



**Mark Farman, Dept of Plant Pathology,
Healthcare Genomics Center, University of Kentucky**

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Phylogenomics and Genome-Enabled Molecular Diagnostics For Blast Diseases

Genome sequencing has transformed the field of phylogenetics to provide unprecedented insights into organismal evolution. This is especially so in the case of the fungus, *Magnaporthe oryzae*, a serious pathogen of rice and wheat, along with other cereal crops and grasses. Though *M. oryzae* exists as several distinct, host-specialized populations, the relationships between the different forms have been unclear due to a paucity of informative markers. In 2011, *M. oryzae* was discovered on a single wheat plant in Kentucky, raising a concern that the disease had been introduced from South America. While traditional molecular markers were unable to resolve the origin of the causal organism, genome sequence data clearly pointed to an endemic *Lolium*-infecting population as the probable source. Motivated by the powerful genetic resolution afforded by whole genome data, we developed a genome-based forensics platform for *M. oryzae*. Here, an understanding of fungal genome organization and dynamics was of critical importance in the choice of comparative analysis tools, and in the interpretation of data. I will highlight the most important considerations and will describe the use of our platform to characterize isolates collected from the 2016 wheat blast outbreak in Bangladesh. Finally, I will provide a critical assessment of the recent claim that some wheat blast pathogens constitute a new species.