F-71 Genetic Relationship of *Colletotrichum gloeosporioides* and *C. acutatum* Isolated from Apple, Pepper and Black locust. Jung Nam Kim[1], Se Hoon Choi[2], Yoon Soo Do[2], Jae Youl Uhm[2], Jung Sup Shin[3], Moo Ill Yeo[2] [1]Research Institute of Technogreen , Yongin 641-41, Korea; [2]Department of Agricultural biology, Kyungpook National Unibersity Daegu, 702-701, Korea; [3]Agricultural Research Center, HankookSamgong, Osan 235-6, Korea.

As the apple, pepper and black locust on which anthracnose occurs are sometimes grown in closely related area, the similarity of the pathogenic fungus was analyzed. The pathogenic fungi isolated from the three host plants were subjected to species analysis by the reaction against benzimidazole fungicides. Among the 390 isolates originated from apple, 35% were *Collectotichum acutatum* that is completely insusceptible to benzimidazole and others were *C. gloeosporioide* among which 7% were benzimidazole-resistant. The 101 isolates from black locust was divided into *C. gloeosporioides* and *C. acutatum* at the rate of 21% and 79%, respectively. In the reciprocal inoculation of the 3 host plants with nit-mutants derived from each of them, the inoculation of apple and pepper with the two fungal species from black locust and that of pepper plant with the two species from apple were successful, but other inoculations were unsuccessful. The genetic similarity among the isolates from the three hosts was examined by RAPD. The similarity among the isolates within the same species derived from same host plant was so high that formed a group. The group of *C. acutatum* from apple and that of *C. gloeosporioides* from black locust showed relatively high similarity at about 70% level. However, the isolates of *C. gloeosporioides* from apple showed lower similarity with those of *C. acutatum* from the same host than those from black locust. The C. acutatum from pepper showed low similarity with those from the other two host.

F-72 Attenuation of virulence of *Burkholderia glumae* and *Erwinia carotovora* by engineered endophyte containing AiiA gene. Hyun-Soo Cho, Soo-Young Park, Hoon Cheong, Seung-Hoon Kang, Jihyun F. Kim, Seung-Hwan Park Laboratory of Microbial Genomics, Division of Genomics and Proteomics Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon, 305-333

Quorum sensing regulates virulence factors depending on the population density manner in many plant pathogenic bacteria. In contrast, some bacterial species such as *Bacillus* spp. secrete counterpart enzymes (refered to as quorum quenching enzyme) that degrade acyl-homoeserine lactones (AHL), Gram-negative quorum sensing signal

molecules, resulting in inhibiting expression of AHL dependent target genes. To apply this quorum quenching mechanisms to manage bacterial diseases in agriculture, we evaluated role of quorum quenching gene by introducing into bacterial endophytes. The endophyte, *Burkholderia* sp. KJ006r was isolated from surface steriled rice plant previosely. Among these plant pathogenic bacteria, *Burkholderia glumae* and *Erwinia carotovora* subsp. carotovora was used as pathosystem for this study due to previous data that virulence of B. glumae and E. carotovora subsp. carotovora tightly controlled by quorum sensing. We constructed *Burkholderia* sp. KJ006r that expressed *Bacillus thuringiensis aiiA* gene by modifying promoter and expression vector. For reducing of pathogenicity of pathogen, we used *Burkholderia* sp KJ006r isolated from rice root. First of all, we constructed promoter probing and expression vector for expression of in *Burkholderia* sp. KJ006r. Through searching the promoter, aiiA gene was expressed behind TPR promoter originated from *Burkholderia* sp. KJ006r. *In vitro*, the engineered *Burkholderia* sp. KJ4114r-AiiA was successfully degraded N-hexanoyl-L-homoserine lactone while vector control did not show any activity. In vivo assay, *Burkholderia* sp. KJ4114r-AiiA significantly reduced disease severity caused by both *B. glumae* and *E. carotovora*. Our results indicate that the engineered endophytic bacteria harboring *aiiA* gene could be used a novel mean to manage bacterial pathogens that, upto date, can be difficult to control by other control methods such as chemical application.

F-73 Two putative isocitrate lyase genes (*GzICL1* and *GzICL2*) are required for virulence and sexual development in *Gibberella zeae*. Seung-Ho Lee[1], Sung-Hwan Yun[2], and Yin-Won Lee[1]. [1]School of Agricultural Biotechnology, Seoul National University and center for Agricultural Bio-materials, Seoul 515-742, Korea; [2]Division of Life Sciences, Soonchunhyang University, Asan, Choongnam 336-745, Korea.

Isocitrate lyase (ICL) is one of two enzymes consisting of the glyoxylate pathway that are involved in the metabolism of two-carbon compounds such as acetate. Recent studies on *Leptosphaeria maculans* and *Magnaporthe grisea* revealed that the *ICL* genes were essential for disease development by these phytopathogenic fungi. To elucidate the function of ICL in the cereal head blight fungus *Gibberella zeae*, we identified two orthologs of the *ICL* gene, designated *GzICL1* and *GzICL2* from the *G. zeae* genome database. Transgenic strains of *G. zeae* deleted for either of two *GzICL* (designated *delGzICL1* and *delGzICL2*, respectively), or for both (*delGzdII*) were generated using a gene replacement strategy. Transgenic *delGzICL1* strains were normal compared with its wild-type progenitor except ascospore formation; they produced