

a. Project Title

Population genomics of diversity, adaptation, and gene flow in American chestnut

b. Summary

Across eastern North America, genetically diverse populations of American chestnut have adapted to environmental conditions that differ markedly from north to south and from high to low elevations. Common garden studies have investigated adaptations of American chestnut growing in the coldest parts of the species' range. However, we are aware of no published information on adaptation of American chestnut to environments in the southernmost part of its range. We propose a population genomics study to elucidate the adaptive significance of gene flow from chinquapin to American chestnut in the southeastern U.S.

c. Principal Investigator(s)

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Term Research Assistant

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d. Duration of Project

August 2021 – July 2022

e. Total Amount Requested

\$10,000

f. Short and Long Term Goals

Short Term Goals

- Identify southern American chestnut with alleles that were naturally introgressed from chinquapin.
- Use machine learning analyses of herbarium specimens to quantify variation in American chestnut leaf morphology across its range.
- Use population genetic statistics to determine whether alleles introgressed from chinquapin into American chestnut have been under positive selection.
- Test for a statistical relationship between leaf morphology variation and introgression from chinquapin in American chestnut populations.

Long Term Goals

- Share coordinates of introgressed American chestnut with TACF science staff for future scionwood collection and breeding.
- Share data and results with Virginia Tech and TACF collaborators that can facilitate the identification of genes of adaptive significance for restoration breeding.

g. Narrative

Introduction

An understanding of locally adaptive genetic variation can prove critical to the success of species conservation and restoration efforts. In reforestation projects, for example, locally sourced trees often exhibit greater survival, health, and productivity than trees from distant sources due to local adaptation to climate (Flanagan et al. 2017). If local adaptation exists but is not taken into consideration, restoration plantings may not thrive under local environmental conditions. For example, some restoration plantings in the Great Basin have used seed sources that were not locally adapted to planting sites, despite being native species, which has caused poor establishment of plantings founded from distant seed sources (Flanagan et al. 2017).

Hybridization and introgression between species (or lower taxa) can provide a means for adaptive genetic variation to move rapidly from one species to another, thus allowing recipients of this genetic variation to thrive in new habitats or changing environments. Such cases of adaptive introgression have been documented in organisms ranging from humans, Neanderthals, and Denisovans (Huerta-Sanchez et al. 2014; Yair et al. 2021), to killifish species (Oziolor et al. 2019), to corn and highland teosinte (Calfee et al. 2021). The cases of introgression from highland teosinte into corn are particularly interesting. Alleles introgressed from highland teosinte into high elevation corn populations were shown to co-localize with quantitative trait loci (QTL) and genes associated with or controlling early flowering, macrohairs on leaves and stems, and anthocyanin-based pigmentation – all traits which have been shown experimentally to confer adaptive advantages at high elevations (Calfee et al. 2021).

Multiple population genetic and phylogenetic studies of American chestnut over the past decade have found evidence that American chestnut has hybridized with its sister species, North American chinquapin (Kubisiak and Roberds 2003; Shaw et al. 2012; Li and Dane 2013; Perkins et al. 2021; A. Sandercock, Virginia Tech, pers. comm., Aug. 2021). Claims from the older of these studies, which relied largely on chloroplast DNA data, are less compelling than when first published, because so-called “chinquapin chloroplast haplotypes” documented in American chestnut chloroplasts may also be an artefact of incomplete lineage sorting. Recent work, using nuclear genome-wide data, has provided resolution not possible in earlier studies. In a STRUCTURE analysis (Pritchard et al. 2000) of genome-wide single-nucleotide polymorphism (SNP) data, Perkins et al. (2021) identified chinquapins in northern Florida that contained up to 15% American chestnut ancestry. Most recently, our collaborators at Virginia Tech and The American Chestnut Foundation have performed ADMIXTURE analyses (Alexander et al. 2009) on the *Castanea* species reference panel, which contains whole genome resequencing data for each of the 7-10 *Castanea* species worldwide, including American chestnuts and chinquapins we (M.T. Perkins and J.H. Craddock) have sampled from the southeastern United States. Preliminary ADMIXTURE analysis showed that: some Ozark chinquapin samples have ~10-13% ancestry from American chestnut; some *Castanea alabamensis* samples have up to 7% ancestry from American chestnut; and two American chestnuts we sampled from areas sympatric with *C. alabamensis* may have a small amount of *C. alabamensis* ancestry (A. Sandercock,

Virginia Tech, pers. comm., Aug. 2021). In the work by Perkins et al. (2021) and work for the *Castanea* reference panel, the number of sequenced plants from these populations of sympatric American chestnut and *C. alabamensis* was low, however. Expanding the number of sequenced plants from these sympatric populations will allow us thoroughly characterize admixture between American chestnut and chinquapins.

The cases of admixture between American chestnut and chinquapin have all been documented in or near the southern part of American chestnut's distribution, where the species often co-occurs with chinquapin. Curiously, we have observed that American chestnuts growing in Alabama and middle Tennessee tend to have more shallow leaf serrations and broader leaves than American chestnuts at higher latitudes and elevations, both traits that cause American chestnut leaves to appear similar to chinquapin in these areas. These anecdotal observations await statistical verification. The degree of leaf serration and total leaf area has been shown to respond to climate in other species, particularly in red maple, where common garden studies have shown that variation in these leaf traits between northern and southern populations was explained largely by genetic variation (69-87% of total variance) and to a lesser extent by phenotypic plasticity (6-19% of total variance) (Royer et al. 2009). Royer et al. (2009) and others have hypothesized that leaf teeth are an adaptation to colder climates. The above observations and results prompt the following questions: Is leaf variation in southern populations of American chestnuts the result of introgression from chinquapin? Is variation in American chestnut leaf shape across the range due to local adaptive differences?

Research Questions

Taken into consideration with known instances of adaptive introgression in other species, the findings of admixture between American chestnut and chinquapin listed above provide impetus to investigate the roles of hybridization and adaptation in shaping American chestnut population structure, particularly as it relates to restoring the species throughout the entirety of its former range. Towards this goal, we have been sampling wild American chestnut and chinquapin from South Carolina, Tennessee, Georgia, Alabama, Arkansas, and Missouri since 2015. We have shared the DNA extracts and leaf samples with our Virginia Tech and TACF collaborators. We ask the following questions:

1. What is the frequency of admixture with chinquapin in populations of American chestnut growing in the southeastern United States?
2. Do introgressed alleles confer an adaptive advantage to American chestnut in southern populations?
3. Does introgression from chinquapin explain a portion of the morphological variation we observe in American chestnut in the south?

Methods

Using our existing funds at the University of Tennessee at Chattanooga, we will coordinate with collaborators at Virginia Tech to perform whole genome resequencing of approximately 100 American chestnut and chinquapin samples. Our focus will be on expanding the number of sequenced plants in populations where American chestnut occurs in sympatry with *C. alabamensis* and Allegheny chinquapin. These leaf samples and DNA extracts have been collected over the past few years and were mailed to Virginia Tech in 2019, 2020, and early 2021. Sequencing is planned for this fall, with data expected to arrive later in the year. Collaborators at Virginia Tech will use the same sequencing library protocol for our samples that

they have used for the *Castanea* reference panel. We will combine our data with whole genome data already produced for the *Castanea* reference panel by Virginia Tech and TACF; this existing dataset includes American chestnut sampled across its range.

We will use bwa mem software (Li 2013) to align sequencing data from our samples to v1.1 of the American chestnut reference genome (https://phytozome-next.jgi.doe.gov/info/Cdentata_v1_1). We will use GATK software (McKenna et al. 2010) to identify genomic locations where single nucleotide differences exist between the reference genome and samples (i.e., SNPs) and will extract sequence pileup using samtools software (Li et al. 2009). We will use SNP datasets and sequence pileup data for population genetic analyses. We will infer a phylogenetic tree and perform population structure analyses to determine the evolutionary relationships between samples, which will be necessary steps for subsequent analyses. Using phylogenetic relationships determined in the previous step, we will perform ABBA-BABA tests for gene flow (Patterson et al. 2012) between American chestnut and chinquapin. We will then estimate ancestry tracts across chromosomes (i.e., local ancestry) using a hidden Markov model (Corbett-Detig and Nielsen 2017). Local ancestry estimates will allow us to determine if alleles from chinquapin are found in the same genomic locations in multiple American chestnut populations. This scenario would be consistent with natural selection favoring chinquapin ancestry in key regions of American chestnut's genome, which would support the hypothesis of adaptive introgression. We will also calculate Tajima's *D* genome-wide (Korneliussen et al. 2013) to measure patterns of natural selection across the genome. Highly negative values of Tajima's *D* correspond to an excess of low-frequency polymorphism, which would be expected if chinquapin alleles were under strong positive selection in admixed American chestnut.

Since 2006, samples we have collected for DNA extraction at UTC have been accompanied by herbarium vouchers, which are used to validate species identity in cases of unexpected results. These herbarium vouchers are being scanned this fall to obtain high resolution images, which are uploaded to the SERNEC database (<https://www.serneportal.org/portal/>), a repository of herbarium specimen images open to the public. We will use the machine learning methods in the software LeafMachine (Weaver et al. 2020) to extract data on leaf area and leaf serration in plants used in the population genetic analyses. We will test for morphological differences between northern and southern American chestnut populations. We will also test for a relationship between chinquapin ancestry in American chestnut and variation in leaf traits.

Outcomes and Impact

The proposed work is designed to address gaps in knowledge regarding American chestnut population structure and adaptation to the diverse environments in which the species grows. Compelling results have been presented on American chestnut's adaptation to environments in the coldest parts of its range (e.g., Gurney et al. 2011; Saielli et al. 2014). However, there are no published studies on adaptation of American chestnut to conditions in the southernmost part of its range. Studies by Gurney et al. (2011) and Saielli et al. (2014) used the common garden method. Our study will differ from the studies in Vermont by our use of population genomics, but our work may provide a starting point for common garden studies using southern germplasm that has been characterized at the genomic level. Evidence of adaptive introgression will guide germplasm conservation efforts by identifying American chestnut with alleles "pre-adapted" for the southern U.S. that can be targeted for scionwood collection and

eventual breeding. These trees may prove to be particularly valuable as climate across American chestnut's range becomes warmer (Zolkos et al. 2015). Although a genome-wide association study (GWAS) of correlations between leaf traits and genetic variation is beyond the scope of our 11-month timeline, we will share all results, data, and code with collaborators at Virginia Tech and TACF throughout the course of the project. Collaborators can leverage knowledge of high introgression loci in American chestnut with GWAS and landscape genomic studies already underway to refine the search for genes involved in adaptation of American chestnut to environments in the southeastern U.S. Beyond the impacts listed above, this work benefits the science objectives of TACF in that 100% of the funds requested will be used towards salary to conduct analyses on data already generated with TACF funds or to be generated with UTC funds. TACF grant funds we request will allow us to further our knowledge of germplasm that has already been identified by TACF as a high research priority.

References

- Calfee, E., D. Gates, A. Lorant, M.T. Perkins, G. Coop, and J. Ross-Ibarra. Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. Submitted to *PLoS Genetics*. Preprint available at *bioRxiv*, doi: 10.1101/2021.03.05.434040
- Corbett-Detig, R., and R. Nielsen. 2017. A hidden Markov model approach for simultaneously estimating local ancestry and admixture time using next generation sequence data in samples of arbitrary ploidy. *PLoS Genetics* 13(1):e1006529
- Flanagan, S.P., B.R. Forester, E.K. Latch, S.N. Aitken, and S. Hoban. 2018. Guidelines for planning genomic assessment and monitoring of locally adaptive variation to inform species conservation. *Evolutionary Applications* 11(7):1035-1052.
- Gurney, K.M., P.G. Schaberg, G.J. Hawley, and J.B. Shane. 2011. Inadequate cold tolerance as a possible limitation to American chestnut restoration in the northeastern United States. *Restoration Ecology* 19(1):55-63.
- Huerta-Sánchez, E., X. Jin, Z. Bianba, B.M. Peter, N. Vinckenbosch, Y. Liang, X. Yi., M. He, M. Somel, P. Ni, and B. Wang. 2014. Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. *Nature* 512(7513):194-197.
- Korneliussen, T.S., I. Moltke, A. Albrechtsen, and R. Nielsen. 2013. Calculation of Tajima's *D* and other neutrality test statistics from low depth next-generation sequencing data. *BMC Bioinformatics* 14(1):1-14.
- Kubisiak, T.L., and R.H. Roberds. 2003. Genetic variation in natural populations of American Chestnut. *Journal of the American Chestnut Foundation* 16: 43-48.
- Li, H. 2013. Aligning sequence reads, clone sequences and assembly contigs with bwa-mem. arXiv [q-bio], May 2013. arXiv: 1303.3997.
- Li, X., and F. Dane. 2013. Comparative chloroplast and nuclear DNA analysis of *Castanea* species in the southern region of the USA. *Tree Genetics & Genomes* 9: 107-116.
- McKenna A., M. Hanna, E. Banks, A. Sivachenko, K. Cibulskis, A. Kernysky, K. Garimella, D. Altshuler, S. Gabriel, M. Daly, and M.A DePristo. 2010. The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. *Genome Research* 20:1297-303.
- Oziolor, E.M., N.M. Reid, S. Yair, K.M. Lee, S.G. VerPloeg, P.C. Bruns, J.R. Shaw, A. Whitehead, and C.W. Matson. 2019. Adaptive introgression enables evolutionary rescue from extreme environmental pollution. *Science* 364(6439):455-457.
- Patterson, N., P. Moorjani, Y. Luo, S. Mallick, N. Rohland, Y. Zhan, T. Genschoreck, T. Webster and D. Reich. 2012. Ancient admixture in human history. *Genetics* 192(3):1065-1093.
- Perkins, M.T., T. Zhebentyayeva, P.H. Sisco, and J.H. Craddock. 2021. Genome-wide sequence-based genotyping supports a nonhybrid origin of *Castanea alabamensis*. *Systematic Botany* 46(3): in press. Preprint available at *bioRxiv*, doi: 10.1101/680371

- Pritchard, J.K., M. Stephens, P. Donnelly. 2000. Inference of population structure using multilocus genotype data. *Genetics* 155: 945-959.
- Royer, D.L., L.A. Meyerson, K.M. Robertson, and J.M. Adams. 2009. Phenotypic plasticity of leaf shape along a temperature gradient in *Acer rubrum*. *PLoS One* 4 (10), e7653.
- Saielli, T.M., P.G. Schaberg, G.J. Hawley, J.M. Halman, and K.M. Gurney. 2014. Genetics and silvicultural treatments influence the growth and shoot winter injury of American chestnut in Vermont. *Forest Science* 60(6):1068-1076.
- Shaw, J., J.H. Craddock, and M.A. Binkley. 2012. Phylogeny and phylogeography of North American *Castanea* Mill. (Fagaceae) using cpDNA suggests gene sharing in the Southern Appalachians (*Castanea* Mill., Fagaceae). *Castanea* 77: 186-211.
- Weaver, W.N., J. Ng, R.G. and Laport. 2020. LeafMachine: Using machine learning to automate leaf trait extraction from digitized herbarium specimens. *Applications in Plant Sciences*, 8(6), p.e11367.
- Yair, S., K.M. Lee, and G. Coop. 2021. The timing of human adaptation from Neanderthal introgression. *Genetics* 218(1), iyab052.
- Zolkos, S.G., P. Jantz, T. Cormier, L.R. Iverson, D.W. McKenney, and S.J. Goetz. 2015. Projected tree species redistribution under climate change: implications for ecosystem vulnerability across protected areas in the eastern United States. *Ecosystems* 18:202-220.

h. Timeline

| | | |
|-------------------|--|--|
| UTC Funds | Aug. 2021 – Oct. 2021 | Prepare voucher specimens and upload images to SERNEC database; Generate whole genome resequencing data for ~100 American chestnut and chinquapin samples to add to <i>Castanea</i> reference panel |
| | Oct. 2021 – Dec. 2021 | If not completed, finish voucher specimen scanning; Align sample sequences against American chestnut reference genome and generate SNP and sequence pileup data |
| TACF Funds | Jan. 2022 – Mar. 2022 | Analyze phylogenetic relationships and population structure of American chestnut and chinquapin samples; Perform ABBA-BABA tests for gene flow. Train machine learning model to extract leaf traits and begin trait measurements |
| | Mar. 2022 – May 2022 | Estimate local (chromosome-scale) ancestry in admixed samples. Calculate Tajima's <i>D</i> . Test for relationship between admixture and leaf trait variation |
| | May 2022 – June 2022 | Prepare first drafts of articles for <i>Chestnut</i> magazine and a peer-reviewed journal |
| | July 25, 2022 (30 days after funding period conclusion) | Submit final financial report and final narrative report to TACF. |

i. How Results Will be Measured and Reported

As results are produced, we will share data, results, and code with our collaborators at Virginia Tech (A. Sandercock, J. Holliday) and the American Chestnut Foundation (J. Westbrook, P.H. Sisco). To facilitate such discourse, one of us (Hill Craddock) initiated the “Chinquapin Working Group” earlier this year. By July 25, 2022, one month after the conclusion of the funding period, we will submit a final financial report and a final narrative report for publication in *Chestnut* magazine. We will work to prepare a first draft of a full-length paper by June 25, 2022, which will be written for eventual submission to a refereed journal. We will share this first draft and later versions of the full-length paper as they are completed with TACF.

j. Breakdown of How and When Funds Will Be Spent

| Expense | TACF Amount Requested |
|--|------------------------------|
| Salary for Taylor Perkins (20 hrs/wk × \$20/hr × 25 weeks (10 Jan. 2022 – 25 June 2022)) | \$10,000 |
| <i>Total</i> | \$10,000 |

k. Curriculum Vitae

Matthew Taylor Perkins

Phone: 423-314-4063

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[Google Scholar profile](#)

Education

| | |
|--|-----------|
| M.S. Environmental Science | 2014-2016 |
| University of Tennessee at Chattanooga | |
| B.S. Biology , University Honors, Honors in Biology, <i>cum laude</i> | 2007-2012 |
| University of Tennessee at Chattanooga | |

Relevant Work History

| | |
|--|---------------------|
| Adjunct Instructor, Biology, Geology & Environmental Science, University of Tennessee at Chattanooga | Aug. 2021-present |
| Instructor for Principles of Biology I laboratory | |
| Term Research Assistant, University of Tennessee at Chattanooga | June 2021-present |
| Perform botanical and genomics research on North American <i>Castanea</i> species, supervised by Dr. Hill Craddock | |
| Graduate Research Assistant, University of Florida | Aug. 2020-Dec. 2020 |
| Perform simulations of genomic prediction breeding program designs using R and computing clusters; laboratory rotation supervised by Dr. Marcio Resende | |
| Laboratory Manager, University of California, Davis | Apr. 2019-Aug. 2020 |
| Perform population genomic analyses and prepare RNAseq and whole-genome sequencing libraries as part of research on local adaptation in maize; supervised by Dr. Jeffrey Ross-Ibarra | |
| Adjunct Instructor, University of Tennessee at Chattanooga | Aug. 2017-Dec. 2017 |
| Instructor for Principles of Biology I lecture | |
| Laboratory Technician, Tennessee Aquarium Conservation Institute | 2017-2019 |
| Conservation genetics of the Cumberland Darter; supervised by Drs. Anna George and Bernard Kuhajda | |
| Graduate Research Assistant, University of Tennessee at Chattanooga | 2014-2016 |
| Phylogenetics of the North American chestnut species; supervised by Dr. Hill Craddock | |
| Visiting Scholar, Clemson University Genomics Institute | Jan. 2015-June 2015 |
| Quantitative genetics of resistance to Phytophthora root rot in chestnut; supervised by Drs. Tatyana Zhebentyayeva (Clemson U.) and Paul H. Sisco (American Chestnut Foundation) | |
| Undergraduate Honors Researcher, University of Tennessee at Chattanooga | 2011-2012 |
| Horticultural study of mycorrhizal assemblages of chestnut roots; supervised by Drs. Hill Craddock, Jennifer Boyd, and Joey Shaw | |

Publications (*undergraduate co-author)

Preprints (in review)

- Calfee, E., D. Gates, A. Lorant, **M.T. Perkins**, G. Coop, and J. Ross-Ibarra. Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. Submitted to *PLOS Genetics*. Preprint available at *bioRxiv*, doi: 10.1101/2021.03.05.434040

In press or in print (refereed)

1. **Perkins, M.T.**, T. Zhebentyayeva, P.H. Sisco, and J.H. Craddock. Genome-wide sequence-based genotyping supports a nonhybrid origin of *Castanea alabamensis*. *Systematic Botany* 46(3): in press. Preprint available at *bioRxiv*, doi: 10.1101/680371

2. Lozano, R, E. Gazave, J. P.R. Dos Santos, M.G. Stetter, R. Valluru, N. Bandillo, S.B. Fernandes, P.J. Brown, N. Shakoor, T.C. Mockler, E.A. Cooper, **M.T. Perkins**, E.S. Buckler, J. Ross-Ibarra, and M.A. Gore. 2021. Comparative evolutionary genetics of deleterious load in sorghum and maize. *Nature Plants* 7(1):17-24.
3. Craddock, J.H., **M.T Perkins**. 2019. Chestnut (*Castanea* spp. Miller) breeding. Book chapter in *Advances in Plant Breeding Strategies: Nut and Beverage Crops Vol. 4*. (J.M. Al-Khayri, S. Mohan Jain, D.V. Johnson, eds.), pp. 105–156. Springer Nature Switzerland AG, Basel. DOI: 10.1007/978-3-030-23112-5_5
4. Zhebentyayeva, T., P.H. Sisco, L.L. Georgi, S.N. Jeffers, **M.T. Perkins**, J.B. James, F.V. Hebard, C. Sasaki, C.D. Nelson, and A.G. Abbott. 2019. Dissecting resistance to *Phytophthora cinnamomi* in interspecific hybrid chestnut crosses using sequence-based genotyping and QTL mapping. *Phytopathology* 109(9):1594–1604
5. **Perkins, M.T.**, A.C. Robinson*, M. Cipollini, and J.H. Craddock. 2019. Identifying host resistance to *Phytophthora cinnamomi* in hybrid progeny of *Castanea dentata* and *Castanea mollissima*. *HortScience* 54(2):221–225

Articles for a General Audience

- **Perkins, M.T.**, T. Zhebentyayeva, P.H. Sisco, and J.H. Craddock. 2021. *Castanea alabamensis*: rediscovery of a lost American chestnut relative. *Chestnut: The Journal of the American Chestnut Foundation* (in press)
- Sisco, P., **M.T. Perkins**. 2020. Male-sterile F₁ trees as long-term controls in seed orchards. *Chestnut: The Journal of the American Chestnut Foundation* 34(2):23–25
- Hein, K.M.*, **M.T. Perkins**, J.W. Westbrook, and J.H. Craddock. 2019. Early screening to detect resistance to *Phytophthora cinnamomi* in backcross Chinese-American chestnut hybrids. *Chestnut: The Journal of the American Chestnut Foundation* 33(1):27–30

Awards and Distinctions

Janie Leonard Bryan Award “for outstanding botanical research” Cullowhee Native Plant Conference, 2018
 Graduate Student Research Award, UTC Chapter of Sigma Xi, 2016
 Outstanding Graduate Student award, UTC Dept. of Biol. and Environ. Sci., 2016
 Earl Core Student Research Award, Southern Appalachian Botanical Society, 2016
 Graduated with University Honors, 2012
 Graduated with Departmental Honors in Biology, 2012
 UTC Chancellor’s Scholarship, 2007-2012
 UTC Brock Scholarship (Honors Program scholarship), 2007-2012

Funding

Research grants

- Support from the Environmental Science Graduate Student Award (\$500), Apr. 2016
- Southern Appalachian Botanical Society’s Earl Core Student Research Award (\$500), Mar. 2016
- Arkansas Natural Heritage Commission grant (\$4600) for phylogenetic study of the North American *Castanea* (with Dr. Joey Shaw), Jan. 2016
- American Chestnut Foundation external grants program award (\$5000) to fund research on *Phytophthora* resistance in chestnut (with Dr. Hill Craddock), Oct. 2015
- Provost Student Research Award to partially fund research on genetics of *Phytophthora* resistance in chestnut (\$1000), Mar. 2015

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August 2021

EDUCATION

UNIVERSITA' DI TORINO

Dottorato di Ricerca in Colture Arboree, 1992

Thesis title: Investigations in *Corylus avellana* L. and *Castanea* spp. on: rooting of cuttings using ectomycorrhizal fungi, pollination and germplasm of chestnut.

OREGON STATE UNIVERSITY

Master of Science in Horticulture, 1987

Thesis title: Cryopreservation of pollen.

INDIANA UNIVERSITY

Bachelor of Arts in Fine Arts and Biology, 1983

Areas of concentration: Printmaking (etching and lithography) and Botany.

EXPERIENCE

UTC DEPT. BIOLOGY, GEOLOGY, AND ENVIRONMENTAL SCIENCE

Robert M. Davenport Professor in Biology, July 2008 to Present.

Robert M. Davenport Associate Professor in Biology, August 2002 to July 2008.

Robert M. Davenport Assistant Professor in Biology, January 1999 to July 2002.

Assistant Professor, August 1996 to December 1998.

RECENT EXTERNAL GRANTS

The American Chestnut Foundation (2019) with Trent Deason and Erin Taylor, \$5,230

The American Chestnut Foundation (2016) with Taylor Perkins, \$5,000

The Chestnut Project at Dollywood (2000-2015, continuing support, \$15,000/year)

The American Chestnut Foundation (2008) with Bethany Baxter, \$13,000

The American Chestnut Foundation (2006) with Joey Shaw, \$6,000

Bettie J Smith Family Limited Partnership (2002-2015, continuing support, \$6000/year)

RECENT PUBLICATIONS

REFEREED JOURNALS

Perkins, M.T., Zhebentyayeva, T., Sisco, P.H., and Craddock, J.H. (2021) Genome-wide sequence-based genotyping supports a nonhybrid origin of *Castanea alabamensis*. *Systematic Botany* 46(3) in press. Preprint available at: bioRxiv 680371;
<https://doi.org/10.1101/680371>

Perkins, M.T., Robinson, A.C., Cipollini, M, and Craddock, J.H. (2019) Identifying host resistance to *Phytophthora cinnamomi* in hybrid progeny of *Castanea dentata* and *Castanea mollissima*. *HortScience* 54(2): 221-225. <https://doi.org/10.21273/HORTSCI13657-18>

Georgi, L., Craddock, J.H., Bevins, D., Kling, R., and Hebard, F. (2014) Grafting chestnuts. *J. Amer. Chestnut Foundation* 28(1): 20-23.

Sisco, P.H., Neel, T.C., Hebard, F.V., Craddock, J.H., and J Shaw, J. (2014) Cytoplasmic male sterility in interspecific hybrids between American and Asian *Castanea* species is correlated with the American D chloroplast haplotype. *Acta Hort.* 109:215-222.
<https://doi.org/10.17660/ActaHortic.2014.1019.32>

Shaw, J. Craddock, J.H. and Binkley, M.A. (2012) Phylogeny and phylogeography of North American *Castanea* Mill. (Fagaceae) using cpDNA suggests gene sharing in the Southern Appalachians. *Castanea* 77(2):186-211. <https://www.jstor.org/stable/pdf/23274390.pdf>

BOOK CHAPTERS

Craddock, J.H. and Perkins, M.T. (2019) Chestnut *Castanea* spp. Miller) Breeding. Chapter 5 in: Al-Khayri, J.M., Jain, S.M., and Johnson, D.V. (Eds.). *Advances in Plant Breeding Strategies: Nut and Beverage Crops*. Volume 4. Springer. ISBN 978-3-030-23111-8

Craddock, J.H. (2009) USA. Pages 168-174 in: Avanzato, D. (ed.) *Following Chestnut Footprints (Castanea spp.) - Cultivation and Culture, Folklore and History, Tradition and Uses :: Sulle Orme del Castagno - Coltura e Cultura, Folclore e Storia, Tradizioni e Usi*. Scripta Horticulturae (ISHS) Number 9. 175 pp. ISBN 978-90-6605-632-9

Craddock, J.H. (2007) Chestnut Relatives. In: Bolgiano, C. (ed) *Mighty Giants: An American Chestnut Anthology*. Images from the Past, and The American Chestnut Foundation. 296 pp. ISBN 978-1884592485

CONFERENCE PROCEEDINGS, PUBLISHED ABSTRACTS, ETC.

Perkins, M.T., J. Harris, J. Shaw, and J.H. Craddock. (2018). Chloroplast DNA phylogenetics of the North American *Castanea*. Meeting of the Association of Southeastern Biologists. March 29-April 1 2017. Montgomery, Alabama. Abstract in: *Southeastern Biology*. In press.

Perkins, M.T., J. Shaw, and J.H. Craddock. (2016). Phylogeographic examination of *Castanea* Mill. (Fagaceae) morphotypes in the eastern United States. Meeting of the Association of Southeastern Biologists. March 31-April 3 2016. Concord, NC. Abstract in: *Southeastern Biology* 63(2): 163.

Hein, K., Perkins, M.T. and Craddock, J.H.. (2017) Implementing early screening methods to detect resistance to *Phytophthora cinnamomi* in first-backcross Chinese-American chestnut hybrids. Technical Report to USDA NE-1333: Biological improvement of chestnut through technologies that address management of the species, its pathogens and pests. September 2017, Maggie Valley, NC.

Craddock, J.H. (2014). The return of the chestnut -- a tree crop archetype | Hill Craddock | TEDxUTChattanooga. The YouTube version has been viewed more than 21,500 times: https://www.youtube.com/watch?v=bz_NgKnVKxE

Harris, A., Shaw, J. and Craddock, J.H. (2012). A Flora of Bendabout Farm, Bradley County, Tennessee and Survey of Native *Castanea dentata* (Marsh) Borkh. (Fagaceae, American Chestnut). Poster. 2012 American Chestnut Summit. The American Chestnut Foundation and the USDA Forest Service. Asheville, NC. 19-21 October 2012.

Lyon, A., Boyd, J and Craddock, J.H. (2012) Investigating the shade tolerance of *Castanea dentata*, *C. mollissima*, and their hybrids. Poster. Posters at the Capitol, Legislative Plaza, Nashville, TN.

Perkins, T. and Craddock, J.H. (2012). The effect of mono- and di-potassium salts of phosphorous acid on mycorrhiza formation in *Castanea dentata*. Poster. American Chestnut Summit. The American Chestnut Foundation and the USDA Forest Service. Asheville, NC. 19-21 October 2012. <http://www.acf.org/pdfs/summit/Proceedings.pdf>

HONORS

Dr. John R. Freeman Memorial Award for Excellence in Teaching, April 2008

UTNAA 2002 Outstanding Teacher of the Year

UTC Student Government Association 2000 Outstanding Teacher of the Year

I. Conflict of Interest or Commitment Statement

Hill Craddock is on the TACF Board of Directors, and has served, in the past, on the External Grants Committee. He will recuse himself from the review panel for the current round of proposals.