**Genome improvement of *Magnaporthe oryzae* strains Guy11 and U233**

1Chloe DeGiorgio, 2Diksha Satish, 1Mark Farman, 3Jerzy Jaromczyk, 4Patrick Calie, and 2Claire Rinehart

1Department of Plant Pathology, University of Kentucky, Lexington, KY 40546

2Department of Biology, Western Kentucky University, Bowling Green, KY 42101

3Department of Computer Science, University of Kentucky, Lexington, KY 40506

4Department of Biological Sciences, Eastern Kentucky University, Richmond, KY 40475

 *Magnaporthe oryzae* is a pathogenic fungus responsible for rice blast disease. The terminal ends of *M. oryzae* chromosomes are unstable which allows for frequent rearrangement of the genome, a property that may be useful for adaptation. High-quality genome assemblies are required to investigate this mechanism. The genomes of *M. oryzae* strainsGuy11 and U233 were selected for improvement with the goal of producing chromosome-level assemblies. Using MUMplot, the Guy11 and U233 contigs were aligned to two chromosome-level assemblies of *M. oryzae* strains (70-15 and LpKY97). The MUMplot data guided efforts to arrange and connect contigs, find mis-assemblies, and identify translocations. MinION raw reads of the Guy11 and U233 assemblies were used to verify MUMplot data. Raw read coverage was viewed in the Integrative Genomics Viewer, and BLAST reports gave information on connections. The subterminal regions of strain 70-15 were also used to guide the arrangement of Guy11 contigs, as these regions of 70-15 have been characterized, and 70-15 is a progeny strain of Guy11.

 The final number of Guy11 contigs was reduced from 33 to 23, and the number of U233 contigs was reduced from 49 to 43. In both genomes, mis-assemblies were found and corrected, and *Escherichia coli* DNA contamination was discovered. U233 had seven translocations in its assembly, but none were present in Guy11. Identifying the telomere-containing contigs enables future study of the terminal and subterminal regions of the genomes. The refined genomes can be used for reference-based assembly using Illumina reads to further improve other genome sequences.