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.