The Emerging Chromosomes of the American and Chinese Chestnuts

by

For 30 years now, scientists have worked to lend the natural blight-resistance of Chinese chestnut trees to the American chestnut.

With the advent of molecular biology, the possibility of transferring specific genes that may confer blight resistance is a tantalizing promise, but as Nurul Faridi, a U.S. Forest Service research geneticist explains, “There is a lingering knowledge void, and until recently, we haven’t even known about the general, much less specific, characteristics of the American chestnut chromosomes.”

Faridi and his colleagues at the Southern Research Station Forest Genetics and Ecosystems Biology unit have been working with Penn State University, Clemson University, and The American Chestnut Foundation to map and characterize the American chestnut genome. Ultimately, they plan to integrate the entire DNA sequence of both American and Chinese chestnut to a physical map of their chromosomes.

American chestnut's genome is hard to study. At 780 million base pairs of DNA, it is actually quite small for a forest tree. Pine trees, for example, have 20 to 30 billion base pairs, about 25 times more than chestnut. “Given that the chestnut genome is relatively small, it would seem to be easier to study, but it has consistently proved difficult until Faridi’s lab refined the necessary cytogenetic techniques,” remarked Dana Nelson, project leader of the research unit.

Faridi and his colleagues used fluorescent probes that bind to specific DNA sequences, and identified all twelve American chestnut chromosomes. Knowing how the genome is organized into chromosomes is a crucial step towards developing blight-resistance, and Faridi and his team also identified the exact chromosomal location of important genes and groups of genes.

Genes that are close to each other in the chromosome are often inherited together, as a group. These genes are said to be linked, and understanding genetic linkage is important for predicting how genes and traits they endow, such as blight resistance, will be passed along through generations. “We’ve assigned all twelve linkage groups to their individual chromosomes,” says Faridi. “As far as we know, this is the first time linkage groups of a tree species have been assigned.”

Faridi and his colleagues have also identified the physical locations of important protein-synthesis genes, and they have characterized the structural organization of the chromosome associated with linkage group B. The rest of the chromosomes are being characterized in the same way in Faridi’s lab at College Station, TX.
“In the future, we aim to combine the genetic sequences of both American and Chinese chestnut with the physical arrangement of their chromosomes and linked genes,” says Faridi. “This information will accelerate breeding efforts and ultimately help to return the American chestnut tree to our forests.”

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