

RESTORING GREEN ASH (*FRAXINUS PENNSYLVANICA*): BREEDING FOR RESISTANCE TO THE EMERALD ASH BORER (*AGRILUS PLANIPENNIS*)

Jennifer L. Koch¹, David W. Carey¹, Mary E. Mason², Therese M. Poland³, Kathleen S. Knight¹, Jeanne Romero-Severson⁴, Charles Tubesing⁵, and Roger Gettig⁵

The invasion of emerald ash borer (EAB) (*Agrilus planipennis*) threatens the survival of green ash (*Fraxinus pennsylvanica*) in the United States, where it is extensively used for soil conservation, rural water management, and in urban green spaces. It is also one of the most common hardwood species in riparian forests of eastern North America. Long term monitoring of permanent plots in EAB infested natural forests identified surviving green ash trees, or “lingering” ash trees, that had maintained healthy canopies for at least 2 years after all other ash trees (>10 cm DBH) had died. EAB egg bioassay experiments confirmed that these trees possess an increased level of resistance due to multiple types of host defense responses, including mortality of early instar larvae, development of larvae having significantly lower weights, and reduced adult feeding preference of foliage. Fifty-five lingering green ash trees have been accessioned and a replicated clone test has been established to assess field performance of 42 of these. We are employing a polycross breeding strategy and to date, 16 full-sibling families resulting from crosses between 8 mother trees and 15 different father trees have been produced. Additional families will be added as select parent trees begin to flower. Bioassay evaluation of seedling progeny from 7 different lingering x lingering families, 2 susceptible x susceptible families, 1 susceptible x lingering family and 1 susceptible open-pollinated family demonstrated variation both within and between families. Between 15 to 40 percent of lingering x lingering progeny had a more effective defensive response to EAB than either parent, a result expected if the two parents employ different mechanisms based on allelic variants at more than one gene. Polycross progeny are being further evaluated in field trials that also include progeny from susceptible x susceptible and susceptible x lingering families as reference populations to allow for analysis of genetic gain.

¹Northern Research Station, USDA Forest Service, Delaware, OH 43015, (jennifer.koch@usda.gov).

²Department of Evolution, Ecology and Organismal Biology, The Ohio State University, Columbus, OH 43210.

³Northern Research Station, USDA Forest Service, East Lansing, MI 48910.

⁴Department of Biological Sciences, University of Notre Dame, Notre Dame, IN 46556.

⁵The Holden Arboretum, Kirtland, OH 44094.