

NC STATE UNIVERSITY 2020 & 2021 Annual Report

2020-21 CAMCORE ANNUAL REPORT

International Tree Breeding and Gene Conservation

Department of Forestry & Environmental Resources College of Natural Resources North Carolina State University Raleigh, North Carolina 27695-8008, USA

Telephone: 919.515.6424

Email:

info@camcore.org

Gary R. Hodge grh@ncsu.edu Juan Lopez jllopez@ncsu.edu Juan José Acosta jjacosta@ncsu.edu woodbridge@ncsu.edu William C. Woodbridge Romeo Jump rjump@ncsu.edu Robert M. Jetton rmjetton@ncsu.edu W. Andrew Whittier wawhitti@ncsu.edu J. Robert McGee rmcgee@ncsu.edu Elmer A. Gutiérrez egutierrez3161@gmail.com

Website: camcore.cnr.ncsu.edu

Table of Contents

EXECUTIVE SUMMARY (English) RESUMEN EJECUTIVO (Español) RESUMO EXECUTIVO (Portugués) MUHTASARI WA TAARIFA KUU (Kiswahili) RINGKASAN EKSEKUTIF (Bahasa Indonesia)	1 2 3 4 5
YEAR IN REVIEW Message From the Director 2020-21 Camcore Membership	6 7
BREEDING & TREE IMPROVEMENT Expanding the Camcore Eucalyptus Portfolio <i>Eucalyptus</i> Hybrid Project Multi-site Corymbia Analysis in Africa Multi-site Corymbia Analysis in Africa Pine Hybrid Project Update Hybrid Tree Genetic Parameters Teak Update Gmelina Update Towards Adelgid Resistant Fraser Fir Members Take Charge of Camcore Wood Sampling Efforts	8 9 10 11 13 17 17 18 19
SPECIES CHARACTERIZATION Early growth performance of <i>P. patula x P. tecunumanii</i> F2 seedlings Wood and Pulping Properties and Sampling Strategy for Acacia crassicarpa Eucalypt Species Wood Properties Expanding the Global NIR Model with <i>E. pellita</i> and Other Species Cutting Production of <i>Pinus tecunumanii</i> and <i>P. maximinoi</i> in Hydroponic Hedges Forest Health Program Update	20 24 28 31 32 34
DEVELOPMENT OF ENABLING TECHNOLOGIES Preliminary Results of Within-family Genomic Selection in <i>P. taeda</i> Full-Sib BLUP Analysis using SAS or R The Use of a Slingshot and Rope Saw to Collect Pollen and Seed Can the Nano NIR Predict Solid Wood MFA and MOE? New Methods for <i>Eucalyptus</i> Pollen Testing The Use of UAV Drones for Pine Pollination Handheld NIR and Image Analysis to Measure Foliage Nutrient Content in Eucalypts Potential Use of Ground Lidar & Photogrammetry for Measurement of Genetic Tests	36 39 40 41 44 46 47 50
CONSERVATION & GENETIC DIVERSITY 21 Pine Species Lesser-known Species With Potential for Plantation Establishment . 2020-21 Seed Collections in Central America 2020-21 Camcore Domestic Conservation Update Assessment of Carolina Hemlock Populations Hemlock Restoration Silviculture Research Update	52 53 54 56 58
CAMCORE NEWS ITEMS Webinars, Mini-Conferences, and Virtual Visits	62 64 65 66 67 68

EXECUTIVE SUMMARY

- 1. In 2020-2021, we made important acquisitions of *Eucalyptus* provenance and family collections to expand our genetic portfolio to 24 species.
- 2. Clones from five different *Eucalyptus* hybrid combinations were planted in 35 trials in South Africa and Colombia. By the end of 2022, we hope to have seed in Raleigh from 10 to 15 new hybrid combinations produced in Phase 2 of the breeding program.
- 3. Good progress was made in the full-sib hybrid pine breeding projects. For *P. patula x P. tecunumanii*, progeny from 113 families were planted in 13 field tests by the end of 2021. For *P. tecunumanii x P. greggii*, seed from 114 families was received in Raleigh. For *P. caribaea x P. tecunumanii*, we began pollen collections for full-sib family breeding.
- 4. Early growth data for F2 *P. patula x P. tecunumanii* hybrid seedlings produced from open-pollinated F1 parents suggest that this might be a useful strategy for inexpensive production of hybrid seed for commercial plantations.
- 5. Acacia crassicarpa grown in Indonesia has mediumhigh wood density (481 kg/m³), high pulp yield (53.8%), and medium lignin content (29.4%). Assessments of whole-tree wood properties using breast-height samples (1.3 m) combined with samples at 25% commercial height (roughly 4.5 m) give very good results for all wood properties, while breast-height samples alone give good predictions for most (but not all) traits.
- 6. We expanded the global eucalyptus NIR model with additional samples of *E. pellita* and 102 samples from an array of minor species, including four *Corymbia* species.
- 7. A study of *P. maximinoi* and *P. tecunumanii* hedges indicated that increasing the size of hedges and decreasing the frequency of cutting harvests may lengthen the lifespan of the hedges and increase the cumulative number of cuttings produced over the long term.
- 8. Preliminary results from a study to investigate the potential of genomic selection within full-sib families in *P. taeda* are very encouraging. The data indicate that we can make within-family selections for volume with good predictive ability and high genetic accuracy.
- 9. A study using artificial inoculation of *Eucalyptus* seedlings with the pathogen *Austropuccina psidii* demonstrated important variation among species. All species showed some level of infection by *A*.

psidii, but *E. benthamii*, *E. badjensis*, and *E. smithii* had overall high levels of susceptibility, while *E. camalduensis*, *E. globulus*, and *E. longirostrata* had the highest levels of resistance.

- The inexpensive DLP NIRscan Nano can be used to predict solid wood properties (Density, Microfibril Angle (MFA) and Modulus of Elasticity (MOE)) from increment core strips.
- 11. Conservation seed collections of threatened US species pitch pine, Table Mountain pine, and red spruce were completed. Conservation seed orchards of eastern hemlock, Carolina hemlock, and Table Mountain pine were planted in western North Carolina and eastern Tennessee.
- 12. A study using artificial infestation of Fraser fir clones and seedling families with balsam woolly adelgid (BWA) was able to identify genetic differences in tolerance among clones.
- 13. Encouraging results were found in studies looking at the efficacy of different silvicultural treatments to re-establish eastern and Carolina hemlock in natural forests. There are important impacts of light availability, canopy gap size, and reduction of competition around re-introduced hemlock seedlings, and these factors will be critical in future restoration efforts for these species.
- 14. There were many other important accomplishments in 2020-2021. We began investigation of Terrestrial Lidar and Photogrammetry for the measurement of genetic trials. We established a teak conservation bank / breeding orchard in Guatemala. Luis Ibarra studied the genetic architecture of two hybrid forest tree populations using two of the largest datasets ever analyzed. An algorithm was developed to allow the analysis of a full-sib progeny test dataset using a general linear mixed model software package lacking a pedigree function. Juan Lopez completed a literature review of 21 potential pine species for future Camcore collections.
- 15. And finally, during the pandemic we made good use of Zoom to maintain contact with members. We held 23 webinars on various topics with a total attendance of 1,312 people, and we held two mini-conferences for Camcore members on hedge and rooted cutting management in *E. dunnii* and sub-tropical pines. We also made 58 virtual technical visits with 21-member companies from 11 countries, interacting with 443 people. We are thankful for that technology, but will be even more thankful when we are able to visit with you again live and in person!

RESUMEN EJECUTIVO (Español)

- 1. En 2020-2021, realizamos importantes adquisiciones de colecciones de procedencias y familias de *Eucalyp-tus* para ampliar nuestro portafolio genético a 24 especies.
- Se plantaron clones de cinco combinaciones diferentes de híbridos de Eucalyptus en 35 ensayos en Sudáfrica y Colombia. Para finales de 2022, esperamos tener en Raleigh semillas de entre 10 y 15 nuevas combinaciones híbridas producidas en la Fase 2 del programa de mejora.
- Se han hecho buenos progresos en los proyectos de cría de pinos híbridos full-sib. En el caso de *P. patula x P. tecunumanii*, la progenie de 113 familias se plantó en 13 pruebas de campo a finales de 2021. Para *P. tecunumanii x P. greggii*, se recibieron semillas de 114 familias en Raleigh. Para *P. caribaea x P. tecunumanii*, se iniciaron las recolecciones de polen para la reproducción de familias completas.
- 4. Los primeros datos de crecimiento de plántulas híbridas F2 de *P. patula x P. tecunumanii* producidas a partir de progenitores F1 de polinización abierta sugieren que ésta podría ser una estrategia útil para la producción económica de semillas híbridas para plantaciones comerciales.
- 5. La Acacia crassicarpa cultivada en Indonesia tiene una densidad de madera media-alta (481 kg/m3), un alto rendimiento de pulpa (53,8%) y un contenido medio de lignina (29,4%). La evaluación de las propiedades de la madera de todo el árbol utilizando muestras a la altura del pecho (1,3 m) más muestras al 25% de la altura comercial (aproximadamente 4,5 m) da muy buenos resultados para todas las propiedades de la madera, mientras que las muestras a la altura del pecho por sí solas dan buenas predicciones para la mayoría de los rasgos (pero no todos).
- 6. Ampliamos el modelo NIR global de eucalipto con muestras adicionales de *E. pellita* y 102 muestras de una serie de especies menores, incluyendo cuatro especies de *Corymbia*.
- 7. Un estudio de setos de *P. maximinoi y P. tecunumanii* indicó que el aumento del tamaño de los setos y la disminución de la frecuencia de las cosechas de esquejes puede alargar la vida de los setos y aumentar el número acumulado de esquejes producidos a largo plazo.
- 8. Los resultados preliminares de un estudio para investigar el potencial de la selección genómica dentro de familias de hermanos completos en *P. taeda* son muy alentadores. Los datos indican que podemos hacer selecciones dentro de las familias para el volumen, con la buena capacidad de predicción y una alta precisión genética.
- 9. Un estudio utilizando la inoculación artificial de plántulas de Eucalyptus con el patógeno Austropuccina

psidii demostró una importante variación entre especies. Todas las especies mostraron algún nivel de infección por *A. psidii*, pero *E. benthamii*, *E. badjensis* y *E. smithii* tuvieron en general altos niveles de susceptibilidad, mientras que *E. camalduensis*, *E. globulus* y *E. longirostrata* tuvieron los mayores niveles de resistencia.

- El económico DLP NIRscan Nano puede utilizarse para predecir las propiedades de la madera maciza (densidad, ángulo de microfibrillas (MFA) y módulo de elasticidad (MOE)) a partir de tiras de núcleo incrementales.
- 11. Se completaron las colecciones de semillas de conservación de las especies estadounidenses amenazadas de pitch pine, Table Mountain pine, y red spruce. Se plantaron huertos semilleros de conservación de eastern hemlock, Carolina hemlock, and Table Mountain en el oeste de Carolina del Norte y el este de Tennessee.
- 12. Un estudio en el que se utilizó la infestación artificial de clones y familias de plántulas de abeto Fraser con balsam woolly adelgid (BWA), permitió identificar diferencias genéticas de intolerancia entre los clones.
- 13. Se han encontrado resultados alentadores en estudios que analizan la eficacia de diferentes tratamientos silvícolas para restablecer eastern y Carolina hemlock en bosques naturales. Hay importantes impactos de la disponibilidad de luz, el tamaño del dosel y la reducción de la competencia alrededor de las plántulas de hemlock reintroducidas, y estos factores serán críticos en los futuros esfuerzos de restauración de estas especies.
- 14. Hubo muchos otros logros importantes en 2020-2021. Comenzamos la investigación de Lidar Terrestre y Fotogrametría para la medición de ensayos genéticos. Establecimos un banco de conservación de teca/huerto de cría en Guatemala. Luis Ibarra estudió la arquitectura genética de dos poblaciones de árboles forestales híbridos utilizando dos de los mayores conjuntos de datos que no habían sido analizados. Se desarrolló un algoritmo para permitir el análisis de un conjunto de datos de prueba de progenie de hermanos completos utilizando un paquete de software de modelo lineal mixto general que carece de una función de pedigrí. Juan López completó una revisión bibliográfica de 21 especies de pinos potenciales para futuras colecciones de Camcore.
- 15. Y por último, durante la pandemia, hicimos un buen uso de Zoom para mantener el contacto con los miembros. Celebramos 23 webinars sobre diversos temas con una asistencia total de 1.312 personas, y realizamos dos mini conferencias para los miembros de Camcore sobre la gestión de setos y cortas enraizadas en *E. dunnii* y pinos subtropicales. También realizamos 58 visitas técnicas virtuales con 21 empresas asociadas de 11 países, interactuando con 443 personas. Estamos agradecidos por esta tecnología, pero lo estaremos aún más cuando podamos volver a visitarles en persona!

RESUMO EXECUTIVO (Português)

- 1. Em 2020-2021 fizemos importantes aquisições de procedências e famílias de eucaliptos para ampliar nosso portfólio genético para 24 espécies.
- Clones de cinco diferentes combinações híbridas de eucalipto foram plantados em 35 experimentos na África do Sul e Colômbia. Até o final de 2022, esperamos ter sementes em Raleigh de 10 a 15 novas combinações híbridas produzidas na Fase 2 do programa de cruzamentos.
- 3. Um bom progresso foi feito nos projetos de melhoramento de pinus com famílias híbridas de irmãos completos. Para *P. patula x P. tecunumanii*, progênies de 113 famílias foram plantadas em 13 experimentos de campo até o final de 2021. Para *P. tecunumanii x P. greggii*, sementes de 114 famílias foram recebidas em Raleigh. Para *P. caribaea x P. tecunumanii*, iniciamos coletas de pólen para a geração de famílias de irmãos completos.
- 4. Dados de crescimento inicial de mudas híbridas F2 de *P. patula x P. tecunumanii* produzidas a partir de polinização aberta de genitores F1 sugerem que esta pode ser uma estratégia útil para a produção barata de sementes híbridas para plantios comerciais.
- 5. Acacia crassicarpa cultivada na Indonésia tem densidade de madeira média-alta (481 kg/m3), alto rendimento de polpa (53,8%) e teor médio de lignina (29,4%). A avaliação das propriedades da madeira ao nível de árvore inteira usando amostras tomadas à altura do peito (1,3 m) e a 25% da altura comercial (aproximadamente 4,5 m) fornecem resultados muito bons para todas as propriedades da madeira, enquanto amostras tomadas somente à altura do peito fornecem boas predições para a maioria (mas nem todas) das características.
- 6. Expandimos o modelo global de NIR com amostras adicionais de *E. pellita* e 102 amostras de uma variedade de espécies secundárias, incluindo quatro espécies de *Corymbia*.
- Um estudo em matrizes de *P. maximinoi* e *P. tecunumanii* indicou que o aumento do tamanho do mini-jardim e a diminuição da frequência da colheita de estacas pode prolongar a vida útil das matrizes e aumentar o número cumulativo de estacas produzidas no longo prazo.
- 8. Os resultados preliminares de um estudo para investigar o potencial da seleção genômica dentro de famílias de irmãos completos em *P. taeda* são muito promissores. Os dados indicam que podemos fazer seleções dentro da família para o volume com boa capacidade preditiva e alta acurácia.
- Um estudo utilizando inoculação artificial de mudas de eucalipto com o patógeno *Austropuccina psidii* demonstrou importante variação entre as espécies. Todas as

espécies apresentaram algum nível de infecção por *A. psidii*, mas *E. benthamii*, *E. badjensis* e *E. smithii* tiveram altos níveis gerais de suscetibilidade, enquanto *E. camalduensis*, *E. globulus* e *E. longirostrata* tiveram os mais altos níveis de resistência.

- O barato DLP NIRscan Nano pode ser utilizado para predizer propriedades da madeira sólida (Densidade, Ângulo Microfibrilar e Módulo de Elasticidade) a partir de amostras de bagueta.
- 11. Foram concluídas as coletas de sementes para conservação das espécies americanas ameaçadas "pitch pine", "table mountain pine" e "red spruce". Pomares de conservação de Cicuta Oriental (eastern hemlock), Cicuta da Carolina (Carolina hemlock) e "table mountain pine" foram plantados no oeste da Carolina do Norte e no leste do Tennessee.
- 12. Um estudo utilizando infestação artificial de clones e famílias de abeto-de-fraser (Fraser fir) com o pulgão lanoso do bálsamo (balsam wooly adelgid – BWA) foi capaz de identificar diferenças genéticas entre clones quanto à tolerância ao inseto.
- 13. Resultados promissores foram encontrados em estudos que analisaram a eficácia de diferentes tratamentos silviculturais para restabelecer a Cicuta Oriental (eastern hemlock) e a Cicuta da Carolina (Carolina hemlock) em florestas naturais. Existem impactos importantes da disponibilidade de luz, tamanho da abertura do dossel e redução da competição em torno de mudas de cicuta reintroduzidas, e esses fatores serão críticos em futuros esforços de restauração para essas espécies.
- 14. Houveram muitas outras realizações importantes em 2020-2021. Iniciamos a investigação de LIDAR terrestre e fotogrametria para a medição de ensaios genéticos. Estabelecemos um banco de conservação/pomar de teca na Guatemala. Luís Ibarra estudou a arquitetura genética de duas populações de árvores florestais híbridas usando dois dos maiores conjuntos de dados já analisados. Um algoritmo foi desenvolvido para permitir a análise de um conjunto de dados de teste de progênie de irmãos completos usando um pacote de modelo linear misto sem uma função de pedigree. Juan Lopez completou uma revisão da literatura de 21 espécies potenciais de pinus para futuras coleções da Camcore.
- 15. E por fim, durante a pandemia fizemos bom uso do Zoom para manter contato com os membros. Nós realizamos 23 webinars sobre diversos temas com uma participação total de 1.312 pessoas, e realizamos duas miniconferências para membros da Camcore sobre manejo de matrizes e mudas clonadas por estaquia em *E. dunnii* e pinus subtropical. Também realizamos 58 visitas técnicas virtuais com 21 empresas associadas de 11 países, interagindo com 443 pessoas. Somos gratos por essa tecnologia, mas ficaremos ainda mais agradecidos quando pudermos visitá-lo novamente ao vivo e pessoalmente!

MUHTASARI WA TAARIFA KUU (Kiswahili)

- 1. Mnamo 2020-2021, tulifanya ununuzi muhimu wa asili ya mikaratusi na makusanyo ya familia ili kutanua jalada letu la kijeni hadi kufikia spishi 24.
- Kloni kutoka mseto ya mikaratusi tano ya mchanganyiko maalum zilipandwa katika majaribio 35 nchini Afrika Kusini na Colombia. Ni matumainiyetu kuamwishonimwa mwaka2022, tutakuwana mbegukatika Raleighkutoka michanganyiko mipya 10 hadi 15 itakayozalishwa katika awamu ya pili ya program ya uzalishaji
- 3. Maendeleo mazuri yalipatikana katika miradi ya chotara za aina zote za misonobari. Kwa *P. patula x P. tecunumanii*, vizazi kutoka kwa familia 113 vilipandwa katika majaribio 13 kufikia mwisho wa 2021. Kwa *P. tecunumanii x P. greggii*, mbegu kutoka kwa familia 114 zilipokelewa Raleigh. Kwa *P. caribaea x P. tecunumanii*, tulianza kukusanya chavua kwa ajili ya uzalishaji wa familia kamili.
- 4. Taarifa ya awali ya ukuaji wa mapema kwa F2 *P. patula x P. tecunumanii* miche chotara inayozalishwa na wazazi wa F1 iliyochavushaji wazi inaashiria kuwa hii inaweza kuwa mkakati muhimu kwa uzalishaji wa bei nafuu wa mbegu mseto kwa mashamba ya kibiashara.
- 5. Acacia crasicarpa inayokuzwa Indonesia ina msongamano wa wastani wa kuni (481kg/m3), mavuno mengi ya rojo ya ubao (53.8%, na kiwango cha wastani cha lignin (29.4%). Tathmini ya sifa za mti mzima kwa kutumia sampuli za urefu wa matiti (1.3m) pamoja na sampuli za urefu wa kibiashara wa 25% (takriban mita 4.5) hutoa matokeo mazuri kwa sifa zote za mbao, wakati sampuli za urefu wa matiti pekee hutoa utabiri mzuri wa sifa nyingi (lakini sio zote).
- 6. Tulipanua muundo wa kimataifa wa mikaratusi ya NIR kwa sampuli za ziada za *E. pellita* na sampuli 102 kutoka kwa safu ya spishi ndogo, ikijumuisha spishi nne za *Corymbia*.
- Utafiti wa kingo za *P. maximinoi* na *P. tecunumanii* ulionyesha kuwa kuongeza ukubwa wa ua na kupunguza marudio ya uvunaji wa kukata kunaweza kurefusha maisha ya ua na kuongeza idadi ya vipandikizi vinatakavyozalishwa kwa muda mrefu.
- 8. Matokeo ya awali ya utafiti wa kuchunguza uwezekano wa uteuzi wa jeni ndani ya familia kamili katika *P. taeda* yanatia moyo sana. Data inaonyesha kwamba tunaweza kufanya uteuzi wa kiasi ya miti ndani ya familia kwa uwezo mzuri wa kutabiri na usahihi wa juu wa kinasaba.
- 9. Utafiti kwa kutumia chanjo bandia ya miche za mikaratusi na pathojeni Austropuccina psidii, ilionyesha tofauti muhimu kati ya aina. Aina zote zilionyesha kiwango fulani cha maambukizi na A. psidii lakini E. benthamii, E. badjensis, na E. smithii zilikuwa na viwango vya juu vya kuathirika kwa upesi kwa ujumla, wakati E.

camalduensis, *E. globulus*, na *E. longirostrata* yalikuwa na viwango vya juu zaidi vya upinzani.

- 10. DLP NIRscan Nano ya bei nafuu inaweza kutumika kutabiri sifa za mbao ngumu (Density, Microfi bril Angle (MFA) na Modulus of Elasticity (MOE)) kutoka kwa vipande vya msingi vya nyongeza.
- 11. Mkusanyiko wa mbegu za uhifadhi wa misonobari ya aina mbalimbali za Marekani yaliyo hatarini, misonobari ya Table Mountain, na misonobari nyekundu ilikamilishwa. Bustani za mbegu za uhifadhi za hemlock ya mashariki, Carolina hemlock, na Table Mountain pine zilipandwa magharibi-kaskazini mwa Carolina na mashariki mwa Tennessee.
- 12. Utafiti uliotumia uvamizi wa bandia wa mimea ya Fraser fir clones na familia za miche zilizo na balsam woolly adelgid (BWA) uliweza kutambua tofauti za kijeni katika utofouti wa ustahimilivi kati ya kloni tofouti.
- 13. Matokeo ya kutia moyo yalipatikana katika tafiti zinazoangalia ufanisi wa matibabu tofauti ya kitamaduni ili kurejesha hemlock ya mashariki na Carolina katika misitu ya asili. Kuna athari muhimu za uwezo wa kupatikana kwa mwanga, saizi ya kipenyo cha kivuli, na kupunguzwa kwa ushindani karibu na miche ya hemlock iliyorejeshwa tena, na mambo haya yatakuwa muhimu katika urejeshaji wa matokeo ya baadaye ya spishi hizi.
- 14. Kulikuwa na mafanikio mengine mengi muhimu mwaka wa 2020-2021. Tulianza uchunguzi wa Terrestrial Lidar na Photogrammetry kwa ajili ya kipimo cha majaribio ya kijeni. Tulianzisha benki ya uhifadhi wa teak / bustani ya kuzaliana huko Guatemala. Luis Ibarra alisoma usanifu wa kijeni wa idadi ya miti ya mseto ya msituni kwa kutumia hifadhidata mbili kubwa zaidi zilizowahi kuchambuliwa. Algoriti iliundwa ili kuruhusu uchanganuzi wa mkusanyiko wa data wa jaribio la kizazi kamili kwa kutumia kifurushi cha jumla cha kielelezo cha mchanganyiko cha umri kisicho na utendaji wa ukoo. Juan Lopez alikamilisha ukaguzi wa fasihi wa aina 21 za misonobari zinazo uwezo kwa ajili ya makusanyo ya baadaye ya Camcore.
- 15. Na hatimaye, wakati wa janga hili tulitumia vyema Zoom kudumisha mawasiliano na wanachama. Tulifanya mikutano 23 kutumia mitandao zenye mada mbalimbali iliyohudhuriwa na jumla ya watu 1,312, na tulifanya maelewano mawili ya mkutano mdogo kwa wanachama wa Camcore juu ya ua na usimamizi wa kukata mizizi katika *E. dunnii* na misonobari ndogo ya tropiki. Pia tulifanya ziara 58 za kiufundi na kampuni zenye wanachama 21 kutoka nchi 11, tukishirikiana na watu 443. Tunashukuru kwa hiyo teknolojia, lakini tutashukuru zaidi tutakapoweza kukutembelea tena moja kwa moja na ana kwa ana!

RINGKASAN EKSEKUTIF (Bahasa Indonesia)

- 1. Pada tahun 2020-2021, kami mengakusisi material dari beberapa provenance (sumber geografis) dan family, dari spesies Eukaliptus, untuk memperkaya koleksi genetik kami menjadi 24 spesies.
- 2. Klon-klon dari lima Eukaliptus hibrida yang berbeda telah ditanam pada 35 percobaan di Afrika Selatan dan Kolombia. Pada akhir tahun 2022, tahap ke-2 dari program pemuliaan kami, diharapkan akan ada 10 hingga 15 benih hibrida baru yang diproduksi di Raleigh.
- 3. Ada kemajuan baik dari proyek pemuliaan "full-sib" pinus hibrida. Untuk proyek persilangan *P. patula* x *P. tecunumanii*, keturunan dari 113 family telah ditanam di 13 uji-lapangan pada akhir tahun 2021. Untuk proyek persilangan *P. tecunumanii* x *P. greggii*, benih dari 114 family telah diterima di Raleigh. Sementara itu, untuk proyek persilangan *P. caribaea* x *P. tecunumanii*, pengumpulan serbuk sari untuk program pemuliaan telah dimulai.
- 4. Data pertumbuhan awal generasi ke-2 dari persilangan *P. patula x P. tecunumanii*, yang berasal dari penyerbukan terbuka generasi ke-1, menunjukkan bahwa metode ini merupakan metode yang murah untuk memproduksi benih hibrida dalam skala besar.
- 5. Acacia crassicarpa yang ditanam di Indonesia memiliki kerapatan kayu sedang-tinggi (481 kg/m3), hasil pulp yang tinggi (53,8%), dan kandungan lignin yang sedang (29,4%). Penilaian menunjukan bahwa kombinasi sampel kayu setinggi dada (1,3m) dan 25% dari tinggi komersial (sekitar 4,5m) mampu memprediksi sifat kayu keseluruhan pohon dengan baik, sedangkan sampel setinggi dada saja mampu memprediksi sebagian besar sifat kayu keseluruhan pohon.
- 6. Kami memperluas model NIR Eukaliptus global dengan menambahkan sejumlah sampel dari *E. pellita* dan 102 sampel dari beberapa spesies lain, termasuk empat spesies *Corymbia*.
- 7. Studi tentang kebun pangkas *P. maximinoi* dan *P. tecunumanii* menunjukkan bahwa peningkatan ukuran tanaman dan penurunan frekuensi panen dapat memperpanjang umur tanaman dan meningkatkan jumlah stek yang dihasilkan dalam jangka panjang.
- 8. Penelitian mengenai potensi seleksi genom dalam "full-sib" family *P. taeda* menunjukkan hasil awal yang menjanjikan. Data mengindikasikan bahwa seleksi pohon dalam family yang sama memberikan hasil prediksi yang baik dan akurasi genetik yang tinggi.
- 9. Kajian inokulasi buatan pada bibit Eukaliptus dengan patogen Austrouccina psidii menunjukkan

adanya respon yang berbeda antar spesies dengan tingkat infeksi yang bervariasi. Secara keseluruhan, *E. benthamii, E. badjensis*, dan *E. smithii* memiliki tingkat kerentanan yang tinggi, sedangkan *E. camalduensis, E. globulus*, dan *E. longirostrata* memiliki tingkat ketahanan yang paling tinggi.

- 10. Alat DLP NIRscan Nano yang relatif murah dapat digunakan secara lansung pada sample bor riap kayu, untuk memprediksi sifat-sifatnya seperti kerapatan kayu, sudut microfibril dan modulus elastisitas.
- 11. Koleksi benih dalam rangka konservasi spesies-spesies terancam di AS (pinus pitch, pinus table mountain, dan spruce merah) selesai dilakukan. Kebun benih dari hemlock timur, hemlock carolina, dan pinus table mountain telah dibangun di bagian barat Carolina Utara dan timur Tennessee.
- 12. Penelitian mengenai serangan buatan dari serangga balsam woolly adelgid (BWA) pada klon dan anakan Fraser fir mampu menentukan varisai tingkat ketahanan dari klon-klon tersebut.
- 13. Penelitian perlakuan silvikultur dalam upaya membangun kembali hutan alam hemlock timur dan hemlock carolina menunjukkan hasil yang menjanjikan. Ketersediaan cahaya, ukuran celah kanopi dan meminimalisir persaingan berpengaruh besar terhadap pertumbuhan hemlock. Faktor-faktor tersebut berperan penting dalam upaya restorasi hemlock di masa depan.
- 14. Ada banyak pencapaian penting lainnya di tahun 2020-2021. Kami memulai penelitian mengenai pemanfaatan Lidar Terestrial dan Fotogrametri dalam pengukuran percobaan genetik. Kami mendirikan kebun konservasi/kebun benih jati di Guatemala. Luis Ibarra mempelajari arsitektur genetik dari data dua populasi pohon hibrida terbesar yang pernah dianalisis. Beliau mengembangkan algoritma untuk menganalisis data dari uji keturunan "full-sib" menggunakan model linier campuran umum dari perangkat yang tidak memiliki fungsi analisis arsitektur genetik. Juan Lopez mematangkan tinjauan literatur 21 spesies pinus yang berpotensi untuk koleksi Camcore di masa depan.
- 15. Dan terakhir, di masa pandemi ini, 23 webinar yang mencakup berbagai topik telah diselengarakan dengan baik melalui Zoom. Total kehadiran yaitu sebanyak 1.312 orang. Kami juga mengadakan dua konferensi tentang manajemen kebun pangkas dan stek dari *E. dunnii* dan beberapa pinus sub-tropis. Kami menyelenggarakan 58 kunjungan virtual ke 21 perusahaan anggota, dari 11 negara dan berinteraksi dengan 443 orang. Meski demikian, kami sangat berharap dapat melakukan kunjungan secara langsung.

YEAR IN REVIEW

OxfordLanguages

Words of an

unprecedented

vear

Message From the Director

Every year, the Oxford English Dictionary chooses a word of the year, which is typically a new word or phrase that has entered the language, or one that has significantly increased in frequency of usage around the world. In 2020, OED concluded that "the year cannot be neatly accommodated in one single

word". Instead, they selected an array of words, including *coronavirus, lockdown, shelter-in-place, social distancing, bubbles, follow the science, doom scrolling, remote working, in-person, essential worker*, and *unmute*. All of these words reflect something of what Camcore experienced in 2020 and 2021, but the word that I heard the most, at least in the first

six months of the pandemic, was *unprecedented*, which means something that has never happened, been done, or been known before. Much of what we as Camcore did over 2020 and 2021 were things we have never done before, but despite the challenges, we had two successful years.

The Camcore staff did not travel during 2020 and 2021, a huge change from our normal 6 to 10 international trips per year. Instead we met with members using Zoom, Microsoft Teams and Google Meet, and we learned to unmute when we wanted to speak. We made 58 virtual technical visits to members, where we discussed Camcore research and breeding, as well as company-specific research and breeding programs. We also took the opportunity to begin offering forest genetics education and training, a new strategic goal identified in our 2019 Annual Meeting in Portugal. We offered a total of 23 webinars on various topics, attended by an average of 57 people per session. In addition, we held two virtual mini-conferences for Camcore members on rooted cutting propagation in pines and eucalypts.

As a group, we made excellent progress in a number of breeding and research projects. This is due to the fact that forestry was deemed an *essential indus*-*try* in almost all countries, and member research teams were able to contiue with field work. In our pine full-sib hybrid breeding projects, pollen collection and crossing continued for the *Pinus greggii x P. tecunuma-nii* hybrid, and for the *P. patula x P. tecunumanii* hybrid, 13 field tests were established in South Africa. In the eucalypt hybrid breeding projects, 24 new clonal trials were planted in 2020-21, bringing the total number of field trials to 35. In addition, crossing continued for Phase 2 of this project, with seeds collected from 15 new hybrid combinations, with another 10 to 15

expected in the future. In the area of *Eucalyptus* species characterization for wood properties, our members took over all aspects of the field sampling, with only *remote* guidance from the Camcore staff.

I am also very proud of the work that the Camcore staff was able to accomplish during this time. We

expanded the global *Eucalyptus* NIR model, initiated research on the use of NIR for *Eucalyptus* foliage nutrient analysis, and on the use of terrestrial lidar for genetic test measurement. We continued pollen and seed imports and exports, conducted genetic analyses, and our graduate students all made significant progress on their research. Much of this work is fearment

tured in this annual report.

Finally, despite the economic and financial challenges faced by industry worldwide, we were able to attract new members into the program in 2020 and 2021. Forest First (Colombia) joined the program as an Active Member in early 2020. Forest First is a greenfield Eucalyptus project in the eastern llanos of Colombia. In 2021, Suzano (Brazil) rejoined Camcore as an Active Member, effective in 2022. In early 2022, as this report was going to press, Arauco Brazil (sister company of Arauco Chile and Arauco Argentina) joined Camcore. This will give us five strong members in Brazil, creating the opportunity for significant synergy of breeding and research in that country. Also of note, is that at the 2020 virtual Advisory Board Meeting, we approved a new membership category called Small Active Member, for companies with less than 15,000 ha of managed plantation. Small Active Members will pay 1/2 the full annual dues, will have access to genetic material, and will contribute to breeding, testing, and research. At the end of 2021, we approved ACOFORSA (Guatemala), a forestry management organization, as our first Small Active Member. Shortly afterward, we approved Plantabal Baltek (Ecuador) as our second Small Active Member. Plantabal grows plantation balsa for parent company Baltek, which produces strong and lightweight composite building materials for high-value end-products.

In summary, it was a strange and *unprecedented* two years. In keeping with that theme, there was no 2020 Annual Report; instead this is a two-year Annual Report (2020-2021). We accomplished much over the past two years, but we are hopeful that in 2022 we will return to more normal working conditions. Visiting you and your trees *in-person* is one of the best parts of our job, and we hope to see you all soon.

Gary Hodge, Director

YEAR IN REVIEW

2020-21 Camcore Membership

Active & Associate Members

1999

2004



Argentina

- Arauco Argentina SA ٠
- Bosques del Plata, SA (Associate) ٠



Brazil

DI	aZII	
٠	Arauco Brazil	2022
٠	ArborGen (Associate)	2013
٠	Bracell	2019
٠	Klabin, SA	1987
٠	Suzano	2022
٠	WestRock Brazil	1993



Chi	ile	
٠	Arauco Bioforest	1991
٠	CMPC Forestal Mininco (Associate)	1991

China

٠	Guangdong Academy of Forestry	
	(Associate)	2013

Colombia

•	ForestFirst Colombia SAS	202
•	Smurfit Kappa Colombia, SA	198
Ecu	ador	



Ghana

Miro Forestry Ghana 2017 ٠

Plantabal Baltek (Small Active)



Belize

Ministry of Agriculture, Forestry, Fisheries ٠ and the Environment



- **El Salvador** ٠
- Centro Nacional de Tecnología Agropecuaria (CENTA)
- Guatemala Instituto Nacional de Bosques (INAB)



Indonesia **APRIL** Indonesia ٠ Araya Bumi Indonesia ٠ Sinarnas Forestry ٠ Kenya Kenya Forest Research Institute ٠



Mexico

Proteak Uno SA de CV ٠

Guatemala

٠

ACOFORSA (Small Active)

2022

2018

2019

2017

2005

2011

2006

2018

Republic of South Africa

•	MTO group Ltd	2006
٠	Mondi South Africa	1988
•	PG Bison Holdings Pty Ltd	2006
•	SAFCOL	1983
٠	Sappi Forests	1988
•	York Timbers	2010



United States of America

- ٠ USDA Forest Service (Associate) 2006
- Uruguay Montes del Plata - EuFores SA ٠ Lumin ٠

Honorary Members



Honduras

Universidad ESNACIFOR ٠

Mexico



Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias (INIFAP)

Nicaragua

Instituto Nacional Forestal (INAFOR) ٠

20 80

2022

Expanding the Camcore Eucalyptus Portfolio

Camcore was founded in 1980 with a goal to conserve genetic diversity of pine species of Central America and Mexico. Many of these species had potential as commercial plantation options, so were of interest to our industry partners. Camcore attracted new members over the years, many of which also had interest in *Eucalyptus*. We began working with eucalypts in 1996 with rangewide collections of *Eucalyptus urophylla* in Indonesia, followed by collections of *E. pellita* and *E. dorrigoensis* from 2009 to 2011. We also made a strategic decision to acquire genetic resources of more eucalypt species, including many of the most important commercial species. By the end of 2012, we had acquired provenance and family collections of 15 commercially important *Eucalyptus* and *Corymbia* species.

In 2018, we began efforts to further expand our portfolio. We commissioned Jakob Butler and Brad Potts of the University of Tasmania (Australia) to conduct a literature survey and recommend a number of lesserknown species with commercial potential. This comprehensive document, including some 3000 literature references, is available to members on the Camcore website. Using this survey, at the Annual Meeting in 2019, we conducted an exercise to rank the various species to prioritize future seed acquisitions.

In 2020 and 2021, we acquired a number of important provenance and family collections, which brings our portfolio to 24 species (Table 1). Most of these were purchases of seed from the CSIRO Australian Tree Seed Centre including *E. camaldulensis, E. tereticornis* and *E. saligna*, three of the "Big Nine" commercial species in the world. Additional species purchased were cold-tolerant *E. viminalis, E. benthamii*, and *E. macarthuri*, dry-site adapated *E. propinqua*, and the tropical species *Corymbia henryi*. However, additional species were obtained from other collaborators.

Eucalyptus amplifolia offers good growth and frost tolerance. We obtained 38 improved family seed-lots from Florida Fast Growing Trees, working with Don Rockwood (retired from the Univ. of Florida).

Eucalyptus robusta is a highly adaptable subtropical species, that tolerates flooding, and acidic and saline soils. We acquired 80 improved seedlots of *E. robusta* in collaboration with IPEF (Instituto de Pesquisas e Estudos Floestais) in Brazil, facilitated by Dr. Paulo Henrique Muller. Camcore will distribute the seed to our members for test establishment, and we will work with IPEF in the future on test measurement, data analysis, and publication of results.

Eucalyptus smithii is a cold-tolerant species, with very good wood properties, somewhat similar to *E. globulus*. We obtained small bulk seedlots from two seedling

seed orchards in Australia managed by Seed Energy. We also received donations of improved *E. smithii* from two South African members: from Mondi, a large bulk orchard seedlot, and from Sappi, a set of 61 family seedlots. In addition to those donations, we received a commitment from Lumin (Uruguay) to make a donation of family seedlots of *E. dunnii* and *E. saligna* from tested populations in Uruguay. Those species perform well in Uruguay, but the company has decided to focus future breeding on other species with wood properties more suited to their final product. Camcore performed a BLUP analysis and identified good families and candidates for selection. The genetic tests are being thinned, and we hope to collect seed in 2022 and 2023. We expect from 100 to 150 family seedlots of each species.

The donations of genetic material from Mondi, Sappi, and Lumin are much appreciated, and it is important to also note earlier donations of 139 improved *E. grandis* families from Smurfit Kappa Colombia, and Mondi, Sappi, and SAFCOL in South Africa. All of the seed acquistions discussed above, and all of these donations to the program become shared Camcore genetic material, material that all members have rights and access to utilize in the future. These donations reflect a belief among our members that a strong Camcore will benefit everyone. This broad and diverse portfolio of genetic resources provides a strong base upon which to build our pure species and hybrid breeding programs for the future.

 Table 1. Camcore Eucalyptus genetic resources through 2021.

 Species in bold are the "Big Nine" well-known commercial species. Provs = number of provenance or sources, Fams = number of family seedlots.

Species	Provs	Fams	Climate Region	Subgenus	Section
E. amplifolia	1	38	wet subtropics	Symphomyrtus	Exsertaria
E. brassiana	6	25	wet tropics	Symphomyrtus	Exsertaria
E. camaldulensis	14	84	subtropics	Symphomyrtus	Exsertaria
E. propinqua	1		dry subtropics	Symphomyrtus	Exsertaria
E. tereticornis	6	86	subtropics	Symphomyrtus	Exsertaria
E. grandis	13	168	wet subtropics	Symphomyrtus	Latoangulatae
E. longirostrata	4	45	dry subtropics	Symphomyrtus	Latoangulatae
E. pellita	6	99	wet tropics	Symphomyrtus	Latoangulatae
E. robusta	1	80	wet subtropics	Symphomyrtus	Latoangulatae
E. saligna	5	120	wet subtropics	Symphomyrtus	Latoangulatae
E. urophylla	62	1116	subtropics	Symphomyrtus	Latoangulatae
E. badjensis	2	30	cool temperate	Symphomyrtus	Maidenaria
E. benthamii	4	36	cool temperate	Symphomyrtus	Maidenaria
E. dorrigoensis	5	34	cool temperate	Symphomyrtus	Maidenaria
E. dunnii	2	36	cool temperate	Symphomyrtus	Maidenaria
E. globulus	9	175	cool temperate	Symphomyrtus	Maidenaria
E. macarthurii	3	20	cool temperate	Symphomyrtus	Maidenaria
E. nitens	5	40	cool temperate	Symphomyrtus	Maidenaria
E. smithii	4	61	cool temperate	Symphomyrtus	Maidenaria
E. viminalis	1		cool temperate	Symphomyrtus	Maidenaria
C. citriodora (Ccc)	1	30	subtropics	Corymbia	Maculatae
C. henryi	1		subtropics	Corymbia	Maculatae
C. maculata	1	30	subtropics	Corymbia	Maculatae
C. torelliana	2	32	subtropics	Corymbia	Septentrionales

Eucalyptus Hybrid Project

The first phase of *Eucalyptus* hybrid crosses started in 2012, when 12 members with eucalypt research and operational programs decided to work under Camcore's guidance. In 2017, most of the Camcore members had done some work with the genus and decided to initiate a second phase. In both phases, the idea was to test many hybrid combinations, establish progeny and/or clonal tests, and select the best clones for commercial propagation. Camcore members continued making progress in both phases during 2020 and 2021. In previous annual reports, we provided detailed information about the program background. In this report, we limit the information to advances accomplished in the last two years.

First phase

In South America, Arauco Chile and CMPC planted progeny trials and Klabin, Lumin and Smurfit Kappa Colombia established hybrid-seedling selection blocks (HSSB) with the seeds received from the crosses made by the 12 participating members. Smurfit cut their HSSB and planted three clonal trials with E. grandis x E. globulus, E. grandis x E. pellita and E. urophylla x E. pellita in 2020 (Table 2, see also photo on p. 45). Lumin and Klabin will cut their HSSB in 2022 and Arauco Chile will cut the progeny trials in 2024 to test the best clones in clonal trials. Other hybrids planted in the progeny trials and blocks are *E. grandis* x *E. benthamii*, *E. grandis* x *E. saligna*, *E.* urograndis x *E.* dunnii, *E.* urophylla x *E.* dunnii, and E. nitens x E. pellita.

South African members propagated hybrid plants in the nursery after screening them in the HSSB. Their great accomplishment was the establishment of 32 clonal trials in the last three years as shown in the table below. Selected clones in the trials will be available for the 12 members taking part in the first phase of this program.

Second phase

Many members made pollen collections, pollen shipments, controlled pollination and capsule harvesting in 2020 and 2021. Smurfit Kappa Colombia provided seeds of 20 families of E. grandis x E. urophylla; WestRock, 20 families of E. dunnii x E. benthamii; Sappi, 13 families of the same hybrid; York, 10 families of E. grandis x E. nitens; and Klabin, 10 families of E. urograndis x E. dunnii, eight families of C. torelliana x C. citriodora, and two families of C. torelliana x C. henrvi. There are also seeds of 25 families of E. grandis x E. nitens received from Mondi. All these seeds are already in Camcore's cold room in Raleigh. Sinarmas in Indonesia collected seeds of several hybrids that will be shipped to the US in the first months of 2022; these hybrids are E. pellita x E. dunnii, E. pellita x E. urophylla, E. pellita x E. globulus, (E. pellita x E. camaldulensis) x E. dunnii, and (E. pellita x E. camaldulensis) x E. globulus. Montes Del Plata in Uruguay will ship seeds of E. dunnii x E. dorrigoensis in the first semester of 2022. In the second half of 2022, Camcore will be able to start distributing seeds of all these hybrids to the interested members, whose land has potential for growth and adaptation of the various hybrids.

MTO in South Africa made crosses of *E.* grandis x *E.* benthamii in 2021 and is making more crosses in the beginning of 2022. KEFRI in Kenya crossed *E.* urophylla x *E.* camaldulensis in 2021. Sappi made crosses of *E.* dunnii x *E.* amplifolia. Arauco Bioforest in Chile is making crosses of

Table 2. Eucalypt hybrid clonal trials planted by Camcore members in 2019, 2020, and 2021.

Hybrid		Sapp	i	I	Mond	i	S	AFCC)L	Me	erens	ky		York			SKC		Total
	19	20	21	19	20	21	19	20	21	19	20	21	19	20	21	19	20	21	
GraxGlo	2			2	2	3			1					2			1		13
GraxSmi	1	1		1		1			1		1			2					8
GraxDun	1	1		1				1	1					2					7
GranxPel	1					1	1		1	1							1		6
UroxPel																	1		1
Total	5	2		4	2	5	1	1	4	1	1			6			3		35

Eucalyptus globulus x E. benthamii, and will make crosses of *E. nitens x E. smithii* with pollen that will be provided by Sappi. APRIL Indonesia will make crosses of *E. pellita x E. grandis* and *E. pellita x E. urophylla* with pollen received from Klabin. Proteak in Mexico is crossing *E. urophylla x E. grandis* and Mondi in South Africa *C. torelliana x C. maculata*. Finally, Arauco Argentina is waiting for pollen production of *E. longirostrata*

Multi-site Corymbia Analysis in Africa

Corymbia, comprising over 113 tree species, is a sister genus to Eucalyptus. Known as spotted gums (C. citriodora, C. maculata and C. henryi) and cadaga (C. torelliana), these Corymbia species are of commercial importance in the Australian states of Queensland and New South Wales due to their superior survival and growth across a broad range of edaphic and climatic conditions. Our members Sappi amd Mondi from South Africa and former members Merensky (South Africa) and Chikweti (Mozambique) participated in the African Camcore Corymbia species trial series. Members planted two trials for each of three Corymbia species. In 2020, we performed an across-site analysis for each species in the region, to estimate genetic parameters, and to rank families. For our and *E. major* in its own trials to produce seeds of *E. grandis* x *E. longirostrata, E. urophylla* x *E. longirostrata* and *E. grandis* x *E. major.* By the end of 2022 and beginning of 2023, Camcore members will have seeds of at least 22 hybrid combinations to be tested in clonal trials.

Congratulations to all Camcore members who have been working hard to make this program successful, especially with all the challenges present during these two years of the pandemic.

analysis, we used diameter at breast height at 3 years of age (DBH3). DBH was standardized by rep and site to a mean of 100% and a standard deviation proportional to the observed coefficient of variation. Single-site linear mixed models were estimated and tests with low heritability (h²) and survival were excluded. A multiple-site linear mixed model was used to estimate genetic parameters including, h², Type B genetic correlations (r_{Bq}) to assess GxE, and family ranks (BLUPs). The results are summarized in the table below. This information has been used by Sappi to convert some of their tests into seedling seed orchards. In the near future, we expect to replicate this analysis with the Corymbia tests that were established in South America.

Species	Test	Region DBH3 HT3 DBH5 H		HT5	h²	r _{Bg}		
	Sappi	Zululand, S.Africa	12.2		14.0			
	Mondi1	Zululand, S.Africa	8.0	8.1	10.3	10.3		
C. maculata	Mondi2	Zululand, S.Africa	8.5	7.1	10.7	10.0	0.23	0.62
	Merensky	Limpopo, S.Africa	9.7	13.4				
	Chikweti	Mozambique	6.2	6.1				
	Sappi1	Zululand, S.Africa	12.0		13.8			
	Sappi2	Zululand, S.Africa	8.9				0.34	0.74
C to vollion o	Mondi1	Zululand, S.Africa	6.4	4.7	7.8	5.6		
C. toreillana	Mondi2	Zululand, S.Africa	6.4	4.2	8.7	6.2		0.74
	Merensky	Limpopo, S.Africa	9.2	11.2				
	Chikweti	Mozambique	4.4	4.0				
	Sappi	Zululand, S.Africa	13.1		14.9			
C. citriodora	Mondi1	Zululand, S.Africa	7.7	7.3	10.1	10.6	0.04	
	Mondi2	Zululand, S.Africa	8.1	6.6	10.4	10.8	0.34	0.76
	Merensky	Limpopo, S.Africa	9.4	12.4				

Summary of growth data and genetic parameters for *Corymbia* trials in Africa. Traits were DBH (cm) and Height (m) for ages 3 and 5 years, and genetic parameters are heritability (h^2) and Type B genetic correlation (r_{eq}).from a multiple-site analysis.

Pine Hybrid Project Update

Camcore members continue to work on the pine hybrid program. Advances in the *Pinus patula* x *P. tecunumanii*, *P. tecunumanii* x *P. greggii* and *P. caribaea* x *P. tecunumanii* hybrids were made during 2020 and 2021. In this and previous annual reports, there is detailed information about the development of this program, including results from the 90 bulk pine hybrid trials planted by members.

P. patula x P. tecunumanii

Sappi and Mondi were very busy propagating *P. patula* x *P. tecunumanii* plants in their nurseries. In addition to the hybrid seed sown by Mondi in 2018, Sappi sowed three batches of the hybrid seed in its Shaw Research Centre Nursery in February and March of 2020. This seed was collected from crosses made during 2013 to 2015.

Sappi produced 4,532 germinants, representing 97 crosses made in South Africa and 16 crosses made in Colombia. A total of 113 families were available for hedges (Report by Lelethu Sinuka, Wayne Jones and Noku Maplanka, July 2020). Sappi moved the seedlings to Mondi's Mountain Home nursery in June 2020, where the plants were managed for four months and converted to hedges in October. These hedges together with the ones previously grown by Mondi in 2019 and 2020 (seeds sown in July and October of 2018) were the source of cuttings for the progeny trials in South Africa.

Based on the seedlings available at Mondi in October 2020, Camcore staff in Raleigh recommended bulking the 36 families with fewer than 11 genotypes per family and keeping the identity of the 76 families with 11 or more genotypes per family for hedge management. Rooted-cutting propagation started in February 2021. Good families within the bulk lots in the trials can still be identified, since all the parents have been fingerprinted.

With the inventory of rooted cuttings sent to Camcore in August 2021, Camcore staff helped Mondi to optimize the distribution of plants to members for progeny trials. The number of families per trial for each member varied between 55 and 61, with an average number of trees close to 3,900 per trial. The test design was 3-tree row plots, and with full-sib families in 6, 9 or 12 replications, depending on the number of plants available. The idea of the design is to facilitate conversion of the progeny trials to seedling seed orchards at eight years of age for production of F2 seeds. The South African members planted 13 trials in 2021 and will plant four more in the beginning of 2022. Great work!

P. tecunumanii x P. greggii

Smurfit Kappa Colombia progressed in making crosses of *P. tecunumanii x P. greggii* in its seed orchards, work that commenced in 2016 and ended in 2020. In July 2020, Martha Salas of SKC sent us an inventory of the hybrid seeds already collected from previous years' crosses. From a total number of 78,540 seeds harvested, 17,550 were filled (22%), representing 114 families of the hybrid. We developed a seed distribution plan for members to define the number of seeds available to ship to Argentina, Brazil, and Colombia. Each member will receive enough seeds to establish and manage hedges for vegetative propagation for planting trials. We already have the seeds here in Raleigh and we will send them to the members in the first half of 2022. The first set of progeny trials will be planted in 2023 with the same design used for P. patula x P. tecunumanii in South Africa and with the same intent to convert them into seedling seed orchards for F2 seed production.

Once the members receive and germinate the seeds in their nurseries, we will meet with them to look at the number of seedlings per family to define a propagation plan for bulks and individual families. Genetic markers will be used to fingerprint the parents of both species in the Colombia and Brazil seed orchards in order to verify cross ID in the progeny trials.

Smurfit Kappa Colombia will collect one more batch of cones in the *P. tecunumanii* seed orchards from additional hybrid families at the end of 2022 and will send them to Camcore US. The seeds will then be distributed for the establishment of more progeny trials. Very exciting progress!

P. caribaea x P. tecunumanii

We have been talking about the exciting potential of the *P. caribaea* x *P. tecunumanii* hybrid for a few years now. Volume growth and stem



Jadrian Matroos of MTO working on the establishment of a full-sib *P. patula* x *P. tecunumanii* trial in the southern Cape of South Africa in 2021.

form of the trees have been measured in multiple Camcore hybrid trials with excellent results. In 2021, we met with several members and defined two main projects with this hybrid.

The first project is focused on the establishment of small pilot plantations to provide better knowledge of the hybrid performance and management in commercial stands and in the nursery. Mondi, Sappi and Safcol provided pollen of Pinus caribaea var. hondurensis from 18 males in their own seed orchards to Camcore. York Timbers used part of the pollen for more than 100 crosses made on 10 females of P. tecunumanii in its Goedgeloof seed orchard in August 2021. Lizette De Waal with York sent the rest of the pollen to Camcore US for distribution to other members. Currently, we are in the process of exporting this pollen to Klabin, Brazil, where it will be used for crosses with P. tecunumanii in 2nd generation trials that show good flowering. Arauco Argentina will also receive part of the pollen to make crosses with P. tecunumanii in its clonal seed orchard. Once the hybrid seeds are produced, they will be shipped to participating members for the establishment of pilot plantations. Sappi and Mondi took advantage of the opportunity to do a flowering assessment in their P. caribaea seed orchards during pollen collection in order to learn more about the species. Now these companies have better knowledge of male and female flowering times as well as the number of female strobili per tree. This is useful information for the implementation of a mating plan.

The second project is a full-sib breeding effort, similar to work described above for the previous two hybrids. The objective is to produce seeds of 300 full-sib families for the establishment of progeny trials to identify and deploy the best families for commercial stands. The crosses will be made in the three seed orchards of P. caribaea var. hondurensis owned by Mondi, Sappi and SAF-COL. Other members in South Africa and South America will provide pollen of low- and high-elevation P. tecunumanii. Camcore members will meet early in 2022 to define the mating plan in order to start pollen collections and crosses in 2022 and 2023. Some crosses with P. caribaea var. bahamensis will be made to include some individuals of this hybrid as controls in the progeny trials. The progeny trials will be converted to seedling seed orchards for F2 seed production.

This hybrid shows great adaptability to different environmental conditions and may be a promising alternative taxon. In view of global warming, we think this could be an excellent option for Camcore members in the future.

Hybrid Tree Genetic Parameters

Luis Ibarra recently completed his PhD dissertation on the genetics of hybrid trees. Luis' full dissertation is available on the Camcore website and in the NC State library, and manuscripts are being prepared for publication in peerreviewed journals. This report provides a brief summary of some of the important results.

Introduction

Camcore has been working with pine hybrids since 2005, and with eucalypt hybrids since 2012. Hybridization offers the opportunity to combine desirable traits from different species into new varieties, and hybrid forest trees have shown great potential in many environments. However, the genetic control of hybrid tree performance is not well understood. Here we report results from large studies of two important tree hybrids: *Pinus patula* x *P. tecunumanii* in South Africa, and *Eucalyptus globulus* x *E. nitens* in Chile.

Eucalyptus globulus x E. nitens

In Chile, the most common hardwood species used across the country are *E. globulus* and *E.* nitens. Both species are well adapted to the Chilean environments and climates. The choice between E. nitens and E. globulus for commercial plantations depends mainly on the environment. Eucalyptus globulus is considered the premium species for pulp and paper production due to its good growth and excellent overall pulpwood properties. However, the relatively poor frost tolerance of this species in the south of the country restricts its use. On frost-prone sites, E. globulus is replaced by E. nitens, a more frost-tolerant species which also exhibits extremely fast growth. Hybridization of these two species offers the chance to combine the best traits of the two species, and this effort has been a focus of the breeding program of Arauco Bioforest.

Materials and Methods

A large clonal population of *E. nitens* x *E. globulus* hybrids (GloNi) was produced by the breeding program of Arauco Bioforest. The population had more than 1200 clones derived from 28 full-sib families formed with a mating design crossing 12 *E. nitens* mothers and 8 *E. globulus* fathers.

Clonal trials were planted in 12 locations in the

Arauco region and 17 tests in the Valdivia region. The Arauco region has mean annual precipitation (MAP) of 1360 mm, a minimum mean monthly temperature around 6.5 °C, and an average of 3 frost days per year. The Valdivia region has MAP = 1900 mm, a minimum mean monthly temperature around 3.6 °C in the coldest months of winter, and an average of 10 frost days per year. Arauco is better suited for E. globulus, and Valdivia is better suited for E. nitens. All tests were 10-replication Randomized Complete Block designs with single-tree plots. Traits measured at 8 years of age were height and DBH (used to estimate volume), along with three important wood traits (predicted with NIR models): basic density (kg/m³), pulp yield (%) and Specific Consumption (m³ wood/ton pulp). Volume data from each test site was standardized to a mean of 100%.

Quantitative genetic analysis was done using a linear model with fixed effects for site and replication, and random effects for General Hybridizing Ability for E. globulus and E. nitens (GHA_{GLO} and GHA_{NIT}, respectively), Specific Hybridizing Ability (SHA), and Clonewithin-family (Clw), along with the corresponding genetic x environment interaction terms. These random effects are analogous to General and Specific Combining Ability (GCA and SCA) in the pure species context. A parent model was used for the analysis to allow for the possibility of different contributions of genetic variance from the two parent species. Analyses were conducted with ASREML, and variances associated with all random effects were estimated, along with genetic parameters broad-sense (clonal) heritability (H²) and clonal Type B genetic correlation to measure GxE.

Results and Discussion

In both regions, mean performance of the GloNi hybrids was intermediate to pure species *E. globulus* and *E. nitens* for volume growth and all wood traits. However, for all traits, total clonal genetic variation was substantial, and there is potential for large genetic gain from clonal selection. Clonal heritability was generally high for both volume and wood traits in both regions (Table 3). For volume, clonal heritability was $H^2 > 0.50$ in both regions, and for the wood traits mean clonal heritability was $H^2 = 0.50$ in Arauco, and $H^2 = 0.38$ in Valdivia. For all traits, there was very little GXE across tests within region, with clonal Type B genetic correlation ranging from $r_{BG} = 0.86$ to 0.99.

Table 3 also presents the breakdown of total clonal genetic variance into the various levels

Table 3. Genetic parameters of *E. nitens* **x** *E. globulus* hybrids. Estimates are from combined site analysis for standardized volume (stVol), Basic density (BD), Specific Consumption (SC), and Pulp Yield (PY) in Arauco and Valdivia regions. GHA_{NIT} or GHA_{GLO} is the General Hybridizing Ability variance due to *E. nitens* female or *E. globulus* male. SHA is the Specific Hybridizing Ability variance. Clw is the clonal variance within family. G is the total genetic variance. Genetic variation is expressed in units of genetic standard deviations (σ). H² is the broad-sense heritability, r_{BG} is the type-B genetic correlation for total genetic (clonal) variance.

Region			Ge	H ²	r _{bg}			
	Trait	GHA _{NIT}	GHA _{GLO}	SHA	Clw	G		
Arauco	stVol (%)	21.06	-	-	39.89	45.10	0.54	0.92
	BD (kg/m ³)	4.50	6.76	-	7.91	11.34	0.36	0.93
	SC (m ³ /ADt)	0.04	0.08	0.04	0.10	0.14	0.53	0.99
	PY (%)	0.29	0.53	0.32	0.59	0.90	0.6	0.92
Valdivia	stVol (%)	27.37	-	-	42.75	50.76	0.51	0.89
	BD (kg/m ³)	3.59	3.56	1.81	5.91	7.99	0.22	0.86
	SC (m ³ /ADt)	0.05	0.04	0.02	0.07	0.10	0.36	0.86
	PY (%)	0.43	-	0.14	0.54	0.70	0.55	0.94

of genetic effects. In Table 3, genetic variation is expressed in units of genetic standard deviation (σ) , as the σ values are in the measurement units of the trait, and are directly related to the potential for genetic gain from the different sources of genetic variation. For volume, Clone-within-family (Clw) was the largest source of genetic variation (Table 3). However there was also important variation for GHA_{NIT} , but zero variation estimated for GHA_{GLO} . In other words, there were some *E. nitens* parents which on average produced hybrid clones with superior volume growth, while there was no impact of E. globulus parents on hybrid progeny volume growth. For wood properties, Clone-within-family variation had the most impact for all traits in both regions, and SHA variation, while present, was relatively small. Also, for most traits there was important variation associated with both GHA_{NIT} and GHA_{GLO}. Interestingly, in the Arauco regions (where E. globulus is better adapted than E. nitens), the variation associated with GHA_{GLO} was larger than for GHA_{NIT} for all three wood traits. In the Valdivia region (where E. nitens is better adapted than E. globulus), GHA_{NIT} variation was roughly equal to GHA_{GLO} variation for basic density and specific consumption, and much larger for pulp yield (due to a zero estimate for variation of GHA_{GLO}).

Finally, there were estimates of pure species GCA available from the Arauco breeding programs, and these were compared with the GHA

14

estimates. For volume growth, the correlation of GCA-GHA was r = 0.68 and 0.69 for *E. nitens* parents in the two regions. This correlation could not be estimated for *E. globulus* due to a zero estimate for GHA_{GLO} variance for volume. For wood traits, there was a strong correlation of GCA-GHA (r = 0.82 to 0.99) for *E. globulus* parents in the Arauco region, and a strong correlation for *E. nitens* parents in the Valdivia region (r = 0.88 to 0.92).

Pinus patula x P. tecunumanii

In South Africa, *Pinus patula* has been the primary commercial pine species for over 100 years. The species exhibits very good growth and excellent wood quality, is cold tolerant and adapted to a wide range of climatic conditions across the country. A limiting factor for its continued use in the country is its susceptibility to pitch canker fungus (*Fusarium circinatum*), which has become an established pathogen over the past two decades. Research indicates limited genetic variation for tolerance to the pathogen within the species.

Pinus tecunumanii is a tropical/subtropical species widely distributed in Mexico and Central America. In South Africa, *P. tecunumanii* is replacing *P. patula* (PAT) on some sites due to its faster growth, better drought tolerance, higher wood density, and high tolerance to *F. circinatum*. There are two subpopulations or varieties, high elevation (TECH) and low elevation (TECL). In general, the varieties exhibit similar characteristics, but TECH

Table 4. Genetic parameters of *P. patula x P. tecunumanii* hybrids. Hybrids with high-elevation and low-elevation *P. tecunumanii* were studied (TECH and TECL, respectively). Estimates are from combined site analysis for standardized volume (stVol) and Modulus of Elasticity (MOE). GHA_{PAT} or GHA_{TEC} is the General Hybridizing Ability variance due to *P. patula* female or *P. tecunumanii* male. SHA is the Specific Hybridizing Ability variance. Clw is the clonal variance within family. G is the total genetic variance. Genetic variation is expressed in units of genetic standard deviations (σ). H² is the broad-sense heritability, r_{BG} is the type-B genetic correlation for total genetic (clonal) variance.

Company	Hybrid	Trait		Gen		H ²	r _{bg}		
			GHA _{PAT}	GHA _{TEC}	SHA	Clw	G		
SAFCOL	PATxTECH	stVol (%)	8.71	-	11.20	na	25.50	0.31	0.71
		MOE (Gpa)	0.66	0.34	0.43	na	1.36	0.20	0.76
	PATxTECL	stVol (%)	7.15	9.32	5.00	na	19.40	0.18	0.72
		MOE (Gpa)	0.64	0.37	0.61	na	1.60	0.22	0.71
Sappi	PATxTECL	stVol (%)	7.36	11.10	1.30	19.4	23.80	0.24	0.91

is typically intermediate between TECL and PAT for most traits.

The interspecific hybridization of *P. patula* with *P. tecunumanii* offers the potential to combine the well-known advantages of these species. This report summarizes some results from the breeding progams of SAFCOL and Sappi Forests.

Materials and Methods

The SAFCOL hybrid population consisted of seedlings from full-sib families of both hybrid varieties. For PATxTECH, there were 40 full-sib families derived from 20 PAT and 11 TECH parents. For PATxTECL, there were 97 full-sib families derived from 17 PAT and 15 TECL parents. Field tests at SAFCOL used a randomized completed block design, with 6 replications per site, and plots of 1x6 trees per family. In these tests, 8-year measurements for growth were taken, along with measurements of Modulus of Elasticity (MOE) measured on standing trees using the TreeSonic acoustic wave velocity tool. Five tests were established, but one test was at a much higher elevation than the others, and it represents a different environment. The results of the other four tests will be discussed here.

The Sappi hybrid population was clonally replicated progeny of the PATxTECL hybrid. There were 271 clones from 30 full-sib families derived from 5 PAT and 11 TECL parents. Two tests were established using an Alpha-lattice design with 3 replications per site and plots of 1x4 trees. There was an average of 127 clones per full-sib family, and 12 ramets per clone. In these tests, 8-year measurements of growth were taken.

Quantitative genetic analysis was done as described above for the GloNi hybrids. For the Sappi data, the linear model included random effects for General Hybridizing Ability for *P. patula* and *P. tecunumanii* (GHA_{PAT} and GHA_{TEC}, respectively), and Specific Hybridizing Ability (SHA), and Clone-within-family (Clw), along with the corresponding genetic x environment interaction terms. For the SAFCOL data, the Clone-within-family terms were deleted from the model. Analyses were conducted with ASREML, and variances associated with all random effects were estimated, along with genetic parameters broad-sense (clonal) heritability (H²) and clonal Type B genetic correlation to measure GxE.

Results and Discussion

In general, the PATxTECL hybrids showed slightly better growth and higher MOE than the PATxTECH hybrids, reflecting the differences between the two *P. tecunumanii* varieties.

The PATxTECH variety was studied only in the SAFCOL seedling tests. For 8-year volume growth, there was substantial total genetic variation, with $H^2 = 0.31$, and moderately low GxE (R_{BG} = 0.71) (Table 4). Table 4 also presents the breakdown of total genetic variation into the model sources, and these are expressed in genetic standard deviations (σ), as mentioned above for the GloNi analysis. There was important variation due to P. patula parentage (GHA_{PAT}), however, there was a zero estimate for variation of GHA_{TECH}, indicating that the P. tecunumanii (high-elevation) parentage has no impact on the hybrid volume growth. For this hybrid, it appears that SHA variation is very important, as it is substantially larger than the variaton of GHA_{PAT}. For MOE, GHA_{PAT} was the most important source of genetic variation, followed by SHA. Variance of GHA_{TECH} was detected, but it was of lower imporance than the other two sources.



Figure 1. GHA vs GCA relationship for standardized volume in the SAFCOL hybrid population of *P. patula* x *P. tecunumanii*. A: *P. patula* GHA vs GCA on *P. patula* x *P. tecunumanii* (LE). B: *P. patula* GHA vs GCA on *P. patula* x *P. tecunumanii* (LE). C: *P. tecunumanii* GHA vs GCA on *P. patula* x *P. tecunumanii* (LE). The relationship of *P. patula* x *P. tecunumanii* (LE) was not plotted since there was a zero estimate for variance of GHA_{PAT}.

The PATxTECL variety was included in both the SAFCOL seedling progeny tests, and in the Sappi clonally-replicated progeny tests. Volume data was available for both datasets, and the genetic parameter estimates are similar, giving extra confidence in the results. Broad-sense heritability for volume was moderate ($H^2 \approx 0.20$) and genotype x environment interaction was moderately low ($r_{BG} = 0.72$ to 0.91). The largest source of genetic variance for volume is GHA_{TECI}, but GHA_{PAT} is also very important. In both datasets, SHA variance for volume was detected, and was moderate in the SAFCOL tests, and very low in the Sappi tests. The Sappi tests also allowed the estimation of Clone-within-family variance, and this was moderately high. Genetic theory allowed the use of these parameters to estimate epistatic genetic variance, and it appears that this is low. In other words, the Clone-within-family variance appears to be mostly due to the additive effects inherited from the two parents. For the wood trait MOE, variance of $\mathrm{GHA}_{\mathrm{\scriptscriptstyle PAT}}$ and SHA effects was high, and variance of GHA_{TEC} was moderate.

Pure species GCA estimates from the Sappi breeding program were available, and there are useful GCA-GHA correlations for volume ($r \approx$ 0.67) for TECL parents and PAT parents of both types of hybrid progeny (Figure 1). For MOE, pure species GCA for the *P. patula* parents was a good predictor of GHA for both hybrid types (r =0.56 for hybrids with TECH, and r = 0.72 for hybrids with TECL). Interestingly, there was zero GCA-GHA correlation for TECL parents for MOE.

Summary and Outlook

These quantitative genetics studies are among the largest populations of hybrid trees ever examined in the literature, both in terms of number of parents and crosses, and in field tests. Despite this, the genetic parameters must be interpreted with some caution. A simulation experiment done as part of this research indicated that a mating design of 24 parents per species gave generally reliable parameter estimates. Smaller designs, say with 12 parents per species, may sometimes at random produce very misleading parameter estimates. Nevertheless, some general conclusions can be drawn from these two real-life tree hybrid experiments. The data indicate that different parent species can contribute different amounts of genetic variance to hybrid progeny, depending on the trait and the environment. In some cases, a parent species may have very little impact (perhaps zero) on variation among hybrid progeny for a given trait. Some knowledge of hybrid genetic architecture can be used to guide hybrid mating strategy, such as determining the number of parents, and numbers of crosses per parent. In addition, there will often be some correlation between pure species GCA and hybrid GHA. These GCA-GHA correlations can be used to help guide selections of parents that will tend to produce better hybrid crosses in future F1 hybrid mating designs.

Teak Update

A great accomplishment in the teak program in 2020 and 2021 was the establishment of a Camcore conservation bank in Guatemala. A set of 99 trees was selected in a four-hectare provenanceprogeny trial in 2019, with the excellent trees coming mainly from Indonesia and Costa Rica sources. In 2020 and 2021, Elmer Gutiérrez and Josué Cotzojay collected scions of these trees and used them to make grafts. A conservation bank of 2 ha was planted with 5 ramets from each of the 99 selected clones in a flat area with very fertile and welldrained soils in the Department of Escuintla. Elmer coordinated and supervised all the activities required for the establishment of the bank: plant transportation, weeding, harrowing, tracing, planting, and fertilizing. We expect a small harvest of seed from this bank as early as the end of 2022.

Out of the 152 selected trees of teak in a progeny-provenance trial in Colombia, 36 clones have been propagated through rooted cuttings at Smurfit Kappa Colombia for the establishment of a conservation bank on the company's land, probably by the end of 2022. Thanks to SKC for safeguarding this valuable Camcore genetic material.

Gmelina Update

Using seeds of *Gmelina arborea* collected from the Camcore clonal seed orchard in Forestal Monterrey Colombia in 2018, four progeny trials were shipped to Miro Forestry Ghana, two to KEFRI in Kenya, and one to Sinarmas in Indonesia during 2019, 2020 and 2021. The seeds are being used for the establishment of 2^{nd} generation progeny trials. Miro Forestry Ghana also planted the 55 Camcore clones of *G. arborea* received from Forestal Monterrey in 2018 in two clonal trials located on different sites in May of 2020. Smurfit Kappa Colombia received the same 55 clones, propagated them through rooted cuttings and planted them in a conservation bank.

In conversations with Olman Murillo, Director of GENFORES in Costa Rica, we agreed to exchange selected clones of the species for mutual benefit to both programs. GENFORES will receive 50 clones selected by Camcore from provenance–progeny trials and Camcore will receive 60 clones selected in Costa Rica. The



Elmer Gutiérrez standing in the Camcore teak conservation bank in Escuintla, Guatemala.

In 2021, seeds of teak collected from the Guatemalan progeny trials were sent to KEFRI for 2nd generation trials in Kenya. In 2022, we expect to complete a BLUP analysis of four teak trials for Proteak, Mexico. We expect a candidate list of 450 trees to make a final selection of between 80 and 100 trees. With the selections from Colombia, Guatemala and Mexico, Camcore will have more than 200 clones available for clonal trials.

clones of GENFORES were selected from clonal trials that were established with seeds from seven provenances in Southeast Asia, plantations in Costa Rica, and a Ston Forestal's clonal seed orchard. The material will be shipped directly from Costa Rica to Colombia and vice versa.



Conservation bank of *Gmelina arborea* planted by Smurfit Kappa Colombia.

Towards Adelgid Resistant Fraser Fir

Austin Thomas recently completed his PhD dissertation on the biology of the balsam woolly adelgid, which attacks Fraser fir, a native species of North Carolina. Austins' dissertation is available on the Camcore website and in the NC State library, and manuscripts will be published in peerreviewed journals. This report provides a summary of one aspect of Austin's work, genetic resistance to the adelgid.

Introduction

Fraser fir, Abies fraseri, (Pursh) Poir., is a tree endemic to the Southern Appalachians and natural stands are found only in a few isolated populations at high elevations. Fraser fir is also the premier Christmas tree species grown in North Carolina and is prized for its superior form, branch density, and post-harvest needle retention. The species is threatened by an introduced phloemfeeding insect, the balsam woolly adelgid, Adelges piceae, Ratzeburg (BWA), and has experienced severe decline throughout its natural range in the 1960s and 1970s with smaller subsequent waves of mortality. The introduction of BWA has also necessitated increasing pesticide usage among Christmas tree growers in order to protect their product. Despite multiple attempts to introduce classical biocontrol agents to control BWA in both natural stands and Christmas tree plantations since the 1960s, none of these introductions have been successful. Host resistance breeding has remained largely unexplored, and was a focus of Camcore's work in this area starting in 2014.

Materials and Methods

The balsam woolly adelgid induces a myriad of negative responses on fir, causing gouting on branches, loss of apical dominance, reduced growth, the formation of abnormal wood called rotholz, and, ultimately, tree mortality. All of these host tree responses were assessed on 37 Fraser fir clones from 14 open-pollinated families and natural stand selections. Ramets of the clones were grafted onto potted rootstock in 2014, artificially infested with BWA in 2016, and evaluated in 2018. Trees were then re-infested and re-evaluated again in 2019. In addition to the five major negative host responses, changes in foliar chemistry related to BWA infestation were evaluated in needle samples collected over a 20-week period in 2019. Finally, lateral meristem tissue sampled pre-infestation and post-infestation were analyzed via RNASeq.

Results and Discussion

A broad range of responses to BWA infestation were observed among families and clones. Clonal response ranged from apparent extreme susceptibility with substantial ramet mortality to putative resistance, where no significant reduction in the growth rate of infested trees was observed and almost no gouting was present on any individual ramet. Family heritability estimates based on this single site analysis ranged from $h_{\rm f}^2 = 0.14$ for loss of apical dominance to $h_{\rm f}^2 = 0.85$ for gouting density. There was a stark contrast between the poorest and best performing clones. The highest performing clones were noticeably healthier looking trees that could be visually identified among other study trees from a distance of 10 or so feet.

Clones were grouped into three performance categories (good, intermediate, and poor) based on their performance assessments for further foliar chemistry and RNASeq analysis. Foliar concentrations of two sesquiterpene compounds in particular, camphene and humulene, were found to be induced two-fold and four-fold respectively after 20 weeks of BWA infestation in good performing clones. No significant changes in foliar sesquiterpene concentrations were found in intermediate or poor performance groups, or in uninfested controls. This finding of increased foliar sesquiterpene concentrations in healthy BWA-infested Fraser fir is in line with observations made by Carlo et. al. (2006) in natural stands. It is not clear that sesquiterpenes are the mechanism of observed putative resistance to BWA. However, the consistent correlation between induced foliar sesquiterpenes and apparent BWA resistance means that foliar chemical analysis may be a useful tool for rapidly and inexpensively screening Fraser fir trees for resistance in future breeding cycles.

Surprisingly, RNASeq analysis of lateral meristem tissue pre- and post-BWA infestation did not reveal any transcription factors specifically related to sesquiterpene synthesis. However, a small subset of differentially regulated genes (DEGs) was identified in poor and good performance categories. Significant differential expression of genes related to a phloem feeding insect (PFI) response and associated salicylic acid (SA) signaling, along with upregulation of genes related

to guaiacol synthesis, indole-3-acetic acid (IAA) inactivation, and cell wall remodeling, were found only in good performing, putatively resistant clones. We believe these data provide evidence that good performing clones exhibit a highly targeted defensive response to BWA attack that is absent in poor performing clones.

Outlook

In collaboration with the NCSU Christmas Tree Genetics Program, Camcore hopes to facilitate additional research relating to BWA resistance in Fraser fir in the near future. To truly confirm BWA resistance in good-performing Fraser fir clones and families, studies of adelgid fecundity and survival on putatively resistant fir are required. Also, a more extensive, multi-site progeny trial is warranted before attempting to integrate BWA resistance into the selection process for the next generation of improved Fraser fir Christmas trees.



Artificial infestation of Fraser fir clones in the screening study. Grafted clones are in pots below the wooden frame supporting Fraser fir logs naturally infested with BWA. Crawlers (mobile first stage nymphs) hatch from eggs on the logs and "rain down" onto the grafts below to initiate infestations for the study.

Members Take Charge of Camcore Wood Sampling Efforts

From 1980 to 2000, Camcore only occasionally sampled wood quality, and the results were generally limited to density determined from cores or wedges. The samples were extracted by members and sent to Raleigh for analysis. In the early 2000s, Camcore expanded research to include NIR-estimated chemical components. Extracting and processing wood shavings with drills was easier than using solid wood pieces, and this became the standard method to produce wood powder samples for NIR scanning. The Camcore team also tested and deployed the Fakkop TreeSonic acoustic wave sampler and the IMF Resistograph drill to estimate wood MOE and density, respectively. Since 2015, Camcore has been routinely using these non-destructive sampling methods in 8-year-old pine hybrid trials and 5-year-old euc species trials. Typically, a member of the Raleigh staff would travel to visit a member and work with a company team of 5 to 10 workers to do the sampling. The heavy equipment, including the Resistograph, TreeSonic probes, increment borers, and multiple drill bits was carried from the US, and always drew much curiosity from airport security! In recent years, some members have been buying their own equipment, either a resistograph, and/or TreeSonic



Mthokozisi Brian Ntshangase (right) with the Tree Sonic, and Mthokozisi Nicholas Zondi (left) with the Resistograph in a Sappi trial in KwaZulu-Natal, South Africa.

unit. In 2020, several sampling trips were canceled due to travel restrictions, so members began to complete the wood studies without on-site help from a Raleigh staff member. Companies used equipment they already had or borrowed from nearby members. In some cases, we shipped equipment to members from Raleigh. We hope that members will continue to build their inventory of sampling tools because mailing the heavy yet delicate equipment is undesirable. We still process and scan wood samples in the lab at Raleigh but our members are becoming self-sufficient in the field sampling work.

Early Growth Performance of *Pinus patula x P. tecunumanii* F2 Seedlings

Introduction

Camcore has been working with pine hybrids for nearly 20 years. We began by breeding and testing a wide array of interspecific combinations as bulks. Results of growth and wood property measurements have shown that pine hybrids have great commercial potential. In nearly every environment, we have found one or more hybrids that are superior to (or as good as) the primary pure species commercial option for that environment. Camcore has begun collaborative full-sib hybrid breeding projects for three different pine hybrids (*P. patula* x *P. tecunumanii*, *P. greggii* x *P. tecunumanii*, and *P. caribaea* x *P. tecunumanii*.

Compared to working with pure species, commercial deployment of pine hybrids is likely to be more challenging. One option is to identify desirable full-sib hybrid crosses, and to use vegetative propagation of rooted-cutting hedges established with limited amounts of F1 hybrid seed produced by controlled pollinations. This approach will work, and the vegetative propagation methodology is well known, but it can be expensive as it requires a substantial amount of manual labor. Another option for commercial production of hybrid plantations is the use of open-pollinated F2 hybrid seed, analogous to the use of pure-species seed orchard seed. Limited use of F2 material (with generally good results) has been reported for Pinus rigida x P. taeda in Korea (Hyun, 1976; Dungey, 2001) and P. elliottii x P. caribaea in Australia (Nikles, 2000; Dungey, 2001). The hybrid of P. patula x P. tecunumanii has shown excellent growth, very good wood properties, and resistance to the pitch canker pathogen, Fusarium circinatum, across a wide range of environments, and particularly in South Africa where P. patula has been the most important pure species. This study describes an experiment where F1 hybrid families and F2 advanced hybrid families of the Pinus patula x P. tecunumanii low-elevation hybrid (PPTL) were compared in a progeny field experiment for early growth at three years of age. Full results of this study are reported in Nel et al. 2021, Southen Forests.

Material and Methods

A series of five clonal PPTL progeny trials were established in South Africa by Sappi from 2008 to 2010. Rooted cuttings were produced from seedling hedges of twenty-five different F1 hybrid families produced via controlled pollination. Seedling hedges of multiple clones per family were tested. One of the clonal F1 PPTL trials was selected to conduct an experiment to evaluate F2 outcrossed hybrid seed. This trial is well isolated from outside pine pollen sources, being surrounded predominately by eucalypt plantations. Open-pollinated F2 seed was collected from five of the hybrid F1 families in 2015 and the seed was used for the establishment of the experiment reported here (Table 5). Subsequent seed harvest operations were also conducted in 2016, 2017 and 2018 and seed yield information is reported here.

Table 5. Families included in the mixed-model analy-sis of the full and reduced datasets. F1 families listedin blue, F2 families in red.

Hybrid Family	Туре	Full Dataset	Common Ancestry Dataset
PT1x1_F1	F1	Х	
PT1x2_F1	F1	Х	
PT2x1_F1	F1	Х	
PT2x3_F1	F1	Х	
PT3x1_F1	F1	Х	
PT3x4_F1	F1	Х	Х
PT4x1_F1	F1	Х	
PT4x4_F1	F1	Х	Х
PT5x3_F1	F1	Х	
PT5x4_F1	F1	Х	
PT4x4_F2	F2	Х	Х
PT3x4_F2_A	F2	Х	Х
PT3x4_F2_B	F2	Х	Х
PT4x5_F2	F2	Х	
PT1x5_F2	F2	Х	

Field Experiment Details

The F1 versus F2 PPTL hybrid progeny trial was established in May 2016 (latitude 25°37' S, longitude 30°48' E, altitude 1009 m above sea level) with a warm temperate climate with mean annual rainfall of 1014 mm and a mean annual temperature of 17.5 °C. The trial design was an alpha-lattice design with six replications and sixtree line plots, planted at 3 x 2m spacing. The trial consisted of 16 treatments in total, five F2 PPTL seedling families, ten F1 PPTL cutting families and a single P. patula open-pollinated seed orchard mix seedling control. Survival, tree height (H) and over-bark diameter at breast height (DBH) were measured at 36 months after planting, and a volume index (V) was calculated as V = 0.00003 $(DBH^2 * H).$

Data Analysis

Since *P. patula* was represented by a single open-pollinated bulk seedlot, and the two hybrid types were represented by multiple random families, we first used a very simple linear model to compare *P. patula* to the two hybrid types. The model included only Type as a fixed effect, and least squares means (LS means) were used to compare *P. patula* to both F1 and F2 hybrids.

A linear mixed model was then used to examine differences between the two hybrid types (F1 and F2), and among hybrid families within types:

where Type = the fixed effect associated with taxon/propagule (*Patula*, F1 Hybrid, or F2 Hybrid).

Statistical significance tests for the fixed effect Type were done, and the genetic variance associated with Family(Type) was estimated. For the two hybrid types F1 and F2, LS means and standard errors and confidence intervals (CI 95%) were calculated and plotted. For the random effect Family(Type), the variance component (σ^2_{fam}) was estimated, and also used to calculate a family-level genetic coefficient of variation (GCV_{fam}):

$$GCV_{fam} = 100\% * (\sigma_{fam} / \bar{y}_{type})$$

where \bar{y}_{type} = trait mean for either the F1 or F2 Type. Family BLUPs and associated standard errors of prediction (SEP) were calculated for each family. Predicted family means (\bar{y}_{fom}) were calculated as

$$\bar{y}_{fam} = \hat{g} + \bar{y}_{type}$$

where \hat{g} = the family BLUP. A 95% confidence interval was calculated as ±1.96 SEP, and the predicted family means and confidence intervals were plotted with box-and-whisker plots. Finally, uniformity of growth performance for height, DBH, and volume for the different hybrid types was compared using a pooled within-family coefficient of variation (CVw) for the F1 and F2 hybrids.

The analyses described above were done with two populations: 1) the full dataset, with ten F1 and five F2 hybrid families, and 2) a reduced common ancestry dataset with the *P. patula* control plus three F1 and two F2 hybrid families only from the same original F1 *P. patula* x *P. tecunumanii* crosses (Table 6).

Results

Seed Yield

Seed yields per cone were determined for the harvest years from 2015 to 2018. Across years, there was large variation in seeds per cone, with means ranging from 7 to 16 seeds per cone. Across clones and years, there was also large variation in the range of seeds per cone, varying from 0 to 42 seeds per cone. Seed germination information was also available for the 2015 harvest year, for the seed used in the establishment of the field experiment. The mean seed germination was 66% and ranged from 10 to 86% for the different clones that yielded seed.

Growth Traits

For the growth traits HT36, DBH36 and VOL36, there were no significant differences between the F1 and F2 hybrid treatments, for both the full population and the common ancestry subsets of data (Table 6). All growth traits were higher for the F1 families, although these were not significantly different. There were, however, highly significant (p < 0.01) differences between the *P. patula* control and the F1 and F2 PPTL hybrid treatments, for both full and sub-datasets.

Uniformity

Table 6 presents the pooled within-family coefficients of variation (CVw) for the two hybrid

types, which gives some indication of uniformity. For the full data set, there is no indication that the F1 hybrids have greater uniformity than the F2 hybrid families. With the smaller subset of data representing only common F1 family ancestry, the results are similar.

Discussion

For the growth traits analysed, the results show that the hybrid propagule type (F1 vs F2) does not seem important, with non-significant differences between F1 and F2 in the full and subdatasets (Table 6, Figure 2). Both hybrid types produced substantially higher tree height and volume than the *P. patula* control (Figure 2). Selecting good F1 hybrid families based on general combining ability of the parent (*P. patula* and *P. tecunumanii*) selections should therefore also produce good F2 hybrids, as is the case with the *P. elliottii* x *P. caribaea* hybrid in Australia (Kain, 2003) as well as the *P. rigida* x *P. taeda* hybrid in Korea (Hyun, 1976).

Compared to F1 progeny, there is a possibility of increased variance (decreased uniformity) in F2 progeny due to segregation of homozygotes in the F2 generation. However, the pooled withinfamily coefficients of variation (CVw) showed no important tendency for F2 progeny to be less uniform than F1 progeny, at least for the growth traits examined in this study (Table 6). This result corresponds well to results with larger populations of the *P.* elliottii x *P. caribaea* hybrid in Queensland (Kain 2003), where F1 and F2 populations were compared for 12-year-old height and DBH on two sites, with very similar values for both mean growth and within-family variation.

In this experiment, the mean open-pollinated seeds per cone yield was rather low (7 and 16 seeds per cone), compared to yields from commercial controlled hybrid pollinations (mean seeds per cone was 27), and seed yields for the pure species *P. patula* and *P. tecunumanii* low elevation (22 and 30 filled seeds per cone, respectively) (Dvorak et al., 2000a; Dvorak et al., 2000b). The seed yield for F2 hybrid seed is likely to increase significantly as the F1 trees age and pollen production increases.

Due to the impact of F. circinatum on the post-establishment survival of pure P. patula in Southern Africa, there is increasing demand for hybrid seed. The PPTL hybrid seed is expensive. involving manual labor for controlled pollinations and the production of rooted cuttings. In addition, hedges of PPTL can only be used for a limited time (approximately 5 years) before maturation sets in and they must be replaced with new seedlings. A PPTL hybrid seed produced via controlled pollination costs around 20 times more than an open pollinated P. patula seed, and the cost of rooted cuttings are also double compared to that of seedlings. F2 hybrid seed would be a much cheaper option to consider for hedge establishment, and depending on seed production, could also be considered for large-scale seedling production.

Conclusion

The early results from this study indicate that the growth of the F2 PPTL hybrid is encouraging and is not significantly different than the F1 hybrid performance. Both the F1 and F2 hybrid outperformed the pure *P. patula* control. These early results should be monitored further to determine if this trend continues, and this question should be further examined with larger populations. However, it appears that the F2 hybrid offers the opportunity to produce tolerance to *F. circinatum* and better growth than *P. patula* at a much lower cost than the deployment of the F1 PPTL hybrid.

Table 6. Summary of linear mixed model results for statistical differences between *P. patula* x *P. tecunumanii* hybrid types (F1 vs F2), and genetic variance among families within hybrid types (GCVfam), and within-family phenotypic coefficient of variation (CVw) for different *P. patula* x *P. tecunumanii* hybrid types (F1 vs F2).

Population	F1	F2	Trait	Type Differences	Family-level	F1 CV _w	F2 CV _w
	families	families		F1 ≠ F2	GCV _{fam}		
Full	10	5	HT36	p = 0.1435	7%	22.5%	19.8%
			DBH36	p = 0.3442	6%	25.8%	23.7%
			VOL36	p = 0.1739	20%	54.6%	61.5%
Common	2	3	HT36	p = 0.9492	5%	21.8%	17.8%
F1 ancestry			DBH36	p = 0.8192	0%	29.3%	23.5%
			VOL36	p = 0.7534	8%	57.1%	57.4%

Figure 2. Common-ancestry population BLUPs for 36-month height and volume for families of *P. patula* x *P. tecunumanii* hybrids (F1 and F2). LS Means ± standard error for hybrid families were estimated with a linear mixed model approach for the sub-population of five F1 and F2 families with common F1 full-sib parentage, treating Type as a fixed effect and hybrid family within Type as random. Mean ± standard error for the *P. patula* bulk control was estimated separately.



Wood and Pulping Properties and Sampling Strategy for Acacia crassicarpa

Acacia crassicarpa is a fast-growing tree species largely used in South East Asia for kraft pulp and paper production. Other possible products include dissolving pulp, chemicals, fuels, polymers, and biofuels.

To improve kraft pulp production efficiency, one of the main breeding objectives is to improve wood quality to optimize cellulose yield and chemical consumption during the pulping process. In general, phenotyping for pulping traits or wood quality traits is expensive and time-consuming, requiring laboratory facilities and technical expertise. Tree breeders want to efficiently characterize families and clones for selection. Usually, families and clones are ranked using an average value across multiple trees/ramets measured for a particular trait with an indirect measurement method. Ultimately, the goal is to develop a rapid, inexpensive, and accurate selection protocol.

In this study we evaluated wood density, screened kraft pulp yield, α-cellulose, carbohydrate composition, and lignin content and composition (S/G ratio) for 240 wood samples representing six stem positions taken from 40 rotation-age A. crassicarpa trees. The specific objectives were to (1) assess variation in important wood and pulping properties of Acacia crassicarpa; (2) estimate phenotypic correlations among different wood quality and pulping traits, and (3) understand within-tree longitudinal patterns of variation and its impact on whole-tree level phenotyping. With this comprehensive set of wood and pulping property estimates, recommendations could be made to develop efficient sampling procedures for different phenotyping objectives.

Materials and Methods

Field Trials

The field trials used were two *A. crassicarpa* progeny trials established by the breeding program of Asia Pacific Resources International Limited - APRIL. The tests were located in Pelalawan Regency, Riau Province, Indonesia, and the design for both tests was an 8-replication randomized complete block design with 10 trees per plot (two rows of five trees). The genetic entries were 25 open-pollinated families from a clonal breeding orchard with 2nd generation selections from Papua New Guinea provenance.

A total of 40 trees were sampled at age 50 months using destructive sampling. Trees were felled, and commercial heights measured to a 4.5 cm diameter. Bole positions corresponding to 1.3 m, and 0%, 25%, 50%, 75%, and 100% of the commercial height were then marked (Figure 3). At all bole positions, two discs (2.5 cm of thickness) were collected. One disc was used to measure disc basic density (DBD), from the other disc, wedges were ground to produce woodmeal for NIR spectrometry sampling and wet chemical analysis. The remaining billets from each log were chipped to provide chips for basic density (CBD) and screened kraft pulp yield (KPY) measurements, and whole-tree composite basic density and composite screened kraft pulp yield.

For each of the 240 samples, wet chemistry was done at the University of British Columbia using 5 grams of wood meal. Traits measured included insoluble lignin content (INS), acid-soluble lignin (SOL), total lignin (LIG), arabinose (ARA), galactose (GAL), glucose (GLU), mannose (MAN), rhamnose (RHA), xylose (XYL), and Syringyl-Guaiacyl Ratio (S/G). Other traits measured by APRIL staff included Alpha cellulose



Figure 3. Destructive sampling for direct measurement of wood properties and corresponding laboratory analyses performed at each position along the tree bole. The figure is a schematic and not to scale and is intended for illustration only.

(α CEL), and screened kraft pulp yield (KPY).

For each bole section (i.e., the log in between the positions where discs were taken), we calculated the frustum volume and its mean wood property by averaging the lower and upper measures weighted by their areas. Within-tree variation for each of the traits was examined. The whole-tree phenotypes were estimated as the average value of all bole sections weighted by their volumes. Pearson's correlation (r) of all pairwise combinations of variables at the whole-tree level were calculated. The precision of reduced sets of sampling positions to predict the whole-tree phenotype was investigated by comparing simple linear regression models with positions taken singly, in pairwise, and in three-way combinations. For pairwise and three-way combinations, the predictor was the mean value of the corresponding positions. The "reliability" of the whole-tree value prediction was assessed using the model R². All statistical analyses were done using R software.

Results

Growth and Wood Properties

For the 40 trees, mean volume was 0.257 m³, total tree height was 21.3 m, commercial height was 17.9 m, and DBH was 18.2 cm. The volumetric proportions of each bole section are presented in Figure 4.

Mean whole-tree wood properties are presented in Table 7. The basic density mean values were 481.7 kg/m³ for disc basic density, 467.3 kg/ m³ for chips basic density, and 474.8 kg/m³ for composite chips basic density. As expected, the range for basic density was wide, on the order of 157.5 kg/m³. The mean screened kraft pulp yield was 53.8%, the same value was observed for the composite KPY, both with a 7% range. The mean alpha cellulose content was 44.4%, with an 8.4% range. The two major carbohydrates were glucose, with mean 50.4% and 5.6% range, and xylose, with mean 13.8% and 2.4% range. The contents of the minor carbohydrates mannose, galactose,



Figure 4. Graphical representation of the volumetric proportion of the average tree bole sections.

arabinose, and rhamnose were 1.31%, 0.62%, 0.26%, and 0.23%, respectively. Mean total lignin was 29.35%, with a range of 4.4%, whereas insoluble lignin was 27%, and acid-soluble lignin was 2.35%. The mean lignin monomers syringil-guaiacyl ratio was 1.67, with a range of 0.3.

At the species level, *Acacia crassicarpa* can be described as having medium-high wood density (DBD = 481 kg/m3), high pulp yield (KPY = 0.538) and medium lignin content (LIG = 0.294). The basic density and lignin values found in this study are consistent with previous results reported in the literature. Compared with another important acacia species, *A. mangium, A. crassicarpa* seems to have higher basic density, higher pulp yield, and lower lignin. Compared with eucalypts, the *A. crassicarpa* in this study had lignin and cellulose contents roughly similar to *urograndis* hybrids, kraft pulp yield similar to *E. globulus*, and S/G ratio lower (i.e. , worse for kraft pulping) than most eucalypts.

Within-tree variation

Table 7. Descriptive statistics of whole-tree level disc basic density (DBD), chips basic density (CBD), composite chips basic density (CBDc), screened kraft pulp yield (KPY), composite screened kraft pulp yield (KPYc), alpha cellulose (α CEL), glucose (GLU), arabinose (ARA), galactose (GAL), rhamnose (RHA), xylose (XYL), mannose (MAN), total lignin (LIG), insoluble lignin (INS), acid-soluble lignin (SOL) and syringyl-guaiacyl ratio (S/G).

Variable	units	N	Mean	SD	CV	
DBD	kg/m ³	40	481.7	34.4	7.1%	
CBD	kg/m³	40	467.3	31.3	6.7%	
CBDc	kg/m ³	37	474.8	31.6	6.7%	
KPY	%	40	53.8	1.6	3.0%	
KPYc	%	39	53.8	1.5	2.9%	
αCEL	%	40	44.4	1.7	3.9%	
GLU	%	40	50.4	1.6	3.1%	
ARA	%	40	0.26	0.06	23.1%	
GAL	%	40	0.62	0.11	17.6%	
RHA	%	40	0.23	0.05	24.1%	
XYL	%	40	13.8	0.5	3.5%	
MAN	%	40	1.31	0.29	22.0%	
LIG	%	40	29.4	1.0	3.5%	
INS	%	40	27.0	1.0	3.7%	
SOL	%	40	2.35	0.18	7.8%	
S/G		40	1.67	0.08	4.6%	

The pattern of within-tree variation (from base to top) is not the same for all wood properties. Although there is much variability among individual trees, Figure 5 shows the general trend for four important wood traits: disc basic density, glucose, xylose and insoluble lignin content. Most of the chemical traits show a relatively constant value up the stem (e. g., glucose content (GLU) or S/G ratio), but some show a distinct trend (e. g., insoluble lignin content (INS) decreases from a mean of 28.6% at the base to 25.3% at the top. As one might expect, basic density shows a marked decrease from the base (528 kg/m³).

Phenotypic Correlations Among Traits

Phenotypic correlations among whole-tree wood property values were examined. For wood density, very high positive relationships (R > 0.90) were apparent between disc basic density, chips basic density, and the composite CBD, indicating that regardless of the measurement method, similar estimates were obtained at the whole-tree level. Similarly, the KPY and the KPYc have a correlation of R = 0.93, showing strong evidence that the chips composite may be a resource-wise sampling strategy, especially for expensive phenotyping traits, such as pulp yield. The wood basic density was positively correlated with pulp yield, alpha cellulose, arabinose, galactose, and rhamnose; and negatively correlated with mannose and soluble lignin. The alpha cellulose content was strongly associated with glucose (0.70), and both traits negatively correlated with lignin content (R = -0.48 and -0.60, respectively). Correlations among carbohydrates, arabinose, galactose, and rhamnose were positively correlated among themselves. Galactose was related to density, to all other sugars, and lignin. Xylose was not associated with any trait other than galactose.

The correlation between total lignin and insoluble lignin was R = 0.97, demonstrating that the insoluble lignin is the major component driving the complete lignin response. Total lignin was negatively associated with glucose, alpha cellulose, and pulp yield, showing consistency among the data, with the antagonistic relationship expected between lignin and pulp yield-related traits. The lignin monomers ratio (syringil-guaiacyl) was only significantly correlated with the carbohydrate mannose.

Kraft pulp yield was correlated with alpha cellulose (R = 0.35), glucose (R = 0.48), and galactose (R = 0.43), and negatively correlated with insoluble lignin (-0.49). The S/G ratio was only significantly correlated with mannose, a minor carbohydrate, indicating that for the *Acacia crassicarpa* germplasm studied, the S/G ratio



Figure 5. Box plots of wood property at different sampling heights (x-axis) for diameter, disc basic density (DBD), glucose (GLU), xylose (XYL), insoluble lignin (INS), and syringyl-guaiacyl ratio (S/G).

did not greatly influence the pulp yield or its related traits (although it may have important impact on the cost of the pulping process). This significant and favorable correlation of high basic density with high pulp yield is not typically seen in eucalypts, where zero correlation or lower values have been reported.

Sampling Positions

The study provided information about the reliability of sampling wood properties at different positions along the bole of the tree (1.3 m, and 0%). 25%, 50%, 75%, and 100% of commercial height) in order to predict whole-tree values. In general, when comparing a single sample position, the 1.3 m and 25% heights were the most reliable to predict the whole-tree value. However, pairwise and three-way combinations of sample positions increased the correlations. Figure 6 summarizes results for four important wood traits (DBD, GLU, XYL, and INS). For DBD, the 1.3 m alone gave a reliability of $R^2 \approx 0.84$ with whole-tree density. however, 1.3 m and 25% together increased reliability to $R^2 \approx 0.95$. For the carbohydrates and insoluble lignin content, a single sampling position was less useful to predict whole-tree properties. For glucose, 1.3 m was the best position alone with $R^2 = 0.69$. When the mean value of 1.3 m and 25% was used, the reliability increased to $R^2 = 0.87$. For the traits of xylose and insoluble lignin content, there were even more dramatic improvements in reliability from including the 25% sampling height to go with the 1.3 m sample position.

Additional sample positions at 0% (and higher positions on the stem), did not produce any substantial improvement in the correlation with wholetree values.

Conclusions

The wood and pulping properties estimates for 2nd generation *Acacia crassicarpa* trees demonsrate the suitability of this species for efficient pulp production, with lignin contents, carbohydrates contents, and kraft pulp yields in the range of the hardwoods commercially planted around the world.

Wood property sampling is typically done at breast height (1.3 m) on the stem, and the current data suggest that this will generally give good results for A. crassicarpa. From a practical point of view, the additional positions that could be sampled in standing trees are 0%, and 25% of commercial height. Even though sampling at the 25% position (roughly 4.5 m) may require substantial additional effort, for most traits, the addition of the 25% significantly improved the correlations, indicating its importance to have higher precision in predicting whole-tree properties. A strategy of sampling standing trees at breast height and 25% of the commercial height, and using the mean value of those positions will give a very high degree of accuracy for individual whole-tree level phenotyping for all wood traits.



Figure 6. Reliability of different wood sampling options to predict whole-tree wood properties. Bar plots show Reliability = R^2 of a linear regression between sample value and whole-tree value. Sample options include one sample at breast height (1.3 m), and combinations of samples from 1.3 m with samples at 0% and/or 25% commercial height.

Eucalypt Species Wood Properties

Our *Eucalyptus* breeding program started in 1996 with the introduction of E. urophylla. As of 2021, we have distributed to our members more than 500 trials including tropical, subtropical and temperate Eucalyptus and Corymbia species. We have expanded our suite of species and diversified our genetic base so that our members can select material that is more resistant to disease, drought or frost, and can identify new species that can be used as hybrid partners for increased productivity. Since 2017, we have assessed wood properties on our Eucalyptus and Corymbia studies. A set of tests, with minimum age of five years, has been selected for field measurements to evaluate species wood properties. In this article, we present the characterization for all studies measured to date in Chile, Colombia, South Africa and Uruguay.

Materials and Methods

During 2020-2021, we measured four Camcore tests. One test in Colombia established by Smurfit Kappa Colombia in 2012, and three tests in South Africa planted in 2013, two by Mondi and one by Sappi. So far, we have sampled 14 trials, and have evaluated over 2,700 trees. We intended to sample between 25-30 trees per species per site. However, due to mortality, tree size or shape, smaller numbers of trees were available for some species (Table 8). In this report we present results of physical and chemical characteristics of wood in 28 pure species and hybrids. On each sampled tree, field measurements and wood samples were made at breast height to evaluate the following wood properties:

Species	Chile		Col.	Col. South Africa							Uruguay				Total
	Arauco		SKC	Merensky		Mondi		Sappi		Lumin		MDP]	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	
C. citridora var. variegata				30											30
C. citriodora											24				24
C. henryi					15										15
C. maculata											25		30		55
E. badjensis	30										23		30		83
E. benthamii	30	30		15		60			30		25	25	30	30	275
E. brassiana										10					10
E. cladocalyx							8								8
E. drepanophylla				15											15
E. dunnii		18				65			30			25	30	60	228
E. globulus	44	16											30		90
E. globulus bicostata	29														29
E. grandis			90	30	60	30		30	30	60	19	45			394
E. grandis x E. cam.			30		30			29		30	10	10			139
E. grandis x E. nitens						45									45
E. grandis x E. urophylla			30	30	30		30	29		30	10	10			199
E. longirostrata				30	15		29								74
E. macarthurii		30				30			30			25		30	145
E. major				30											30
E. moluccana				30			31								61
E. nitens	31	29				20									80
E. pellita			30	30				30		30					120
E. propinqua							26								26
E. saligna		29				60			30			25		30	174
E. sideroxylon													30		30
E. smithii		30				30			30			22		30	142
E. urophylla			30	30	30			20		30					140
E. urophylla x E. grandis			30		30			29							89
Total	164	182	240	270	210	340	124	167	180	190	136	187	180	180	2750

Table 8. Species samples available for expansion of the Camcore global eucalypt NIR model in 2020 and 2021.

<u>Modulus of Elasticity (MOE)</u>: In its simplest form, MOE measures wood stiffness, and it is a good overall indicator of strength. We estimated MOE using the TreeSonic. This tool measures the stress wave propagation time in the stem of standing trees. With this time and the distance between device sensors, fiber direction velocity is calculated, which correlates very well with MOE and yield strength of wood.

<u>Resistance</u>: We used the IML-Resistograph to get the resistance profile of the tress. The IML-Resistograph system measures the drilling resistance of a thin needle that is inserted into the wood under constant drive. While drilling, the required energy is measured; this resistance is directly proportional to the density of the tree. Resistance profiles were adjusted by friction and bark resistance was excluded from the data before calculation of mean core resistance. <u>Wood Chemistry</u>: we used hand drills to collect wood shavings for NIR prediction of percentages of lignin, guaiacyl lignin (Lignin_G), syringyl lignin (Lignin_S), glucose, xylose, minor sugars (0_sugars) and the ratio S/(S+G). Oven dried samples were ground into woodmeal and scanned with a FOSS 6500 NIR spectrophotometer; spectra generated for each sample was used in the Camcore's Global *Eucalyptus* NIR models

For the statistical analyses, we built a generalized linear model (GLM) for each trait (resistance, MOE, and NIR predicted variables) and evaluated the significance of the modeled trait. If variation between species was detected, comparisons of the species LSMEANS were conducted. In addition, we conducted a principal component analysis (PCA) on the Estimated Marginal Means (LSMEANS) to reduce the complexity of our highdimensional data and to observe trends and

Table 9. Species LS means for wood property traits.Samples derived from 14 mixed-species trials in Chile, Colombia,South Africa and Uruguay.

Species	Code	Resis-	MOE	Glucose	Lignin	Soluble	Insol.	Xylose	Minor	Spct
		tance		(%)	(%)	Lignin	Lignin	(%)	Sugars	(%)
		(x100)				(%)	(%)		(%)	
C. citridora Variegata	C.CIT.V	20.54	14.36	48.84	21.48	16.68	4.80	15.68	14.00	77.66
C. citriodora	C.CIT	21.10	16.67	48.18	20.56	15.87	4.69	14.96	16.30	77.20
C. henryi	C.HEN	19.37	14.71	50.00	22.51	17.12	5.40	13.33	14.16	76.03
C. maculata	C.MAC	19.91	14.79	48.02	20.49	15.97	4.52	15.41	16.07	77.96
E. badjensis	BAD	18.32	12.46	46.26	22.58	17.77	4.82	14.42	16.73	78.67
E. benthamii	BEN	16.47	12.90	47.11	26.59	19.96	6.62	11.93	14.38	75.09
E. brassiana	BRA	15.21	16.27	49.56	26.43	19.26	7.17	10.69	13.32	72.87
E. cladocalyx	CLA	17.62	12.52	46.41	28.20	19.66	8.54	12.42	12.97	69.71
E. drepanophylla	DRE	28.62	16.48	48.69	24.05	18.18	5.86	14.79	12.48	75.61
E. dunnii	DUN	16.98	14.96	49.90	22.06	17.42	4.64	14.09	13.95	78.97
E. globulus	GLO	20.48	15.22	47.93	21.00	17.15	3.85	14.55	16.52	81.67
E. globulus bicostata	GLO.B	20.72	12.08	48.04	22.34	17.54	4.79	14.53	15.09	78.54
E. grandis	GRA	15.74	14.59	48.75	25.24	18.56	6.69	12.17	13.84	73.51
E. grandis x E. cam.	GRAxCAM	16.80	14.33	48.32	25.67	19.18	6.48	12.11	13.90	74.75
E. grandis x E. nitens	GRAxNIT	17.93	14.72	48.61	23.25	17.88	5.37	13.45	14.68	76.92
E. grandis x E. urophylla	GRAxURO	15.83	15.08	48.36	26.22	19.17	7.05	12.16	13.26	73.11
E. longirostrata	LON	19.21	14.92	45.40	25.84	20.62	5.22	13.00	15.76	79.80
E. macarthurii	MAC	17.90	12.18	47.68	24.85	19.06	5.78	12.79	14.68	76.72
E. major	MAJ	20.87	14.13	48.24	27.99	20.62	7.38	11.71	12.06	73.65
E. moluccana	MOL	29.85	15.42	50.15	20.72	16.33	4.39	14.39	14.74	78.81
E. nitens	NIT	19.55	12.86	45.29	22.34	17.36	4.98	15.58	16.79	77.69
E. pellita	PEL	17.40	15.54	47.26	29.47	20.26	9.21	10.70	12.57	68.75
E. propinqua	PRO	17.47	12.80	47.02	28.65	19.73	8.92	12.35	11.98	68.85
E. saligna	SAL	15.52	13.80	47.39	25.98	19.28	6.70	12.57	14.06	74.23
E. sideroxylon	SID	24.76	11.58	45.65	24.84	18.78	6.05	14.26	15.25	75.63
E. smithii	SMI	19.74	15.28	47.61	21.74	17.47	4.28	13.98	16.66	80.32
E. urophylla	URO	17.41	12.72	47.34	26.83	19.34	7.48	12.61	13.23	72.11
E. urophylla x E. grandis	UROxGRA	17.78	15.16	48.08	26.59	19.64	6.95	11.84	13.50	73.86

patterns between the species and the measured traits (Figure 7). NIR prediction of wood traits, statistical analyses and graphical representations were conducted using the R programing environment.

Results and Outlook

Interestingly, for all modeled traits, the variation associated with species (or hybrids) was significant (P-values below 0.001), indicating that statistical differences were observed. Obtained LSMEAN values are presented in Table 9, as a reference for our readers to describe the variances between species and across traits. Perhaps more relevant is the graphical representation of the wood traits in the PCA biplot, which allow us to identify desirable species (or hybrids) in terms of their physical and chemical wood properties. The biplot graph presented in Figure 7, depicts over 78 % of the total variation of our data. The biplot's origin (0,0) represents the congruence of species wood property values in the new projected space. The x-axis discriminates species by their percentage of sugars, resistance and lignin: species to the right of the biplot's origin have higher sugar percentage and resistance (wood density), while species located to the left have a higher lignin content. Similarly, the biplot y-axis discriminates species in terms of MOE and glucose, species above the origin have higher values of Glucose and MOE.

Species exhibiting high percentages of glucose, xylose, and resistance are *E. drepanophylla*, *E. moluccana*, *E. dunni*, *C. citriodora*, and *C. henryi*. Species with high levels of xylose and intermediate levels of glucose are *E. globulus*, *E. smithii*, and *C. maculata*. For *E. grandis* and its hybrids (except *E. grandis* x *E. nitens*), lignin and glucose content and MOE values are above average, while xylose and minor sugars content and S_pct (the ratio of S/(S+G)) are below average. *E. nitens* and *E. badjensis* have high xylose, but low glucose content, MOE and lignin. *E. urophylla*, *E. saligna* and *E. benthamii* have similar lignin



Figure 7. Principal Component Biplot of *Eucalyptus* species Least Squares Means for wood property traits. Wood samples were taken from 14 mixed-species trials in Chile, Colombia, South Africa, and Uruguay.

values to *E. grandis* and its hybrids, but inferior glucose content and MOE. *E. pellita*, *E. propinqua*, *E. cladocalyx* and *E. major* showed the highest lignin percentages, intermediate glucose and MOE values, and low xylose, S pct, and resistance.

With the addition of these four tests in 2020 and 2021 we are building a very valuable data set that is helping our group to identify the potential that some species can bring to our breeding programs as alternative species or as hybrid partners and guide our breeding and testing efforts. In 2022 we plan to assess four more trials in South America (Argentina and Uruguay) and two more trials in South Africa.



Resistograph measurements being taken by Alex Plaza and Martha Salas of Smurift Kappa Colombia for the the eucalpyt species wood characterization study.

Expanding the Global NIR Model with E. pellita and Other Species

We have been working on development of our global Eucalyptus NIR model since 2012, and we have prediction models for soluble lignin, insoluble lignin, SG ratio, glucose, xylose, and minor sugars. Building an NIR prediction model is a costly process since each sample requires both spectral information and laboratory measurements (wet chemistry). We have worked with the University of British Columbia (Dr. Shawn Mansfield) for wet chemistry determination, pre-selecting a subset of samples that cover a wide range of spectral variation. Our first global model included 186 samples distributed across four projects: 50 samples of *E. urophylla* (project with several members), 50 samples of E. dunnii (work with Lumin, Uruguay), 50 samples of *E. globulus* and *E. nitens* (project with CMPC, Chile), and 36 samples of *E. grandis* (work with Smurfit Kappa Colombia). In 2019, as part of a project with Mondi and Merensky, we expanded our global model by includ-



2021 Global NIR model predictions for lignin for *Eucalyptus* species (green), *Corymbia* species (black), and *E. pellita* (yellow).

ing 102 samples of 10 species (*E. badjensis, E. benthamii, E. dorrigoensis, E. macarthurii, E. pellita, E. saligna, E. smithii, C. citriodora, C. maculata, C. henryii, and C. torelliana*), all species were represented by 10 samples (except *E. smithii*). In 2021, we selected 50 *E. pellita* samples from a population of 550 trees provided by Sinarmas Forestry in Indonesia. All samples were scanned with our FOSS 6500 NIR machine and we used the Kennard-Stone algorithm (KS) to select 50 samples that represented the spectral variation of the population. Our current global NIR prediction model has 338 samples representing seven *Eucalyptus* species and four *Corymbia* species. We believe our models are sufficiently robust and precise to be very useful in breeding programs for any *Eucalyptus* (and probably *Corymbia*) species.

Cutting Production of *Pinus tecunumanii* and *P. maximinoi* in Hydroponic Hedges: Resting Effects

Smurfit Kappa Colombia (SKC) decided to use the family forestry approach for mass-production of the best crosses of *P. tecunumanii* and *P. maximinoi*. This was primarily due to seed supply limitations and the growing market for cement sacks in Colombia. SKC's nursery expanded pine propagation capacity by establishing hydroponic hedges on sand beds using the current system for eucalypts. During the first two years, the pine hedges looked healthy and were very productive, however, hedges expressed a decline in productivity during years 3 and 4 (see photo below). As a consequence, pines hedges were moved from sand beds to bags for operational production.

Experimental Design and Analysis

Camcore recommended conducting an experiment in the nursery for *P. maximinoi* and *P. tecunumanii* to refine SKC's protocol for vegetative propagation. The main goals of the experiment were to refine the optimum combination of nutrients, hedge height, hedge spacing, and harvest frequency, as well as the evaluation of hedge lifespan. Hedges of both species were planted on sand beds using an experimental design that included two planting spacings (10 cm x 15 cm and 20 cm x 15 cm), two hedge heights (15 cm and 25 cm), two nutritive solutions (100% Hoagland and 60% Hoagland), and two frequencies of harvesting (every 2 weeks or every 4 weeks). Treatment combinations are presented in Table 10. The experiment was conducted at SKC's Vivero Rancho Grande, in the municipality of Restrepo (Lat: 3° 51' 22" N, Lon: 76° 30' 32" W), with elevation of 1,453 m.a.s.l and yearly rainfall of 1,205 mm. Sand beds were established in February 2016, and measurements were taken monthly from July 2016 to December 2020, with a total of 57 evaluations during 4.75 years.

Measured traits were the number of cuttings produced by hedge and their rooting percentage, the later was calculated on a subsample of the cuttings produced by each treatment combination. For each monthly evaluation, treatment productivity was estimated by calculating the number of effective cuttings using the following expression:

Effective Cuttings = (Total cuttings)(Area Conversion Factor)*(Rooting Percentage)*

where:

- *Total cuttings* = sum of cuttings produced monthly (weeks 2 and 4)
- Area Conversion Factor = 0.95 for spacing of 20 cm x 15 cm (35 hedges on 1.05 m²)
- = 1.19 for spacing of 10×15 cm (56 hedges on 0.86 m^2)
- *Rooting Percentage* = estimated with information on the first 27 monthly evaluations

For each trait and every evaluation time, descriptive analyses and summary plots and tables were generated. In addition, generalized linear models were fitted to the data and factor differences were evaluated for each species on every monthly assessment. All analyses were conducted in R.



Pine hedges decline in vigor over a four-year period
SPECIES CHARACTERIZATION

120000	1.	1000000	Treatment	Combination
Factors	Levels	Notation	1	B1.T.20x15.25.2W
Nutrient	Hoagland 100%	B1	2	B1.T.20x15.15.4W
Regime	Hoagland 60%	B2	3	B1.T.10x15.25.4W
8	Hougiana 00%		4	B1.T.10x15.15.2W
Hedge	20 x 15 cm	20x15	5	B1.M.20x15.15.4V
Spacing	10 x 15 cm	10v15	6	B1.M.20x15.25.2V
	10 x 15 cm	10/13	7	B1.M.10x15.15.2V
Hedge	25 cm	25	8	B1.M.10x15.25.4V
Height	45	45	9	B2.M.10x15.15.2V
	15 cm	15	10	B2.M.20x15.15.4V
Harvest	2 weeks	2W	11	B2.M.10x15.25.4V
frequency	-	-	12	B2.M.20x15.25.2V
nequency	4 weeks	4W	13	B2.T.10x15.25.4W
	P. tecunumanii	2W	14	B2.T.20x15.25.2W
Species		+	15	B2.T.10x15.15.2W
	P. maximinoi	4W	16	B2.T.20x15.15.4W

Table 10.	Factors and levels studied in the pine hedge	
managem	ent study	

eatment	Combination
1	B1.T.20x15.25.2W
2	B1.T.20x15.15.4W
3	B1.T.10x15.25.4W
4	B1.T.10x15.15.2W
5	B1.M.20x15.15.4W
6	B1.M.20x15.25.2W
7	B1.M.10x15.15.2W
8	B1.M.10x15.25.4W
9	B2.M.10x15.15.2W
10	B2.M.20x15.15.4W
11	B2.M.10x15.25.4W
12	B2.M.20x15.25.2W
13	B2.T.10x15.25.4W
14	B2.T.20x15.25.2W
15	B2.T.10x15.15.2W

Results

Significant differences were observed in all monthly evaluations. During the first 12 monthly evaluations, production of mini-cuttings was very irregular, and as a consequence, treatment rankings were not stable. Interestingly, we observed that starting at measurement 14 the experimental data consistently showed that best treatment combinations for Pinus maximinoi and P. tecunumanii were treatments 8 (B1.M.10x15.25.4W) and 13 (B2.T.10x15.25.4W), respectively (Figure 8), indicating that the optimum factor combination to maximize the effective number cuttings per square meter is obtained when hedges were 25 cm tall, planted with a spacing of 10 cm x 15 cm and cuttings were harvested every 4 weeks.

We also learned that there are important differences between these two species: first, productivity (measured as the number of effective cuttings) was always higher in *P. tecunumanii* than *P. maximinoi*, in fact the effective cuttings yield was almost double. Second, nutritional requirements are different between species, maximum productivity for P. maximinoi was achieved in Bed1 (complete Hoagland solution), whereas maximum productivity for P. tecunumanii was found in Bed2 (60% concentration of Hoagland solution). For all treatments, mortality gradually increased, and we found that the higher mortalities were always reached on treatment combinations including biweekly harvests (mortality data not presented). In contrast, lower mortality rates were obtained when cutting collections were made every 4 weeks.

We expect that by applying these operational modifications to SKC's pine propagation protocol, the lifespan of hedges and their



Pine hedges in the sand beds, note the different hedge heights and spacing.



Figure 8. Effective number of cuttings at 24 and 57 months of hedge production. Treatment Combinations with maximum number of cuttings per m² are presented in blue for *Pinus maximinoi*, and green for P. tecunumanii.

productivity efficiency will increase. In addition, the implementation of a system in which hedges are established in individual containers within the sand bed, will help control mortality and hedge renovation.

Forest Health Program Update

Forest health, and specifically issues related to invasive species, continues to be a global concern for forest managers worldwide. Recent estimates indicate global economic costs due to damages from invasives over the last 50 years equal at least \$1.2 trillion USD (Zenni et al. 2021. Neobiota 67: 1-9). Camcore members have experienced this impact first hand as newly arrived insects and diseases affecting pines and eucalypts have caused extensive mortality and yield losses and required shifts to alternate species or new hybrids.

During our strategy session at the 2019 Camcore Annual Meeting in Portugal, these ongoing impacts led Camcore to list forest health, in particular, research and extension activities related to forest insects and disease, as a top priority for the program over the next 10 years. Although Camcore has conducted research on pests and pathogens over the years (e.g. Fusarium circinatum and Thaumastocoris peregrinus), this is the first time the program has had dedicated staff resources in this area. Robert Jetton, who has worked with Camcore for 16 years as project leader for Camcore's domestic conservation efforts in the United States, now fills the role of Camcore Forest Health Specialist. Robert will spend 30% of his annual effort supporting Camcore members on pest and disease issues with the other 70% of his time dedicated to forest health research and teaching activities within the Department of Forestry and Environmental Resources at NCSU. Trained as a forest entomologist, Robert also has a good working knowledge of forest pathology and a genuine excitement for working with Camcore members and building our forest health program. The following sections of this article provide a brief overview of Robert's vision for Camcore's forest health program and updates on some of our ongoing pest and disease research projects.

Program Overview

Camcore's forest health program was started during the COVID 19 pandemic and has not yet benefited from in-person visits with our members as we shape the program direction. While it is still a work in progress, we have defined four areas where we feel we can make important contributions to Camcore members: (1) on-site consultations as part of regular Camcore technical visits, (2) creation of a Forest Health link on the Camcore webpage where we will post well-curated and reliable resources (fact sheets, diagnostic guides, important scientific literature, etc.) on important insect and disease issues, (3) forest health education and training opportunities through Camcore webinars and mini conferences, and (4) special research projects on the biology, impacts, and management of important and emerging forest pests and pathogens impacting Camcore members. As always, we welcome input from our members on specific topics you would like to see addressed in the above program areas or for additional program areas you think are important.

Sentinel Plantations Project

Sentinel plantations (a.k.a. sentinel plantings, sentinel trees) established for the specific purpose of monitoring the impacts of insects, diseases, and other disturbance agents on tree health are being utilized increasingly around the world. Of particular interest is their application to post-border surveillance for the early detection and documentation of newly arrived pests and pathogens, determination of their invasive potential, and evaluation of likely impacts on commercial forestry operations. Developed by Robert Jetton and Arnulf Kanzler (then with Sappi), Camcore's Sentinel Plantations Project was first introduced at the 2017 Annual Meeting in Sweden. The plan is to establish a series of small pine and eucalypt species trials across the Camcore membership with interested members planting 2 trials each year on a 3- to 5-year rotating basis.

As of the end of 2021, Camcore members in South Africa and Indonesia have established sentinel trials and are collecting insect and disease monitoring data. The first trials were planted by Sappi in 2019, with one eucalypt and two pine tests established. Detailed reports on results from these trials through the end of 2020 are available in the 2019 Annual Report and Jolanda Roux's presentation at the 2020 Annual Meeting (available on the Camcore webpage). Some interesting findings so far from the eucalypt sentinel trial include a higher abundance and severity of pests and diseases on Eucalyptus species compared to Corymbia species, and also the fact that Teratosphaeria destructans (Destructans leaf blight) had most severe impact on *E. grandis* and *E. urophylla* at year 1.

SPECIES CHARACTERIZATION

Sinarmas established three sentinel trials in 2021 well distributed across the company's landholdings to monitor for pest and disease issues in the north (Riau), south (Jambi), and east (East Kalimantan). The exact treatments in each trial vary somewhat, but all include some combination of bulk eucalypt species from Camcore, commercial eucalypt clones from Sinarmas, *Acacia mangium*, *A. crassicarpa*, an *Acacia* hybrid, and species from the company's native tree species program. The first pest and disease evaluations in these trials are scheduled for early 2022.

While only a few sentinel trials have been established to date, we believe sentinel plantings provide valuable information and we are committed to seeing our members continue to participate in this project. However, we also recognize some of the challenges these trials present and the need to refine the process. Some challenges, like the time required to conduct field evaluations, can be helped by reducing the size of the plantings. Others, like the need for people skilled in pest and disease diagnostics and the difficulties of accessing the crown of trees as they age and grow taller, will require more thought and creativity as we refine the process. One alternative is rather than establishing purpose-built sentinel trials is to incorporate insect and disease evaluations into our progeny trial protocols, allowing for additional data capture without the need to plant new tests. Other approaches to sentinel plantings are also possible, and we welcome suggestions.

Austropuccinia Screening Study

Over the past few years, Camcore has been collaborating with Smurfit Kappa Colombia (SKC) and FABI to understand the importance of *Austropuccina psidii* to Camcore's eucalypt breeding program. The pathogen causes the disease commonly called Myrtle rust, and it infects plants exclusively within the *Myrtaceae*, a host range that includes 78 genera and 522 species. First described in the late 1800s and known to infect and cause outbreaks in *Eucalyptus* and *Corymbia* species in Brazil since the mid 1900s, it was not until the early 2000s that the pathogen began a rapid global spread and was recognized as a threat to native and non-native *Myrtaceae* worldwide.

The goal of our study was to test the relative susceptibility of twelve commercial *Eucalyptus* species from Camcore's breeding program to infection by *A. psidii*. The experiment was carried out in 2018 under controlled conditions in SKC's forest health laboratory near Restrepo, with genetic material of the twelve species provided by Camcore and *A. psidii* resistant and susceptible clones as controls provided by SKC (see 2018 Camcore Annual Report for species lists and detailed methodology).

A manuscript on this study was recently submitted to a forestry journal and will be shared with Camcore members when published. Here we share a few important results from the study. All eucalypt species inoculated showed some level of infection by A. psidii, but there were clear differences in general susceptibility. Eucalyptus benthamii, E. badjensis, and E. smithii had overall high levels of susceptibility, while E. camalduensis, E. globulus, and E. longirostrata had the highest levels of resistance. Within species, some individuals were classified as asymptomatic or as having a successful hypersensitive defensive response, while others showed low, medium, and high susceptibility. This provides evidence that for most species tested, damage due to A. psidii infection can likely be avoided by selection and breeding of disease-tolerant planting stock.

Field Screening Studies in Colombia

In 2019, Camcore and SKC established field trials at two locations in Colombia for species-level screening of Eucalyptus genetic material for susceptibility to the pathogens Chrysoporthe cubensis and Ceratocystis neglecta. Two trials were planted at Cedral farm in the cooler, higher elevation SKC North Zone where both pathogens are being tested, and a single trial was planted at Vanessa farm in the warmer, low-elevation SKC South Zone where C. cubensis is being tested. The Cedral trials include 12 eucalypt species while the trial at Vanessa has 11 (for species lists, see Robert Jetton's presentation from the 2020 Virtual Camcore Annual Meeting which is available on the Camcore webpage). All trials include pathogen-resistant and susceptible clones from SKC's breeding program as controls.

Although these trials were planted in 2019, a series of unfortunate circumstances, including wild-fires and the need to re-isolate pathogens for inoculation, caused field inoculations to be delayed until December 2021. Field evaluations will be conducted in March 2022. A full report on the results of the study will be presented at the 2022 Camcore Annual Meeting and the next edition of the Camcore Annual Report.

Preliminary Results of Within-Family Genomic Selection in Full-Sib Familes of *Pinus taeda*

Introduction

<u>Genomic selection</u> (GS) refers to the use of high-density molecular marker data on candidate genotypes to help make selection decisions in a breeding program. Developing the capacity to do genomic selection in a breeding program is a somewhat complex process, but can be briefly summarized as follows.

- 1. GS models work best if they are developed and then applied to a specific population of genes. This means that the breeder must identify a relatively small effective population of interest containing the valuable genotypes that will be carried forward in the cycles of breeding and selection.
- 2. Dense molecular marker information and accurate phenotypic data and/or genetic value predictions must be available for a number of specific candidates.
- 3. Statistical models must be built that identify informative molecular markers that can be used to identify good genotypes with an acceptable level of precision.
- 4. The statistical models can then be used to make selections in new untested progeny and/ or advanced generations of progeny candidates following cycles of breeding.

There are a number of factors impacting the accuracy of GS, including the number of molecular markers and their distribution across the genome, the heritability of the trait of interest, the accuracy of the phenotypic / genetic value predictions on the calibration population, the size of the training population (i.e., the number of progeny to build the statistical model), and the effective size (N_e) of the breeding population. The last factor is extremely important. In general, it will be much more difficult to produce good GS models for N_e = 50 or 100 than for N_e < 10.

Family Forestry and Genomic Selection

In forest tree improvement, one common method of deploying improved genetic material into commerical plantations is through the use of full-sib families. Outstanding parents and full-sib families are identified through progeny testing, and then these full-sib families are reproduced through controlled pollination (CP), a somewhat time consuming and expensive process. The limited amount of CP seed is then used to produce hedges, which are used to produce rooted cuttings for planation establishment.

In this study, the objective is to examine the potential of GS for within-family selection in specific full-sib families. The idea would be to use a family-specific GS model to select a sub-set of superior progeny within that family, and only use those genotypes for commercial planation establishment. This means that the effective population size is $N_e = 2$, which should facilitate the development of accurate GS models. The experiment will focus on five commercial full-sib *P. taeda* families developed by the breeding program of WestRock in Brazil. This report provides preliminary results for three of the full-sib families.

Materials and Methods

A set of five full-sib families (derived from 9 parents) was identified. Progeny of the these five families were available in 6-year-old progeny tests, (along with other related and unrelated families). There were from 70 to 85 progeny per full-sib family. Height and DBH data were taken, along with IML resistograph measurements (an indirect measure of wood density). The bark-to-bark readings of resistance were projected into a circle representing breast-height Disk Density. Breast-height wood samples were taken, ground into woodmeal, scanned with a Foss 6500 NIR spectrometer, and Cellulose and Lignin content were predicted using the Camcore global pine model. Foliage samples were taken, DNA extraction was done by Dario Grattapablia (EMBRAPA), and molecular marker analysis was done using the ThemoFisher P. taeda Pita50K SNP chip. Custom genotype clustering was performed using the Axiom Analysis Suite from ThermoFisher. Clustering analysis was performed using TF best practice recommendations. There were some 16,000 informative SNP markers for this particular set of families.

Phenotypic and geneotypic data was availalble for 75, 80 and 85 full-sib (FS) progeny of Families 1, 2, and 3, respectively. In addition, pertaining to full-sib Family 1, data was available for 350 half-sib (HS) progeny related to one of the two parents. GS modeling was done using the SNP markers and within-family phenotypic deviations for each trait as the variable of interest. For a given full-sib family, within-family phenotypic deviation is directly related to the within-family genetic deviation.

Bayesian whole-genome regression models were implemented to assess the predictive ability of markers. Methods included Bayesian ridge regression, and Bayes A, B, and C (alphabet models). Bayesian Ridge Regression is statistically equivalent to genomic BLUP, i.e. a BLUP analysis accounting for different degree of relatedness among family members. Each Bayesian alphabet model makes different initial assumptions about the sizes and numbers of marker effects to estimate breeding values. For the GS training models, the model parameters were 30,000 burn-in and 75,000 total iterations.

Two GS model building approaches were examined: a FS-only approach, and a FS+HS approach. In the FS-only approach, for each of the full-sib families, a model was built using only the full-sib data, with 10% of data randomly set to missing and the remaining 90% was used to predict the phenotypes.

The FS+HS approach was examined only for full-sib Family 1. For each scenario, 10% of the full-sib progeny were randomly set to missing and then genetic value predicted with the remaining 90% of the full-sib data plus the half-sib relatives.

In all cases, each scenario was repeated 50 times to estimate the average predictive ability for each scenario for each trait. There were two key metrics to examine the quality of the GS models. First is Predictive Ability = $Corr(y_w, \hat{y}_w)$, where (\hat{y}_w) = the predicted phenotype from the GS model, and y_w = within-family deviation. Second is Predictive Accuracy = $Corr(g_w, \hat{g}_w)$, where \hat{g}_w = the predicted genotype, and g_w = the true breeding value. Predictive Accuracy can be calculated from Predictive Ability as follows:

 $Corr(g_{w},\hat{g}_{w}) = Corr(y_{w},\hat{y}_{w}) / h_{w}$ where h_{w} = the square root of the within-family heritability of the trait, and the following h^2 and h^2_{w} were assumed:

Volume: $h^2 = 0.30, h^2_w = 0.21$

Lignin, Cellulose, Density: $h^2 = 0.40$, $h^2_w = 0.31$

Results and Discussion

The SNP markers used worked well to resolve family structure and identify deviations from the expected pedigree relationships (Figure 9). One ramet of the putative parents was also genotyped, this allowed confirmation of parentage of the families.

FS-only Models

In general, all four GS algorithms tested gave similar average Predictive Ability for a given full-sib family-trait scenario. For example, for-Family 1 - Volume, average $Corr(y_w, \hat{y}_w)$ across the 50 repititions of that scenario were $Corr(y_w, \hat{y}_w) =$ 0.38, 0.42, 0.36, and 0.38, for Bayes Ridge Regression, Bayes A, Bayes B, and Bayes C respectively. Similarly, for Cellulose, the averages were $Corr(y_w, \hat{y}_w) =$ 0.33, 0.30, 0.26, and 0.26, respectively. This was seen for all traits and for the other two families, as well as the Family 1 FS+HS scenario. Therefore, the remainder of the discussion will focus on the Bayes Ridge Regression results.



Figure 9. Genomic relationship matrix for families of *P. taeda* showing three full-sib families of commercial interest, and seven other full-sib families with one parent related to FS Family 1. Darker colors indicate a higher degree of relatedness.

Table 11. Mean Predictive Ability (Corr(y_w, \hat{y}_w)) and mean Predictive Accuracy (Corr(g_w, \hat{g}_w)) of within-full-sib family genomic selection in *P. taeda*. Data are for four traits and three distinct full-sib families. Two scenarios for training data were examined: full-sib data only (FS-only) in families 1, 2, and 3, and full-sib plus half-sib data (FS+HS) for family 1. Values presented are average Corr(y_w, \hat{y}_w) and Corr(g_w, \hat{g}_w) over 50 repeated analyses using a random 10% of the FS data as validation, and 90% of the FS data (+HS data) as the training data set.

Family,	N	N	$\textbf{Predictive Ability (Corr(y_w, \hat{y}_w))}$			Predictive Accuracy (Corr(g _w ,ĝ _w)				
Training Data	IN _{fs}	IN _{hs}	Volume	Lignin	Cellulose	Density	Volume	Lignin	Cellulose	Density
Family 1, FS-only	75		0.38	0.10	0.33	-0.16	0.83	0.17	0.57	-0.28
Family 1, FS+HS	75	350	0.45	0.12	0.20	0.33	0.98	0.21	0.35	0.57
Family 2, FS-only	80		0.57	0.22	0.17	0.31	1.24	0.38	0.30	0.54
Family 3, FS-only	85		0.33	0.17	0.02	0.14	0.72	0.30	0.03	0.24
Mean, FS-only			0.43	0.15	0.18	0.16	0.94	0.27	0.31	0.27

Table 11 presents the results of the GS modeling for the three full-sib familes. There was substantial variation in Predictive Ability among the four different traits, and the patterns were similar for all families. Volume gave the best response, with average Predictive Ability ranging from $Corr(y_w, \hat{y}_w) = 0.38, 0.57$ and 0.33 for Families 1, 2, and 3, respectively. Cellulose content was the next best trait, with $Corr(y_w, \hat{y}_w) = 0.33, 0.17$, and 0.02. Lignin content gave similar Predictive Ability to Cellulose, but was more uniform across the families, with $Corr(y_w, \hat{y}_w) = 0.30, 0.22$, and 0.17 for families 1, 2, and 3, respectively. Disc Density gave variable results with $Corr(y_w, \hat{y}_w) = -0.16$, 0.31, and 0.14.

FS+HS Model

The addition of data from 350 half-sib progeny to the 75 full-sib progeny available for Family 1 did result in better models, at least for three of the four traits (Table 11). For volume, $Corr(y_w, \hat{y}_w)$ increased from 0.38 with FS-only data, to $Corr(y_{w}, \hat{y}_{w}) = 0.45$ with FS+HS data. For Lignin, there was only a very small improvement, from $Corr(y_{w}, \hat{y}_{w}) = 0.10$ to 0.12. Surprisingly, for Cellulose, the Predictive Ability actually decreased, going from $Corr(y_w, \hat{y}_w) = 0.33$ with FS-only data, to $Corr(y_{w}, \hat{y}_{w}) = 0.20$ with FS+HS data. The trait that had the largest increase with the addition of the half-sib data was Disk Density, where Predictive Ability went from $Corr(y_w, \hat{y}_w) = -0.16$ to $Corr(y_w, \hat{y}_w) = 0.33$. It is important to note that these improvements in Predictive Ability came from inceasing the number of progeny genotype from 75 in the FS-only model to 425 in the FS+HS

model. It seems likely that increasing the number of full-sibs (if possible) would be a more costefficcient way to improve the GS models.

Table 11 also presents estimates of Predictive Accuracy for the different GS scenarios. The estimates were derived assuming a typical value for the narrow-sense heritability for these traits in *P. taeda*. The genomic accuracy $(Corr(g_{w}, \hat{g}_{w}))$ is an estimate of the correlation between the true withinfamily genetic value and the predicted genetic value from genomic selection. Since this is actually a genetic correlation which ranges between zero and unity, this parameter is intuitively easy for breeders to understand and explain. The mean Predictive Accuracy for volume, averaged over the three FS-only scenarios, was $Corr(g_w, \hat{g}_w) = 0.94$. This indicates that we can make within-family selections for volume with a very high degree of accuracy. This is a very exciting result, since volume growth is, by far, the most valuable trait in a forest tree breeding program. For all three wood traits, mean accuracy was $\text{Corr}(g_w, \hat{g}_w) \approx 0.30$. This is somewhat lower than might have been expected, given that wood property traits typically have higher heritability than growth traits.

Summary and Outlook

Work is ongoing, both to gather FS data for two more families, and possibly to include additional data from HS progeny for all five families. Further analytical work will also be done, including other model building and validation strategies. The preliminary results are very encouraging, and suggest that it should be possible to build good within-family GS models among *P. taeda*.

Full-Sib BLUP Analysis Using SAS or R

Background

The use of linear mixed models is widespread in the analysis of genetic data, in particular progeny test data of animals and plants, including forest trees. Mixed models are well suited for genetic data analysis, using fixed effect estimates to adjust phenotypic data (e.g., for the environmental effects associated with test and replication) during the prediction of the random genetic effects that are of primary interest to breeders. Breeders commonly use software programs that combine the Restricted Maximum Likelihood (REML) estimation of variance components associated with random effects in the model and the use of those variance component estimates to both estimate the fixed effects (with Best Linear Unbiased Estimates, BLUEs) and predict the random effects (Best Linear Unbiased Predictions, BLUPs).

Most genetic improvement programs use progeny tests that contain offspring arising from known or controlled matings among a set of parents, and these offspring or progeny are measured for commercial traits of interest. For a diploid organism (like trees) and full-sib progeny test data (i.e., for all progeny, both parents are known), an appropriately constructed linear model must account for the fact that female parents and male parents are both sampling the same distribution of additive genetic effects. In addition, for a monoecious plant species, an individual plant genotype can produce both female and male reproductive structures. So, in a given progeny data set, the same parental genotype could be the female parent of some progeny and the male parent of other progeny. A proper analysis of this kind of data set would typically require a dedicated genetic software package (e.g., ASREML, Echidna, MTDF-REML, SeleGen, or WOMBAT) that can form a pedigree matrix or a numerator relationship matrix.

However, mixed model packages or procedures are also available in a number of generalpurpose statistical software packages, in both commercial packages, such as SAS Proc Mixed, or in open-source programs, such as the R lme4 package. Most of these packages do not have a pedigree matrix or numerator relationship option, and do not have the capacity to equate female and male random terms in the linear model to represent the same additive genetic effect. Breeders who need to analyze full-sib genetic datasets and who are familiar with general-purpose statistical packages, but are less familiar with or lack access to other software might benefit from an alternate approach.

An Alternate Approach

We developed an algorithm that allows for analysis of full-sib genetic datasets using generalized mixed-model software programs. The algorithm involves artificially doubling the dataset, so that each observation is in the dataset twice, once with the original female and male parent identification, and once with the female and male parent identities switched, and then analyzing the data with a parent model including female and male parents as random effects. For the parent models, breeding values of all progeny are then predicted as a function of the mid-parent breeding value, plus an adjustment for Mendelian sampling of additive genetic alleles affecting the trait of interest (effectively equivalent to the Reduced Animal Model, where the predicted BVs for progeny are obtained by back-solving from the parental BVs).

The algorithm was examined using a simulated full-sib dataset representing a typical forest tree breeding population (40 parents, 80 full-sib crosses, 4 tests, and 6000 trees). Five different analytical approaches were compared. First, we used the dedicated genetic software program ASREML and an individual tree model (*ASR_ind*), and this was identified as the "standard" or baseline model for comparison. The second approach used ASREML with a function within the program that properly specified the parent pedigree, along with a Mendelian adjustment to predict progeny BVs. Finally, three models with the doubled-dataset algorithm and a parent model (ASREML, SAS Proc Mixed, and R lme4) were examined.

Comparison of Results

Variance components, genetic parameters, and BLUPs of parental breeding values, progeny breeding values, and full-sib family specific combining abilities were compared across the five different linear models/software. Genetic parameter estimates were essentially identical across all analyses (e.g., heritability ranged from $h^2 = 0.220$ to

0.223, proportion of dominance variance ranged from $d^2 = 0.057$ to 0.058). Most importantly, BLUP predictions of breeding values from all five models were essentially identical, for both parents and progeny. The correlations between BLUPs from the baseline analysis (ASREML with an individual tree model) and the doubled-dataset/parent models using SAS Proc Mixed or R lme4 were never lower than R = 0.99999, and the correlation among BLUPs of SCA effects for full-sib families was never lower than R = 0.99997. Furthermore, in all cases, the linear regression coefficients were essentially one, and the linear regression intercepts were essentially zero. These data indicate that breeding values for parents, SCA effects for fullsib families, and breeding values for progeny from the doubled dataset / parent models are functionally identical those from ASR ind, thus regardless of the linear model used, there will be no differences in terms of selection decisions, and no differences in genetic gain predictions for a population of selected genotypes.

Conclusion

Breeders who need to analyze a full-sib progeny test dataset, and who wish to do so using a general linear mixed model software package lacking a pedigree function, can accomplish this analysis using a doubled dataset and a model including female and male parents as random effects. This approach will provide variance component estimates, genetic parameter estimates, breeding value predictions for both parents and progeny, and solutions to all other important random effects that are, for all practical purposes, identical to the results that would be obtained from an analysis using individual-tree data and a dedicated genetic software program with a pedigree function. A full description of the algorithm and the results can be found in Hodge & Acosta 2020, Forests, and the SAS and R code to conduct the analysis is available on the Camcore website.

The Use of a Slingshot and Rope Saw to Collect Pollen and Seed

Normally, the collection of pollen or seed involves tree climbing, which can be time-consuming, somewhat expensive, and for some companies is severely restricted for safety reasons. Camcore has been testing the use of a new tool, the slingshot and rope saw, to harvest flower-bearing tree branches in high, hard-to-reach crown positions, or on steep sites inaccessible to mobile elevated

work platforms. The slingshot is used to launch a rope high into the crown, then a guide rope pulls the rope saw into position to cut the branch. Camcore acquired this equipment with the idea of testing techniques and obtaining experience in different uses here in the USA in nearby pine and *Eucalyptus* seed stands and orchards. The tool was first used by Camcore in mid-2019 to collect immature *Pinus taeda* top cones for embryo extraction. In 2020, we used the tool to collect pine scion for grafting and laboratory experiments on sterile transfer. Finally, in spring 2021, *Eucalyptus amplifolia* pollen was collected from a seed orchard in Valdosta, Georgia.

In one of our webinars from fall 2021 (available on the Camcore website), Romeo Jump presented the equipment components, applications, and methods to operate the slingshot and rope saw for pollen collection. After the seminar, several members expressed interest in procuring this equipment for various applications, including DNA collection, and to attach ropes to the tree for safe felling. This method requires some skill and practice, but definitely has potential to be useful in a breeding program as a faster and less expensive option to collect pollen and seed.



Carlos Poz aims the slingshot during a collection of *Eucalyptus amplifolia* pollen in Valdosta, Georgia, in spring 2021.

Can the Nano NIR Predict Solid Wood MFA and MOE?

In the 2019 Annual Report, we reported on a promising new NIR device, the Texas Instruments DLP NIRscan Nano EVM. This device was used to produce very satisfactory models for protein content and fiber content of forage crops, applications that should be very similar to the prediction of chemical content of woodmeal samples. In 2020, we conducted an experiment to examine if the Nano would have utility to predict important properties on solid wood samples. A full manuscript of this research will be prepared and submitted to a scientific journal, but will be summarized briefly here.

Materials and Methods

Background

From 2005 to 2008, Camcore conducted a large experiment to study the juvenile wood properties of a number of important tropical and subtropical pine species. In the experiment, increment core samples were taken in 6 countries, across 22 sites, from 19 taxa (species, varieties, and hybrids), and 2244 trees.

Foss NIR Scanning and Silviscan

Two traits of interest in that experiment were Microfibril Angle (MFA) and Modulus of Elasticity (MOE). Increment cores were sawn with a double-bladed saw to produce 2 mm thick radial slices. The resulting "planklets" or "strips" were NIR scanned using a Foss 6500 in consecutive 10-mm windows from pith to bark. This work was done by Laurie Schimleck (then at the University of Georgia) using a specially constructed module to attach to the Foss designed to allow scanning of increment core strips. In total, 1737 increment core strips were scanned, with an average of 8.4 scanning windows per strip.

A subset of 370 core strips representing multiple species, sites and countries was sent to Paprican (Canada) for X-ray analysis on a Silviscan machine to measure density, MFA, and MOE on the same 10-mm windows scanned for NIR (see Figure 10). This subset was used to develop NIR models that were then used to predict density, MFA, and MOE on the remaining samples.



Figure 10. A typical increment core strip and the 10-mm windows used for Silviscan X-ray measurements and NIR scanning.

Nano NIR Scanning

In 2020, a module was built to allow scanning increment core strips with the Nano, and the same 370 core strips and windows were scanned with the Nano. In the intervening time, one strip had been lost, and a few window segments had been damaged, but the sample set was 99% identical to that which had been scanned with the Foss and the Silviscan. NIR model development was performed using the Camcore data analysis pipeline written in R (R Core Team, 2016). The pipeline examines several spectral transformations (including Multiplicative Scatter Correction (MSC), Standard Normal Variate (SNV) and Detrend (DT), and second derivative of Savitzky-Golay smoothing with two different window sizes of 5 and 7 points (SG5 and SG7), followed by partial least squares regression (PLS) and leave-one-out (LOO)



The plastic case developed to allow use of the DLP Nano NIR to scan increment core strips.

Table 12. Comparison of NIR model fit statistics for the prediciton of solid wood properties using increment core strips. Two devices were compared: the Foss 6500 and the DLP Nano. Traits were Density, Microfibril Angle (MFA), and Modulus of Elasticity (MOE).

Trait	Mean	Range	Foss			Nano			
			R ² _{cv}	R _{cv}	SECV	R ² _{cv}	R _{cv}	SECV	
Density	450 kg/m ³	250 to 800	0.71	0.84	47	0.56	0.75	58	
MFA	7°	5 to 45	0.82	0.91	3.1	0.65	0.81	4.4	
MOE	25 Gpa	2 to 22	0.86	0.93	1.5	0.72	0.85	2.2	

cross-validation. The final model chosen was the one that maximized the cross-validation R^2_{CV} with a small number of latent variables as a secondary criterion. Fit statistics for the Foss and Nano were then compared to evaluate the performance of the new device.

Results and Discussion

Table 12 shows the comparions between the fit statistics for the Foss and the Nano NIR models for the three wood property traits. In general, the laboratory-grade Foss machine produced good to very good models. For density, the R² of cross-validation was $R^2_{CV} = 0.71$, $R^2_{CV} = 0.82$ for MFA, and $R^2_{CV} = 0.86$ for MOE. The Nano models were satisfactory to good: the R² of cross-validation was $R^2_{CV} = 0.56$ for density, $R^2_{CV} = 0.65$ for MFA, and $R^2_{CV} = 0.72$ for MOE (Figure 11). On average, the Foss models had an R^2_{CV} that was 0.15 higher than the Nano models.

One of the reasons a breeder would be interesting in scanning increment core strips in this manner would be to investigate the pith-to-bark profiles of these important wood traits. It is well known that most pine species show a very distinct trend from pith to bark. Lower-strength wood (i.e., lower MOE) is found near the pith (due to lower density and higher MFA), and strength increases moving out to the bark (higher MOE due to higher density and lower MFA). This occurs in the juvenile core or inner wood of a tree; eventually the tree will begin producing "mature wood", with more constant wood properties. However, in fastgrown commercial pine plantations, juvenile wood makes up a substantial proportion of the total wood harvest at rotation age. Thus, the pattern of pith-to-bark variation is important, and a possible breeding objective could be earlier production of mature wood.

We examined the pith-to-bark profiles of a number of indiviudal trees, comparing the Silviscan measurements, the Foss NIR predictions, and the Nano NIR predictions. Figure 12 illustrates the MOE profiles of one tree of P. tecunumanii, one P. elliottii x P. caribaea, and one P. taeda sampled in Argentina. Regardless of whether using the Silviscan X-ray data (the red circles in Figure 12), the Foss NIR predictions (the blue triangles), or the Nano NIR predictions (the green squares), the general profiles of a particular tree are very similar. The Nano NIR predictions are less precise than the Foss predictions, and for any given window of measurement, a moderately large prediction error is possible (for example, note window 9 for the *P. tecunumanii* sample in Figure 12). Nevertheless, since there are a large number of windows for each tree, these errors tend to cancel out, and accurate pith-to-bark profiles will still be produced. In general, the results suggest that breeders would be able to use the Nano predicition profiles to identify desirable genotypes without significant loss of efficiency.

Conclusions and Implications

The Nano NIR device appears to be useful for working with solid wood samples, in addition to its utility to measure more typically used woodmeal. As it is inexpensive and easily portable, there should be opportunities for tree breeders to inocorporate this device into their wood testing protocols.



Figure 11. NIR prediction models for MOE, MFA, and Density using the DLP Nano on solid wood strips.



Figure 12. Pith-to-bark MOE profiles for three trees developed using three methods: Silviscan x-ray measurements (red circles), Foss NIR predictions (blue triangles), Nano NIR predictions (green squares).

New Methods for Eucalyptus Pollen Testing

Due to interest among the members in improving pollen quality, Romeo Jump presented a series of webinars in 2020 and 2021 on testing *Eucalyptus* and pine pollen quality following conventional protocols of *in vitro* germination and staining methods. These webinars were presented as video tutorials where step-by-step laboratory procedures for testing pollen were demonstrated. After the webinars, many members expressed interest in further research of new alternatives to evaluate pollen quality.

Preliminary studies were developed in 2021 with the use of the Impedance Flow Cytometer (IFC), a high-tech device that applies principles of flow cytometry to detect and measure physical and chemical characteristics of cell populations. IFC results on viability have proven to be highly correlated with in vitro germination testing using pollen of some commercial crops. This technology was developed by Amphasys AG, a Swiss company that works on providing mobile cell analysis solutions. The IFC was on loan from Amphasys to the NCSU P. taeda Tree Improvement Program to be used in pine pollen applications. To define the protocol for Eucalyptus pollen testing using the IFC, pollen samples from a single Eucalyptus amplifolia tree, recently collected, were used to test rehydration time, an important step for IFC's sample preparation. For rehydration, individual samples were poured into open microcentrifuge tubes and placed inside a wet chamber for 0, 15, 30, 60 or 120 minutes. Viability percentage of samples did not differ considerably, but the graphed results showed that the separation between viable and dead pollen grain populations was more visible as the time of rehydration increased.

Experiments to compare pollen quality testing using an in vitro method versus Amphasys' IFC were carried out. Sample lots were obtained from fresh pollen of Eucalyptus amplifolia collected in 2021 in Georgia, 1-year-old stored pollen of E. benthamii from Uruguay and 2-year-old pollen of Corymbia henryi from Brazil. Two samples of each pollen lot were obtained for a total of 26 samples. The first 13 samples were tested using the in vitro agar method and germinated grains were counted after 48 hours. Germination percentage was recorded for each sample. The other 13 samples were tested using Amphasys' IFC device with 60 minutes of rehydration for each sample. For this test, the IFC pumps the prepped pollen sample through a highly sensitive microchip where pollen grains align individually and travel along a microchannel, exposing each grain to an electric current flow that is interrupted by passing grains. The microchip records the individual electric impedance signature of 10,000 grains showing each measurement on a scatter plot for pollen viability and size. IFC sample running takes around 2 minutes.

Both methods, *in vitro* and IFC, showed similar results of viability for each sample in this experiment, indicating that Amphasys' IFC has potential to be used as a fast, reliable alternative to test pollen quality. Camcore will continue performing research to validate new methods for *Eucalyptus* and pine pollen testing.



Figure 13. Steps to test Eucalyptus pollen samples using Amphasys' Impedance Flow Cytometer in the lab.



Figure 14. The graphed reults for pollen analysis by Impedance Flow Cytometry. Blue points indicate the impedance signature of each pollen grain. Y-axis on the scatter plot (Amplitude) represents an estimate of grain size, while X-axis (Phase) is an estimate of viability.



Ten-month-old clonal trials of hybrid *E. grandis x E. globulus, E. grandis x E. pellita* and *E. urophylla x E. pellita* planted by Smurfit Kappa Colombia in 2020. These trials are part of the Camcore Eucalyptus hybrid project (see article in this document on p. 9)

The Use of UAV Drones for Pine Pollination

Controlled pollination (CP) is a critical component of many forest tree breeding programs, and in some cases, is an important part of commercial production of improved material for plantation establishment. Currently, almost all CP techniques are very labor intensive, and often require tree climbing, and/or the use of heavy machinery in seed orchards. The use of small aerial robots with partial or complete autonomous operation conceivably could provide a cheaper, safer, and more efficient method to make CP crosses.

Current work in robotic pollination can be divided into two distinct groups: 1) "bee-replacers" aimed at mass pollination of flowers, and 2) systems aimed at pollinating plants that need artificial pollination such as vanilla planted in a greenhouse. NCSU-Camcore PhD student Piyush Pandey is working on a project that incorporates a mechanical design of a pollinating device mounted on an unoccupied aerial vehicle (UAV), as well as the design of a perception and control system for the aerial pollinator. Specifically, his project is aimed at the design of a low-cost pollinating device that can successfully inject pollen into a paper exclusion bag in *P. taeda* seed orchards.

To date, the mechanical design of the pollination device has been completed and tested. All parts other than the motors are 3D-printed using a polyactic-acid (PLA) filament, and an updated design of the manipulator has been created to include an injector "claw" that is mounted on a mobile Steward platform that is used to orient the injector to the required pose based on the detected position of the pollination bag. To integrate the pollinating device with the UAV, a simulation study is being conducted for the large-scale navigation of the UAV in the orchard. The large-scale navigation for visiting trees is based on the GPS coordinates of the trees to be pollinated. Initial work on the creation of a loblolly pine tree model for a simulation study has been completed. The modeling of a quadcopter system with a front-facing stereovision camera as well as the creation of a small orchard world for Gazebo simulation has been completed. The system architecture diagram is shown in the figure below. Though this is likely to be long-term project, we are excited about this work and we will keep our members updated about Piyush's progress.



Use of Handheld NIR and Image Analysis to Measure Foliage Nutrient Content in Eucalypts

Camcore has been working with NIR models for prediction of wood chemical and physical traits for more than 20 years, and we have developed global NIR models for wood characterization of pines and eucalypts. We have also used NIR to differentiate between pure and hybrid species and to confirm clonal identity in the nursery. Recently, we used NIR to develop nutrient foliage content models for nursery-grown teak seedlings with benchtop and handheld NIR devices. During our 2019 annual meeting in Portugal, Camcore's Technical Committee approved a research proj-

ect to test the efficiency of our handled devices (MicroPhazir and DLP_Nano) to predict foliar nutrient content in *Eucalyptus* seedlings.

Materials and Methods

Seeds of Eucalyptus urophylla x E. grandis were sown in the Tree Improvement Program's covered mist house at the Horticulture Field Lab at NC State University in the late summer of 2021. The experiment was conducted during late summer and early fall 2021. Seed originated from a family bulk collection and was contributed by our Mexican member Proteak. A total of 200 seedlings were grown in individual 1.25-quart square pots filled with washed silica river sand, with a particle size of 0.8 to 1.2 millimeters. Seedlings were irrigated daily as required. Germination culminated after ten days from sowing, and fertilization was initiated using a complete Hoagland's solution which provides all essential nutrients for plants grown hydroponically. Each seedling received 50 ml of the complete Hoagland's daily. After 40 days, the seedlings were divided into five lots of 40, and each lot started to receive one of five different fertilizer treatments. One lot continued receiving the same complete Hoagland's solution (T1), the other lots received a modified Hoagland's solution adjusted to supply either 50% of N-P-K (T2), 10% of N (T3), 10 % of P (T4), or 10% of K (T5). All plants received 50 ml of their fertilization treatment daily.



Figure 15: Foliage collection and preparation for scanning.

Two foliage collection and scanning events were carried out at 15 and 30 days after starting the fertilization treatments. For each event, 20 seedlings of each treatment were selected randomly. From each seedling, we harvested the first four leaf pairs attached to the stem, starting with the topmost pair with a width greater than 15 mm. The four pairs were labeled and arranged on a blue tray in preparation for scanning (Figure 15).

We used three different scanning devices. First, we placed the tray inside a chamber to be scanned with the Resonon Hyperspectral camera, followed by NIR spectral scans of each of the eight leaves using Thermo Fisher Scientific's MicroPhazir, and Texas Instrument's DLP Nano, as depicted in Figure 16. The scanned leaves and the remaining foliage from each seedling were placed in labeled paper bags, sealed, and submitted to the North Carolina Department of Agriculture & Consumer Services (NCDA&CS) for wet-laboratory foliar nutrient determination.

Data Analysis

Spectral information was converted into datasets according to the scanning device. For the hyperspectral camera (Resonon), the resulting hypercube was segmented by differentiation of green pixels (black and white segmentation) and aggregated datasets were generated per leaf pair, in which only information from the white shape was considered and averaged (Figure 17). For



Figure 16. Leaf scanning methods: left = hyperspectral camera, center = ThermoFisher MicroPhazir, right = Texas Instruments DLP Nano.

MicroPhazir and DLP Nano, datasets by leaf pairs were creating by averaging NIR spectra of both leaves.

For each scanning instrument, raw spectral data was used to generate 10 databases: 4 sets with average spectral information on each leaf pair, 3 sets with average information combining two consecutive pairs, 2 sets with average information combining three consecutive pairs and 1 set with average information of all four pairs (whole-plant scanning).

Models for predicting foliage nutrients were developed using our data analysis pipeline written in the R environment. The pipeline is separated into two phases: spectral transformation and outlier detection, followed by model training, crossvalidation, and model selection.

In the first phase, different mathematical transformations, including scatter corrections, spectral derivatives, and combinations of the former (pairs of transformation), were applied to the raw spectra to remove scattering associated with diffuse reflection and improve the subsequent regression analysis. Scatter correction transformations included multiplicative scatter correction (MSC), standard normal variate (SNV), and detrend (DT). Spectral derivative methods included Savitzky-Golay transformation calculated with second-order polynomial and second derivative at two different window sizes of five and seven smoothing points (SG5 and SG7). Pairs of transformations included SNV+DT, MSC + DT, SNV + SG, MSC + SG, and DT + SG. On each transformed dataset, outliers were determined and removed by calculating Local Outlier Factors (LOFs).

In the second phase, model selection, outlier-free datasets for all transformations and the raw spectra were used to compute models between the spectral data and the laboratory determined foliage nutrients. For model fitting, we used partial least squares regression (PLS) with factors (latent



Figure 17. Schematic of the hyperspectral image date extraction for four leaf pairs.

		2	Mi	croPhazir				Resonon Hyperspectra				DLP Nano						
Irait	Database	Factors	R ² _cal	RMSEP_cal	R ² _c-v	RMSEP_c-v	Database	Factors	R ² _cal	RMSEP_cal	R ² _C-V	RMSEP_c-v	Database	Factors	R ² _cal	RMSEP_cal	R ² _c-v	RMSEP_c-v
AI																		
В	SG7	1	0.1512	5.2717	0.10638	5.409	DT	1	0.2683	4.8945	0.2281	5.027						
Ca	DT_SG7	2	0.6265	0.1462	0.59789	0.1516	SNV	3	0.5302	0.1639	0.4628	0.1752	NIR	4	0.585	0.1541	0.5409	0.162
Cu	SG7	4	0.6447	2.7869	0.56607	3.079	NIR	5	0.5766	3.042	0.4558	3.447	DT	4	0.484	3.3597	0.3639	3.728
Fe	NIR	1	0.1182	17.2575	0.08497	17.58			0000	1717-1	0.000							
Fe:Mn		2(2)																
к	DT	1	0.3022	0.2734	0.25319	0.2828	DT	1	0.064	0.3167	0.01684	0.3245	DT	1	0.231	0.2871	0.19329	0.2939
Mg	SG7	3	0.6206	0.0363	0.579	0.03827	SG7	3	0.5478	0.0397	0.4517	0.04367	NIR	4	0.604	0.0371	0.565	0.0389
Mn																		
N	MSC_SG7	4	0.933	0.2664	0.9139	0.3018	MSC	7	0.8675	0.3746	0.8305	0.4235	DT	4	0.78	0.4831	0.717	0.5471
N:K	SG7	4	0.6087	0.4951	0.52074	0.5477	SNV	2	0.4167	0.6044	0.3687	0.6287	DT	1	0.232	0.6938	0.1945	0.7101
N:S	DT	3	0.6454	1.5414	0.5725	1.692	NIR	3	0.6584	1.5128	0.617341	1.601	SG7	2	0.646	1.5405	0.5097	1.81
Na	DT	1	0.2657	0.0816	0.21895	0.08415	DT_SG7	1	0.1642	0.0871	0.11607	0.08952	SNV	1	0.208	0.0847	0.16339	0.08709
Р	MSC	1	0.1195	0.0578	0.07249	0.05936	SNV	7	0.3449	0.0499	0.197034	0.05539		(1942) (
S	SG7	4	0.7969	0.0207	0.7489	0.02302	DT	5	0.7046	0.025	0.6425	0.02749	MSC	4	0.679	0.0261	0.6126	0.0286
Zn	DT	1	0.295	4.9472	0.25538	5.084			1000	12121)	DT	1	0.261	5.0647	0.21554	5.217

Table 13. Selected models for whole plant scanning.

variables) ranging from 1 to 20, and model performance was evaluated by leave-one-out cross-validation (LOO). The optimum number of latent variables was selected using the "one-sigma" approach, in which the model with the lowest number of latent variables is selected based on the root mean squared error of prediction (RMSEP) that is within one standard error of the model with the absolute minimum RMSEP. Desirable models are those with a small number of latent variables that maximize the coefficient of determination (R²c-v), and minimize the root mean squared error of prediction by cross-validation (RMSEPc-v).

Results and Outlook:

In this article we only present the results obtained for the first foliage scanning and collection. Predictive foliar nutrient models were developed for each of 16 macro and micro nutrients and ratios (N, P, K, Ca, Na, S, Zn, Al, B, Cu, Fe, Mg, Mn, Fe:Mn, N:K, N:S). More than 130,000 model combinations were examined for this study (3 instruments, 16 nutrients, 14 transformations (including raw spectra), 10 aggregated databases per transformation, and 20 factors per model). Consistently, we found that better models are obtained when a higher percentage of the plant was scanned. In other words, higher R²c-v, and lower RMSEPc-v were achieved when databases included combined information of several leaf pairs. In fact, the best models were obtained using the datasets with average information of all four pairs (whole plant scanning). Selected models for whole plant scanning are presented in Table 13. Adequate models were found for N (and N ratios), S, Ca, Cu, Mg. The length of the green bar represents the value of the cross-validated R², the longer

the green bar the better the predictive power of the model. Note that in general, the R²c-v for the MicroPhazir models were higher than the ones found with the hyperspectral data or with the DLP Nano, however there is a clear correspondence between all instruments, as the length of green bars follows a consistent pattern. Interestingly, models selected for DLP Nano were similar to Resonon hyperspectral camera. Regardless of the instrument, the dataset or the amount of information used for the model, we were not able to find acceptable equations to model the foliage content of the remaining elements (Al, B, Fe, Fe:Mn, K, Mn, Na, P, Zn).

The preliminary results of this study indicate that near infrared spectroscopy and hyperspectral imaging of seedlings across their height can be used to predict foliar levels of N, N:K, N:S, S, Ca, Cu, and Mg in E. urograndis seedlings with a reasonable level of accuracy. All devices produced usable models for some nutrients. The MicroPhazir NIR models were the best, and the results obtained with the DLP Nano and the Resonon Hyperspectral camera were similar. It is worth mentioning that there is a highly significant difference in the cost of the devices; the MicroPhazir costs about 25x and the Resonon hyperspectral camera about 50x the cost of the DLP Nano. Unfortunately, predictive models for the remaining macro and micronutrients using NIR or hyperspectral imaging were poor and will need further investigation to prove useful. In 2022, we will complement this study by analyzing the information for the second foliage collection, scanning and wet chemistry determination. Additionally, we will study the usefulness of NIR handheld scanners and possibly hyperspectral data for pines and acacias.

Potential Use of Ground Lidar & Photogrammetry for Measurement of Genetic Tests

At the 2019 Annual Meeting in Portugal, the Camcore Advisory Board identified a number of research topics to focus on over the next ten years. One of those topics was the potential use of new imaging technologies for genetic trial assessment. Many forestry companies around the world are investigating or using aerial photogrammetry and lidar as tools for forest inventory, and in some cases, to measure tree height in research trials. Our interest in Camcore is more toward the use of images taken from ground level to measure tree diameters, stem straightness, stem taper, branch characteristics, etc. In 2021, we took our first steps toward investigating how to use this technology to measure genetic trials.

Genetic Trials

Working with a friend of Camcore, Bob Purnell, we identified two *P. taeda* genetic trials owned by Weyerhaeuser Company, and part of the NC State-Industry Tree Improvement Program (NCSU-TIP) breeding program. The tests are in eastern North Carolina and were 14 years old at the time of measurement, with tree heights and diameters roughly similar to 8-year-old subtropical pines. The tests were measured for height, DBH, and straightness by Weyerhaeuser contractors using traditional techniques in August 2021, and then were assessed with two different imaging technologies.

Photogrammetry

Our ground photogrammetry work built on a method developed by Edgar Alberto Agudelo del Rio (Beto) in his MS research at the Universidad Católica de Manizales in Colombia. Beto is an employee of Smurfit Kappa Colombia, and he spent two weeks with us in North Carolina to assist with this project.

The method involves the use of a UAV drone-camera system, but rather than flying the drone, the device is mounted on a pole and carried through the stand. The specific device we tested was a DJI AIR 2s with a 20 MP camera and a Gimbal stabilization system, mounted on a 4.6 m pole. In July 2021, we measured both trials by walking



DJI Air 2s drone (propellers removed) and the mounting device that fits onto a telescoping pole.

every row and column taking more than 7000 photos per test. The images are being processed with special software (Software Pix4Dmapper and Técnicas SfM - Structure from Motion) to create a 3D point cloud of data. The total cost of the devices for this work was less than US\$ 2500, and the field measurements took 2 days with a crew of 4 people to completely measure the two 1.5 to 2.0 ha genetic



Beto Agudelo (SKC) and Gary Hodge (Camcore) using the polemounted DJE Air 2s.



A typical image from the drone camera in the forest genetics trial.

trials.

Lidar

Our lidar work was done with NCSU graduate student Travis Howell. Travis is a forester with a BS and MS degree from NC State. He is currently employed full time with a landscape architecture and surveying company in the Raleigh area, and he works with lidar on a daily basis. He has recently begun a PhD program at NCSU, working with the three industry research programs here: Camcore, NCSU-TIP, and the Forest Productivity Cooperative.

For this work, we utilized the Leica BLK 360. This ground lidar device is mounted on a tripod, and takes a 360° lidar image + panoramic color photos. Each 360° reading returns about 54 million data points from roughly a 50 m radius around the center. Readings were taken from 27 to 30 locations in the two trials, and resulting data were stitched into 3D point clouds in a similar manner as described above. The cost of the device is currently around US\$ 20,000, and the field measurements took 1 day with a crew of 2 people to completely measure the two 1.5 to 2.0 ha genetic trials.

Data Quality and Outlook

Once a 3D point cloud has been developed, it is possible to measure traits of interest "manually" using tools and widgets with the specialized software. We expect that the data that can be extracted will be of very high quality, and will be highly correlated with traditional field data. For example, we extracted DBH data for 37 trees from a 25 m radius plot. Correlation between field DBH and lidar DBH was very high, with R = 0.97.

We expect to be able to extract much more useful data as well, for example,

- diameters at different heights, which can be used for determining taper and more accurate stem volume,
- commercial height to an 8 cm diameter,
- stem sweep or other straightness data, and
- branching characteristics.

A focus for 2022 will be to work on automated data extraction using special code written in R, Python, or other coding language. This will eliminate the need for operators to "hand process" the data in the office.

In the long term, there are a number of



Travis Howell and Juan José Acosta (NCSU) with the Leica BLK 360 ground lidar device.

research questions of interest. Some of these are technical, such as determining optimal measurement strategies to use in the field, and determining what kind of data can be extracted automatically and reliably. There are also important genetic questions. Will this method of progeny test measurement process be more efficient in terms of cost and time? Can this data be more useful to measure "economic volume", and perhaps be tied to mill yield models? We are very excited about the potential of these technologies, and are hopeful that they will be part of our tool kit in the future.



<u>Left</u>: Image from lidar + photographic scanning with the Leica BLK 360. <u>Right</u>: Point cloud image of a single tree, with stem section up to 4 m height highlighted.

21 Pine Species: Lesser-known Species With Potential for Plantation Establishment

In the 2019 Camcore annual meeting in Portugal, we decided to complete a literature review of pines, a project similar to the report on eucalypt species written for Camcore in 2018 by Jakob Butler and Brad Potts of the University of Tasmania. In December of 2020, Juan Lopez sent the document on pines to all the members and made a presentation at the 2020 Camcore annual meeting.

The article on 21 species of pines provided information about taxonomy, morphology, native range and climate, environmental tolerances, insects and diseases, and commercial history. None of the 11 species of pine covered in the Camcore book "Conservation and Testing of Tropical & Subtropical Forest Tree Species by CAMCORE Cooperative" published in year 2000 were included in this manuscript. However, there were 11 other species of pine that have been tested in Camcore trials, that were not included in the 2000 Camcore book, that are part of this new literature review. Some of these species may have commercial potential as hybrid partners and information on growth and adaptation is available. Several Camcore members have trials and conservation banks of these species with pollen and seeds accessible if desired. Ten additional species in this document, never tested by Camcore, show some potential as pure species for Camcore members.

Seven of the 21 species show a mean annual increment (MAI) over 20 m3/ha/year: Pinus douglasiana, P. kesiya, P. leiophylla, P. luchuensis, P. massoniana, P. merkusii and P. Species like P. kesiya, P. pseudostrobus. merkusii, P. massoniana and P. luchuensis have been planted successfully in some Southeast Asian countries. Some of the limiting factors in species such as P. kesiya and P. pseudostrobus are the frequencies of stem forking, heavy branches, and large knots. Pinus massoniana shows frost and drought tolerance in addition to fast growth and good wood quality. Growth potential of Pinus douglasiana from Mexico looks very

promising in several countries. This species might be an excellent hybrid partner for *P. maximinoi* or *P. pseudostrobus*; species that belong to the same taxonomic group. *Pinus merkusii*, with high wood density, should grow well in tropical regions.

Species with a MAI between 10 and 20 m³/ha/year are *P. echinata, P. muricata, P. lambertiana, P. palustris* and *P. ponderosa* from the United States as well as *P. teo-*



derosa from the United from a natural stand in Mexico.

cote. P. michoacana and P. montezumae from Mexico. Pinus ponderosa is frost and drought hardy and has potential in areas with dry summers and wet winters. Pinus lambertiana is a frost-hardy species. Pinus echinata and P. palustris are part of the same taxonomic group (Australes) as P. taeda, P. elliottii and P. caribaea and might be possible hybrid partners with those species. Pinus muricata is a close relative of P. radiata and might be a possible hybrid partner. *Pinus teocote* is reported to be frost and drought tolerant and might hybridize well with P. patula, P. tecunumanii, P. greggii, P. leiophylla and P. herrerae. Pinus michoacana is drought hardy and has good structural timber. Pinus montezumae has shown good growth and form in plantings in South Africa. Seeds of the last two species can be collected in some areas of Guatemala.

Six species with low growth (less than 10 m³/ha/ year) that have been tested by Camcore might have some use as hybrid partners. *Pinus arizonica, P. cooperi, P. ayacahuite, P. durangensis, P. engelmannii* and *P. hartwegii* are frost hardy and two of these, *P. cooperi* and *P. engelmannii* are drought tolerant.

At the beginning of 2022, we sent a survey to the members asking for the level of interest in establishing new trials with these species, so that we can start coordinating seed collections and purchases in 2022.

2020-2021 Seed Collections in Central America

In 2020 and 2021, Camcore made Pinus tecunumanii seed collections in four natural stands, one in Guatemala (San Jerónimo) and three in Honduras (Villa Santa, Los Planes and San Esteban). In addition, seed collections of P. tecunumanii were made in a Camcore seedling seed orchard established in La Lagunilla farm in Jalapa, Guatemala by Grupo DeGuate and the National Institute of Forests (INAB) (Table 14). Because of the pandemic and the restrictions on transit circulation enforced by the Guatemalan government, Elmer and Josué could only make seed collections in two sites in 2020, Villa Santa and Los Planes. In 2021, the government removed the restrictions and they were able to go back to these two stands as well as the other sites shown in the table. No seed collections of P. maximinoi were made in 2021 because seed production was very poor. In the second half of 2021, Elmer and Josué dedicated much time to the establishment of the teak conservation bank in Guatemala (see article Teak Update in this report).

Our seed collection efforts focus on populations that are poorly represented in Camcore members' trials, conservation banks, and seed storage in Raleigh. In some of the natural stands in Central America, where we made seed collections, the trees are competing with cattle and agricultural crops which, together with fires and insect attacks, contributes to a decrease in the life expectancy of the forests. Conservation of forests species continues to be one of the main objectives of Camcore. In the natural forest, the best phenotypes are selected for seed collections and the seeds are sent to Camcore members in different countries where



Josué Cotzojay and staff from La Lagunilla farm, collecting seeds in the Camcore *P. tecunumanii* seedling seed orchard.

they are used for the establishment of additional progeny tests and ex situ conservation banks.

In 2020, we renewed the agreement we have with INAB for mutual benefit to both organizations. In the operational plan for 2021, we provided INAB with seeds of 1st and 2nd generation P. tecunumanii and Tectona grandis for the establishment of 2nd and 3rd generation progeny trials in Guatemala. INAB shared the seeds with several universities and a small landowner in Guatemala to plant trials on their land in the second half of 2022 or first half of 2023.

Country	Species	Provenance	Status	Latitude	Longitude	Trees
Guatemala	P. tecunumanii HE	San Jerónimo	Critically Endangered	15° 03' N	90° 18' W	15
	P. tecunumanii 2 nd gen SSO	La Lagunilla	-	14° 43' N	89° 57' W	11
Honduras	P. tecunumanii LE	Villa Santa	Vulnerable	14° 12' N	85° 38' W	20
	P. tecunumanii LE	Los Planes	Vulnerable	14° 47' N	87° 50' W	20
	P. tecunumanii LE	San Esteban	Endangered	15° 17' N	85° 40' W	8

Table 14. Summary of seed collections completed in Central America in 2020 and 2021.

2020-21 Camcore Domestic Conservation Update

Seed Collections

Throughout 2020 and 2021, Camcore has continued to make significant progress in our domestic gene conservation efforts. Most recently this work included collections of seed from natural populations of both pitch (*Pinus rigida*) and Table Mountain pine (*P. pungens*) and red spruce (*Picea rubens*) from the southern portion of the species range (Table 15).

Pitch pine cone production is irregular with large crops being produced every three to nine years. Unfortunately, our work with this species began in 2018 and we have yet to encounter a bumper crop. While production has been down, we have been able to collect from a total of 19 trees from four populations in South and North Carolina.

From 2010 to 2016, Camcore collected seed a total of 269 individual mother trees of Table Mountain pine from 39 populations in 8 states. While both Camcore and the USFS are pleased with these numbers, we have agreed to collect additional cones from populations in South Carolina in order to help with restoration efforts by the USFS. In 2020, we collected 21 new mother trees from five populations. Both the recent pitch and Table Mountain pine cones have been sent to the USFS Ashe Seed Extractory where the seed was extracted and cleaned.



Pitch pine cone collections at Daniel Branch, SC, November 4, 2020



Jason Hollifield (USFS) assisting in a pitch pine collection at Callas Gap, SC, in October 2020

During the fall of 2021 we were able to add to our red spruce conservation efforts with collections from 50 new mother trees from two populations in Tennessee and two in Virginia. These collections bring us to a total of 187 individual mother trees collected in 22 populations across the southeastern United States. Recently collected cones were shipped to the USFS Ashe Seed Extractory for processing. Thanks are extended to the Appalachian Trail Conservancy (ATC) for providing field assistance with the 2021 red spruce collections. Camcore's recent red spruce collections are being made in collaboration with the Southern Appalachian Spruce Restoration Initiative (SASRI) for which Andy Whittier of Camcore serves on the steering committee. SASRI is a partnership of private, state, federal, and non-governmental organizations that recognize the importance of high-elevation spruce ecosystems and is dedicated to restoring these systems in ecologically appropriate locations.

Species	Common Name	Provs	Families	Year	Producing
Pinus rigida	Pitch pine	4	19	2020	Yes
Pinus pungens	Table Mountain pine	5	21	2020	No
Picea rubens	Red spruce	4	50	2021	No
Tsuga caroliniana	Carolina hemlock	Orchard	66	2020	No
Tsuga caroliniana	Carolina hemlock	Orchard	41	2021	No

Table 15. Camcore domestic seed collections in 2020 and 2021.

Conservation Orchards

In addition to the collections of seed from threatened tree species in the eastern US, we have made great strides in putting this material back into the ground in the form of conservation seed orchards (Table 16). These orchards are an invaluable resource and will allow us to maintain fresh germplasm for years to come for use in restoration and research efforts. Our first domestic conservation orchard was established in 2008 in northwestern NC. Every year since 2016 we have been able to collect seed from this orchard. Seed from the earliest collections were not viable, but more recent collections have yielded seed that has germinated and is now growing in our western NC greenhouse.

In late January 2020, twenty workers from Camcore and the USFS successfully planted nearly 1000 conifer seedlings into seed orchards located in western North Carolina and eastern Tennessee. On January 22, we established both a 301 seedling eastern hemlock seed orchard and a 167 seedling Table Mountain pine orchard at the USFS Beech Creek Genetic Resource Management Area (GRMA) located outside Murphy, North Carolina. The following day these plantings were duplicated in nearby Chilhowee, Tennessee at the Chilhowee Genetic Resource Management Area.

These four seed orchards mark an important step forward in Camcore's domestic conservation

efforts and are hopefully the first of several more conservation plantings done in collaboration with the USFS. Future seed produced will be shared by Camcore and the USFS. Genetic material produced in these orchards will be instrumental in the conservation, restoration, and research of these threatened conifers endemic to the eastern US.

It should be noted that establishment of these seed orchards would not have been possible without an impressive team from the USFS that helped with the planting. In addition to the planting crew, we would like to particularly acknowledge Robin Taylor (USFS, retired), Jason Rodrigue (USFS), and Drew McCarley (USFS) for helping to get this project implemented and in the ground.

Continuing the success with the Beech Creek and Chilhowee seed orchards, we established a 500 seedling Carolina hemlock orchard at Crossnore, North Carolina in March of 2020. Space for this orchard was provided by the NC Forest Service. In addition to the NCFS we are thankful for volunteers from the Hemlock Restoration Initiative that were instrumental in helping us to plant this orchard. Future conservation planting plans include a red spruce and a Fraser fir seed orchard using seedlings currently growing in our western NC greenhouse, as well as an Atlantic White Cedar conservation orchard located along the southeastern coast of the US.

Orchard	Common Name	Location	# Trees	Established	Producing
UMRS	Carolina hemlock	Laurel Springs, NC	400	2008	Yes
UMRS	Carolina hemlock	Laurel Springs, NC	315	2012	No
Beech Creek	Eastern hemlock	Murphy, NC	301	2020	No
Beech Creek	Table Mt pine	Murphy, NC	167	2020	No
Chilhowee	Eastern hemlock	Chilhowee, TN	298	2020	No
Chilhowee	Table Mt pine	Chilhowee, TN	167	2020	No
Crossnore	Carolina hemlock	Crossnore, NC	509	2020	No

Table 16. Camcore domestic gene conservation orchards.



USFS Beech Creek Orchard Planting Team: Jason Rodrigue, Heather Luczak, Tim Lamb, Gary Kaufman, Sarah Bridges, Mike Hennigan, Dave Perez, Danny Skojac, Justin Seaborn, Dan Slovak, Mike Brod, David Ralston, Drew McCarley, Alexandria Perrier, Cheyenne Ada and Robin Taylor

Assessment of Carolina Hemlock Populations

Carolina hemlock (*Tsuga caroliniana*) is an endemic conifer located in isolated pockets across the southern Appalachian Mountains of the United States. Most Carolina hemlock populations are found in the mountains of western North Carolina with a few additional disjunct pockets in Georgia, South Carolina, Tennessee, and Virginia. Throughout its range, Carolina hemlock, much like the sympatric eastern hemlock (*T. canadensis*), is threatened by the exotic hemlock woolly adelgid (HWA, *Adelges tsugae*).

Faced with possible population losses, Camcore, in partnership with the USFS, has embarked on an effort to conserve genetic material from Carolina hemlock before it becomes scarce. These seed collection conservation efforts led to the confirmation of 32 distinct Carolina hemlock populations. Through discussions with different organizations and landowners this initial population list grew to include 143 reported natural populations. This number was later revised down to 127 due to the fact that some of the sites had been reported multiple times with different names.

Utilizing our expanded list of Carolina hemlock populations, Camcore and the USDA Forest Service embarked on a collaborative effort to assess the status of the species across its range. The three primary objectives of this study are to delineate and census all known populations of the species, quantify HWA infestation levels across the range while determining the efficacy of insecticide applications in treated populations, and lastly, to establish long-term monitoring transects in a subset of representative populations. Results from this assessment will identify new locations of Carolina hemlock that should be targeted for conservation as well as populations that should have silvicultural, chemical, and biological control strategies implemented to reduce HWA impacts.

From our database of 127 reported sites, Camcore has visited 106 sites and confirmed 74 as containing naturally occurring Carolina hemlock. This work has led to the discovery of several populations in central Virginia that were significantly farther north of our original collections in 2003. Rangewide health varies from terrible to healthy. Carolina hemlock growing in full sun or with exposed canopies often contains greater amounts of and darker green foliage. Improved health also appears to be correlated with chemical treatments. Both exposure and insecticidal treatments also tend to improve cone production which will be useful in future conservation efforts. Greater exposure and improved Carolina hemlock health correspond with data from another study Camcore is currently conducting in which gaps created

around HWA-infested eastern hemlock trees appear to improve foliar density and overall crown health despite persisting HWA infestations. Overall, Carolina hemlock health is generally better than that of eastern hemlock occurring in the same region. There were no obvious trends in health across elevation or latitude. In sites with low intensity fires, Carolina hemlock typically fares well. In 2022 we plan to both visit the remaining sites and implement our long-term monitoring protocols on a subset of populations.

Building on our efforts to assess all known Carolina hemlock populations, Camcore is working with Dr. Jodi Forrester (Associate Professor of Forestry at NCSU) and MS student Elle Gossman to establish an additional monitoring program for Elle's work will examine Carolina hemlock. twenty populations across the species range and assess the vulnerability of the species using longterm growth, climate, and insect infestation pattern data. This work will produce rangewide establishment, growth and mortality pattern information for Carolina hemlock ecosystems using inventory and tree-ring data. We will compare these results with multi-year trends from the Forest Inventory and Analysis (FIA) program data to assess large-scale inventory performance of this rare and vulnerable species.



NCSU student Elle Gossman cores a Carolina hemlock tree in southwestern Virginia.



NCSU students Elle Gossman and Casey Wofford examine a Carolina hemlock tree along the Appalachian Trail in snowy southwestern Virginia.

At each of our twenty sites, crown ratings and branch tip sampling will be assessed on individuals across four permanent plots distributed throughout each site. In addition to crown and HWA ratings, an intensive inventory will be completed to characterize the plant community in the Carolina hemlock populations. We will also be taking and analyzing increment core samples from a subset of dead or declining hemlock trees in order to supplement existing tree-ring data from another recent study.

In the summer of 2021, Andy Whittier assisted Elle in her preliminary visits to 20 Carolina hemlock populations spanning the latitudinal range of the species. During these visits we recorded species composition and took core samples within each of the four plots per population. In winter of 2021 and 2022 we revisited each of these populations in order to quantify HWA levels and tree health in the populations.

Hemlock Restoration Silviculture Research Update

Camcore's efforts to conserve the threatened species eastern hemlock (Tsuga canadensis) and Carolina hemlock (Tsuga caroliniana) have long formed the foundation of our domestic conservation program. Through our funding partnership with the USDA Forest Service, these were the first tree species native to the United States to which we applied our expertise in genetic resource conservation, and as documented in previous editions of the Camcore Annual Report, we have accomplished much to help secure the future of these species since our first seed collections in 2003, nearly 20 years ago! We have assembled the largest and most diverse genetic resources for the species that exist outside of native stands, described patterns of genetic and adaptive variation across the geographic ranges, developed seed handling and preservation protocols, defined seed germination and nursery guidelines, and established conservation seed orchards at multiple locations in the southern Appalachian Mountains.

Ultimately, the goal of all of this effort is for the hemlock genetic resources conserved by Camcore to be used for the restoration of both species to areas of the eastern United States where they have been extirpated by the invasive insect hemlock woolly adelgid (Adelges tsugae, HWA). While species restoration to native habitats is a noble goal, it is also not an easy one for species like eastern and Carolina hemlock. Both are considered keystone species in their native environments, meaning they exert a large influence over the microclimate and soil conditions in the forests they occupy and, by association, all other plant and animal species that occur in those forests. Removal of these keystone trees from their natural environments means the ecosystem that supports them is altered at a fundamental level and restoring them to these locations will likely require more than simply planting seedlings and hoping for the best.

There is relatively little information in the scientific literature on how to restore hemlock to their native environments, so in 2015 the Camcore domestic conservation program began a collaboration with USDA Forest Service Research Entomologist Dr. Albert E. "Bud" Mayfield on a series of field studies designed to explore the silvicultural strategies needed to maintain hemlocks as part of

the eastern North American forests. Two studies, referred to below as Hemlock Restoration 1 and Hemlock Restoration 2, are focused on restoration of hemlocks via seedling planting. The third study, Hemlock Target-tree Release, is focused on retaining naturally established eastern hemlock in suppressed and intermediate canopy positions in forests that have been heavily impacted by HWA. While these studies all differ in their objectives, designs, and locations, they do share one common hypothesis: increased sunlight exposure and resource availability via silvicultural manipulation of the surrounding forest canopy benefits the establishment, growth, crown health, and carbon balance of hemlocks in HWA impacted forests (see Brantley et al. 2017. For. Ecol. Mgmt. 385: 150-160 and Mayfield & Jetton. 2020. Ag. For. Entomol. 22: 309-318 for review of our preliminary research on this topic). The following sections provide brief updates on each of the three field studies.

Hemlock Restoration 1

This study was established in 2015 and is focused on the reintroduction of eastern hemlock via seedling planting at two locations in western North Carolina: DuPont State Recreational Forest and Cold Mountain Game Land. It tested the effects of two overstory forest canopy treatments (canopy gap versus thinned), white-tailed deer (an ungulate herbivore similar to gazelles and impalas) exclusion, fertilization, and competition control via herbicides on the establishment, survival, and early growth of seedlings planted in replicated blocks. Canopy treatments were reapplied annually as needed to maintain moderated light environments. Deer exclusion fences were checked monthly and damage from tree falls and other factors repaired. Fertilization and herbicide treatments were applied in April and June of each year, respectively, and tree heights and basal diameters were measured and recorded once immediately after planting (March 2015) and then annually in November at the end of each growing season of the study. Seedlings received insecticide protection from HWA during the first four growing seasons of the study. A mixed-model, repeated-measures analysis of variance was used to evaluate the main effects of canopy, deer exclusion, fertilization, competition

control, time, and all two- and three-way interactions. Treatment effects on hemlock seedling height and basal diameter growth were similar, so for brevity only the results for height are reported here.

In November 2018, after four years in the field, survival across the entire study was 91%. The largest differences in seedling growth were between the canopy treatments, with average height nearly 70 cm greater in the gaps versus under the thinned canopy (Figure 18). Within the gaps, seedling-level treatments where competing vegetation was controlled with herbicide alone (H) or in combination with fertilization (F+H) resulted in significantly higher seedling height growth compared to fertilization alone (F) treatments that did not differ from the controls. Under the thinned canopy, seedling-level treatments had no effect on seedling growth. There were no differences in

seedling establishment, survival, or growth between the deer exclusion treatments.

A general takeaway from this study is that planting eastern hemlock in a canopy gap should have substantial benefits for tree growth, but those benefits may be outweighed by the need for repeated intervention to control competing vegetation. Land managers with fewer resources to support restoration efforts may be more accepting of slower growth under a thinned or intact canopy where less care and feeding of the seedlings is feasible. A manuscript with a complete analysis and more in-depth discussion of the results from this study is currently being prepared for submission to a peer-reviewed journal in 2022. In the meantime, we continue to maintain these study plots and are transitioning them to a new project to evaluate the integration of silvicultural management with chemical and biological control of HWA.



Figure 18. Height growth responses of eastern hemlock seedlings to canopy, fertilization, and herbicide treatments over four growing seasons in western North Carolina.

Hemlock Restoration 2

This study was established in 2020 and is focused on the reintroduction of eastern and Carolina hemlock via seedling planting on the Pisgah National Forest near Asheville, North Carolina. It is located within a larger research area where scientists with the USDA Forest Service are using the expanding gap silviculture or "Femelschlag" technique to study the regeneration of oaks (Quercus spp.). Our study is located in 8 small 0.1 ha canopy gaps that were cut on the site where we are testing the main effects of hemlock species, insecticides, competition control, and light exposure gradients on the early growth of planted hemlock seedlings. Within each gap we planted 144 seedlings in a 4seedling by 36-seedling transect alternating between eastern and Carolina hemlock (72 seedlings per species) with a spacing of $2x^2$ m between seedlings (Figure 19). Transects run north to south across the gaps capturing the light gradient from forest interior at the north through the center of the gap and again into forest interior at the south. Half of the seedlings per species in each transect are receiving insecticide protection from HWA while the other half are not. Gaps are grouped into pairs where one gap per pair is receiving competition control via herbicides and the other gap is not. Each pair of gaps is grouped with another smaller,



Figure 19. Lauren Gonzalez and Andy Whittier collecting seedling growth data in one of the herbicide treated gaps on the Pisgah National Forest.

36-seedling plot in the nearby forest interior where the same species, insecticide, and herbicide treatments are replicated.

Although much has already been accomplished at this new study site, this second hemlock restoration experiment is still in its early stages. Field activities at the site will accelerate during 2022 as this study is the foundation of the research project for Lauren Gonazalez, a new Camcore PhD student working with Robert Jetton. In addition to basic growth measurements, Lauren will also be incorporating more advanced analysis techniques related to soils and seedling ecophysiology.

Hemlock Target-tree Release

This study was established in 2017 and was designed to develop and validate a silvicultural tool that improves the health and sustainability of established eastern hemlock infested with HWA. Individual "target" eastern hemlocks (i.e., suppressed or intermediate trees with moderate to good crown health) were released by removing or girdling other stems competing for sunlight directly above and near the target trees. Increased sunlight was expected to improve hemlock crown health, enhance new foliage production, and reduce HWA settlement rates relative to unreleased trees.

Twenty-one replicate sites were established in the Appalachian Mountains on State and National Forest lands in North Carolina, Georgia, Tennessee, Virginia, and Maryland and were divided into three latitude groups: South (34.7°N -35.7°N; NC, GA, TN), Central (36.7°N - 37.7°N; VA) and North (38.7°N - 39.7°N; MD). The experimental unit to which treatments were applied was an individual understory or midstrory eastern hemlock tree at the center of a canopy gap or in the forest interior. Treatment plots were spaced by a distance ≥ 1.5 times dominant tree height to achieve independence in terms of moderated light environment. Within each replicate, five gap treatments were applied in late 2017 to early 2018 by varying both the size of the canopy gap (Large vs. Small) and the method of gap creation (Fell vs. Girdle), plus a "no gap" Control. Small gaps were created by removing all trees overhanging the target hemlock dripline, whereas large gaps expanded on the small gap by adding 25% of the dominant tree height to the gap radius. HWA density index, percent new shoots, and percent branch dieback

(semi-annually), plus crown condition ratings (annually) were measured on the target hemlock at the center of each gap through winter 2021. Target hemlock DBH was measured in 2017 and 2021. Within each Latitude Group, a mixed-model, repeated-measures analysis of variance was used to evaluate the effects of Treatment and Year-Season, and their interaction (Treatment x Year-Season). For brevity, results for only the South latitude group are reported here.

In the South latitude group, the interaction of Treatment x Year-Season had a significant effect on all dependent variables analyzed (Figure 20). No variables differed by treatment at the time the gap treatments were applied. In the first summer post-treatment (2018 2), HWA densities in the Large Fell treatment were significantly lower than all other treatments (Figure 20A). However, by summer 2020, the Control group had lower HWA densities than all other treatments (Figure 20A). presumably due to the lack of new shoots on Control trees during this period (Figure 20B). From 2019 to 2021, hemlocks in the Large Fell treatment produced significantly more new shoots than those in the Control treatment (Figure 20B), despite having similar or higher densities of HWA than the Control treatment (Figure 20A). The Large Fell treatment also had significantly lower foliage transparency (= better crown health) than the Control treatment by winter 2021, with other treatments intermediate (Figure 20C). Branch dieback, expressed as the percentage of dead shoot tips, increased steadily in the Control treatment over time and was higher than all other treatments by winter 2021 (Figure 20D).

This project demonstrated that small canopy gaps, particularly the Large Fell treatment, improved crown health and new shoot production of midstory hemlocks infested with HWA in the South latitude group. In the

Figure 20. Mean hemlock woolly adelgid (HWA) population index (A), percent new shoots (B), percent foliage transparency (C) and percent dead branch tips (D) on eastern hemlock trees in the SOUTH latitude group for silvicultural Treatment and Year_Season (1=winter, 2=late spring).

South, the Large Fell treatment resulted in consistently higher new shoot production, lower foliage transparency, and lower branch dieback than the control throughout the study. Similar trends were evident in the North latitude group, but were less consistent in the Central latitude group, where HWA densities were highly variable and treatment replication was lower than in the other regions (5 reps vs. 9 in South and 7 in North). The results indicate that incorporating silvicultural release of hemlock through small gaps is worth considering as a management strategy against HWA that could be integrated with existing tactics. A manuscript with more in depth discussion of the results from this study is currently being prepared for submission to a peer-reviewed journal in 2022.



Webinars, Mini-Conferences, and Virtual Visits

Webinars

One of the long-term priorities identified by Camcore members in our 2019 strategy meeting in Porto, Portugal, was for Camcore to take a bigger role in members' education and training. The COVID-19 pandemic situation has encouraged us to find creative ways to keep our program in good health and our members engaged. Camcore offered a series of webinars covering various topics from breeding strategy to data analysis to forest health to laboratory procedures. Since July 2020, our group has presented a total of 23 webinars. To date, webinars had a live attendance of 1,312 people, with a mean attendance of 57, a maximum of 88 and a minimum of 35 participants. These seminars have been well received and appreciated by our members. Webinar topics are presented in the table below.

Camcore webinars have been a very costeffective way to train our global members. Juan José Acosta scheduled, hosted and moderated all webinars. Webinar materials (videos, slides, programing codes, databases, etc.) were posted to our website by Andy Whittier and are available to our members under the "Camcore Seminar" tab.

Webinar Topics, 2020 - 2021	Speaker	Session	Date
Clonal Testing and Deployment	Gary Hodge	1	15-Jul-20
Breeding for non-breeders #1		8	3-Mar-21
Breeding for non-breeders #2		13	19-May-21
Breeding for non-breeders #3		19	11-Aug-21
Breeding for non-breeders #4		23	6-Oct-21
Introduction to R and Experimental Design Analysis in R	JJ Acosta	2	29-Jul-20
Using the R-NIR Pipeline	1	11	14-Apr-21
Data Aggregation and Summary with R		15	16-Jun-21
Fancy Graphics with R		16	30-Jun-21
Using the Resisto -R Pipeline		18	28-Jul-21
Financial analysis in forestry and tree breeding	Juan Lopez	3	12-Aug-20
Introduction to Kraft Pulping		9	17-Mar-21
The Use of Linear Programming in Forest Management		14	2-Jun-21
Integrated Forest Pest Management	Robert Jetton	4	26-Aug-20
Forest Health Monitoring		12	5-May-21
Framework for Forest Health Monitoring in Commercial Forestry Operations		20	25-Aug-21
Excel Methods - Using text formulas	Willi Woodbridge	5	9-Sep-20
Using the DLP nano NIR		10	31-Mar-21
Managing Data with Pivot Tables and LOOKUP Functions in Excel	1	21	8-Sep-21
Field Wood Sampling Techniques (TreeSonic and Resistograph)	Woodbridge & Jump	17	14-Jul-21
<i>Eucalyptus</i> pollen viability tests	Romeo Jump	7	7-Oct-20
Pine Pollen Testing and the Use of the Slingshot / Rope Saw for Pollen Collection		22	22-Sep-21
Safety practices when climbing trees	Andy Whittier	6	23-Sep-20

CAMCORE NEWS ITEMS

Rooting Cuttings of Eucalyptus dunnii

In addition to our Webinars, during 2020 and 2021, we conducted two mini-conferences. In October 2020, Gary Hodge organized a workshop about rooting cuttings of *Eucalyptus dunnii* for clonal production or family forestry. The idea behind this event was to invite member experts in this area to give a short presentation of their protocols for rooting of *E. dunnii*. We then had a time of open discussion, questions and answers. The workshop was conducted via Zoom with 27 participants from 6 companies in 4 countries. Conference topics and presenters are shown below:

E. dunnii Rooted Cutting Seminars	Speaker	Date
Welcome and Overview	Gary R. Hodge, Camcore	2-Oct-20
E. dunnii cuttings - Sappi Experience	André Nel, Sappi	
E. dunnii Propagation at Mondi	Mmoledi Mphahlele, Mondi	
Eucalyptus dunnii at Klabin	Leticia Miranda, Klabin]
E. dunnii Vegetative Propagation & Rooting at WestRock	Mara Luana Engel, WestRock	

Rooted Cuttings of Pines

The next year, in June 2021, Camcore organized a two-day workshop about pine rooting. During the workshop, protocols for hedge management, and for rooting plantlets were shared. In addition, speakers presented information regarding the production rates, rooting success, and life span of the hedges. The workshop was conducted via Zoom, and was very well attended, with 84 participants the first day, and 75 participants the second day, representing all Camcore member companies. The mini-conference program is given below, and mini-conference materials (videos, and slides) were posted to our website and are available to our members under the "Camcore Seminar" tab. It is our intention to continue offering virtual webinars and mini-conferences in 2022.

P. taeda Rooted Cutting Seminars	Speaker	Date
<i>P. taeda</i> Rooted Cuttings, Hedge Management, Rooting, and Clonal Multiplication	Barry Goldfarb, NCSU	3-Jun-21
Cutting Production of <i>Pinus tecunumanii</i> and <i>Pinus maximinoi</i> in Hydroponic Hedges	JJ Acosta, Camcore & Martha Salas, SKC	
Cuttings Experience in Southern Cape, South Africa	Andre van der Hoef, Sinarmas	
Klabin: Propagation Research	Leticia Miranda , Klabin	
Sappi: Pine Hybrid Propagation	Damien Naidu, Sappi	10-Jun-21
Mondi: Pine Hybrid Propagation	Marius du Plessis, Mondi	
Producción de Plantas de Pino Clónales	Rodolfo Calquin, Arauco Chile	
Rooting Pine Cuttings	Carlos Gioia, Arauco Argentina	

Camcore Virtual Technical Visits

Faced with the impossibility of making visits in person due to the COVID-19 pandemic, Camcore decided to carry out virtual technical visits with our members during 2020-2021. The main objective of those virtual visits was to support our cooperators research goals, provide technical advice and review Camcore-related research projects. In addition, virtual technical visits allowed all members of our staff to interact with our global partners, which is critical to build a strong, diverse and inclusive program.

Our group had a very full agenda, we met 58 times with 21-member companies from 11 countries, and interacted with 443 people. Our staff members gave technical presentations in many of those meetings, and when possible, we provided written reports to the members summarizing recommendations made during our virtual visits.

2021 & 2022 Virtual Annual Meetings

Each year Camcore holds an annual meeting that lasts for 10 to 14 days, hosted by the companies in one of the member countries. The purpose of the meeting is to plan research and breeding, discuss results, and conduct the business of the program, but also to make field visits in the host country learning about everything from nurseries to forests to mills. Generally, activities are about $\frac{1}{3}$ indoor meetings and $\frac{2}{3}$ field visits.

The pandemic made us change the format of our annual meeting. For 2020 and 2021, the annual meetings were six virtual sessions over a two-week period, using Zoom. Camcore has members all over the world, so we scheduled the sessions to allow participation from in multiple time zones, with sessions starting at local times ranging from 6:30 am in

Graduate Programs and Training

- Luis Ibarra completed his PhD program in 2021, and returned to Arauco Bioforest in Chile, where he will serve as Chief of Tree Improvement Stategy. His dissertation focused on hybrid quantitaive genetics and breeding (see p. 13 in this Annual Report).
- **Colin Jackson** continued his PhD work at NC State, funded jointly by Camcore and the NC State University *P. taeda* Tree Improvement Program. His work is focused on the development of the tropical pine SNP chip, and quantatitative genetic analysis and genomic selection on 2nd generation *P. taeda* families in the WestRock breeding program in Brazil (see initial results on p.36 in ths Annual Report). Colin plans to finish his PhD in mid-2022.
- **Gustavo Martins** (APRIL, Indonesia) began his PhD program in 2020 and completed one full semester at NCSU. He returned to Indonesia for work in 2021, and will return to NC State in 2022 to complete his PhD program. His work will focus on *Acacia crassicarpa*, with chapters on wood properties and sampling strategies (see p. 24 in this Annual Report), seed orchard dynamics, and genomic selection.
- **Romeo Jump** (Camcore) continues to make progress toward his MS degree in forestry, while working fulltime as the Camcore Seed and Pollen Lab Manager. He has completed most of his coursework, and will concentrate on his research in 2022. His project will look at the use of NIR spectroscopy to assess foliage nutrient content in *Acacia* and pine seedlings.
- **Piyush Pandey** is a PhD student funded by the Biological and Agricultural Engineering Department, working closely with Camcore and the NC State University *Pinus taeda* Tree Improvement Program (NCSU-TIP). He is working on the use of imaging technology and robotic

Mexico to 8:30 pm in Indonesia. We recorded the sessions and posted meeting materials (slides, chat and videos) in the Camcore website, so if members had conflicts and couldn't attend live, they could go back and view the presentations.

We typically have 35 to 50 people attend a live, in-person annual meeting. The virtual format allowed participation of many more people. We broke all attendance records. We averaged 87 participants/session over the past two years!

In 2022, we are hopeful that we can return to a live annual meeting, and tentative plans are to meet in South Africa in early November. But we hope to take advantage of what we learned the past two years, and open some of the our indoor technical sessions to virtual participants.

drones for tree breeding applications (see p. 46 in this Annual Report).

- **Travis Howell** began a PhD progam in 2021, supported by the three forestry industrial cooperative research programs at NC State (Camcore, NCSU-TIP, and Forest Productivity). His work will focus on the use of advanced imaging technology for forest mensuration, inventory, and genetic trial measurement (see article in this Annual Report). During his PhD program, Travis will continue as a full-time employee with a civil engineering firm in North Carolina.
- Austin Thomas completed his PhD in 2021. His ressearch was on the physical and chemical responses of elite Fraser fir genotypes to infestation by balsam woolly adelgid (see p. 18 in this Annual Report), and ecosystem analysis and genetic health analysis of a relict population of eastern hemlock near Raleigh, NC. Austin has taken a postdoctoral position with the USDA Forest Service and the University of Kentucky.
- **Dominic Manz** began a PhD program with the Camcore domestic conservation program in May 2020 (right at the beginning of COVID!). His project will look at management of elongate hemlock scale insect infestation in Fraser fir Christmas tree plantations. Prior to his PhD studies, Dominic completed a BS degree in Forestry at NCSU.
- Lauren Gonzalez began a PhD program in 2021 under the supervision of Robert Jetton. Her research will focus on the management of hemlock woolly adelgid and conservation of eastern and Carolina hemlock. She will study the effects of canopy condition, competition control, and chemical and biological pest management on the establishment and early growth of hemlock seedlings planted for restoration.

Changes in Camcore

- **Ricardo Austin** moved to Chile to take a new position as the Arauco Chile Forest Operations Manager. **Javier Maestropaolo** replaced Ricardo as the Forest Manager in Arauco Argentina.
- Juan Schapovaloff is the new Forest Operations Sub manager in Arauco Argentina, and Carlos Gioia is now the Chief of Research and Development, Genetics and Biotechnology.
- Mário César Gomes Ladeira left Klabin to join Bracell as the Forest Research and Development Senior Manager. Bruno Afonso Magro replaced Mario in Klabin as the new Forest Research Manager.
- **Sebastián Fernández** replaced **Eduardo Rodríguez** as the new Bioforest Manager in Arauco Chile.
- Mauricio Hernán Ramírez is the new Tree Improvement Manager in Bioforest.
- Luis Ibarra returned to Chile after finishing his PhD at NC State, and is now working as the Chief of Tree Improvement Strategy in Bioforest.
- Kevin Cazalet retired from Forest First in Colombia after working for the company as The Chief Technical Officer for several years.
- **Ray Risco**, based in the US, is the Chief Operating Officer of Forest First as part of the Operational Leadership Team of the company.
- **Liliana Perafán**, who worked as data manager with the Forestry Division of Smurfit Kappa Colombia, retired in 2021.
- **Gildardo Montenegro** retired from Smurfit Kappa Colombia after working with the company for many years in Forest Research.
- Alvaro Durán with APRIL Indonesia was promoted to the position of Research Manager.
- Adriano Almeida is now the new Tree Improvement Manager in APRIL Indonesia.
- Nhora Isaza, who had retired from Smurfit Kappa Colombia in 2018, was hired by Sinarmas Forestry in 2021 to work as Acacia Breeding Researcher.
- **Arnulf Kanzler** left Sinarmas Forestry in 2021 and was replaced by **Albertus Bambang Herdyantara** as the new Forest Improvement Program Leader.
- **Ben Pienaar**, the Chairman of the Camcore Advisory Board, is now the Forest Research and Development Manager at Mondi Forests.
- Marius du Plessis has a new position in Mondi Forests as the Forest Research Programme Manager.
- **Mmoledi Mphahlele**, Tree Breeding Programme Manager at Mondi Forest, finished his PhD on Genome Sciences/Genomics at The University of Pretoria in South Africa.
- Fanele Mabaso moved from York Timbers to Mondi Forest, where she works now as a Pine Breeding Forester.

- **Tracy Le Roux** returned to Sappi after a three-year absence, and is now working as a Principal Research Officer in The Forest Shaw Research Centre in Howick.
- **Willie Brink** retired from MTO Forestry in South Africa after working as the Forestry Technical Services Manager for several years.
- **Vourinus Coetzee** retired from SAFCOL on March 2021, after working as a Centre Manager of the company for many years. **Dumisile Chibi** is acting in his position until someone is named permanently.
- **Ebby Chagala-Odera** retired from KEFRI in Kenya after working many years as Deputy Director, Forest Research Support Services. The new contact with Camcore in KEFRI is **Stephen Fredrick Omondi**, who was named as Deputy Regional Director, Central Highlands Eco-Region Research Programme.
- **Juan Pedro Posse** left Lumin and has taken a role as Regional Director for INIA (Instituto Nacional de Investigación Agropecuaria, Uruguay).
- **Paola Molina** (Lumin) has returned to tree improvement after several years as Nursery Manager for the company. She is now Nursery and Tree Improvement Manager, and will be working closely again with Camcore going forward.
- **Fernando Gutiérrez** (Lumin), formerly the Silviculture and Technology Manager, is now in charge of Forest Research for the company.
- **Martím Terra**, who was in charge of Research and Development in Montes del Plata, Uruguay, left the company in June 2020 to pursue new opportunities.
- Mónica Heberling became the Chief of Tree Improvement of Montes del Plata in 2020, reporting to **Diego Carrau**, the Forest Manager.
- **Barb Crane** retired from the USDA Forest Service and was replaced by **Marcus Warwell**, who is now the new Region 8 Geneticist based in Atlanta GA.
- **Robert Jetton** with Camcore is now an Associate Professor in the Department of Forestry & Environmental Resources (FER) at NC State University working 33% of his time for Camcore on pests and diseases research and 67% for FER.
- **Erin Sills** was named as the permanent Department Head of FER on June 30, 2021. She replaces **Tom Gower**, who went back to his activities as a Professor after several years working in the administrative position until July 2020.
- Myron Floyd became the Dean of College of Natural Resources (CNR) at NC State University in August 2019, replacing Mary C. Watzin who had the position for seven years. She retired from NC State in December 2021.
- José Fidel Alvarado is the new Chief of the Seed Bank in UNACIFOR, Honduras. He replaced Oscar Leveron, who now is a full-time professor at the university.

CAMCORE NEWS ITEMS

Passings of Friends

Neville Dension, longtime Director of Research for Mondi Forests, died in October 2021. Neville earned an MS degree at NC State in 1973, studying under Bruce Zobel, and he became a leader in the development of forestry research in South Africa. Neville was a great friend and supporter of Camcore, and he served on our Advisory Board and as Chair of the Executive Committee. More important, however, than

his many forestry accomplishments, is that Neville was a wonderful person, always humble, kind, and enthusiastic. He and his wife Liz are famous for their hospitality, joy, and love of life -- including rugby, gardening, friends, and family. He will be greatly missed by all who knew him.





Geoff Galloway, Research Forester with Sappi from 1989 to 2018, passed away in



August 2021. For most of his career, Geoff worked in the subtropical zone near Kwambonambi in Zululand developing hybrid eucalypts. Geoff was always known for his consistent work ethic and passion for tree breeding. He was very particular about trial design, data capture and results, which ultimately delivered a number of winning *E. grandis x E. urophylla* varieties. Geoff was also deeply committed to his family, church, and community. We will miss his friendship and enthusiasm.

Piet van Zyl, CEO of York Timbers since 2009, died suddenly in July of 2021. Piet was a strong supporter of Camcore, the Forest Molecular Genetics Programme at the University of Pretoria (UP), and other forestry research in the country. In early 2020, South Africa implemented a very strict Covid-19 lockdown, and many York employees did not qualify for government relief payments. Piet was instrumental in establishing the York Solidarity Fund, entirely with contributions from employees, management, and the York Board, to raise sufficient money to ensure than no employees went without income during the lockdown. Our condolences go out to his family and friends.



Publications and Papers

Publications

- Acosta JJ, Castillo MS, Hodge GR (2020). Comparison of Desktop and Handheld Near-Infrared Spectroscopy Devices to Determine Forage Nutritive Value. Crop Science. 2020; 60: 3410- 3422. https://doi.org/10.1002/ csc2.20264
- Bakken, K.A., J.A. Forrester, D.J. Mladenoff, Z. Leggett, J. Juzwil, and R.M. Jetton. 2021. Mortality patterns following a hickory decline event: is density reduction key to maintain bitternut hickory? Forest Ecology and Management. 485: 118956.
- Bekewe PE, Castillo MS, Acosta JJ, Rivera R. (2020), Defoliation management effects on nutritive value of 'performer' switchgrass. Crop Science. 2020; 60: 1682- 1689. https:// doi.org/10.1002/csc2.20036
- Caballero M, Lauer E, Bennett J, Zaman S, McEvoy S, Acosta JJ, Jackson C, Townsend L, Eckert A, Whetten R, Loopstra C, Holliday J, Mandal M, Wegrzyn J, and Isik F (2021).
 Toward genomic selection in *Pinus taeda*: Integrating resources to support array design in a complex conifer genome. Applications in Plant Sciences. 9 (6): e11439. https://doi.org/10.1002/aps3.11439
- Hodge GR, Acosta JJ (2020). An Algorithm for Genetic Analysis of Full-Sib Datasets with Mixed-Model Software Lacking a Numerator Relationship Matrix Function, and a Comparison with Results from a Dedicated Genetic Software Package. Forests 2020, 11, 1169. https://doi. org/10.3390/f11111169
- Jackson C, Christie N, Reynolds S, Marais C, Tii-kuzu Y, Caballero M, Kampman T, Visser E, Naidoo S, Kain D, Whetten R, Isik F, Wegrzyn J, Hodge GR, Acosta JJ, Myburg AA (2021). A genome-wide SNP genotyping resource for tropical pine tree species. Molecular Ecology Resources. https://doi.org/10.1111/1755-0998.13484
- Lu Y, Walker TD, Acosta JJ, Young S, Pandey P, Heine AJ, and Payn KG (2021). Prediction of Freeze Damage and Minimum Winter Temperature of the Seed Source of Loblolly Pine Seedlings Using Hyperspectral Imaging. Forest Science. 2021. https://doi.org/10.1093/forsci/fxab003
- Martins, GS, Yuliarto M, Antes R, Sabki, Prasetyo A, Unda F, Mansfield SD, Hodge GR, Acosta JJ (2020). Wood and Pulping Properties Variation of *Acacia crassicarpa* A.Cunn. ex Benth. and Sampling Strategies for Accurate Phenotyping. Forests 2020, 11, 1043. https://doi. org/10.3390/f11101043
- Matallana-Ramirez, L.P., K. Goode, M. Bertone, P. Jansta, R. Burks, R. Jetton, and J. Frampton. 2020. Assessing *Mega-stigmus specularis* (Megastigmidae) seed infestation patterns in a Fraser fir (Abies fraseri) clonal seed orchard of the Southern Appalachians. Scandinavian Journal of Forest Research 35: 445-455.
- Matallana-Ramirez, L., K. Goode, N. Moore, R. Jetton, and J. Frampton. 2020. A simple laboratory rearing method for chalcid wasp. Protocols.io. dx.doi.org/10.17504/protocols. io.bb3riqm6.

- Mayfield, A.E. III and R.M. Jetton. 2020. Differential sunlight exposure affects settling behavior of hemlock woolly adelgid crawlers. Agricultural and Forest Entomology 22: 309-318.
- Miniat, C.F., D.R. Zietlow, S.T. Brantley, C.L. Brown, A.E. Mayfield III, R.M. Jetton, J.R. Rhea, and P. Arnold. 2020. Physiological responses of eastern hemlock (*Tsuga canadensis*) to light, adelgid infestation, and biological control: implications for hemlock restoration. Forest Ecology and Management. 460: 117903.
- Mostert, ÄêO'Neill MM, Reynolds SM, Acosta JJ, Lee DJ, Borevitz JO, Myburg AA (2020). Genomic evidence of introgression and adaptation in a model subtropical tree species, *Eucalyptus grandis*. Mol Ecol. 2020; 00: 1- 14. https://doi.org/10.1111/mec.15615
- Mphalele MM, Isik F, Mostert-O'Neill M, Reynolds SM, Hodge GR, and Myburg AA. 2020. Expected benefits of genomic selection for growth and wood quality traits in *Eucalyptus grandis*. Tree Genetics and Genomes 16, 49. doi: 10.1007/s11295-11020-01443-11291.
- Mphalele MM, Isik F, Hodge GR, Myburg AA. 2021. Genomic breeding for diameter growth and tolerance to *Leptocybe* gall wasp and *Botryosphaeria / Teratosphaeria* fungal disease complex in Eucalyptus grandis. Frontiers in Plant Science: 12:638969. doi: 10.3389/fpls.2021.638969.
- Nel A, Acosta JJ, Hodge GR (2021). Initial growth results comparing first generation F1 and advanced-generation F2 *Pinus patula x Pinus tecunumanii* inter-specific hybrid families. Southern Forests: a Journal of Forest Science. https://doi.org/10.2989/20702620.2021.1926370
- Nilsson, O., G.R. Hodge, L.J. Frampton, W.S. Dvorak and J. Bergh. 2020. Growth and Modulus of Elasticity of pine species and hybrid three years after planting in South Africa. In Press, Southern Forests.
- Thomas, A.M., M.E. Johns, and R.M. Jetton. 2021. Characterization of a disjunct population of eastern hemlock *(Tsuga canadensis)* and surrounding plant communities in the North Carolina Piedmont after 65 years of forest change. Southeastern Naturalist. 20(3): 377-398.
- Whittier WA, Hodge GR, Lopez J, Saravitz C, Acosta JJ. (2021) The use of near infrared spectroscopy to predict foliar nutrient levels of hydroponically grown teak seedlings. Journal of Near Infrared Spectroscopy, 29(5):301-310. doi:10.1177/09670335211025649

Other Publications

Nanette Christie, Colin Jackson, Gary Hodge, Juan Jose Acosta, Alexander A. Myburg. 2021. A new DNA marker resource for genome-assisted breeding of pine trees. Technical Note, Timber Industry Presents TIP-Mag, https:// www.forestrysouthafrica.co.za/tip-mag/, p.17-21.

Published Conference Proceedings

Lu Y, Payn KG, Pandey P, Acosta JJ, Heine AJ, Walker TD, and Young S (2020). Hyperspectral Imaging-Enabled High-Throughput Screening of Loblolly Pine (Pinus taeda L.) Seedlings for Freeze Tolerance. 2020 ASABE Annual International Virtual Meeting. 2001072 (doi:10.13031/ aim.202001072).

Conference Presentations

- Mostert-O'neill MM, Reynolds SM, Acosta JJ, Borevitz JO, and Myburg AA (2021). Domestication in progress: How a century of artificial selection has changed the genomes of a wood fibre crop, *Eucalyptus grandis*. Plant Biology 2021 Worldwide Summit. American Society of Plant Biologists, July 19-23, 2021.
- Jackson C, Christie N, Caballero M, Reynolds M, Marais C, Visser E, Naidoo S, Hodge GR, Whetten R, Isik F, Wegrzyn J, Acosta JJ, Myburg AA (2020). Development of a High-Throughput Genome-Wide Genotyping Array for Tropical and Subtropical Pine Species. Plant & Animal Genomes XXVIII Conference, January 11-15, 2020. San Diego, CA
- Hillen, A, Jetton, RM. and Mayfield AE. 2020. Silvicultural and Integrated Management Strategies for Restoring Hemlock to Degraded Southern Appalachian Cove Forests: Phase II. 29th Southern Appalachian Forest Entomology and Pathology Seminar, March 5-6, 2020, Crossnore, NC.
- Hodge, G.R. 2021. (Invited) From Gene Conservation to New Hybrid Varieties: the future of our forests. 9° Workshop Melhoramento Florestal (9th Workshop Forestry Breeding), IPEF - Instituto Pesquisa e Estudios Florestal, Nov. 10-11, 2021.
- Jetton, R.M. 2021. Conservation and restoration of hemlock species in the southern Appalachian mountains threatened by the hemlock woolly adelgid. Pennsylvania-New Jersey Chapter of the American Chestnut Foundation Spring Growers Meeting, April 10, 2021. Meeting held virtually.
- Jetton, R., K. Oten, and S. Jeffries. 2021. Unsolved mystery: the curious case of bumpy beech bark. Southern Appalachian Forest Entomology and Pathology Seminar, March 4, 2021. Meeting held virtually.
- Jetton, R., A. Whittier, K. Potter, L. Campbell, D. Nelson, S. Josserand, and R. Rhea. 2020. Population genetics and conservation of Carolina hemlock. National Forest Health Monitoring Workshop, February 25, 2020, Raleigh, NC.

- Jetton, R.M. and A.E. Mayfield III. 2020. Update on hemlock woolly adelgid silvicultural management research. 6rd Annual Hemlock Woolly Adelgid Program Managers Meeting, July 28, 2020. Meeting held virtually.
- Jetton, R.M. 2020. Host resistance and gene conservation of hemlocks threatened by the hemlock woolly adelgid. Western Maryland Forest Pest Update, March 4, 2020, New Germany State Park, MD.
- Jetton, R., D. Manz, J. Sidebottom, and J. Owen. 2020. New research on elongate hemlock scale. North Carolina Christmas Tree Association Winter Meeting, February 20, 2020, Blowing Rock, NC.

Conference Posters

- Christie N, Jackson C, Reynolds M, Marais C, Visser E, Naidoo S, Kain D, Hodge GR, Wegrzyn J, Acosta JJ, Myburg AA (2020). A genome-wide 50k SNP genotyping array for tropical and sub-tropical pine tree species. Plant Biology 2020 Worldwide Summit. July 27-31, 2020.
- Jackson C, Christie N, Caballero M, Reynolds M, Marais C, Visser E, Naidoo S, Hodge R, Whetten R, Isik F, Wegrzyn J, Acosta JJ, Myburg AA (2020). Development of a High-Throughput Genome-Wide Genotyping Array for Tropical and Subtropical Pine Species. Plant & Animal Genomes XXVIII Conference, January 11-15, 2020. San Diego, CA
- Jackson C, Christie N, Hodge GR, Isik F, Wegrzyn J, Myburg AA, Acosta JJ (2021). Pitro50K: A Genotyping Array for Tropical Pine Species. The 2021 National Association of Plant Breeders (NAPB) annual meeting. August 15-19, 2021. (Virtual). USA.
- Pandey P, Payn K, Lu Y, Acosta JJ, Walker T, Heine A, and Young S (2021), "High throughput phenotyping of loblolly pine: Analysis of hyperspectral images at the plant organ level for fusiform rust disease incidence," in North American Plant Phenotyping Network (NAPPN) Annual Meeting, (Virtual), Feb. 2021.
- Whittier WA, Jetton RM, Hodge GR, Potter KM, Mayfield AEM, Rhea JR. 2020. Assessing Carolina Hemlock Health in the Southern Appalachian Mountains Following Hemlock Woolly Adelgid Infestation. 2020 FHM National Workshop. February 24-27, 2020. Raleigh, NC. USA.
CAMCORE BOARDS AND COMMITTEES

The 2020-21 Camcore Advisory Board

Juan Schapovaloff, Arauco Argentina Mario Cesar Gomes Ladeira, Bracell, Brazil Gisela Andrejow, WestRock, Brazil Carlos Augusto Santos / Bruno Alfonso Magro, Klabin, Brazil Claudio Balocchi, Arauco Bioforest, Chile Nicolás Pombo, Smurfit Kappa Colombia Kevin Cazelet / Ray Risco, ForestFirst Colombia Charlie Bosworth, Miro Forestry, Ghana Agus Kurnia Nugraha, Araya Bumi Indonesia Adriano Almeida, APRIL, Indonesia Andre van der Hoef / Bambang Herdyantara, Sinar Mas Forestry, Indonesia Stephen Omondi, KEFRI Jurgen Stock, Proteak Uno Sapib de CV, Mexico Ben Pienaar, Mondi South Africa Willie Brink / Christel Malek, MTO | group, South Africa Pieter de Wet, PG Bison Holdings, South Africa Nico Olivier, SAFCOL, South Africa André Nel, Sappi Forests, South Africa Lizette de Waal, York Timbers Pty Ltd, South Africa Paola Molina, Lumin, Uruguay Monica Heberling, Montes del Plata, Eufores S.A. Uruguay

<u>College of Natural Resources,</u> North Carolina State University

Myron Floyd, Dean, College of Natural Resources Erin Sills, Professor and Head, Department of Forestry and Environmental Resources

The 2020-21 Camcore Associate Members

Raúl Pezzutti, Bosques del Plata, Argentina Jean-Pierre Lasserre, CMPC Chile Wenbing Guo, Guangdong Academy of Forestry, China Marcus Warwell / Rusty Rhea, USDA Forest Service

The 2020-21 Executive Committee

Chair: Ben Pienaar, Mondi South Africa Claudio Balocchi, Arauco Bioforest, Chile Nicolás Pombo, Smurfit Kappa Colombia Mario Cesar Gomes Ladeira, Bracell, Brazil

The 2020-21 Technical Committee

Chair: Claudio Balocchi, Arauco Bioforest, Chile Byron Urrego, Smurfit Kappa Colombia Fabricio Biernaski, Klabin, Brazil Marius du Plessis, Mondi, South Africa André Nel, Sappi Forests, South Africa Agus Kurnia Nugraha, Araya Bumi Indonesia

The 2020-21 Camcore Honorary Members

Edgardo Reyes Calderon, CENTA, El Salvador Emilio Esbeih, UNACIFOR, Honduras Rony Granados, INAB, Guatemala Bernabé Caballero, INAFOR, Nicaragua Luis Angel Rodriguez del Bosque, INIFAP, México

Rafael Flores Peredo, Instituto de Investigaciones Forestales, Universidad Veracruzana, México

José Abelardo Mai, Ministry of Agriculture, Forestry, Fisheries, the Environment, Sustainable Development, and Immigration, Belize



Back Cover: The 2020 and 2021 Camcore Annual Meetings were done by Zoom. We set records for attendance at an Annual Meeting, and the meetings were interesting and enjoyable, but we will return to live in-person annual meetings as soon as possible!

The Camcore gang: *Top left to right*: Gary Hodge, Juan Jose Acosta, Robert Jetton. *Middle left to right*: Juan Luis Lopez, Andy Whittier, Romeo Jump. *Bottom left to right*: Elmer Guttierez, and Willi Woodbridge.

Front Cover: Lebogang Mphahlele of Sappi doing a 3-month survival count in a full-sib *P. patula x P. tecunumanii* hybrid trial, one of 16 such trials to be planted in South Africa as part of the full-sib hybrid breeding project. This hybrid shows great potential across a wide array of sites and environments with excellent survival, growth and wood peoperties.