

## UC research tests new tool to guide reintroduction of the American chestnut

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This is Yamini Kashimshetty, with leaves from an American Chestnut, in UC's herbarium. Ranked among the top 10 percent of US herbaria on the basis of size, range and scientific value of its unique collection, the UC herbarium holds more than 70,000 specimens. Credit: Dottie Stover, University of Cincinnati

The death of the American Chestnut due to an Asian bark fungus accidentally introduced to the United States had profound environmental and economic consequences since the tree was highly valued for its strong, workable lumber and a variety of wildlife from deer to birds to bears relied upon the chestnut for food.

Ongoing efforts to reintroduce the American Chestnut are labor

intensive and expensive, in part because they rely on genetic cross breeding to produce a tree that is – genetically speaking – primarily an American Chestnut but endowed with the Chinese Chestnut blight-resistance genes. For instance, one recent blight-resistant strain ready for reintroduction is calculated to be 94 percent American Chestnut and six percent Chinese Chestnut.

Since production of genetically cross-bred American Chestnuts for reintroduction is so laborious, University of Cincinnati graduate and undergraduate biology students recently tested a new software tool called NEWGARDEN in order to see how it might guide preserve managers in creating the most-favorable conditions for reintroduction plantings of American Chestnuts.

The results of that testing, "Founder Placement and Gene Dispersal Affect Population Growth and [Genetic Diversity](#) in Restoration Planting of American Chestnut," will be presented by UC biology doctoral student Yamini Kashimshetty at the March 23-25 Midwest Ecology and Evolution Conference, a conference specifically for undergraduate and graduate student research that will draw representatives from the region.

Several years ago, UC faculty members Steven Rogstad of biological sciences and and Stephan Pelikan of mathematical sciences developed the NEWGARDEN computer program in order to not only track but to predict long-term outcomes for newly founded plant populations in terms of population size and genetic diversity.

## **Predicting best planting practices for American chestnuts**

Using the NEWGARDEN software, UC students Kashimshetty and Melanie Simkins input a variety of founder planting scenarios in order to

determine which would best promote a reintroduction population of American Chestnuts to thrive for the next 101 years.

They began with a theoretical restoration preserve of about 25 square kilometers square (or about 9.7 square miles). Using the software, they varied the original placement of 169 founder American Chestnuts to determine which pattern would theoretically lead to the largest population gains and the greatest genetic diversity among that population for the next 101 years. (An original replanting of 169 [trees](#) was selected for this study because previously published studies determined that figure to be the minimum number required to retain a high level of long-term genetic diversity while keeping reintroduction expenses at a minimum.)

Said Kashimshetty, "Due to the expense of producing the hybridized American Chestnuts, we wanted to test and determine potential best practices for reintroducing them. The tests that we are able to do virtually, such as varying different life history characteristics - including pollen and offspring-dispersal distances or varying the placement geometry of founders, cannot be easily done in the real world since large areas, large numbers of trees and replicate experiments lasting 100 years or more would be needed."

So, she added, "To perform multiple real-world variations on a tree like the American Chestnut would be extremely expensive and labor-intensive."

In testing varying reintroduction scenarios with the NEWGARDEN software, the UC team simulated natural population development and found

- To ensure the greatest population growth rate and genetic

diversity retention among the original founders and offspring trees, an original planting of a stand of 169 founders should be 1,500 meters (about 1,640 yards) into the preserve's borders.

Said Kashimshetty, "If you plant near the edge of a preserve, you risk slower population growth and greater loss of genetic variation due to offspring dispersal out of the preserve."

- By simply planting the founder trees 1,500 meters into the preserve and planting the original founder trees in a grid 16 feet apart from one another, the result in 101 years' time should be about 7,000 trees.
- At least 9,000 resulting trees would be possible in 101 years' time by moderate dispersal (manually moving) of offspring seeds or seedlings to greater distances from the founders than would occur naturally.
- If the original stand of trees is planted at the edge of the preserve, it's estimated that the original stand of 169 trees would result in approximately 2,000 resulting trees in 101 years' time. Thus, by planting the trees further into a preserve at 1,500 meters, with proper spacing, it's estimated that 247 percent more trees will result in 101 years' time.
- Even planting the founder trees only 500 meters (1,640 feet) into the preserve vs. planting founders on the preserve's edge would increase the population size by 148 percent in 101 years' time.
- Further, by planting the original founder trees just 500 meters into the preserve, 97 percent of their genetic diversity is preserved. Thus, if the goal is only to preserve genetic diversity without regard for achieving maximum population size, it's sufficient to plant the original stand 500 meters (1,640 feet) into the preserve.

Through such comparative computer modeling, the goal is to provide improved guidelines for the spacing and geometric patterning of founding trees in restoration plantings of American Chestnut, leading to

a more successful return of this threatened but important native to the eastern forests of North America.

Provided by University of Cincinnati

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