THE
AMERICAN
CHESTNUT
FOUNDATION®

Postdoctoral Fellow in evolutionary genomics of blight resistance in *Castanea*
The Holliday lab at Virginia Tech in collaboration with the American Chestnut Foundation is recruiting a postdoc for two years to study the evolutionary genomics of chestnut blight resistance in *Castanea.* At the turn of the 20th century, blight killed approximately four billion American chestnuts (*Castanea dentata*) in the forests of the Eastern United States. Asian *Castanea* species are resistant to chestnut blight whereas the North American and European species are susceptible. Our aim is to develop a basic understanding of the genetic networks underlying blight resistance to enable gene editing to enhance the blight resistance of American chestnut. Specifically, we seek a postdoctoral fellow to take the lead on the following analyses:

- Estimate phylogenies and divergence times among host (*Castanea* spp.) and pathogen (*Cryphonectria* spp.) to test alternative hypotheses about the evolution of blight resistance.
- From whole genome resequence data, detect signatures of positive or balancing selection in blight resistant Asian *Castanea* species that are absent or reduced in susceptible European and North American congeners.
- Use RNA-seq timecourse data to compare gene expression in the stems of Chinese chestnut, American chestnut, and F_1 hybrids of these species. Detect which genes are differentially expressed and determine whether these expression differences are regulated in *cis* or *trans*.
- Compare the annotated chromosome scale reference genomes of American chestnut and Chinese chestnut to detect presence/absence variants, copy number variants, non-synonymous and potentially deleterious alleles in genes and pathways hypothesized to be important for blight resistance.
- Use machine learning approaches to integrate data sources and discover candidate genes involved in resistance. Specifically, integrate QTL mapping of resistance in hybrid populations, differential gene expression analyses, signatures of natural selection, and comparative genomic evidence.

Desired Qualifications
- Ph.D. in population genomics, computational biology, or a related field.
- Experience or desire to learn variant calling, phylogenomics, population genomics, differential gene expression analyses, and machine learning.
- Expertise in R, Python, and Linux scripting and implementation on high performance computing clusters.

Duration: 2 years, Location: Blacksburg, VA, Salary: $55,000 – $57,000 + benefits,
Potential start dates: July 2021 – November 2021
To apply email Jason Holliday (jah1@vt.edu) and Jared Westbrook (jared.westbrook@acf.org) with a cover letter and CV.

50 North Merrimon Avenue, Suite 115 • Asheville, NC 28804 • 828-281-0047 • www.acf.org • chestnut@acf.org