

## THE EVOLVING EFFORT TO RESTORE THE AMERICAN CHESTNUT

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For 30 years, The American Chestnut Foundation (TACF) has pursued backcross breeding to introgress blight tolerance from Chinese chestnut into hybrids that have the timber-type form of American chestnut. The underlying assumptions of the backcross program are 1) blight tolerance is controlled by Chinese chestnut alleles that segregate at two to three loci and 2) that progeny that inherited those alleles can be reliably selected in each backcross generation. To test these hypotheses and to perform genomic selection in backcross seed orchards, we genotyped ~1,200 American chestnut BC<sub>3</sub>F<sub>2</sub> trees. We developed genomic selection models for blight tolerance by genotyping age 10 + trees phenotyped for traits indicative of long-term blight tolerance or whose progeny had been evaluated for blight tolerance. In addition, reference panels of Chinese chestnut and American chestnut were genotyped estimate hybrid index for the BC<sub>3</sub>F<sub>2</sub> trees. We found that blight tolerance phenotypes of individual BC<sub>3</sub>F<sub>2</sub> trees and their progeny were weakly heritable ( $h^2 \sim 0.1$  to  $0.3$ ) and that there is a tradeoff between blight tolerance and the proportion of the genome inherited from American chestnut. On average, selected BC<sub>3</sub>F<sub>2</sub> trees inherited 84% of their genome from American chestnut and had blight tolerance that was intermediate between F<sub>1</sub> hybrids and pure American chestnut. Results suggest that blight tolerance is controlled by more loci than previously assumed. TACF is pursuing multiple alternative routes to ensure restoration success. We are advancing additional backcross lines through fewer backcross generations to find a balance between blight tolerance and American chestnut characteristics. In addition, we plan to outcross transgenic blight-tolerant American chestnuts developed by SUNY-ESF to a diverse collection of wild American chestnut trees. Third, we are pursuing genomic research to identify variants that underlie blight tolerance in Chinese chestnut and to enable additional transgenic and gene editing approaches to developing blight-tolerant populations.