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

fewer perithecia, when selfed. In contrast, *delGzICL2* produced fertile perithecia as many as wild-type, but were slower in hyphal growth on medium containing 0.25% glucose or C_{12} fatty acid (0.25% Tween 20). For virulence on barley heads, both *delGzICL1* and *delGzICL2* caused disease symptoms as severe as wild-type. Interestingly, the *delGzdIl* mutants showed significantly reduced virulence on host plant; they produced no perithecia on mating plates. These results strongly suggest that both *GzICL1* and *GzICL2* genes are required for virulence as well as sexual development in *G. zeae*.

F-74 Microarray analysis of the *Gibberella zeae* cDNA clones obtained by subtractive hybridization against an isogenic *mat1-2* deletion strain. Seung-Ho Lee[1], Sanghyeob Lee[2], Doil Choi[2], Sung-Hwan Yun[3], and Yin-Won Lee[1]. [1]School of Agricultural Biotechnology, Seoul National University, Seoul 151-921; [2]Korea Research Institute of Bioscience and Biotechnology, Taejeon 305-600; [3]Division of Life Sciences, Soonchunhyang University, Asan, 336-745, Korea.

Gibberella zeae is a homothallic ascomycete causing head blight on several cereal crops. Ascospores of this fungus can overwinter within the sexual fruiting body (perithecium) and initiate the primary infection in the next spring. Thus, a greater understanding of sexual development in *G. zeae* is needed for a comprehensive disease control strategy. We have focused on identifying the genes specifically controlled by *MAT* gene, a master regulator of sexual reproduction in *G. zeae*. To do that, we employed suppression subtractive hybridization between self-fertile *G. zeae* Z3643 and an isogenic strain deleted for *MAT1-2* (*delmat1-2*). In total, 1,000 expressed sequence tags (ESTs) were generated from the cDNA subtraction library and 378 EST unigenes were identified. To select the genes expressed under control of *MAT1-2*, we performed a cDNA microarray analysis using the unigenes. Among them, 228 (61.1%) clones were highly expressed in strain Z3643, when grown on mating plates, but not in *delmat1-2*. These included the genes similar to a *Ste12*-like transcription factor, Grg1 protein involved in glucose-repression, a glutamate carboxypeptidase-like protein1, a NADPH-cytochrome P450 reductase, and to several hypothetical proteins. Differential expression of the 15 genes from this collection was confirmed by Northern blot analysis.