

Temporal and spatial meanderings in forest pathology, and fun along the way

Ned B. Klopfenstein^{1*} and many others

First of all, I am both very grateful and extremely humbled to receive the WIFDWC Outstanding Achievement Award, and, of course, I can easily recognize so many other candidates who are more deserving. However, I am extremely happy that Phil Cannon is a co-recipient of this award, because Phil and I have collaborated on diverse projects for about 25 years, and Phil is an exemplary recipient for this award. Unfortunately, I have little idea about what sort of topics I should address here, so I decided to include a bit on various topics.

In past WIFDWCs and other meetings, I think it was Ellen Goheen, Kim Corella, and others who continued a project to track our academic lineages or our forest pathology family tree. Like many other WIFDWC attendees, I come from the Hartig – Meinecke – Boyce academic lineage. I received my Ph.D. in Plant Pathology at Iowa State University, with Harold S. “Sande” McNabb, Jr. as my Major Professor. Sande was known for his work on Dutch elm disease, poplar diseases, teaching forest pathology, and his relentless advocacy for students of diverse backgrounds.

My earliest forest pathology- and mycology-related memories are of Dutch elm disease that began to dramatically change the landscape and aesthetics of cities, small towns, and countrysides across the midwestern USA in the 1950s and 1960s. Subsequently, I also became drawn into the springtime hunts for morel mushrooms that were associated with the dying elm trees in the Iowa forests. These events planted an inspiration for my studies in forest pathology, although I followed a somewhat circuitous route along the way.

Although I wasn’t quite born when Franklin, Watson, and Crick contributed to our understanding of the DNA double helix, many other subsequent landmarks in DNA technology occurred when I was a young, impressionable undergraduate student in biology. In fact, I still remember my inspiration when I first learned about recombinant DNA in a second-year biology class. As a side note, this same biology class in 1973 also had a section devoted to inevitable climate change from burning fossil fuels, which was over 50 years ago. Along the way, I became interested in tissue culture of woody plants, and I became a graduate student in Plant Pathology. As a part of my graduate studies, I took the first university class in genetic engineering, which I found highly interesting. A continuation of my work with tissue culture and genetic engineering led to the genetic engineering of *Populus* hybrids with genes to study pest resistance (Klopfenstein et al. 1991, 1997). In 1989, the first field test of genetically engineered trees was established (Figure 1).

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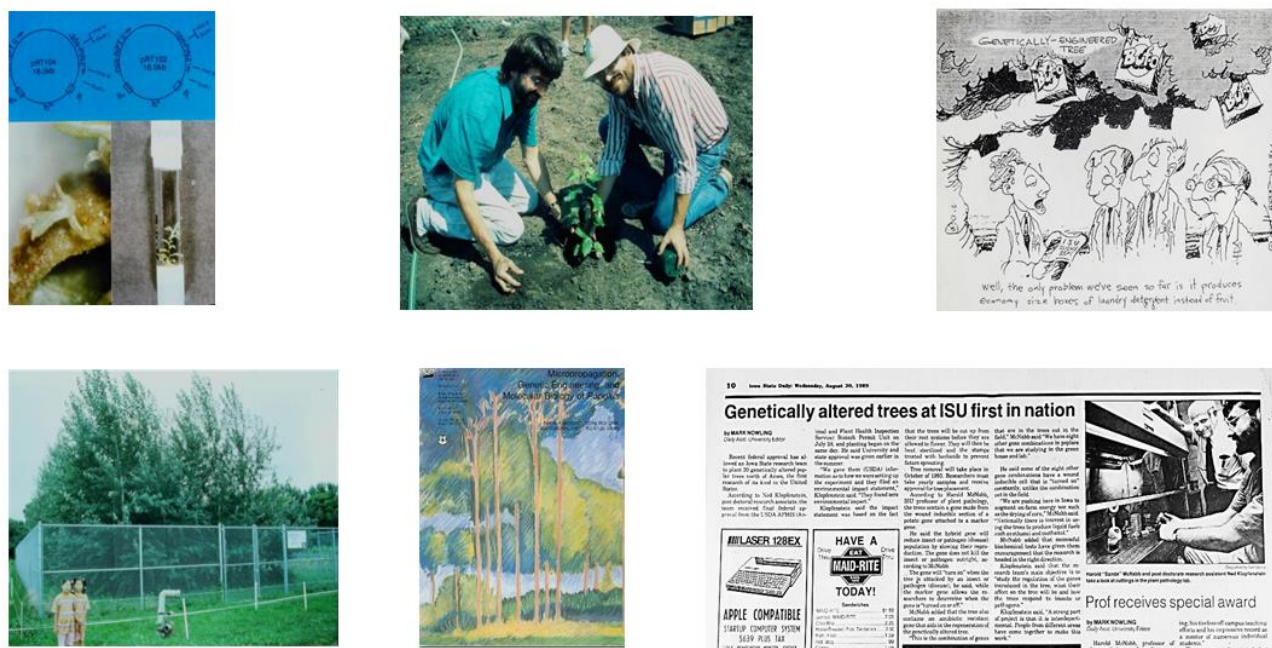


Figure 1: First field test of genetically engineered trees in 1989 (Klopfenstein et al. 1991, 1997).

Subsequently, a large part of my research in forest pathology has focused on diverse aspects of molecular genetics. My collaborative studies in forest pathology have covered diverse topics, such as DNA-based diagnostics of forest pathogens, phylogenetic studies to examine evolutionary relationships among forest pathogens, population genetics of forest pathogens and hosts, genomic and transcriptomic sequencing of forest pathogens to determine genes contributing to pathogenicity, and metagenomics or metabarcoding to examine the roles of associated microbes in forest health. Indeed, I feel quite fortunate to have participated in so many interesting research projects, of which I will briefly mention only a few.

Out of many collection trips, one especially memorable travel was to protected areas at high elevations in Japan to collect white pine blister rust samples. Based on this phylogenetics study, we concluded that the *Cronartium ribicola* that was introduced to North America did not originate from the high-elevation *Pinus pumila* in Japan. Another highlight was when our group traveled with Phil Cannon on a trip to Mexico, where we met Professor Dionicio Alvarado Rosales and conducted surveys for *Armillaria*. This collaboration produced several interesting results, including describing a new species, *Armillaria mexicana*, which appears to be an evolutionary ancestor to all other *Armillaria* species in the Northern Hemisphere (Elías-Román et al. 2018: Figure 2).



Figure 2: *Armillaria* surveys in Mexico (Elías-Román et al. 2018; Kim et al. 2022).

Our collaborative studies on myrtle rust have been both interesting and fun. These studies showed that myrtle rust on eucalypts in Brazil did not emerge via a host jump of the myrtle rust pathogen from guava (Graça et al. 2013). Subsequently, Jane Stewart et al. (2018) determined that the myrtle rust pathogen comprises multiple biotypes that have distinct host associations and different climatic requirements or invasive threats (Figure 3). We also collaborated with Phil Cannon, Colorado State University, and several other international forest health professionals to examine *Phellinus noxius*, the cause of the destructive brown root rot disease on diverse woody hosts in eastern Asia, Australia, and the Pacific Islands. These studies showed that *P. noxius* comprises multiple genetic groups – each with distinct invasive threats (Stewart et al. 2020; Cannon et al. 2022). Subsequent analyses by Olga Kozhar et al. (2022) determined that most recent emergences of brown root rot disease in the Pacific Islands are not the result of a recent invasion by *P. noxius* (Figure 4).



Figure 3: Myrtle rust (caused by *Austropuccinia psidii*) in Brazil and other global regions. Myrtle rust on eucalypts in Brazil did not emerge via a host jump of *A. psidii* from guava (Graça et al. 2013). The myrtle rust pathogen comprises multiple biotypes that have distinct host associations and different climatic requirements or invasive threats (Stewart et al. 2018).



Figure 4: Brown root rot disease (caused by *Phellinus noxius*) surveys in the Pacific Islands. *Phellinus noxius* comprises multiple genetic groups – each with distinct invasive threats (Stewart et al. 2020; Cannon et al. 2022).

Most recent emergences of brown root rot disease in the Pacific Islands likely did not result from a recent introduction of *P. noxius* (Kozhar et al. 2022).

Over the years, I have had the pleasure of working with nearly 400 co-authors from the USA and international institutions from 32 countries. These diverse collaborations are an especially rewarding part of my work. My collaborations with Jane Stewart, Mee-Sook Kim, Geral McDonald, John Hanna, Phil Cannon, Marcus Warwell, Bryce Richardson, Margaret Mmbaga, Girma Tabor, Young Woo Chun, and many others have been a cornerstone for much of my collaborative work, and I feel especially indebted to these folks! As forest pathologists, we all have the pleasure of working in some incredible places in the USA, which is a highlight of our work. In addition, I have also had the pleasure of conducting work internationally, which I also greatly enjoy. My work in forest pathology has included travel to fascinating destinations, such as Puerto Rico, Guam, Northern Mariana Islands, Federated States of Micronesia, Canada, Mexico, Colombia, Brazil, Poland, Turkey, Philippines, Australia, New Zealand, India, Thailand, Hong Kong, Taiwan, Japan, and South Korea. Although I thoroughly enjoy international travel, I am quick to remind younger forest pathologists that international work is essential to remain current in nearly all aspects of forest pathology.

Of course, the colleagues and friends that we meet over the course of our careers are what makes our work and life especially meaningful. Friends and colleagues who have contributed to the quality of various stages of my life and career are too many to mention here, but I trust that they know I am thankful for spending time with them

along the way (Figure 5). As I was preparing for this presentation, I again realize how quickly time passes, but of course, we can all find time for fun along the way (Figure 6).



Figure 5: Friends and colleagues.

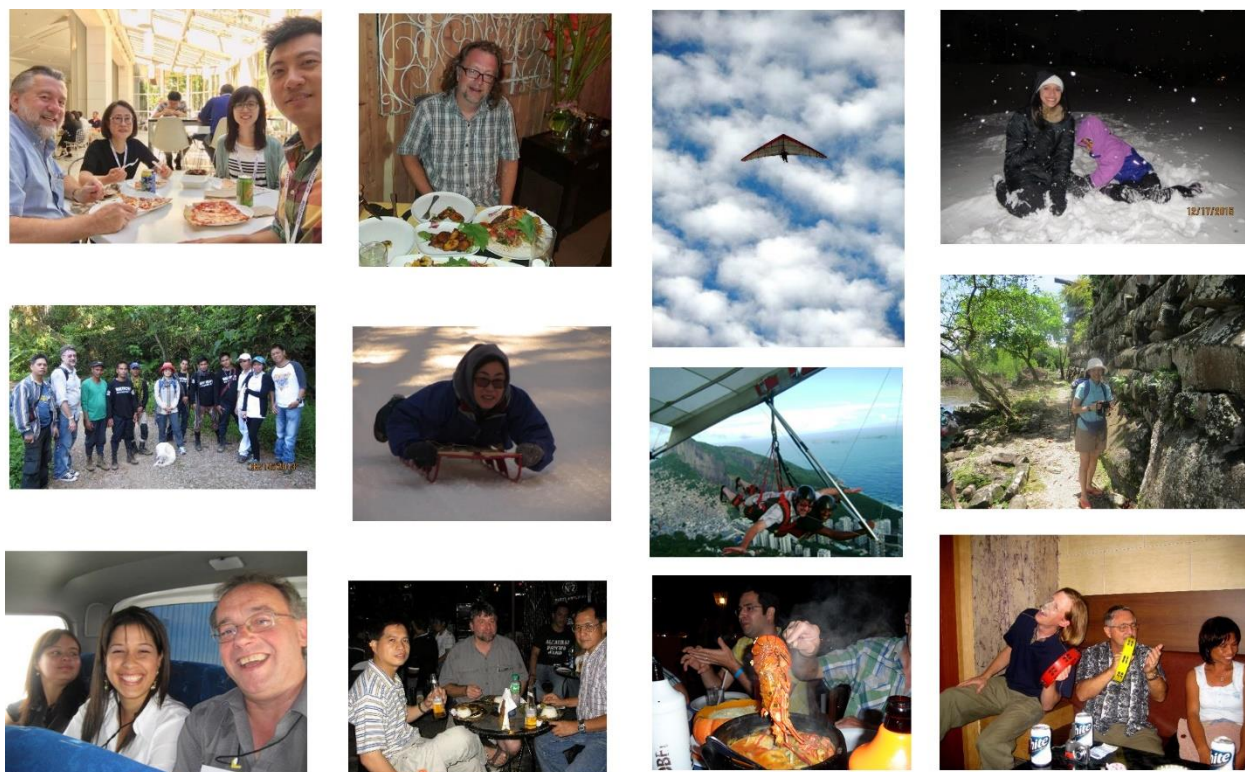


Figure 6: Fun along the way ...

As I mentioned, Phil Cannon and I have collaborated for 25 years, both domestically and internationally (Figure 7). In short, I simply cannot overstate Phil's enormous and diverse contributions to forest pathology. Phil has a tremendous depth of experience in the USA and abroad, and he is extremely knowledgeable about almost any subject in forest pathology. I look forward to continued collaborations with Phil and others.



Figure 7: Phil Cannon in various times and places.

I was advised to provide any perspectives that I learned over the years, but I doubt that I can provide many insights that most of you don't already know. It goes without saying that we need to increase diversity, capacity, inclusion, and collaboration in forest pathology, mycology, and associated disciplines if we want to successfully address future issues in forest pathology. DNA-/RNA-based technologies, environmental metadata, and remote sensing will likely continue to play ever-increasing roles in forest pathology. It also seems likely that paradigms in forest pathology will change as we better understand pathogen variation at the sub-species level and the phytobiome or microbial communities associated with plant disease. And, as everyone already knows, climate change and invasive pathogens will continue to have ever-increasing impacts in forest pathology.

Lastly, I want to reiterate my tremendous appreciation to WIFDWC. I always especially enjoy attending WIFDWC meetings – thank you, everyone!

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