Plant Pathology
COLLEGE OF AGRICULTURAL & LIFE SCIENCES
UNIVERSITY OF WISCONSIN–MADISON

History Note No. 5

April 2026

History Note No. 5 – USDA/ARS Pioneering Research Lab, Plant Disease Resistance Research Unit - 1983-present. Part B - The Second Generation of Scientists/Faculty Members

Upon the retirement of Dr. J. Helgeson in 2003, the USDA terminated the Plant Disease Resistance Research Unit, and the USDA scientists were assigned to either the ARS (Agricultural Research Service) Cereal Crops Research Unit (Leong) or the ARS Vegetable Crops Research Unit (Halterman and Willis) on campus.

Dr. Sally A. Leong (1983-2008) Leong's research interests centered on the molecular biology of filamentous fungi. She studied the high affinity iron transport system of the corn smut fungus *Ustilago maydis,* elucidating the molecular mechanisms of biosynthesis and regulation of biosynthesis of siderophores with the goal of understanding aspects of iron homeostasis in this simple eucaryote and how this affects survival of the pathogen and its interaction with plants. To achieve this goal her research team developed some of the first methods for DNA transformation of *Ustilago* and other fungi, as well as isolated mutants of these fungi, which led to the first cloning and analysis of the genes for these processes in fungi. A second area of research focused on studies of the genome organization of *Magnaporthe grisea*, the causal agent of rice blast disease. Her long-term goal was to understand the molecular bases of host and cultivar specificity and the evolution of cultivar specificity genes in this pathogen and the reciprocal resistance genes in graminaceous hosts of *M. grisea*. Her team identified and cloned the avirulence gene *AVR1-CO39* from *M. grisea* and its complementary disease resistance locus *Pi-CO39 (t)* from rice. Population studies of the fungus showed the widespread occurrence of homologs of *AVR1-CO39* in different host-specific strains of the fungus with rice-infecting isolates often having nonfunctional alleles compared with other grass-infecting isolates. To achieve these goals Leong's team developed a genetic map of the fungus and other tools for fungal genome analysis such as gel electrophoretic karyotyping of intact chromosomes and site-specific genome cleavage with RecA protein. Her team also participated in the sequencing and optical mapping of the rice genome as part of the UW Genome Center and International Rice Genome Sequencing Project. The Leong lab hosted foreign scientists from Japan, India, England, Canada, China and Germany as well as visiting students from China, India, France and The Netherlands.

References:

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Dr. David K. "Kyle" Willis (1968 – 2013) Willis carried out fundamental research on the genetics of the virulence/pathogenicity factors of bacterial pathogens. 1) This involved the characterization of the *gac*S/*gac*A two component genetic regulators that are required for lesion formation by *Pseudomonas syringae* pv. *syringae* on snap beans. 2) Additional genes required for lesion formation by *P. syringae* pv. *syringae* were detected by Tn-5 generated mutations. 3) Conservation of the *gac*S/*gac*A genes among phytopathogenic pseudomonads was researched. 4) The cloning and sequence analysis of the biosynthetic region for tabtoxin (a phytotoxin) of *P. syringae* and the regulation of tabtoxin biosynthesis via the transcriptional activation of the *tbl*A gene were carried out. Later in his career, he used his knowledge of RT-PCR and molecular biology to assist other researchers. Some examples are: a) determination of the copy number of the genes at *Rhg1* associated with nematode resistance in soybean, b) detection of aster yellows phytoplasma in the insect vector, *Macrosteles quadrilineatus,* c) evaluation of type III secreted effector DspE in infection of potato by *Pectobacterium carotovorum,* d) determination of the titer of tomato spotted wilt virus in *Frankliniella occidentalis, and* e) the molecular detection of *Sclerotinia spp*.

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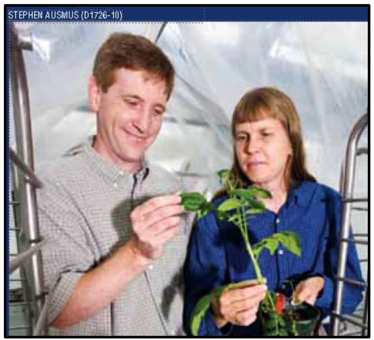
Dr. Dennis A. Halterman (2004 – Present) As a Plant Geneticist, Halterman's career has focused on enhancing the resilience and sustainability of our global potato supply. His foundational research explores the genetic diversity within wild potato relatives, which have naturally developed inherent disease resistance without human intervention.



Dennis Halterman & Shelly Jansky

A significant area of his high-impact research has been the molecular characterization and enhancement of the *RB* gene, a crucial component for robust resistance to late blight in potatoes, first identified by Dr. J. P. Helgeson. Halterman's research is instrumental in understanding how the pathogen *Phytophthora infestans*, particularly through its effector IPI-O4, can suppress RB activity. He elucidated the mechanisms by which *P. infestans* overcomes RB-mediated resistance, identifying variations in RB that enable it to avoid IPI-O4 suppression and improve its durability. This work advanced basic knowledge of plant-pathogen interactions and clarified how RB expression influences the balance between plant growth and disease resistance. These findings underscore the value of RB-containing varieties, now undergoing trials for approval in regions like Africa and India, promising significant reduction of fungicide use.

Advancing plant immunity understanding, Halterman's team uncovered sophisticated regulatory processes, including alternative splicing of potato disease resistance genes, revealing how plants balance growth and immune responses. He also elucidated complex ecological interactions, such as potato virus Y restricting *Alternaria solani* growth during co-infection. These insights are crucial for developing durable and effective disease management strategies.

Beyond his scientific discoveries, Dr. Halterman has served as a pivotal leader in the scientific community, notably as President of the Potato Association of America, and has spearheaded numerous outreach events across the state. His efforts have not only expanded the frontiers of plant genetics but have also translated scientific breakthroughs into tangible benefits for potato breeders and farmers worldwide.

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