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.