Molecular Evolutionary Biology of *Fusarium*

Research in my laboratory focuses on several aspects of the evolutionary biology of *Fusarium*, a large genus of filamentous fungi that represents the single most important group of mycotoxigenic plant pathogens. Fusaria have also emerged within the past two decades as opportunistic pathogens of severely immuno-compromised patients. Members of this genus produce an amazing diversity of toxic secondary metabolites, such as trichothecenes (potent inhibitors of eukaryotic protein synthesis and virulence-associated factors towards sensitive plant hosts), fumonisins (suspected carcinogens) and estrogenic compounds, which pose a serious threat to human and plant health and food safety. One of the primary goals of my research program is to develop molecular epidemiological tools for the rapid detection and identification of the most important fusarial pathogens of plants and humans. To achieve this objective, we have been using multilocus sequence typing (MLST) to identify species limits and to examine their population biology. Knowledge of species limits is essential for understanding their geographic distribution, host range and toxin potential. This information is critical in order to establish successful molecular surveillance programs for economically devastating plant diseases such as *Fusarium* Head Blight (FHB) of wheat and barley and Sudden Death Syndrome (SDS) of soybean (for publications, see below). Just within the past decade, FHB endemics in the upper Midwest of the U. S. have accounted for approximately 3 billion dollars in losses to U. S. agriculture because of low yields and price discounts due to toxin contaminated grain. Research in my laboratory has shown that both of these diseases are caused by several genetically distinct species that are non-indigenous to the United States. Our phylogenetic epidemiological studies are directed at minimizing the threat of inadvertent introductions of foreign FHB and SDS pathogens into the U. S. We are also using MLST to characterize the genetic diversity of medically important fusaria as part of a multi-institution collaborative study. Lastly, some of
my research has focused on the evolution of the Zygomycota and true morels (for publications, see below).
Selected Publications

Evolution of *Fusarium* Head Blight (FHB) and trichothecene mycotoxins


Evolution of the *Fusarium solani* species complex
[including Sudden Death Syndrome (SDS) of soybean]


**Evolution of the Gibberella fujikuroi species complex**  
[mycotoxigenic phytopathogens including most fumonisins toxin producers]


**Evolution of the Fusarium oxysporum species complex**  
[wilt pathogens of many economically important plants]


Web-based Identification of Fusarium


Evolution of the Zygomycota


Evolution of Morels and Truffles (Ascomycota)