

BLIGHT-RESISTANT AMERICAN CHESTNUT TREES: SELECTION OF PROGENY FROM A BREEDING PROGRAM

Shiv Hiremath¹, Kirsten Lehtoma¹ and Fred Hebard²

¹USDA Forest Service, Forestry Sciences Laboratory
359 Main Road, Delaware, OH 43015

²The American Chestnut Foundation, Meadowview Farms,
14005 Glenbrook Ave., Meadowview, VA 24361

ABSTRACT

Introduction of the fungus *Cryphonectria parasitica* into North America in early 1900s resulted in the demise of the American chestnut, which was once the most dominant forest tree in the eastern United States. While the American chestnut (*Castanea dentate*) is susceptible, its counterpart from Asia, the Chinese chestnut, is resistant to the blight-causing fungus. Researchers attempting to restore the American chestnut have focused both on the eradication of the fungus as well as on breeding blight-resistant chestnut trees. Although crosses between the American and the Chinese yield a blight-resistant progeny, often the hybrids have the characteristics of the Chinese tree, which is a dwarf and lacks the superior timber qualities associated with the American chestnut. Therefore, researchers have been using a “back-crossing” technique where the resistant hybrids are successively backcrossed to the original American tree in order to flood more American genes into the hybrid. By repeated back-crosses, it will be possible to generate a blight-resistant chestnut having all the superior traits of the American chestnut.

The American Chestnut Foundation has developed progeny from the third backcross, which by estimation is 15/16 American. However, traditional techniques of determining resistance (by inoculation of the pathogen and assessment) and growth characteristics (waiting to see morphological traits in the mature tree) have proved to be great hindrances to both the pace as well as the degree of success of the program. Progeny selection procedure can be greatly enhanced by utilizing genetic analysis techniques such as PCR and RAPD analyses. Genetic maps of the American and Chinese chestnut trees have been developed and several markers associated with resistance and other traits have been identified. We are using RAPD-PCR analyses to screen progeny for blight resistance and suitable American traits. This method has the capability of precise identification of true resistant types and potentially suitable progeny for use in restoration. Progeny containing none or only a few of the undesirable Chinese traits (0-2) have been selected from the pool and will be used in further analyses. This technique of screening progeny would be a valuable addition to the breeding program and will greatly contribute to the success of the program.