenced, 882 ESTs were considered high quality and further analyzed. Contig assembly generated 442 singletons and a set of 110 consensus sequences including 440 ESTs. *C. acutatum* genes encoding annexin, ADP-ribosylation factor, translation elongation factor, cyclophilin, SnodProt1, and alkaline serine protease were abundantly expressed during conidial germination. A number of genes encoding mold-specific protein, 14-3-3 protein, chitinase and phosphatidylglycerol captured attentions for further analysis.