

Bacteriology and Bacterial Diseases (13 ~ 21)

B-13 Identification of rusty root inducing bacteria in Korean ginseng. Jae Eul Choi¹, Jin Ah Ryuk¹, Jin Hee Kim¹, Chun Hwan Choi¹, Jong Sik Chun², Young Jun Kim³, and Hyang Burm Lee² ¹Division of Plant Sci. & Resources, Chungnam Natl. Univ., Daejeon 305-764, Korea; ²School of Biological Sciences, Seoul Natl. Univ., Seoul 151-747, Korea; ³Division of Biotechnology, Catholic Univ. of Korea, Puchon 420-743, Korea

While the rusty-colored root is common in ginsengs culture and, often results in a severe economic loss, the major factors have not been found. This study was focused on the determination of a potential relationship between rusty root and endophytic bacteria. The number of endophytes was $9.6 \times 10^1 \sim 1.5 \times 10^2$ cfu/g fw in normal ginseng roots compared to $3.7 \times 10^6 \sim 5.1 \times 10^7$ cfu/g fw in rusty ones. Of 31 isolates from rusty ginseng roots, twenty-four isolates repeatedly induced severe to moderate rust on root while seven isolates induced slight rust. The bacteria responsible for rusty ginseng roots were mainly Gram negative aerobic. Rust inducing bacteria were identified as *Agrobacterium tumefaciens*, *A. rhizogenes*, *Burkholderia phenazinium*, *Ensifer adhaerens*, *Lysobacter gummosus*, *Microbacterium luteolum*, *M. oxydans*, *Pseudomonas marginalis*, *P. veronii*, *Pseudomonas* sp., *Rhizobium leguminosarum*, *R. tropica*, *Rhodococcus erythropolis*, *Rh. gloverulus*, *Variovorax paradoxus* on the basis of bacteriological characters and 16S rDNA sequences analysis. The results in this study strongly suggested that the rusty ginseng roots were produced by infection and growth of endophytic bacteria.

B-14 Gene analysis of bacterial blight resistance of principal and differential rice cultivars in Korea. Chun Hwan Choi¹, Xuan Ji Jin¹, Hong Woo Park¹, Tae Kyo Lim¹, Jae Eul Choi¹, Hee Kyeong Kang². ¹Division of Plant Sci. & Resources, Chungnam Natl. Univ., Daejeon 305-764. Korea; ²Dept. of Horticulture, Konju Natl. Univ., Yesan 340-802, Korea

Bacterial blight (BB) caused by *Xanthomonas oryzae* pv. *oryzae* is one of the major diseases of rice globally in the irrigated agroecosystem. Many genes (*Xa1* through *Xa27*) conferring resistance to BB in the different rice growing regions of the world have been identified. *Xa1* resistance gene of Naepungbyeo, Daejinbyeo, and

Hwajinbyeo were derived from Asominori, which resistance originated from Shiga Sekitori 11. *Xal* 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 Kang¹ and Byoung Moo Lee* National Institute of Agricultural Biotechnology, Rural Development Administration, Suwon, 441-707, Korea, ¹Graduate School of Bio and Information Technology, Hankyong National University, Ansong, 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 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