



Report on the Thirty-Fifth Southern Forest Tree Improvement Conference (SFTIC 2019)

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Abstract

The 35th biennial Southern Forest Tree Improvement Conference (SFTIC) was held on the 4th and 5th day of June 2019, in Lexington, KY, USA. The theme of the conference was “Genetics and improvement of forest health and productivity”. Plenary speakers detailed significant progress in understanding forest tree genomes, identifying candidate genes for disease resistance and tree architecture traits and utilizing both genomic selection and genetic modification to advance forest health and productivity. Concurrent and general technical sessions provided additional evidence of progress in these areas as well as information on seed zone development for the eastern USA and species prioritization for conservation and restoration programs, in addition to advanced genome-assisted selection and breeding methods and programs in species of commercial interest including pines and eucalyptus. An interactive poster session provided each poster presenter an opportunity to speak in front of a general session audience and to take Q&A in a traditional poster session format. Pre-conference workshops and a post-conference field tour rounded out the 35th SFTIC with 88 registered for the conference, more than 60 participating in workshops and 33 attending the field tour. The conference program and proceedings are accessible through the SFTIC web site at <http://www.sftic.org>.

Keywords Forest genetics · Tree breeding · Genomics · Biotechnology · Forest health

Introduction

The 35th biennial Southern Forest Tree Improvement Conference was held on the 4th and 5th day of June 2019, in Lexington, KY, USA. The conference was hosted by the Forest Health Research and Education Center and the

University of Kentucky’s Department of Forestry and Natural Resources. The conference offered three plenary sessions, one general session, six concurrent sessions and an interactive poster session. The interactive poster session, new this year, was well received as each poster presenter was given three minutes and three slides to present their work

Footnote: CDN, EMR, JPA, BSC, GFP and Jeffrey W. Stringer served as the Organizing Committee for the 35th Southern Forest Tree Improvement Conference.

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pests with minimal non-target effects and methods of delivery that provide control at appropriate temporal and spatial scales. The availability of genome and transcriptome sequence data has enabled the discovery of species-specific markers, which can be used to track genes through interspecific pedigrees, identify genes associated with resistance and detect targets for silencing approaches in pests.

Plenary session 2 This plenary session included speakers Jill Wegrzyn, University of Connecticut; Margaret Staton, University of Tennessee; and Albert Abbott, University of Kentucky, Forest Health Research and Education Center. Dr. Wegrzyn discussed advances in optical mapping, linking reads, and long-read technologies that are providing tools to resolve the complex, repetitive conifer genomes, which are highly fragmented and error-prone in structural gene annotations. These improvements, combined with the application of recent bioinformatic tools focused on optimizing hybrid genome assemblies and gene annotations, are expected to significantly improve the utility of conifer genomes. Dr. Staton and Dr. Abbott described recent progress in the assembly of a chromosome-scale reference genome for Chinese chestnut (*Castanea mollissima*), with the goal of supporting efforts to restore American chestnut. Five American and five Chinese chestnut genotypes were re-sequenced to enable the analysis of signatures of selection providing insights into the evolution of resistance to *P. cinnamomi* and *C. parasitica* and new information on candidate genes. As indicated here and with other talks, chestnut is becoming a promising platform for leveraging forest tree genotype-to-phenotype research in species restoration.

Plenary session 3 The closing plenary session comprised two presentations that demonstrated the range of research conducted by forest geneticists. Vernon Coffey, American Chestnut Research and Restoration Project (ACRRP) based at SUNY-ESF, covered the history of the devastation of American chestnut by chestnut blight and efforts to restore the species by hybrid breeding. Within this context, he described ACRRP's work on genetically engineering American chestnut trees with an oxalate oxidase (OxO) gene that confers blight resistance on a level equivalent to Chinese chestnut. The ACRRP, led by co-author William Powell, has conducted several ecological risk assessments demonstrating that the OxO-engineered trees do not differ significantly from controls in their impact on environmental variables and non-target organisms. Mr. Coffey also described the project's progress in obtaining non-regulated status for the OxO trees, which would allow wide-scale planting for restoration purposes. Steve McKeand, former Director of the NC State Cooperative Tree Improvement Program, summarized the challenges of maintaining financial support for tree breeding programs, especially when the benefits are long term, such as sustaining forest

health or enhancing carbon sequestration. In his presentation, Dr. McKeand stressed that tree breeders, as a community, should work to raise their profile highlighting specific successes in order to enhance support for tree improvement.

Concurrent technical and poster sessions

Concurrent sessions featured 24 talks in six sessions. These sessions included pine and hardwood genetics and improvement; molecular genetics and biotechnology; disease and insect resistance; gene diversity and conservation; clonal development and production; and breeding, testing and selection. Forest health was a key theme for the 35th SFTIC with several concurrent talks and poster presentations describing ongoing work, including: genetics of blight and root rot resistances in chestnut; emerald ash borer, hemlock woolly adelgid and the potential for long-term surviving trees to harbour genetic resistance; laurel wilt disease in red bay and related species of the Lauraceae family; and important pine issues such as fusiform rust in the southern USA, pitch canker, globally, and the potential for screening and breeding for salt tolerance in slash pine to assist coastal restoration.

On the technology side, speakers discussed advancements in genomic-based tools for genotyping trees in operational breeding programs and applying these data to various questions in breeding, including which trees to select to make more rapid gains per generation and which trees to mate together to provide larger gains in the next generation. Additional work on seed zone development for eastern USA forest trees and new information on pollination bag efficacy and DNA fingerprinting in the southern pines were provided. Finally, a review and an update of active tree improvement programs for various fast-growing hardwoods and potentially woody biomass crop species were provided for cottonwood, sycamore, willow and sweetgum.

A new interactive poster session format was introduced for this biennium's SFTIC. Poster authors participated in a moderated session where each author had three minutes and three slides to present the highlights of their work. This interactive session was followed by a traditional session where authors answered questions from conference attendees. Poster content generally reflected content of the oral presentations and included quantitative and population genetics, research on disease resistance and somatic embryogenesis, molecular analyses (e.g. characterization of genomes, chromosomes and trait variation) and information about programs and tools associated with genetic conservation. Of the 17 posters presented, six were first authored by graduate students.

Career panel, participation and awards

A student-oriented careers panel discussion, organized and led by David Barker, Rayonier, was held on the first evening of

the conference. A diverse panel representing academia, business and government science leaders provided attendees with practical advice on obtaining employment and developing their careers and their lives in an ever-changing and always-demanding job market. The panel shared insights on various strategies used to obtain a desired job, based on the candidate's career interest either in research or academia or field-oriented land management. In addition, the panel imparted experiences on how to maintain an appropriate work-life balance emphasizing its importance in successful career development. The panel encouraged candidates to foster professional flexibility in the workplace, in order to adapt to constant changes, demands, pressures and evolving goals. Finally, the panel expressed to candidates the need to continue to learn, to stretch their boundaries outside their comfort zones, and build a diverse portfolio of employable skills.

Among the registrants, 35 organizations were represented including 15 universities, 9 companies and 11 government agencies. Two participants represented international organizations. The Squillace Award for best overall oral presentation was awarded to Patrick Cumbie, ArborGen, for his talk entitled "Implementation of genomic prediction in a loblolly pine breeding population." The Zobel Award for best student oral presentation was awarded to Colin Jackson, North Carolina State University (student of Fikret Isik and Juan Luis Acosta), for his talk "SNP discovery of tropical and subtropical pines using reduced representation sequencing methods." The van Buijtenen Award for best overall poster and the Belle Baruch Foundation Award for best student poster were awarded to Luis Ibarra, North Carolina State University (student of Gary Hodge), for his poster "Quantitative genetics of hybrid populations of *Eucalyptus nitens* x *E. globulus*: Genetic parameters and implications for breeding strategies." Second and third place student poster awards were given to Stephen Goodfellow, Mississippi State University (student of Randy Rousseau) for his poster "Loblolly pine inter-provenance hybrids and fusiform rust," and Jiali Yu, University of Tennessee (student of Margaret Staton) for her poster "Transcriptomic profiling reveals flower development gene induction during endodormancy to ecodormancy transition in apricot and peach floral buds."

Concluding remarks

Based on various feedback from conference attendees, the 35th SFTIC was a success. The most notable were the plenary sessions covering the inspiring and evolving story of developing disease resistance in American chestnut from genetic mapping and genome sequencing, to phenotypic selection and backcross breeding, to progeny testing and genomic selection, to achieving a high degree of resistance through genetic engineering. Integrating TACF's breeding program with successful products (tested and potentially released events) from the

genetic engineering program of SUNY-ESF puts American chestnut on firm footing for restoration. Important talks in the volunteered sessions outlined recent genetic mapping progress made in *Phytophthora* root rot and blight resistance in chestnut and suggest a path forward for achieving resistance to both diseases in genotypes destined for the American chestnut restoration program. Other plenary session talks discussed the fascinating work on the genetics of crown architecture of trees, the loblolly pine genome and comparisons to other conifer genomes, and past learnings and future directions for cooperative tree improvement in the southern USA and beyond.

The extended offerings of workshops and pre-conference meetings (see Acknowledgements) along with the new, interactive poster session were also important successes for the 35th SFTIC. These sessions allowed additional engagement and learning opportunities for a diverse group of attendees, especially the younger practitioners of tree improvement, both in research and in operations, and those that are transitioning into tree improvement from other fields. We recognize the prominent role that genetics has and will continue to have in integrated pest management strategies to confront current and emerging forest tree pests and pathogens (e.g. emerald ash borer, hemlock woolly adelgid, laurel wilt and pitch canker to name a few that were presented in volunteered talks and the poster session) and the ongoing role of genetics in southern USA pine forestry (and globally for pine and eucalyptus) for both wood products (e.g. loblolly and slash pines) and ecosystem restoration and management (e.g. longleaf, shortleaf and table-mountain pines).

Considerable progress in scientific and technical understanding and achievement has been made since the 31st SFTIC in 2011 (Nelson et al. 2012). At that meeting, the potential of renewable woody biomass for easing carbon emissions was emphasized with the concomitant need for better genetics on the target species to provide increased wood yields. This emphasis has waned some since that meeting, as the technology for utilizing wood in liquid fuels production has lagged. However, this is likely to change in the near future as progress in liquid fuels technology continues to develop and the need for carbon neutral energy remains. In addition, speakers at the 2011 meeting noted the decreasing costs in DNA sequencing and what this could mean for forest genetics and tree improvement. Since then, we have seen the costs continue to decrease and the potential and demonstrated applications increase. For example, the Squillace Award talk focused on implementing genomic selection in an industrial tree improvement program and a plenary session talk discussed the same in a non-profit's program dedicated to species restoration. Clearly the future is bright for forest genetics and tree improvement. The proper integration of new technology with basic know-how and proven strategies for success in plant and animal breeding continues to be relevant for forest trees.

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Reference

Nelson CD, Rousseau RJ, Adams JP, Yuceer MC (2012) Report on the 31st Southern Forest Tree Improvement Conference (SFTIC). *Tree Genet. Genomes* 8:439–441

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