

## DRAFT GENOME SEQUENCE OF MYCOSPHAERELLA DEARNESSII FROM TWO ISOLATES INFECTING LONGLEAF PINE

**B. D. Bartlett<sup>12</sup>, J. H. Roberds<sup>1</sup>, K. C. Showmaker<sup>2</sup>, D. G. Peterson<sup>2</sup>, and C. D. Nelson<sup>13</sup>**

Longleaf pine (*Pinus palustris* Mill.) once occupied over 30 million hectares in the southeastern US, but in recent times has been drastically reduced to an area consisting of 1.2 million hectares. Currently, a restoration effort is underway to increase longleaf pine habitat to a total of 3.2 million hectares. *Mycosphaerella dearnessii* is a fungal pathogen of longleaf pine that could hinder restoration efforts. To better understand the pathogen and develop strategies to limit its damage, a draft genome sequence has been produced. To date, two isolates of the fungus has been sequenced and an assembly of 30Mbp genome sequence with an N50 of 19,120bp has been obtained from one of these. This represents 65% of the estimated genome size of 46Mbp from 12,317 contigs. Gene prediction software has yielded 17,633 protein coding genes. Comparative genomics will be employed to recognize the genes responsible for pathogenicity. Of particular interest is detection of effector protein genes, which are responsible for the fungus entering the plant cell. Knowledge of the pathogen's genome will lead to reduce incidence of the disease and provide a starting point to develop disease-resistant longleaf pine trees.

---

<sup>1</sup>Southern Research Station, Southern Institute of Forest Genetics, USDA Forest Service, Saucier, MS

<sup>2</sup>Institute for Genomics, Biocomputing & Biotechnology, Mississippi State University, Starkville, MS

<sup>3</sup>Forest Health Research and Education Center, University of Kentucky, Lexington KY