

## Plenary Lectures

### PL-1

#### Perspective: Thirty-Eight Years in Plant Pathology (1966-2004)

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My adventure in the United States began when graduate studies began at Mississippi State University in January, 1961. My goal for coming to the United States was to pursue graduate studies in plant genetics and breeding and return home to Korea with a Ph.D. degree. Upon the completion of my Ph.D. degree at Michigan State University in 1966, I had an opportunity to join the Department of Plant Pathology at the University of Illinois and work on the genetics of disease resistance in corn. I took the opportunity and it opened the door for my career as a plant pathologist in the United States. One thing leads to another as more opportunities arose and here I am approaching the end of my career in the United States. For the past thirty-eight years, a lot of changes have occurred in many aspects of plant pathology and that has impacted my activities in research, teaching, extension, administration and outreach. Traditionally, plant pathology is the study of pathogens and environmental conditions that cause disease in plants and the methods of preventing or controlling disease. Other disciplines such as botany, mycology, microbiology, genetics, biochemistry, statistics, agronomy, meteorology, etc. provide the basis for studying plant pathology. Hence, plant pathology departments at most of the Land Grant Universities in the United States have focused their efforts on research and graduate education without having undergraduate programs. All their graduate students are recruited from other disciplines such as biology, agronomy and horticulture. As we go through a period of dynamic change in modern agriculture from the influence of intense economic, technical, political, and social pressure, the impact on plant pathology is great, causing dramatic changes in trends of plant pathology. Furthermore, the increased emphasis on

molecular biology/ biotechnology in plant pathology accelerates the departure from traditional or classical plant pathology where there is already a serious lack in field trained plant pathologists. Consequently, classical plant pathology is diminishing with the elimination of departments or merger with other disciplines. We are at a critical crossroad where we must meet the challenge of sustaining a balance between conventional and non-conventional plant pathology. Plant diseases have had a major impact on mankind. Diseases such as ergotism and late blight of potato have led to the deaths of thousands of people. Diseases such as coffee rust have changed the sociocultural behavior of people. Diseases such as southern corn leaf blight, chestnut blight, and dogwood anthracnose have caused millions of dollars in damage. As the history of mankind unfolds, threats of introducing new diseases in crop production areas, regions or countries exist, such as southern soybean rust which has the potential to be introduced in the United States. Classical plant pathology, studying the dynamics of pathogen, host plant and environment, is an essential basis of managing plant diseases in production fields and must be sustained. Therefore, we must continue to train field oriented plant pathologists.

Although I've been an invited speaker at numerous national and international meetings of professional Korean societies, universities and research institutes during the past years, it is especially gratifying for me to present my perspective on thirty-eight years as a plant pathologist in the United States at the 20<sup>th</sup> Annual Meeting of the Korean Society of Plant Pathology. I am honored and deeply appreciate this opportunity.

### PL-2

#### The Impact of Genomics on Plant Pathology: Looking to the Future

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Major advances in genomics and computational capacities are providing plant pathologists with opportunities to study, develop and apply novel solutions to intractable disease problems. Among these advances are the release of complete genome information for increasing numbers of plant pathogenic microorganisms as well as two model plant species (rice and Arabidopsis), and, the development of high-throughput technologies for comprehensive analysis and validation of gene function. The complete or nearly

complete genome sequences have improved the resolution of comparative genome studies within and among species which are yielding helpful insights into the evolutionary relationships of genes critical to virulence in pathogens and disease resistance in host plants. Comprehensive data from functional genomic analyses are providing unprecedented clues into how pathogens exploit plants, and how plants respond to pathogens or to abiotic stresses. With all of these huge sets of data rapidly accumulating, a crucial

challenge that remains for Plant Pathologists is to develop the capacity to integrate this information with existing knowledge of the biochemistry, physiology, ecology, and epidemiology of the host-parasite interactions such that it can be applied to improve crop production. These improvements may be realized through better diagnostic tools, targeted modifications in host plants to

enhance durable resistance, and superior predictive models of disease development to guide disease management practices. In this presentation, I will suggest a vision of how the advances of genomics will influence plant health in the future, providing illustrative examples from various research approaches.

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### PL-3

## Fungal Hypoviruses and Their Role in the Biological Control of Plant Diseases

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Biological control of fungal diseases of plants is a concept that has been embraced with great enthusiasm. It implies that management strategies can be developed that do not rely on regular, costly applications of fungicides. Even more importantly, it provides a strategy to manage fungi that cannot be controlled using fungicides or other known methods. Unfortunately, there are relatively few examples of successful biological controls that have been demonstrated for fungal diseases of plants. This lack of success has resulted in a waning of effort toward finding biological solutions to plant disease problems. I believe that this retreat from seeking biological management strategies for fungal diseases of plants is premature.

Significant effort has been expended toward seeking biological controls for insect pests, in part, because of the known problems associated with insecticide use. Plant pathologists have never had the array of chemicals available to control plant diseases that have been developed for insect control, thus fungicide use remains low compared with insecticide use world-wide. We are also less aware of the detrimental effects of fungicide use on natural ecosystems than are entomologists in their knowledge of the effects of insecticides, so we expend much less effort than do entomologists in looking for alternatives to pesticides. The effort of the entomologists to find biological controls has been rewarded with numerous successful examples. There is reason to assume that similar efforts to find biological controls of fungi would be met with similar success.

A strategy for biological control of fungi that holds great promise is the use of mycoviruses. As with all known organisms, fungi harbor viruses; some of these have potential in biological control strategies. The most well characterized viruses of fungi that have potential for biological control are the hypoviruses of the chestnut (*Castanea spp.*) blight fungus, *Cryphonectria parasitica*. This group of viruses is a successful naturally occurring biological control for chestnut blight under some circumstances. We do not yet fully understand all of the circumstances that contribute to the success or failure of this biological control.

This type of mycovirus causes its host, *C. parasitica*, to remain in a juvenile state of growth, i.e. to perturb normal developmental processes of the fungus, the results of which are low virulence (hypovirulence), poor asexual and sexual sporulation. Saprophytic growth of the fungus is not affected by the virus, so in culture the fungus grows normally but does not

sporulate or develop the normal pigmentation associated with development. Molecular studies of virus-infected strains of the fungus suggested that a number of genes are transcriptionally down and up-regulated in virus infected strains. Evidence has also been presented that normal cell-signaling processes are perturbed in virus infected strains.

My laboratory has been seeking to understand how the virus is able to perturb developmental processes of this fungus. Our approach has been to examine groups of genes, and their products, that are down-regulated in virus-infected strains to seek commonalities among these perturbed genes. A number of genes were selected based on their differential expression for further characterization. Genes were cloned and their products identified. In most cases, the genes were deleted to study their role in the biology of the fungus. Among the genes identified were the fungal sex pheromones, a cell-surface hydrophobin, and a laccase. The pheromones and hydrophobin are involved in fungal sporulation, and are thus developmentally regulated.

A number of the gene products characterized had common endoprotease recognition sites, suggesting that the preproteins encoded by these genes were processed in the same way during secretion. The recognition sites were the same as those reported for the conserved *kex2* endoprotease of *Saccharomyces cerevisiae*. This endoprotease is known to be involved in the processing a secretion of the alpha pheromone of yeast; a pheromone precursor gene with similar processing sites and signals was found to be down-regulated in virus-infected strains of *C. parasitica*.

These results led us to investigate the secretion of one of the *kex2*-processed proteins in both virus-infected and healthy strains of the fungus. Our results showed that the secretion of the cell-surface hydrophobin, cryparin, is perturbed in the virus-infected strain. Secretion is much slower when the virus is present.

Isolation of the components of the vesicular secretory system of *C. parasitica* showed that the virus genome is found in association with trans-golgi vesicles. The virus lacks a capsid but is able to replicate in association with these fungal vesicles. The trans-golgi vesicles were much more abundant in virus infected strains than they were in uninfected strains. The vesicle fraction that contains the virus vesicles also was enriched for clathrin and an associated adaptor protein. Based on these results, we hypothesize that the virus utilizes a vesicle fraction for its replication and movement that is normally involved in secretion of