

Modeling and Analysis of American Chestnut Blight in North America

Robert F. Allen^{1,*}, Anita D. Baines², Hope E. Anderson³, John Stewart McAlister⁴, Tatum Day Rask⁶, Maia Richards-Dinger⁶

¹*Department of Mathematics & Statistics, University of Wisconsin-La Crosse, La Crosse, WI 54601*

²*Department of Biology, University of Wisconsin-La Crosse, La Crosse, WI 54601*

³*Davidson College, Davidson, NC 28035*

⁴*The Ohio State University, Columbus, OH 43210*

⁵*Pepperdine University, Malibu, CA 90263*

⁶*Lewis & Clark College, Portland OR 97219*

rallen@uwlax.edu

Since the introduction of fungal blight (*Cryphonectria parasitica*), the American chestnut (*Castanea dentata*) has gone from a dominant canopy tree in Appalachian forests to an understory species. The introduction of the hypovirus (*Cryphonectria hypovirus*) to the blight fungus, which reduces pathogen virulence, has improved the survival of some stands of chestnut trees. However, many populations are still declining. In this research, we adapt existing SIR models of the tree-virus-hypovirus system to include new populations of trees seen in stands, as well as new interactions between these populations. These additions provide a more complete and biologically accurate description of the demography of chestnut stands. Our model predicts the existence of sprouts at equilibrium and, in most cases, the disappearance of full-sized chestnut trees, both of which are observed in Appalachian forests. Our model also predicts that, although the hypovirus delays the extinction of full-sized chestnut trees, it does not prevent it.