

Section 4 Abstracts: Ecology and Genetics of the Chestnut Blight Fungus

Mitochondrial DNA Heterogeneity in *Cryphonectria parasitica*. N.K. Van Alfen,¹ C. Bachmann,¹ Y. Wang,² M. Milgroom,³ Y.-C. Liu,³ M.F. Allen,⁴ L. Zhang,¹ N.-T. Wul and E. Gobbi⁵. ¹Department of Plant Pathology and Microbiology, Texas A&M University, College Station, TX 77843; ²Department of Biology, Utah State University, Logan, UT 84322-5305; ³Department of Plant Pathology, Cornell University, Ithaca, NY 14854-5908; ⁴Department of Biology, San Diego State University, San Diego, CA 92182-0057, USA; and, ⁵Istituto de Difesa della Pianta, Università degli Studi di Udine, 33100 Udine, ITALY

The mitochondrial DNA of *Cryphonectria parasitica* is the largest reported from an ascomycete (approximately 145 kbp). Strains of the fungus collected from various parts of the world were examined to determine the relative heterogeneity of the mtDNA. We also examined mtDNA collected in three different field plots: Grimacco, Italy; Accokeek, Md.; and, Linden, Calif. The plot in California was found to be infected by a single clone of the fungus, which is consistent with the history of the infection at this location that is isolated from other infection sites. The fungus at the other locations was found to have extremely heterogeneous mtDNA. A total of 31 haplotypes of mtDNA were detected among the 34 isolates examined from these locations. The nuclear DNA, however, was found to have few single-locus polymorphisms. Most of the heterogeneity detected within populations of the fungus are length mutations. Mapping of some of the mutations shows that the insertion/deletion events responsible for the mutations are not restricted to specific areas of the mtDNA and that most of the inserted/deleted DNA sequences are not typical of repetitive sequences. A mtDNA mutation lineage was constructed from isolates with the

same nuclear DNA fingerprint patterns. The mtDNAs of these closely related isolates differed by a total of at least 7 single-step mutations. The mutations, which of the simplest lineage, are insertional mutations. We conclude from these studies that the mtDNA of this fungus has an unusually high mutation rate.