Hwajinbyeo were derived from Asominori, which resistance originated from Shiga Sekitori 11. *Xa1* resistance gene of Anjunabyeo and Hwayeongbyeo originated from Wase Aikoku 3. The resistance of Cheongcheongbyeo was derived from IR 2035, which resistance may be originated from Peta. Milyang 42 may have multiple resistant genes originated from IR 667, IR 1317, IR 946 and IR 1539. Hangangchalbyeo may have resistant genes originated from KR 51 and TKM 6.

B-15 Disruption of *purD* attenuates virulence of *Xanthomonas oryzae* pathovar *oryzae* KACC10331. Park, Young Jin, Eun-Sung Song, Hee-Wan Kang[1] and Byoung Moo Lee* National Institute of Agricultural Biotechnology, Rural Development Administration, Suwon, 441-707, Korea, [1]Graduate School of Bio and Information Technology, Hankyong National University, Ansung, 456-749, Korea

We constructed a mutant library of *Xanthomonas oryzae* pv. *oryzae* strain KACC10331 by random transposon mutagenesis and identified a purine-auxotrophic mutant (MXO793). MXO793 is disrupted *purD* with transposon containing kanamycin resistance gene and required exogenous purines for growth on minimal media, as well as deficient for virulence on rice. *PurD* gene is encodes phosphoribosylamine-glycine ligase, which is involved in purine biosynthesis pathway. In assays of virulence, MXO793 failed to develop the disease (bacterial blight) on susceptible rice cultivars. These results indicate that *purD* is required for cell-growth as well as virulence in *X. oryzae* pv. *oryzae*.

B-16 The relationship between Type I restriction-modification system and transformation efficiency of *Xanthomonas oryzae* pathovar *oryzae*. Lee, Byoung Moo, Young Jin Park, Eun-Sung Song, Jeong-Gu Kim, Hee-Jung Cho and Gil-Bok Lee National Institute of Agricultural Biotechnology, Rural Development Administration, Suwon, 441-707, Korea

Xanthomonas oryzae pv. *oryzae* (Xoo) causes bacterial blight (BB) in rice. Molecular studies on BB disease caused by Xoo have been facilitated by isolation genes from other *Xanthomonas* species due to the difficulties derived from genetic manipulations including random insertional mutagenesis and marker exchange, especially Korean Xoo strains. Transformation efficiency of bacterial cell was influenced by restriction-modification (R-M) system, a responsible for the attack on

invading DNA, such as bacteriophage and plasmid DNA. We confirmed the presence of Type I R-M related genes of Xoo strains and analyzed the relationship between R-M systems and transformation efficiency.

B-17 Effect of Ca^{+2} Concentration in Nutrient Solution on Development of Bacterial Wilt and Population of *Ralstonia solanacearum* in Xylem of Tomato Seedlings. Inn-Shik Myung, Young-Ki Lee, Ki-Woong Nam, Jong Hyeong Lee, and Jong Min Baek. Plant Pathology Division, National Institute of Agricultural Science and Technology (NIAST), Rural Development Administration (RDA) Suwon 441-707, Korea

The effect of Ca^{+2} concentration in the nutrient solution on the development of bacterial wilt and the population of bacterial pathogen, *Ralstonia solanacearum* in tomato seedlings was examined. Tomato seedlings were cultured in a nutrient solution containing Ca^{+2} at concentration of 2, 5, 10, 15, and 20 mM, and inoculated with the pathogen by clipping method. The disease incidence and disease index were recorded for a period of 9 day. The population of the pathogen in stem of the plant was counted by plating on a medium at 4, 6, and 9 day after inoculation. That xylem vessels were clogged by the pathogen in the Ca^{+2}-treated seedlings was observed by using scanning electron microscopy (SEM) at 6 and 9 day after inoculation. When the plants were cultured in the nutrient solutions containing at above 10 mM, those were resistant to bacterial wilt. The population of the pathogen in the stem and percent of clog in xylem decreased with increasing concentration of Ca^{+2} in the solution. However, even in the presence of Ca^{+2} at a high concentration, infection with the pathogen was observed in the xylem of the plant.

B-18 ToxJ and LysR-type regulator ToxR co-activate *Burkholderia glumae tox* operons encoding toxoflavine biosynthesis and transporter in a synergistic manner. Jinwoo Kim[1], Yongsung Kang[1], Jae-Eun Jeong[1], Yunjung Kim[1], Tomohisa Nagamatsu[2], and Ingyu Hwang[1]. [1]School of Agricultural Biotechnology, Seoul National University, Seoul 151-921, Korea; [2]Faculty of Pharmaceutical Sciences, Okayama University, Tsushima, Okayama 700-8530, Japan.

Burkholderia glumae produces toxoflavin, which is a key pathogenicity factor in rice grain rot and wilt in many field crops. We have previously presented that ToxR, a LysR-type regulator, regulates both *tox* operons (*toxABCDE* and *toxFGHI*) in the presence of toxoflavin as a coinducer. In addition, expression of the operons requires a