15 August 2015

Matthew Taylor Perkins
Department of Biology, Geology, and Environmental Science
University of Tennessee at Chattanooga
317G Holt Hall, 615 McCallie Ave.
Chattanooga, TN 37403

Dear Ms. Fitzsimmons,

Please find attached the proposal "Identifying novel sources of resistance to *Phytophthora* root rot and assessment of a quantitative trait locus for resistance in interspecific *Castanea* hybrids" by M. Taylor Perkins and Dr. J. Hill Craddock of the University of Tennessee at Chattanooga, in collaboration with Dr. Tetyana Zhebentyayeva of Clemson University.

We are requesting $7605.50 for genetic analysis of fifteen families derived from new potential sources of *Phytophthora* resistance. Analysis of a previously identified quantitative trait locus for *Phytophthora* resistance in these families will benefit the American Chestnut Foundation by fostering a better understanding of the genetic determinants of *Phytophthora* resistance in *Castanea*, and we anticipate the results of this study to have direct application in selection of highly *Phytophthora*-resistant progeny throughout the American Chestnut Foundation's southern chapters.

We believe collaboration between the American Chestnut Foundation, scientists at Clemson University, and scientists at the University of Tennessee at Chattanooga will accelerate the incorporation of *Phytophthora* resistance breeding into the American chestnut restoration effort.

Sincerely,

M. Taylor Perkins
Department of Biology, Geology, and Environmental Science
University of Tennessee at Chattanooga

a. Project title: Identifying novel sources of resistance to *Phytophthora* root rot and assessment of a quantitative trait locus for resistance in interspecific *Castanea* hybrids

b. Summary: Root rot, incited by *Phytophthora* spp., is one of the major impediments to American chestnut breeding and restoration in Tennessee. Our primary objectives are to identify sources of *Phytophthora* resistance for use in the Tennessee Chapter's breeding program, and test whether or not the previously identified locus on linkage group E (LG_E) plays a role in *Phytophthora* resistance in American-Asian chestnut hybrids derived from the following novel sources of resistance: *Castanea mollissima* 'Gideon', *C. mollissima* 'Payne', *C. mollissima* 'Amy', *C. mollissima* 'Byron', and *C. mollissima* 'Lindstrom 99'.

c. Principal investigators and institutional affiliations: Dr. J. Hill Craddock and M. Taylor Perkins, Department of Biology, Geology and Environmental Science, University of Tennessee at Chattanooga; Dr. Tetyana Zhebentyayeva, Department of Genetics and Biochemistry, and Genomics and Computational Biology Laboratory, Clemson University

d. Duration of project: 1 November 2015 – 1 November 2016

e. Total amount requested: $7605.50

f. Short and long term goals of the project:

Short term goals: (1) Identification of *Phytophthora*-resistant first-backcross progenies derived from the following novel sources of resistance: *C. mollissima* 'Gideon', *C. mollissima* 'Payne', *C. mollissima* 'Amy', *C. mollissima* 'Byron', and *C. mollissima* 'Lindstrom '99'. (2) With the same progeny, we propose to test the influence of the previously identified LG_E locus on variation in resistance to *Phytophthora* root rot.

Long term goal: To hybridize *Phytophthora*-resistant first-backcrosses with Tennessee chapter 'Clapper' derived *Cryphonectria*-resistant BC3s and other advanced backcross progeny, which possess no resistance to *Phytophthora* root rot.

g. Narrative:

Introduction - The invasive oomycete *Phytophthora cinnamomi* Rands causes a disease in chestnuts and chinquapins (*Castanea* Mill., Fagaceae) that has been called one of the chief obstacles facing American chestnut (*Castanea dentata* Borkh.) restoration (Rhoades *et al.* 2003). The disease, commonly referred to as *Phytophthora* root rot (PRR) and ink disease, incites symptoms of root and collar rot, branch dieback, and defoliation, which eventually kill *C. dentata*. *P. cinnamomi* is thought to have been introduced into North America from Asia in the late 1700s or early 1800s (Jeffers *et al*. 2009; Crandall *et al.* 1945). It subsequently destroyed most *C. dentata* in the Piedmont before the chestnut blight fungus arrived in North America (Sisco 2009) and has since spread, affecting *C. dentata* throughout the southern portion of its range (Jeffers *et al.* 2009).

American chestnut researchers have previously focused on breeding *C. dentata* for resistance to the chestnut blight fungus (*Cryphonectria parasitica* (Murr.) Barr) and have only recently started to find and incorporate sources of PRR resistance into restoration breeding programs (Jeffers *et al.* 2009). Asian congeners of *C. dentata* possess varying levels of resistance to PRR. Thus, cultivars of Chinese chestnut (*C. mollissima* Blume) and Japanese chestnut (*C. crenata* Sieb. & Zucc.) are currently being used to introgress the genes for PRR resistance into a *C. dentata* genetic background. For this purpose, identifying those trees with high levels of PRR resistance has become a critical objective for the American chestnut restoration effort in the southeastern United States (Craddock 2014; Jeffers *et al.* 2009).

Concurrently, study of the genetic determinants underlying PRR resistant phenotypes was initiated by Georgi and Abbott in 2007 (T. Zhebentyayeva, Clemson University, personal communication), with results reported by Kubisiak (2010), Costa *et al.* (2011), Olukolu *et al.* (2012), Zhebentyayeva *et al.* (2014), and Santos *et al.* (2014). The primary approach used by these studies has involved molecular marker: trait association analysis and mapping of the quantitative trait loci (QTL) that influence variation in PRR resistance. Kubisiak (2010) reported a major effect QTL on linkage group E (LG_E) that explained greater than 94% of the variation in PRR resistance in an interspecific BC_1F_1 family (AdairKY1 x GL158). Findings by Zhebentyayeva *et al.* (2014) were in agreement, as a QTL for PRR resistance on LG_E was identified in progeny of a BC_1F_1 cross between *C. dentata* and an F_1 hybrid (*C. dentata* x *C. mollissima* 'Nanking'). Further analysis of progeny from two BC_1F_1 crosses and one BC_4F_1 cross derived from a *C. mollissima* 'Mahogany' source of resistance provided further evidence of a QTL influencing disease resistance on LG_E.

Previous research with other organisms has shown that QTLs are often population specific and even pedigree specific (Allendorf 2013); therefore, an investigation of PRR resistance in other *Castanea* species and cultivars is warranted. To identify PRR resistant germplasm for use in *C. dentata* restoration breeding programs, we will screen 15 families of first-backcross (BC1) and "better-backcross" (open-pollinated seedlings of F1 trees growing in 'Clapper' BC4 orchards) progeny for PRR resistance using a locally isolated strain of *P. cinnamomi* in a controlled tub experiment. Progeny of the crosses are derived from five novel sources of PRR resistance (*Castanea mollissima* 'Gideon', *C. mollissima* 'Payne', *C. mollissima* 'Amy', *C. mollissima* 'Byron', and *C. mollissima* 'Lindstrom 99'), one source already tested by Jeffers *et al.* (2009), Olukolu *et al.* (2012) and Zhebentyayeva *et al.* (2014) (*C. mollissima*'Nanking'), and one source of blight resistance that likely confers no resistance to PRR ('Clapper') (Table 1). The F1 parents of most of our BC1s were selected in PRR symptomatic orchards, and have survived in *Phytophthora*-infested soils for years (unpublished data).

We predict that the major effect QTL on LG_E will influence variation to disease resistance in the progeny, which will be confirmed by analysis of simple sequence repeat (SSR) markers spanning the previously identified region on LG_E. However, the possibility of other loci harboring PRR resistance genes in the genetically diverse *C. mollissima* cultivars must be allowed, and we posit an alternate hypothesis of other PRR resistance loci in these sources, should we not detect the already documented major effect alleles in resistant individuals.

Research Plan

Screening and Phenotyping –In April 2015, we germinated BC_1 seeds in a randomized block design in 229 liter flower pots, along with PRR resistant controls (*C. mollissima*) and PRR susceptible controls (*C. dentata*). In the spring of 2015, in collaboration with S.N. Jeffers and S. Sharpe (Clemson University) we isolated strains of *P. cinnamomi* and an as yet unidentified *Phytophthora* species from three Tennessee Chapter orchards where we have observed PRR symptoms in 'Clapper'-derived advanced backcrosses. In August 2015, we will inoculate the progeny of fifteen crosses with the locally obtained *P. cinnamomi* isolates. Families are being tested in five replicates, each corresponding to one flower pot (i.e., block). In December 2015, we will phenotype individual plants for PRR symptom severity using the rating system developed by Jeffers *et al.* (2009): 0 = healthy, no visible lesions on roots; 1 = lesions on at least one lateral root; 2 = lesions on the tap root or severe root rot on the feeder roots; 3 = severe root rot, plant dead. Additionally, we will measure the following variables (symptoms) where significant effects have been found between genotype and symptom (Santos *et al.* 2014): (1) number of days of survival after root inoculation (2) area of PRR lesion in transverse section of the root collar, expressed as a percentage of total area (3) length of shoot internal lesion. Survival quotients (SQ) will be calculated for each family (Jeffers *et al.* 2009) and all symptom parameters will tested for statistical differences between families. Samples of container mix will be collected to confirm presence of *P. cinnamomi*.

DNA Extraction, parentage analysis, and SSR genotyping - Leaves will be collected from each seedling before inoculation with *P. cinnamomi*. DNA will be extracted from each tissue sample using the modified CTAB method (Zhebentyayeva *et al.* 2014). Each individual will be genotyped with SSR markers for the presence of the major effect quantitative trait locus (QTL) on LG_E identified by Olukolu *et al*. (2012) and Zhebentyayeva *et al.* (2014). Additionally, DNA will be isolated from the parent generation to screen for SSRs to be used in the confirmation of the pollen parents. Because outcrosses affect phenotypic results, these individuals will be eliminated through preliminary SSR screening. Fragment size determination of SSR alleles will be performed with the ABI 3700 instrument (Applied Biosystems) at the Clemson University Genomics & Computational Biology Laboratory.

Expected Outcome – The findings of the proposed study will add to the growing body of work directed to refining the genetic model of PRR resistance in *Castanea.* Confirmation of the role of the LG_E locus in these crosses will allow American chestnut breeders to better understand the inheritance of resistance in *C. mollissima.*

We anticipate that the findings of the proposed research will directly benefit TN-TACF and the American chestnut restoration efforts throughout the Southeast by introducing novel sources of resistance to the breeding programs. Additionally, the BC1 descendants of the *C.*

mollissima cultivars selected for our study may yield an additional benefit to chestnut breeders by improving nut quality in *Phytophthora* resistant populations.

As mentioned above, because F1 parents of our BC1s were selected in symptomatic orchards, we expect to recover many valuable resistant individuals from the families being tested. Introduction of these individuals into other breeding programs throughout the southeast will increase genetic diversity of the PRR-resistant breeding populations currently being developed.

Highly disease resistant crosses that do not possess the LG_E alleles for disease resistance can be replicated in future years for genetic mapping of other potential loci encoding resistance. In turn, these plants may be valuable for pyramiding disease resistance genes in future breeding populations.

Table 1. Interspecific hybrid families to be evaluated for PRR resistance and presence of the major effect QTL on LG_E influencing variation in disease resistance.

Family	**Cross type**	**Potential source of resistance**	**Has this source been tested before?**
TTU A4 x ALA Frames 1	BC_1	*C. mollissima* 'Gideon'	No
TTU A4 x ALA Frames 4	BC_1	*C. mollissima* 'Gideon'	No
TTU A4 x ALA Frames 5	BC_1	*C. mollissima* 'Gideon'	No
TTU A4 x OP	"Better backcross" = F_1 x selected 'Clapper' BC_4	*C. mollissima* 'Gideon'	No
McInturff FF-1 x OP	"Better backcross"	*C. mollissima* 'Nanking'	Yes (Olukolu *et al.* 2012, Zhebentyayeva *et al.* 2014)
McInturff DD-1 x OP	"Better backcross"	*C. mollissima* 'Nanking'	Yes (Olukolu *et al.* 2012, Zhebentyayeva *et al.* 2014)
McInturff II-1 x OP	"Better backcross"	*C. mollissima* 'Nanking'	Yes (Olukolu *et al.* 2012, Zhebentyayeva *et al.* 2014)
TNMac1 x (TNBlo1 x GL103)	BC_4	'Clapper'	Yes (Jeffers *et al.* 2009)
TNSum1 x Neel 6-193	BC_1	*C. mollissima* 'Payne'	No
TNMac1 x Neel 4-195	BC_1	*C. mollissima* 'Amy'	No
TNMac1 x Neel 6-268	BC_1	*C. mollissima* 'Byron	No
TNMac1 x Neel 2-127	BC_1	*C. mollissima* 'Lindstrom '99'	No
Neel 5-238 x ALA Frames 1	BC_1	*C. mollissima* 'Byron'	No
Neel 3-262 x TNCarroll1	BC_1	Unnamed *C. mollissima* seedling	No
Neel 6-268 x AL T3	BC_1	*C. mollissima* 'Byron'	No
C. henryi	Control		No
C. mollissima	Control		Yes
C. dentata	Control		Yes

References

Allendorf FW, Luikart G, Aitken SN. 2013. Conservation and the genetics of populations. Wiley-Blackwell Publishing, West Sussex, UK.

Olukolu, B.A., C.D. Nelson and A.G. Abbott. 2012. Mapping resistance to *Phytophthora cinnamomi* in chestnut (*Castanea* sp.). In: Proceedings of the Fourth International Workshop on the Genetics of Host-Parasite Interactions in Forestry: Disease and Insect Resistance in Forest Trees. Sniezko, R. A., Yanchuk, A. D., Kliejunas, J. T., Palmieri, K. M., Alexander, J. M., and Frankel, S. J., tech. coords. Gen. Tech. Rep. PSW-GTR-240. US Dept. of Agric., Forest Service, Pacific Southwest Research Station. Albany, CA. p. 177.

Costa R, Santos C, Tavares F, Machado H, Gomes-Laranjo J, Kubisiak T, Nelson CD. 2011. Mapping and transcriptomic approaches implemented for understanding disease resistance to *Phytophthora cinnamomi* in *Castanea* sp. BMC Proc. 5 (suppl 7):O18.

Craddock JH. 2014. The Chattanooga report. Technical Report to USDA NE-1333: biological improvement of chestnut through technologies that address management of the species, its pathogens and pests.

Crandall BS, Gravatt GF, Ryan MM. 1945. Root disease of *Castanea* species and some coniferous and broadleaf nursery stocks, caused by *Phytophthora cinnamomi*. Phytopathology 35: 162–180

Jeffers SN, James JB, and Sisco PH. 2009. Screening for resistance to *Phytophthora cinnamomi* in hybrid seedlings of American chestnut. In 4th IUFRO *Phytophthoras* in Forest and Natural Ecosystems. S07.02.09. Goheen EM and Frankel SJ, tech. coords. Gen. Tech. Rep. PSW-GTR-221. US Dept. of Agriculture, Forest Service, Pacific Southwest Research Station. Albany, CA. 334 p.

Kubisiak TL. 2010. QTL analysis of *Phytophthora* resistance in a BC_1 population. NE-1033 Annual Meeting Minutes, 2010, Maggie Valley, NC. p.18.

Rhoades CC, Brosi SL, Dattilo AJ, and Vincelli P. 2003. Effect of soil compaction and moisture on incidence of *Phytophthora* root rot on American chestnut (*Castanea dentata*) seedlings. For. Ecol. Manage. 184: 47-54.

Santos C, Machado H, Correia I, Gomes F, Gomes-Laranjo J, Costa R. 2014. Phenotyping *Castanea* hybrids for *Phytophthora cinnamomi* resistance. Plant Pathol. Early View, Doi: 10.1111/ppa.12313.

Sisco PH. 2009. Outlook for blight-resistant American chestnut trees. In: Dumroese RK; Riley LE, tech. coords. National Proceedings: Forest and Conservation Nursery Associations-2008. Proc. RMRS.

Zhebentyayeva T, Chandra A, Abbott AG, Staton ME, Olukolu BA, Hebard FV, Georgi LL, Jeffers SN, Sisco PH, James JB, Nelson CD. 2014. Genetic and genomic resources for mapping resistance to *Phytophthora cinnamomi* in chestnut. Acta Hort. 1019: 263-270. Proceedings of the Fifth International Chestnut Symposium; Shepherdstown, WV.

h. Timeline:

December 2015	June-July 2016	August 2016	October 2016
Phenotyping of progeny complete.	DNA extracted from progeny and SSR genotyping begins	SSR genotyping completed	Manuscripts in preparation

i. How results will be measured and reported:

A final financial report and a publication-ready final performance report will be submitted to TACF after completion of the grant period. The results of the proposed study will be promulgated to the scientific community through presentation at scientific conferences and publication in refereed journals.

j. Breakdown of how and when funds will be spent:

Method	Amount	Cost per item	Total
DNA extraction (96-well plate format)	550 ind	$1.00*	$550
DNA quantification (picogreen, Biotek Synergy H1 plate reader)	550ind	$1.00*	$550
SSR genotyping using ABI3700	550indx10SSRs=5500/ multiplexed 4SSRs per lane=1375	$2.50	$3437.50
Pay for a UTC graduate student for DNA extraction and genotyping at Clemson (summer 2016)	40 hours per week x 4 weeks	$11 per hour	$1760
Cost for UTC graduate student to transport leaf tissue and other materials to and from Chattanooga and Clemson	1 trip from Clemson to Chattanooga and back per week	$52	$208
Rent for UTC student at Clemson, SC	1 month	$800	$800
Antiobiotics and media for culture of *Phytophthora* isolates		$300	$300
		Total	$7605.50
*Labor not included, funds requested for graduate student			

Disclosure of other funding for this project: We (M.T. Perkins and J.H. Craddock) have received a $1000 Provost Student Research Award from the University of Tennessee at Chattanooga for costs associated with construction of the tub trial and initial culture of the *Phytophthora* isolates.

k. Brief C.V. for each principal investigator:

Curriculum Vitae

Matthew Taylor Perkins
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EDUCATION

M.S. Environmental Science. In progress. University of Tennessee at Chattanooga. GPA: 4.0/4.0

B.S. Biology, minor: Chemistry. 2012. University Honors Scholar, Honors in Biology, *cum laude*. University of Tennessee at Chattanooga. GPA: 3.69/4.0

ACADEMIC and RESEARCH POSITIONS

January 2015 – May 2015 Visiting Scholar, Clemson University Genomics and Computational Biology Laboratory. Principal Investigators: Dr. Tatyana Zhebentyayeva, Dr. Paul H. Sisco

May 2014 – Present Graduate Research Assistant, University of Tennessee at Chattanooga, Department of Biological and Environmental Sciences. Major Professor: Dr. J. Hill Craddock

AWARDS, DISTINCTIONS, and FUNDING

2015 Graduate School Fund Scholarship
2015 Provost Student Research Award ($1000)
2014-present Dollywood Graduate Research Assistantship
2007-2012 University Honors Program/Brock Scholar
2012 Departmental Honors in Biology
2012 Graduated *cum laude* (GPA: 3.69/4.00)
2007-2012 University of Tennessee at Chattanooga William E. Brock, Jr. Scholarship
2007-2012 University of Tennessee at Chattanooga Chancellor's Scholarship
2007-2012 Dean's list

PUBLISHED ABSTRACTS/PROFESSIONAL PRESENTATIONS

Zhebentyayeva, T., M.T. Perkins, M. Staton, S. Jeffers, J. James, P. Sisco, F. Hebard, L. Georgi, B. Olukolu, C.D. Nelson, and A. Abbott. 2015. Genetic mapping of resistance to root rot disease (*Phytophthora cinnamomi*) in chestnut (*Castanea* spp.). The *Phytophthora* working group meeting. 9-10 April 2015. Asheville, NC.

Shaw, J., J. Harris, T. Perkins, and A. Morris. 2015. Molecular genetic studies of Ozark chinquapin(*Castanea ozarkensis*) populations. Annual Meeting of the Ozark Chinquapin Foundation. 13 March 2015. Rogers, AR.

Perkins, M.T. and J.H Craddock. 2014. The effect of phosphite fungicides on mycorrhiza formation in a family of BC_4 Chinese-American chestnut seedlings. Technical Report to USDA NE-1333: Biological Improvement of Chestnut through Technologies that Address Management of the Species, its Pathogens and Pests. 6-5 September 2014, La Crosse, WI.

Perkins, M.T. and J.H. Craddock. 2012. The effect of phosphite on mycorrhiza formation in Chinese-American hybrid chestnuts. Poster at 2012 American Chestnut Summit. 19-21 October 2012, Asheville, NC.

Perkins, M.T. 2012. The effect of phosphite on mycorrhiza formation in American chestnut (*Castanea dentata*). Presented at the Tri-Beta Research Symposium hosted by the University of Tennessee at Chattanooga Department of Biological and Environmental Sciences. 18 April 2012, Chattanooga, TN.

RESEARCH FEATURES/POPULAR PRESS

"Scientists from around world team with Clemson to restore American chestnut trees" by J. Melvin, Clemson University's *The Newsstand*, August 5, 2015.

"For love of a tree" by P. Sohn, *Chattanooga Times Free Press*, June 8, 2012.

PROFESSIONAL MEMBERSHIPS

The American Chestnut Foundation
Association of Southeastern Biologists

RECENT PROFESSIONAL SERVICE

6 October 2012, 5 October 2013 Water quality testing and educational outreach concerning aquatic conservation. Tennessee River Rescue. Chattanooga, TN

May 2012-December 2013 Planting, pollination, assessment of disease severity in chestnut trees, and other work performed in cooperation with the American Chestnut Foundation.

25 September 2012 Educational outreach regarding aquatic ecology and entomology with students and teachers from Normal Park Museum Magnet School at the Chattanooga Nature Center. Hamilton County Water Quality Program.

June 2012 Educated hikers about the ecology of the American chestnut during a group outing in the Cherokee National Forest. Tennessee Wild.

Summer 2012, fall 2012, fall 2013 Taught modules in aquatic ecology, environmental science, and plant communities to Boy Scout groups. Chattanooga Audubon Society.

21 May 2011 Participant in the BioBlitz (specialized in fungi) at the Chattanooga Nature Center and Arboretum.

Curriculum Vitae for J. Hill Craddock
August 2015

Contact

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Education

Dottorato di Ricerca in Colture Arboree (1992), Universitá di Torino, Turin, Italy
Master of Science in Horticulture (1987), Oregon State University, Corvallis, OR
Bachelor of Arts in Fine Arts and Biology (1983), Indiana University, Bloomington, IN

Professional Experience

UC Foundation Robert M. Davenport Professor in Biology, The University of Tennessee at Chattanooga (1996-present, at current rank since July 2008)

Recent Publications

Sisco, PH, TC Neel, FV Hebard, JH Craddock, and J Shaw. (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.

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

Perkins, M.T. and J.H Craddock. 2014. The effect of phosphite fungicides on mycorrhiza formation in a family of BC4 Chinese-American chestnut seedlings. Technical Report to USDA NE-1333: Biological Improvement of Chestnut through Technologies that Address Management of the Species, its Pathogens and Pests. 6-5 September 2014, La Crosse, WI.

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 Mill., Fagaceae). Castanea 77(2):186-211.

Grants/Contracts Awarded

Provost Student Research Award (2015) with Taylor Perkins, $1000
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)

Honors and Awards

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

Biographical Sketch

Tetyana N. Zhebentyayeva
Research Associate Professor
Department of Genetics and Biochemistry,
Clemson University Laboratory for Genomics and Computational Biology
105 Collings St BRC, Office #308
Clemson, SC 29634
Tel: 864-656-4292
E-mail: tzhebe@clemson.edu

Education:
Leningrad State University, USSR, combined BS- MS (Biochemistry)
Leningrad State University, USSR, PhD (Plant Biochemistry)

Positions and Employment:
2011 - current - Research Associate Professor, Genetics & Biochemistry, Clemson University
2003 – 2011 Research Associate, Genetic & Biochemistry, Clemson University
2000 – 2003 Visiting Scientist, Department of Horticulture, Clemson University
1987 – 2003 Staff Senior Research Scientist, Nikita Botanical Garden, Crimea, Ukraine
1981 –1987 Staff Research Scientist, Nikita Botanical Garden, Crimea, Ukraine

Other Experience and Professional Memberships
EUCARPIA (European Association for research in plant breeding); The American Chestnut Foundation

Professional activities
Reviewer for international journals: Tree Genetics and Genomes, Journal of American Society for Horticultural Sciences, HortScience, Scientia Horticulturae, Tree Physiology, Gene, PlosOne.

Ongoing Research Support
1. The American Chestnut Foundation 10/17/2014-10/16/2015
Mapping of resistance to *Phytophthora cinnamomi* (Pc) in interspecific American/ Chinese chestnut populations. PI: T. Zhebentyayeva; co-PIs: CD Nelson, AG Abbott, CA Saski.
2. USDA- AFRS (58-5430-2-313) 8/1/2014-7/31/2016
Data needed for foreign regulatory packages for the PPV resistant transgenic *Prunus domestica* cv. 'HoneySweet'. PI: T. Zhebentyayeva
3. Californian Dried Plum Board (#15-CPB 1) 3/24/2015-3/31/2016
Genomic profiling and development of comprehensive catalogue of plum germplasm using Genotyping-By-Sequencing (GBS). PI: T. Zhebentyayeva; co-PIs: C. Dardick, CA Saski

Funded International collaboration 1/113-12/31/15
1. INIA Spain (#RTA2012-00097-00-00). Genetic and molecular analysis of graft-compatibility and its application to Prunus tree crop breeding; PI: Ana Pina; co-PIs: P. Errea, P. Irisarri, J. Martens,T. Zhebentyayeva
2. The Swedish Research Council (Formas 2014-924) 1/1/2015-12/31/2017.
Understanding of resistance to European cancer in apple: transcriptional responses of genotypes with different levels resistance; PI: L. Gustavsson; co-PIs E. van de Weg, T. Zhebentyayeva.
3. The Royal Swedish Academy of Agriculture and Forestry (H11-0033)
Towards control of European canker in apple: comparison of transcriptomes from healthy and diseased tissue tissue of resistant and susceptible cultivars. PI: Larisa Gustavsson; co-Applicants E. van de Weg, T. Zhebentyayeva

Completed Research Support
NIFA USDA CRIS **(**SC-1700363) 7/1/2008-12/31/2010
Translational genomics of flavonoid pathway genes for improving nutritional value of stone fruits. PI: A.G. Abbott; co-PI: T. Zhebentyayeva

Selected publications (selected from 54 publications, in prep. not included)

BOOK CHAPTERS and invited reviews

1. **Zhebentyayeva T.N**. (1999) Isozyme analysis in breeding of apricot. In: Intensification of the fruit crops breeding (Eds. V.K.Smykov and A.I. Lishchuk). Yalta, 1999, pp.63-73.
2. **Zhebentyayeva T.N**., Ledbetter C., Burgos L., Llácer G. (2012) **Apricots**. In: Handbook of Plant Breeding, Vol. 8, Fruit Breeding. Badenes M.L and Byrne D.H. (Eds.). Springer NY, pp.415-458 (*invited contribution*).
3. Arus P, Verde I., Sosinski B**., Zhebentyayeva TN**, Abbott AG (2012) The peach genome. Tree Genetics & Genomes, 8: 531-547.
4. Abbott AG, **Zhebentyayeva T**, Barakat A, Liu Z. (2015) The genetic control of bud-break in trees. Advances in Botanical Research, **74**: 201-228. doi:10.1016/bs.abr.2015.04.002(*invited contribution*).

REFEREED JOURNAL PAPERS

1. Wang Y., Georgi L.L., **Zhebentyayeva T.N.**, Reighard G.L., Scorza R., Abbott A.G. (2002) High throughput targeted SSR marker development in peach [*Prunus persica* (L.) Batsch.]. Genome, 45: 319-328.
2. **Zhebentyayeva T.N.**, Reighard G.L., Gorina V.M., Abbott A.G. (2003) Simple sequence repeats (SSR) analysis for assessment of genetic variability in apricot germplasm. Theor Appl Genet, 106: 435-444.
3. Horn R., Lecouls A.-C., Callahan A., Dandekar A., Garay L., McCord P., Howad W., Chan H., Verde I., Ramaswamy K., Main D., Jung S., Georgi L., Forrest S., Mook J., **Zhebentyayeva T.N.,** Yu Y., Kim H.R., Jesudurai C., Sosinski B.A., Arús P., Baird V., Parfitt D., Reighard G., Scorza R., Tomkins J., Wing R., Abbott A.G. (2005) Candidate gene database and transcript map for peach, a model species for fruit trees. Theor Appl Genet, 110: 1419-1428.
5. Jung S., Main D., Staton M., Cho I., **Zhebentyayeva T**., Arús P., Abbott A. (2006) Synteny conservation between the *Prunus* genome and both the present and ancestral *Arabidopsis* genome. BMC Genomics, 7: 81.
6. Lalli DA, Abbott AG, **Zhebentyayeva TN**, Badenes ML, Darmsteegt V, Polák J, Krška B, Salava J. (2008) A genetic linkage map for an apricot (*Prunus armeniaca* L.) BC1 population mapping *Plum Pox Virus* resistance. Tree Genetics & Genomes, 4:481-493.
7. **Zhebentyayeva T. N.,** Reighard G., Lalli D., Gorina V.M., Krska B., and Abbott A.G. (2008) Origin of resistance to *Plum Pox Virus* in apricot: what new AFLP and targeted SSR data analyses tell. Tree Genetics & Genomes, 4: 403-417.
8. Bielenberg D.G., Wang Y., Li Z., **Zhebentyayeva T**., Fan S., Reighard G.L., Scorza R., Abbott A.G. (2008) Sequencing and annotation of the evergrowing locus in peach (*Prunus persica* L. [Batsch]) reveals a cluster of six MADS-box transcription factors as candidate genes for regulation of terminal bud formation. Tree Genetics & Genomes, 4: 495-507
9. **Zhebentyayeva T.N.,** Swire-Clark G., Georgi L., Garay L., Jung S., Forrest S., Blenda A., Blackmon B., Mook J., Horn R., Howad W., Arús P., Main D., Tomkins J.P., Sosinski B., Baird W.V., Reighard G.L., Abbott A.G. (2008) A framework physical map for peach, a model Rosaceae species. Tree Genetics & Genomes, 4: 745-756
10. Fan S., Bielenberg D., **Zhebentyayeva T.,** Reighard G., Okie W.R., Holland D. and Abbott A.G. (2010) Mapping quantitative trait loci associated with chilling requirement, heat requirement and blooming data in peach. New Phytologist 185: 917-930.
11. Liang H., **Zhebentyayeva T**., Olukulu B., Wilde D., Reighard G.L., Abbott A.G. (2010) Comparison of gene order in the chromosome region containing a *Terminal Flowering1* homolog in apricot and peach revealed microsynteny across angiosperms. Plant Science, 179: 390–398
12. Ruiz EMV, Soriano JM, Romero C, **Zhebentyayeva T**, Terol J, Zuriaga E, Llácer G, Abbott AG, Badenes ML (2011) Narrowing down the apricot Plum pox virus resistance locus and comparative analysis with the peach genome syntenic region. Molecular Plant Pathology, 12(6): 535–547.
13. Sajer O., Scorza R, Dardick C, **Zhebentyayeva T,** Abbott AG, Horn R (2012) Development of sequence-tagged site markers linked to the pillar growth type in peach [*Prunus persica* L. (Batsch)]. Plant Breeding, 131: 186—192.
14. Pina A., **Zhebentyayeva T.N.,** Errea P., Abbott A.G. (2012) Isolation and molecular characterization of Cinnamate 4-Hydroxylase (C4H) from *Prunus* spp. Biologia Plantarum, 56 (3): 441-450.
15. Soriano JM, Domingo ML, Zuriaga E, Romero C, **Zhebentyayeva T**, Abbott AG, Badenes ML (2012) Identification of simple sequence repeat markers tightly linked to plum pox virus resistance in apricot. Molecular Breeding, **30**:1017–1026.

16. Barakat A, Sriram A, Park J, **Zhebentyayeva T,** Main D, Abbott A (2012) Genome wide identification of chilling responsive microRNAs in *Prunus persica*. BMC Genomics, **13**:481.
17. Fang G-C, Blackmon B, Staton M, Nelson CD, Kubisiak TL, Olukolu B, Henry D, **Zhebentyayeva T**, Saski C, Cheng C-H, Monsanto M, Ficklin S, Atkins M, Georgi L, Barakat A, Wheeler N, Carlson J, Sederoff R, Abbott A (2013) A physical map of the Chinese chestnut (*Castanea mollissima*) genome and its integration with the genetic map. Tree Genetics & Genomes, **9**: 525–537.
18. Kubisiak TL, Nelson CD, Staton ME, **Zhebentyayeva T**, Smith C, Olukolu B, Fang G-C, Anagnostakis S, Hebard FV, Wheeler N, Abbott AG, R.R. Sederoff RR (2013) A transcriptome-based genetic map of Chinese chestnut, (*Castanea mollissima*), and identification of regions of segmental homology with peach (*Prunus persica*). Tree Genetics & Genomes, ***9:** 557-571*.
19. Verde I, Abbott AG, Scalabrin S, Jung S, Shu S, Marroni F, **Zhebentyayeva T**, Dettori MT, Grimwood J et al. (2013) The high-quality draft genome of peach (*Prunus persica*) identifies unique patterns of genetic diversity, domestication and genome evolution. *Nature Genetics*, 45: 487–494 (contribution in 4 chapters: Sequencing and assembly, Linkage mapping, Sequence anchoring and map integration, Repeats analysis, Manual annotation, Gene family characterization and small RNA analysis).
20. Dardick C, Callahan A, Horn R, Carrasco K-R, **Zhebentyayeva T**, Hollender C, Whitaker M., Abbott A, Scorza R (2013) Identification of PpTAC1 as a functionally conserved regulator of axillary shoot growth angle in *Prunus persica* (peach) trees. Plant Journal, **75(4):** 618–630.
21. Zuriaga E, Soriano JM, Zhebentyayeva **T**, Romero C, Dardik C, Cañizares J, Badenes ML. (2013) Genomic analysis reveals MATH gene(s) as candidate(s) for PPV resistance in apricot (*Prunus armeniaca* L.) Molecular Plant Pathology, **14(7)**: 663–677.
22. **Zhebentyayeva T.**, Fan S., Chandra A., Bielenberg D.G., Reighard G.L., Okie W.R., Abbott A.G. (2014) Dissection of chilling requirement and bloom date QTLs in peach using a whole genome sequencing of sibling trees from an F_2 mapping population. Tree Genetics & Genomes, **10**: 35-51.
23. Staton M, **Zhebentyayeva T.,** Olukolu B., Fang G-C, Nelson CD, Carlson JE, Abbott AG. Substantial genome synteny preservation among woody angiosperm species: comparative genomics of Chinese chestnut (*Castanea mollissima*) and plant reference genomes. BMC Genomics (submitted)
24. Santos C, **Zhebentyayeva T**, Serrazina S, Nelson CD, Costa R. Development and characterization of the EST-SSR markers for mapping response to *Phytophthora cinnamomi* in *Castanea* sp. Scientia Horticulturae (in press)

PROCEEDINGS (peer-reviewed)

25. **Zhebentyayeva T.N**., Sivolap Yu. M. (2000) Genetic diversity of apricot determined by isozyme and RAPD analysis. Acta Horticulturae 538: 525-529.
26. **Zhebentyayeva T.N.,** Reighard G.L., Krška B., Gorina V.M., Abbott A.G. (2002) Origin of resistance to plum pox virus in apricot: microsatellite data analysis. Plant Protection Science 38: 117-121.
27. Abernathy D., **T.N. Zhebentyayeva**, A.G. Abbott , S. Vilanova , M.L. Badenes, J. Salava, J. Polák, B. Krška, V.D. Darmsteegt (2004) Molecular genetic mapping of the plum pox virus resistance genes in apricot. Acta Horticulturae 657: 283-288.
28. **T.N. Zhebentyayeva**, R. Horn, J .Mook, A.-C. Lecouls, L. Georgi, G. Swire-Clark, G.L. Reighard, W.V. Baird, A.G. Abbott (2006) A physical framework for the peach genome. Acta Horticulturae 713: 83-88.
29. **T. N. Zhebentyayeva**, D. Jiwan, J.H. Jun, D.A. Lalli, Forrest, S., J. Duncan, A, G.L. Reighard, D. Main, Callahan A., Scorza R. and A.G. Abbott (2007) Exploitation of the structural and functional genomics databases for gene identification in peach. Acta Horticulturae 738: 711-717
30. E. M. Vera-Ruiz, C. Romero, **T. Zhebentyayeva**, A. Abbott, G. Llácer and M. L. Badenes (2010) Towards Sharka containment, the 'Sharco' project: genetic approach. Acta Horticulturae 862:471-477.
31. J.M. Soriano, E. Zuriaga, J. Martínez-Calvo, C. Romero, M.L. Badenes, **T. Zhebentyayeva**, A.G. Abbott. Development of a local physical map for the *Plum Pox Virus* resistance (*PPVres*) locus in apricot. Acta Horticulturae (*in press*)
32. **Zhebentyayeva T**, Staton M, Olukolu B, Chandra A, Jeffers S, James J, Sisco P, Hebard F, Georgi L, Nelson CD and Abbott AG (2014) Genetic and Genomic Resources for Mapping Resistance to Root Rot Disease (*Phytophthora cinnamomi*) in Chestnut. Acta Horticulturae (ISHS) 1019:263-270.
33. C.D. Nelson, W.A. Powell, C.A. Maynard, K.M. Baier, A. Newhouse, S.A. Merkle, C.J. Nairn, L. Kong, J.E. Carlson, C. Addo-Quaye, M.E. Staton, F.V. Hebard, L.L. Georgi, A.G. Abbott, B.A. Olukolu, **T. Zhebentyayeva** (2014) The Forest Health Initiative, American chestnut (*Castanea dentata*) as a Model for Forest Tree Restoration: Biological Research Program. Acta Horticulturae (ISHS) 1019:173-178.

34. Georgi LL, **Zhebentyayeva TN**, Islam-Faridi N, Vining E, Abbott AG, Nelson CD, Hebard FV (2015) The search for genes for resistance to chestnut blight. Chestnut **29**: 16-22.
35. Irisarri P, Errea P, Pina A, Zhebentyayeva T. Genetic determinism of graft compatibility in apricot. Acta Horticulturae (ISHS) (submitted)

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August 15, 2015

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To whom it may concern:

This letter is to indicate that I am willing and able to support DNA extraction, DNA quantification and SSR genotyping of chestnut plant material phenotyped for resistance to Phytophthora cinnamomi by Dr. J. Hill Craddock and M. Taylor Perkins (Department of Biology, Geology and Environmental Science, University of Tennessee at Chattanooga) in the frame of proposal " Identifying novel sources of resistance to Phytophthora root rot and assessment of a quantitative trait locus for resistance in interspecific Castanea hybrids" if proposal successfully funded.

Sincerely,

Tetyana Zhebentyayeva

Tetyana Zhebentyayeva
Research Associate Professor