

Promoting Plant Protection by Root-Associated Microbes

Choong-Min Ryu^{1,2*}

¹Molecular Phytobacteriology Laboratory, Superbacteria Research Center, KRIBB, Daejeon 305-806, Korea

²Biosystems and Bioengineering Program, University of Science and Technology (UST), Daejeon 305-350, Korea

The rhizosphere is a narrow area around plant roots in which root-secreted secondary metabolites and microorganisms co-exist and interact. This area can also be considered as a battle field where beneficial bacteria and deleterious microorganisms compete. Therefore, this specific root area has been a topic of interest for researchers for more than a century. Among the diverse microbial population of the rhizosphere, the beneficial root-associated bacteria, also referred to as plant growth-promoting rhizobacteria (PGPR), have been used to manage plant diseases and promote plant growth and yield. Such a disease control method is referred to as biological control in contrast to chemical control. The biological control strategy was first proposed 50 years ago by Baker and Cook, who defined biological control as “the reduction of the amount of inoculum or disease producing activity of a pathogen accomplished by or through one or more organisms than man” (Baker and Cook, 1974). However, biological control of plant diseases is still in its infancy in comparison to the chemical control method based on market shares. Few biological control agents (BCAs) are currently available on the market. Meanwhile, there is a recent public demand for healthier foods with less contamination from chemical residues, and a great concern for the preservation of the environment. Therefore, a review of recent advances in biological control research including the success and failure of its implementation has been important to avoid repeating the similar mistakes made in the past. Early biological control in the 1970’s–1980’s consisted of screening antagonistic microorganisms for their biological activity, and elucidating their mechanism of action before developing a biological control product. The discovery of PGPR-elicited induced systemic resistance (ISR) in the 1990s shifted the focus of research towards the development of BCAs exhibiting ISR capacity. Genome- and multi-omics-based cutting-edge technologies developed in 2000’s have contributed to our understanding of the molecular mechanisms on the microbial determinants of

biological control and plant responses. Taken together, I introduce the results of 11 studies that used a multi-disciplinary approach to the management of plant diseases with rhizosphere microbes. The papers were organized into four different types as follows: (1) reviews on biological control and ISR, (2) biological control by antagonistic rhizobacteria, (3) biological control by ISR, and (4) induced systemic tolerance to abiotic stresses.

Kwak and Weller reviewed the well-characterized and historically well-defined take-all decline (TAD) that occurred naturally in the north-west United States after long-term continuous monoculture of wheat and barley. The authors review recent research on the role of fluorescent pseudomonads in the suppression of the take-all fungus as a major mechanism of TAD. A second review by Bakker et al. described a different approach to biological control by ISR. From a recent massive microbiome study, the authors raised several important questions such as “Why are not all plants in the state of ISR?” and “What is in it for the eliciting bacteria?”. The answers provide novel insight into our understanding of uncultivated unknown major microbes characterized by recent PhyloChips and NGS-based pyrosequencing technologies, which are likely to become as common as the polymerase chain reaction (PCR) in the future.

Park et al. propose a new approach to overcome the drawbacks of the conventional screening method for the selection of promising BCAs. The study by Sang et al. evaluates the efficacy of four pre-selected antagonistic bacteria against *Phytophthora capsici* using a newly developed assay system referred to as radicle and seedling assay against *P. capsici*. The results of the 3 year greenhouse and field study indicated that the radicle assay is more effective than conventional *in vitro* antagonism-based methods. Li et al. reported a biological control strategy against post-harvest diseases by soaking treatment with *Bacillus amyloliquefaciens* strain 9001 in apple. Diemel et al. present a new screening strategy to select root colonization mutants of *B. amyloliquefaciens* strain FZB42 using green fluorescent protein-tagged wild type and mutants.

Sumayo et al. searched bacterial determinants to elicit

*Corresponding author.

Phone) +82-42-879-8229, FAX) +82-42-860-4488

E-mail) cmryu@kribb.re.kr

ISR from the PGPR strain *Ochrobactrum lupine* KUDC1013 and the secreted bacterial compounds phenylacetic acid, 1-hexadecene, and linoleic acid against *Pectobacterium carotovorum* subsp. *carotovorum* (Pcc) in tobacco seedlings. Ryu et al. recently revealed another dimension of the role of bacteria in eliciting ISR. The main aim of this study was to evaluate the involvement of quorum sensing (QS) in the elicitation of ISR against Pcc and CMV by the PGPR strain *Serratia marcescens* 90-166. Bacteria are not the only ISR triggers, as fungi can also elicit this defense response. Elsharkawy et al. provided new evidence on *Thichoderma asperellum* strain SKT-1-mediated ISR against fungal pathogens and a yellow strain of CMV in *Arabidopsis*.

Induced systemic tolerance (IST) was recently defined in many study that analyzed plant responses to PGPR under abiotic stress conditions. Lim and Kim showed the beneficial effects of PGPR *Bacillus licheniformis* K11 on the drought tolerance of pepper plants. Similarly, Cho et al. reported the results of a genome-wide plant transcriptome study of PGPR-elicited IST in *Arabidopsis*.

This special issue should be of value to scientists and farmers involved in the biological control of pathogens in the field and will hopefully stimulate further investigation into advanced plant disease management. Ultimately, topics in this special issue are aimed to minimize the use of chemicals, which is essential to overcome the recent environ-

mental and health concerns. This issue also introduces a new era and proposes the direction of progress in the field of plant pathology. Especially, the special issues introduce several recent technologies and new concepts such as meta-genome analyses of the plant microbiome, diverse omics techniques (transcriptome, proteome, and metabolome), genome-wide plant responses, and the identification of bacterial determinants important for biological control and ISR (Bakker et al., 2013). The systematic approaches, based on the integration of technology and information, would provide new insight into genes, proteins, and metabolites of rhizobacteria and plants important for the management of plant diseases. Furthermore, in this special issue, several papers emphasize the need for the transfer of such new technologies into the field, where their application in the management of plant diseases constitutes the main objective of the study of “root-associated microbes and plant interactions”.

References

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