# Forest Genetics
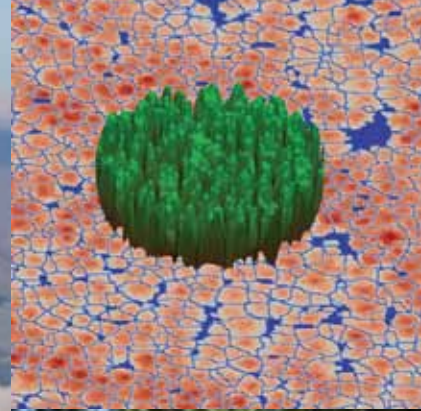# for Productivity Conference
## The next generation

**14-18 MARCH 2016** | ROTORUA | NEW ZEALAND

Handbook

scion
forests · products · innovation

IUFRO

# Welcome

Scion extends a warm welcome to those who have travelled from near and far to attend the Forest Genetics for Productivity Conference; the next generation.

Scion is New Zealand's leader in tree breeding and genomics research. Our relationship with industry helps develop tree improvement programmes, linking science through to the nursery and into the forest.

A Crown Research Institute (CRI), Scion is here to drive innovation and growth in New Zealand's forestry, wood based and biomaterial industries.

Scion is proud to host this IUFRO conference and hopes you have a great stay here in Rotorua – home to natural geothermal wonders, beautiful lakes, outdoor pursuits and a centre of Maori culture.

**scion** ✜
forests · products · innovation

Te Papa Tipu Innovation Park,
49 Sala Street, Rotorua.
Telephone +64 7 343 5899

**OUR VISION**

**Prosperity from trees** *Mai i te ngahere oranga*

**www.scionresearch.com**

## Conference Organising Committee

**Scion staff:** Heidi Dungey (Convenor), Emily Telfer, Lynn Bulman, Christl McMillan, Peter Clinton, Kylie Gunn, Stephanie Byers, Graham Kelly.

## Conference Innovators

The Conference Committee extends thanks to members of the Science Committee:

Heidi Dungey, IUFRO 2.02.20 Southern pines

Michael Stoer, IUFRO 2.02.05 Pacific NW conifers

Shawn Mansfield, IUFRO 2.04.06 Molecular biology of forest trees

Dario Grattapaglia, EMBRAPA

> Deputy Coordinator 2.04.06 – Molecular biology of forest trees
>
> Deputy Coordinator Division 2 IEB –  IUFRO Enlarged Board
>
> Deputy Coordinator 2 2.00.00 – Physiology and Genetics

Brian Baltunis, Weyerhaeuser

Antoine Kremer, INRA

Peter Clinton, Scion

> Deputy Coordinator 8.01.03 – Forest soils and nutrient cycles

Emily Telfer, Scion

Alvin Yanchuk, Ministry of Forests and Range, Canada

> Deputy Coordinator 7.03.11 – Resistance to insects

# Contents

# MINISTRY OF BUSINESS, INNOVATION & EMPLOYMENT
## HĪKINA WHAKATUTUKI

**The Ministry of Business, Innovation and Employment – growing New Zealand for all**

The Ministry of Business, Innovation and Employment's purpose is to grow New Zealand for all.  Our goal is to create a strong and high performing economy without compromising the integrity of our environment and the safety of our workplaces.

We do this by creating an environment that supports businesses to become more productive and internationally competitive, and by increasing opportunities for all New Zealanders to participate in the economy through improved job opportunities and by ensuring quality housing is more affordable.

Using our extensive presence across New Zealand and around the world we will improve access to ideas, investment and trade opportunities that will support businesses to grow and innovate.

With our Crown entity partners we work collaboratively with other government agencies; local government; businesses; industry, sector, union and employer groups; consumer groups; Māori leaders; and scientists to develop and deliver fit-for-purpose policy, services, advice and regulation that support people, businesses, communities and regions to be successful.

We are responsible for delivering a number of initiatives that will help achieve the Government's vision for New Zealand's science and innovation system. Our science investment supports a high-performing science and innovation systems that creates a more diverse, technologically advanced, smart nation.

 As a major supporter of science and innovation in the forestry sector, we are proud to be a sponsor of the 2016 Forest Genetics for Productivity Conference.

**The Conference Organising Committee
wishes to acknowledge and  thank our sponsors,
without whom this conference would not have been possible.**

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**Forest Genetics
for Productivity Conference**
**The next generation**

**14-18 MARCH 2016 | ROTORUA | NEW ZEALAND**

Incorporating the Australasian Forest Genetics Conference

# A very warm welcome

On behalf of the conference committee I am delighted to welcome you to Rotorua for the Forest Genetics for Productivity Conference incorporating the Australasian Forest Genetics Conference.

This is the first international conference on tree genetics held in New Zealand since 1997. The conference provides an exciting opportunity for the New Zealand and international research community to share research findings and to forge new networks, particularly for young and emerging scientists.

Over the next five days participants will hear from international experts and learn about innovations applied to forestry breeding and growing on the global stage. Posters and presentations will cover new technologies such as next generation genotyping, genomics, genotype by environment interactions, plant phenotyping, LiDAR and remote sensing and their application to the development of genetically improved trees.

Increasing forest productivity is a priority not only for the New Zealand forest industry but also globally to meet increasing demand for timber and non-timber products and services. This conference brings together forest industry leaders, scientists and innovators from around the world to help set the scene for the future of this vital industry,

During your stay here, I hope you find time to enjoy the unique setting of Rotorua, which is famous for its natural geothermal wonders, beautiful lakes, outdoor pursuits and centre of Māori culture.

I look forward to meeting you and hope you have a rewarding conference experience.
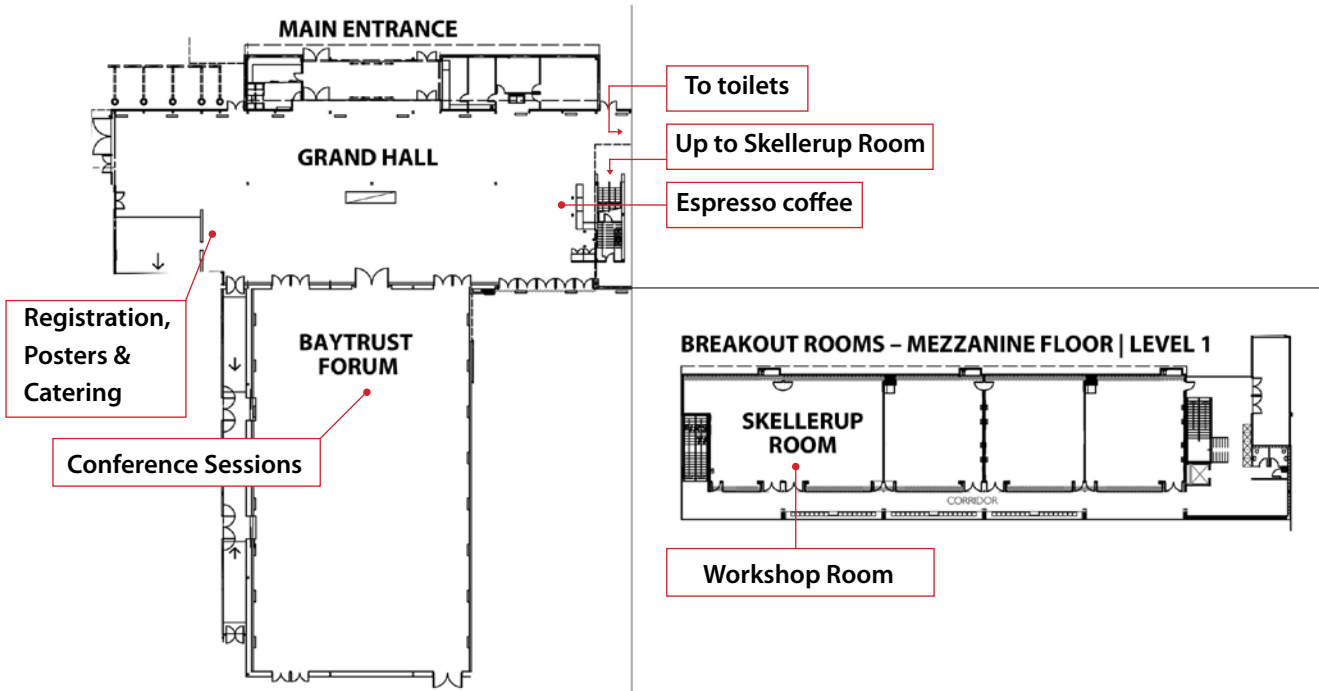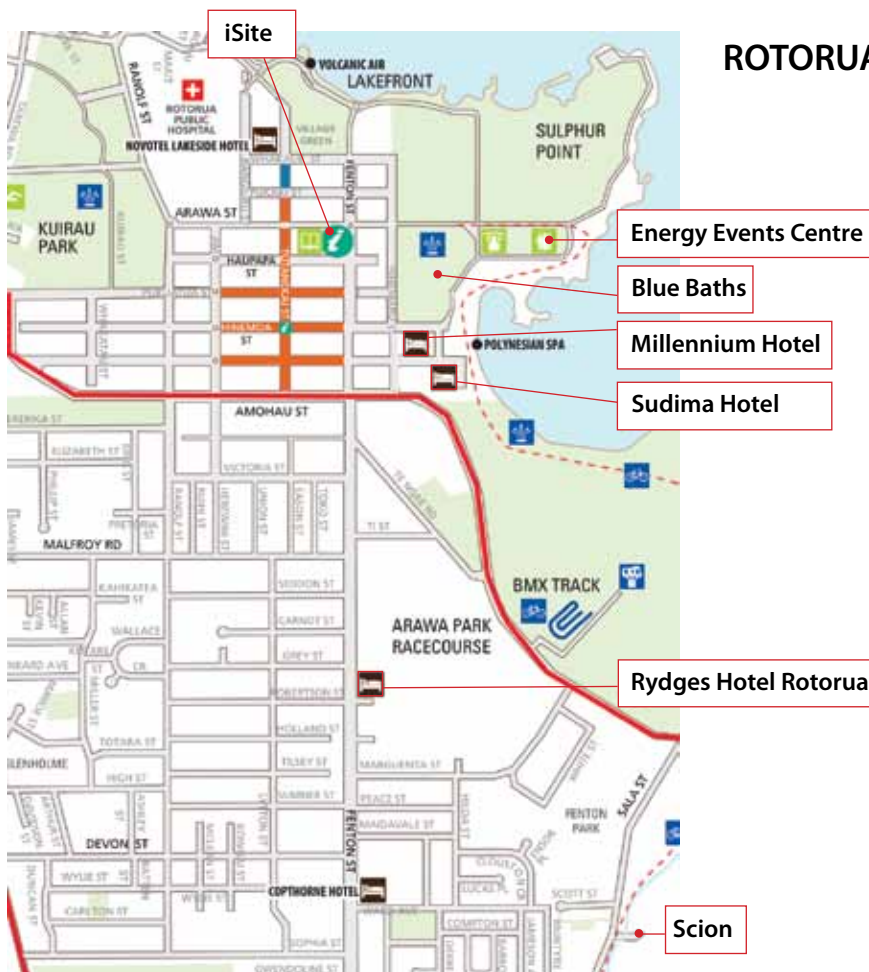
**Heidi Dungey**
*Convenor*

# Maps

## ENERGY EVENTS CENTRE

**GROUND FLOOR**

**MAIN ENTRANCE**

**GRAND HALL**

To toilets

Up to Skellerup Room

Espresso coffee

Registration, Posters & Catering

**BAYTRUST FORUM**

Conference Sessions

**BREAKOUT ROOMS – MEZZANINE FLOOR | LEVEL 1**

**SKELLERUP ROOM**

CORRIDOR

Workshop Room

## ROTORUA

iSite

VOLCANIC AIR

LAKEFRONT

SULPHUR POINT

ROTORUA PUBLIC HOSPITAL

NOVOTEL LAKESIDE HOTEL

VILLAGE GREEN

RANOLF ST

FENTON ST

ARAWA ST

KUIRAU PARK

HAUPAPA ST

HINEMOA ST

Energy Events Centre

Blue Baths

POLYNESIAN SPA

Millennium Hotel

Sudima Hotel

AMOHAU ST

ELIZABETH ST

VICTORIA ST

MALFROY RD

KAHIKATEA ST

WALLACE

GREY ST

CARNOT ST

BMX TRACK

ARAWA PARK RACECOURSE

ROBERTSON ST

Rydges Hotel Rotorua

HOLLAND ST

TILSEY ST

TOTARA ST

SUMNER ST

HIGH ST

PEACE ST

MANGUREITA ST

GLENHOLME

FENTON ST

MADAVALE ST

FENTON PARK

SALA ST

DEVON ST

WYLIE ST

COPTHORNE HOTEL

CARLTON ST

Scion

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# Keynote speakers

**Professor Dario Grattapaglia**

*EMBRAPA & Universidade Católica de Brasília, Brazil*

Dario is a research scientist at EMBRAPA and professor in the graduate programmes of Genomic Sciences at the Catholic University of Brasília and molecular biology at the University of Brasilia. His main areas of research include: forest tree genetics and breeding of sustainable forest tree plantations for energy, pulp, paper and fibre; genomic technologies applied to breeding practice; and population genetics and conservation of tropical trees. He was project leader of the Genolyptus Project (Brazilian Network of Eucalyptus Genomic Research), and co-PI of the International Eucalyptus Genome Sequencing Project.

**Dr Antoine Kremer**

*Research Scientist at INRA, Pierroton, France*

Antoine is a senior scientist at INRA Bordeaux. His research deals with the evolution of genetic diversity and differentiation between natural tree populations, at various hierarchical levels where diversity is expressed (from genes to phenotypic traits). Antoine initiated Europe-wide forestry research as early as the 1980s based on population genetics and evolutionary biology. His current interest addresses microevolution in the context of environmental changes linking genetics, genomics and ecology.

**David Pont**

*Research Scientist, Scion, New Zealand*

David's current research focuses on the detection and characterisation of individual trees in aerial and terrestrial LiDAR data. David has been developing and testing these methods to provide the basis for phenotyping trees in genetics trials, research trials and forest stands using remotely sensed data. David has over 30 years' forestry research experience, specialising in the measurement and modelling of individual tree growth and wood quality and has contributed to the development of models integrating tree growth, branch growth and within-stem wood properties, used to quantify tree, log and product quality.

**Professor Dr Ulrich Schurr**

*Institute Director of IBG-2: Plant Sciences at Forschungszentrum Jülich, Germany*

Ulrich is interested in the performance and optimisation of plants in spatially varying and environmental conditions. In recent years, with his team, he developed non-invasive techniques to quantitatively acquire structural, physiological and molecular data. He founded the Jülich Plant Phenotyping Centre (JPPC), which forms the core of the German Plant Phenotyping Network (DPPN), and coordinates the European (EPPN) and the International Plant Phenotyping Network (IPPN) to develop new methods and innovative experimental concepts for plant phenotyping.

**Dr Jerry Tuskan**

*Group Leader, Plant Systems Biology, BioSciences Division, Oak Ridge Laboratory, TN, USA*

Jerry's research focuses on the genetic basis of tree growth and development including collaborations on the genome sequences of poplar and Populus genomics including the assembly of the draft sequence, comparative genomics and functional gene identification. More recently Jerry has been involved with the development of *Eucalyptus* biofeedstocks. In 2012, he was the fourth award recipient of the Institute of Forest Biotechnology's Forest Biotechnologist of the Year, and in 2014 he was named a Corporate Fellow by UT-Battelle.

**Professor Brian Cullis**

*Inaugural Professor of Biometry, Grains Research and Development Corporation & CSIRO, University of Wollongong, New South Wales, Australia*

Brian is Professor of Biometry at the University of Wollongong, a position co-funded by the Grains Research and Development Corporation and CSIRO. Up until 2011, Brian worked as a biometrician for more than 30 years with NSW Department of Primary Industries. Brian is interested in the design and analysis agricultural and biological data, with his expertise more recently being applied in forestry. Much of his work has involved the analysis of experimental data using linear mixed models, and he is a co-author of the ASReml software package and the R package ASReml-R. Brian has co-authored more than 180 journal articles, has served as a Co-Editor of Biometrics and currently is an Associate Editor of the Australian and New Zealand Journal of Statistics and the Journal of Agricultural Science Cambridge.

**David Balfour**

*Acting CEO, Timberlands, Rotorua, New Zealand*

David has over 30 years' experience in the forest industry. He is a member of the Forest Owners Association Executive, Chairman of the Forest Research Committee, and serves on the Forest Growers Levy Trust Board.

Formally David was Chief Executive of BSW Timber, a Scottish company, which owned five sawmills and stumpage operations. His experience includes forest management, management of harvesting and marketing operations, site manager for a large sawmill and lumber sales. David graduated from Edinburgh University with a BSc (Hons) in Ecological Science. He is a fellow of the Royal Institute of Chartered Foresters (UK) and is an associate member of the NZ Institute of Forestry.

**Dr Robert Banks**

*Director of Animal Genetics and Breeding Unit (AGBU), University of New England, NSW, Australia*

Rob has been involved in the genetic improvement of Australia's extensive meat and livestock industries for over 30 years, in the establishment of the genetic evaluation system for the Australian lamb industry, LAMBPLAN which was then of extended to provide genetic evaluation for the Merino industry. More recently, and in response to rapid advances in genomic technologies, Rob has led the development of Information Nucleus flocks and herds. Intensive phenotying in these populations will help maximise the returns from investing in genomic testing in the Australian red meat industries. Since taking up the role of Director, Rob has guided projects focussed on genetic evaluation of dairy goats and honeybees, as well as contributing to AGBU's portfolio of projects.

Rob is on the board of the Southern Tree Breeding Association.

**John McEwan**

*Senior Scientist, Animal Genomics, AgResearch Invermay, New Zealand*

John is involved in animal genetics and genomics research. His previous and current work includes sequencing genomes and building genotyping platforms including SNP chips and genotyping by sequencing methodologies; trait specialties are host genetics of methane emissions, disease and meat.

# Programme

**Monday 14 March – Bay Trust Forum**

| | |
|---|---|
| 7.00am | Registration desk open |
| 9.00am | Mihi / Karakia<br>Conference Opening<br>**Martyn Dunne**, *Director-General, Ministry for Primary Industries*<br>**Warren Parker**, *Chief Executive, Scion* |
| 10.00am | Morning Tea |
| 10.30am | **KEYNOTE** Overview of current status of genetics and future trends<br>Antoine Kremer |
| 11.15am | **KEYNOTE** Forest Industry Genetic Improvement – Vision, priorities and learning from other species<br>Robert Banks<br>Chair: Heidi Dungey |
| 12.00pm | Lunch |
| 1.00pm | **KEYNOTE** What are the four key questions that New Zealand forestry wants answered by genetics?<br>David Balfour |
| 1.30pm | **INVITED SPEAKER** More urgency in the delivery of commercial benefits from genetic improvement<br>John Butcher<br>Chair: Heidi Dungey |
| | **Theme: Breeding productive and resilient forests** |
| 1.50pm | Realised genetic gain for growth and wood density in New Zealand radiata pine<br>John Moore |
| 2.10pm | *Corymbia* species and hybrids; challenges and potential<br>David Lee |
| 2.30pm | Sampling strategies for wood properties of *Eucalyptus bosistoana* accounting for spatial patterns<br>Luis Apiolaza |
| 2.50pm | Discussion and notices<br>Chair: Alison Stewart |
| 3.00pm | Afternoon tea |

| | Theme: Breeding productive and resilient forests |
|---|---|
| 3.30pm | Productive potential of selected Norway spruce populations from Northern Poland (preliminary study from testing program)<br>**Marcin Klisz** |
| 3.45pm | Investigating efficiency of selection using univariate and multivariate best linear unbiased predictors<br>**Richard Kerr** |
| 4.00pm | When is fast growth costly? Insect herbivory shifts selection patterns in a forest tree<br>**Raul De La Mata** |
| 4.15pm | Improvement of non-key traits in radiata pine breeding programme when long-term economic importance is uncertain<br>**Yongjun Li** |
| 4.30pm | Closing and discussion<br>Chair: Luis Apiolaza |
| 5.30pm | Poster evening |

# Forest Genetics Clonal Varieties Increase Productivity

**FOREST GENETICS™**
creating tomorrows trees

- Substantially increased growth rate, wood quality and Dothi resistance
- Stable performance across a wide range of forest sites
- 30% increase in carbon offsets

**Latest results: Central North Island row plot trial #1**

| Genetics | Volume (dm$^3$/ha) | Dothi (% needles uninfected) | Corewood Stiffness (Gpa) | Wood Density (kg/m$^3$) |
|---|---|---|---|---|
| | age 8.5 | age 5 | age 5 | age 5 |
| Best Variety | 0.26 | 75 | 7.2 | 326 |
| All 10 Varieties | 0.23 | 58 | 5.8 | 316 |
| GF24 Control pollinated (GFPlus 22) | 0.19 | 44 | 3.8 | 322 |
| GF19 Open pollinated | 0.18 | 40 | 3.6 | 315 |

**Latest results: Central North Island large plot trial #2**

| Genetics | Volume (% gain or dm$^3$/ha) | Corewood Stiffness (Gpa) | Wood Density (kg/m$^3$) |
|---|---|---|---|
| | age 9 | age 5 | age 5 |
| Variety A | +15% | 7.9 | 373 |
| Variety B | +38% | 8.1 | 345 |
| Variety C | +17% | 8.1 | 368 |
| GF24-30 Control Pollinated | -0.9% | 5.9 | 318 |
| GF19 Open pollinated | 0.22 | 5.7 | 324 |

**Selection and gain estimates based on:**

| Type of Trial | No. Trials | Years Planted |
|---|---|---|
| 1st Generation Selection | | |
| New Zealand | 26 | 1999-2005 |
| Australia | 20 | 2003-2008 |
| Validation | | |
| New Zealand | 130 | 2000-2015 |
| Australia | 18 | 2007-2013 |

Contact
Mike Carson: 07 357 4244
mike.carson@forest-genetics.com

Christine Te Riini: 027 375 2733

For more information:
www.forest-genetics.com

**Tuesday 15 March – Fieldtrip**

| 8.15am | Depart Rotorua Energy Events Centre |
|---|---|
| 9.15am | Compartment 1061 Kaingoroa Forest<br>A demonstration trial comparing pre-product *Pinus radiata* clones and commercially available open-pollinated and control pollinated seedlots<br>Mike Carson |
| 10.00am | Morning tea |
| 10.45am | Compartment 192 Kaingoroa Forest<br>Operational outplanting of a tested clone and comparison to commercial open pollinated seedlot - Use of clonal material from a grower's perspective.<br>**Dean Witehira** |
| 12.00pm | Compartment 179 Kaingoroa Forest<br>*Cypress* clonal block plantings<br>**Charlie Low** |
| 12.45pm | Lunch |
| 1.30pm | UAV Demonstration<br>**Marie Heaphy** |
| 2.15pm | Compartment 333 Kaingoroa Forest<br>Progeny trials of *Eucalyptus fastigata* and *E. regnans* – discuss the history of the breeding programmes for these two species and gains made to date<br>**Mari Suontama** |
| 3.15pm | Compartment 320 Kaingoroa Forest<br>New Cypress hybrid clones under test improved disease resistance and improved natural durability<br>**Charlie Low** |
| 4.45pm | Return Rotorua Energy Events Centre |

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## Wednesday 16 March – Bay Trust Forum

| | |
|---|---|
| 7.30am | Registration and information desk open |
| | **Theme: Finding the synergies in genotype, environment and silviculture** |
| 8.30am | **KEYNOTE** Genotype x environment interaction in a large MET analysis of *Pinus radiata*<br>**Brian Cullis** |
| 9.15am | Identifying site types for *Pinus radiata* genetic evaluation in Australia<br>**Gregory Dutkowski** |
| 9.35am | Relative impact of mechanical site preparation and stock ideotype on survival and growth of southern pine hybrids aged 15 years<br>**Mark Hunt** |
| 9.55am | Discussion and housekeeping<br>Chair: Peter Clinton |
| 10.00am | Morning Tea |
| | **Theme: Finding the synergies in genotype, environment and silviculture** |
| 10.30am | Increased efficient of breeding value prediction of Swedish Norway spruce breeding program by spatial analysis and dissecting genotype by environment interactions<br>**Zhiqiang Chen** |
| 10.50am | Genotype x site x silviculture interactions in radiata pine: Knowledge, working hypotheses and pointers for research<br>**Rowland Burdon** |
| 11.10am | Simulating realized gain trials by incorporating heritable morphological traits from Douglas-fir progeny tests into growth models<br>**Sukhyun Joo** |
| 11.30am | Influence of site factors on growth and physiology of *Pinus radiata* genotypes, and the implications of silviculture on tree breeding trials<br>**Dean Meason** |
| 12.00pm | Discussion<br>Chair: Keith Jayawickrama |
| 12.05pm | Lunch |
| 1.00pm | Silvicultural value of progeny of European beech provenances under the habitat conditions of Southern Poland<br>**Szymon Jastrzębowski** |
| 1.20pm | Progress with the rolling front in radiata pine<br>**Tony McRae** |
| 1.40pm | Slash x Caribbean pine hybrid genetic improvement in Queensland<br>**Dominic Kain** |
| 2.00pm | Genetic evaluation of Swedish scots pine breeding program<br>**Gunnar Jansson** |
| 2.20pm | Optimising selection in tree breeding with constraints on relatedness and operational flexibility<br>**Tim Mullin** |

| | |
|---|---|
| 2.40pm | Breeding to improve foliar oil yields in *Eucalyptus polybractea*<br>**John Doran**<br>Chair: Greg Dutkowski |
| 3.00pm | Afternoon tea |
| 3.30pm | Genetic control of growth strain in *Eucalyptus bosistonana*: very early screening of a left-censored trait<br>**Nicholas Davies** |
| 3.45pm | Applying experimental design in Swedish forest tree genetics trials<br>**Johan Westin** *(Presented by Richard Kerr on behalf of Johan)* |
| 4.00pm | Screening for red needle cast resistance in radiata pine<br>**Natalie Graham** |
| 4.15pm | Producing forests for the future climate<br>**Simeon Smaill** |
| 4.30pm | Closing and discussion<br>Chair: John Moore |

## Thursday 17 March – Bay Trust Forum

| | |
|---|---|
| 7.30am | Registration and information desk open |
| | **Theme: Genomics and phenomics** |
| 8.30am | **KEYNOTE** Genomic selection in tropical *Eucalyptus* breeding: advantages and challenges<br>Dario Grattapaglia |
| 9.15am | First evaluation of genomic selection for radiata pine<br>Emily Telfer |
| 9.35am | Genetics and genomics of kiwifruit – a breeder's perpective<br>Luis Gea |
| 9.55am | Discussion and housekeeping<br>Chair: Gerald Tuscan |
| 10.00am | Morning tea |
| 10.30am | **KEYNOTE** Phenotyping plants in variable and heterogeneous environment - integrated approaches to mechanistic, high-throughput and field phenotyping<br>Ulrich Schurr |
| 11.15am | **KEYNOTE** The use of LiDAR for phenotyping trees<br>David Pont |
| 11.40am | Lidar update: Improvements and opportunities in using data rich point clouds for forest monitoring<br>David Herries<br>Chair: Elspeth MacRae/Heidi Dungey |
| 12.00pm | Lunch |
| | **Concurrent sessions** |
| 1.00pm | ASREML-R workshop        Skellerup Room<br>**Brian Cullis**<br>**Jaroslav Klapste**<br>**Mari Suontama**         Bioinformatics workshop      Bay Trust Forum<br>**Dan Jones, NZGL**<br>**Emily Telfer** |
| 3.00pm | Afternoon tea |
| | **Concurrent sessions** |
| 3.30pm | ASREML-R workshop *continued*         Bioinformatics workshop *continued* |
| 4.10pm | Closing and discussion |
| 6.30pm | Conference dinner – Blue Baths |

## Friday 18 March– Bay Trust Forum

| Time | Session |
|---|---|
| 7.30am | Registration and information desk open |
| | **Theme: Putting it all together** |
| 8.30am | **KEYNOTE** Frontiers of genomic selection in sheep<br>John McEwan |
| 9.15am | Advanced generation tree breeding: Challenges and opportunities<br>Harry Wu |
| 9.35am | Towards genomic selection for wood properties in *Eucalyptus nitens*<br>Mari Suontama |
| 9.55am | Discussion and housekeeping<br>Chair: Dario Grattapaglia |
| 10.00am | Morning tea |
| 10.30am | **KEYNOTE** Gene discovery through genome-wide association studies<br>Gerald Tuskan |
| 11.15am | Integrated phenotyping: bringing together quantitative data from across disciplines for more informed plant breeding<br>Nari Williams |
| 11.35am | Successful clonal forestry with radiata pine in New Zealand<br>Michael Carson |
| 11.55am | Discussion<br>Chair: Emily Telfer |
| 12.00pm | Lunch |
| 1.00pm | Genetic diversity, conservation and breeding of *Eucalyptus benthamii*<br>David Bush |
| 1.20pm | Landscape community genomics<br>Heidi Dungey |
| 1.40pm | Molecular genetic markers to achieve productive and resilient forests<br>Valerie Hipkins |
| 2.00pm | Future perspectives<br>Heidi Dungey |
| 2.20pm | **WORKSHOP** Solutions to the four questions posed by David Balfour<br>Chair: Emily Telfer |
| 2.40pm | Panel/report back and discussion |
| 3.15pm | Afternoon tea |

## Programme Information

### Speakers' Support Centre

The Speakers' Support Centre is located in the back of the Bay Trust Forum (main plenary room) and will be open from 7.30am to 5.00pm Monday to Friday.

### Oral Presentations

It is important that all speakers check-in their audio visual material at the Speakers' Support Centre at least two hours prior to the commencement of their allocated session. Speakers who are presenting at an early morning session should check-in their audio visual material the day before their presentation.

An audio visual technician will be available to assist with data projection or other technical requirements. If you require assistance from a technician, please ensure you arrange this during one of the breaks prior to your presentation.

### Poster Presentations

Posters will be displayed from Monday 14 March to Friday 18 March. Poster presenters must check-in at the Registration Desk for directions to their allocated poster area. The presenting author must be present at their poster from 5.00pm to 7.00pm on Monday 14 March for the Poster and Trade Evening.

Posters not collected at the conclusion of the conference will be discarded.

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*The NZ Farm Forestry Association wishes all delegates an enjoyable and informative time at the 2016 Forest Genetics for Productivity Conference.*
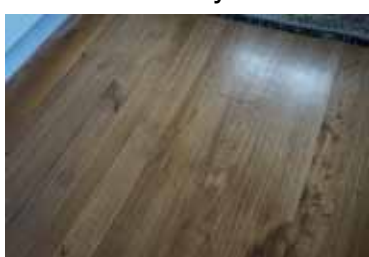




*E.nitens, from standing trees to polished flooring.*

Our members range from Queen Street farmers to rural farmers to researchers and scholars. We can help with the full life-cycle of trees from selection to planting to silviculture to harvesting, and we have regular field days and seminars to see and talk about trees that are in the ground. For more information, contact:

NZ Farm Forestry Association
PO Box 10 349
Wellington 6143
T:   +64 (0)4 472 0432
E:   admin@nzffa.org.nz
W:   www.nzffa.org.nz



*Free copies of our quarterly Tree Grower magazine are available on request.*
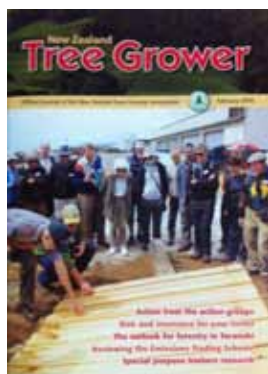


While many NZFFA members grow radiata pine, we also place a strong emphasis on special purpose species, with species-specific action groups for blackwoods, cypress, eucalypt, indigenous, and redwoods.



*Pruning of an adolescent E.quadrangulata.*

Our members grow trees in all parts of New Zealand, with a huge variety of species, growing conditions, and practical experience of which species grow best where.

The NZFFA has represented small forest growers since 1957, and currently advocates for 14,000 forest owners on behalf of the Forest Growers Levy Trust.

# Social Programme

## Poster evening

**Date:**      Monday 14 March 2016
**Time:**      5.30pm - 7.00pm
**Venue:**     History Wall Aisle, Rotorua Energy Events Centre
**Tickets:**   One ticket to the Poster and Trade Evening is included with a full registration.

The Poster evening will be held in the Grand Foyer and History Wall Aisle of the Energy Events Centre.  Join your fellow delegates and sponsors for canapés and drinks to review the day's learning, network or make dinner plans.

## Conference Dinner

**Date:**      Thursday 17 March 2016
**Time:**      6.30pm - 11.00pm
**Venue:**     Blue Baths, Rotorua
**Tickets:**   One ticket to the Conference Dinner is included with a full registration.  Additional tickets can be purchased for $90.00 per ticket from the registration desk.

Join us at Rotorua's historic Blue Baths for a night of fine food and entertainment.

# General Information

## Telephone

Registration and information desk
and after hours (Rachel Cook)          021 918 524

**Hotels**

Millennium Hotel Rotorua              07 347 1234

Rydges Hotel Rotorua                  07 346 3888

Sudima Lake Rotorua                   07 346 0238

**Taxis**

Rotorua Taxis                         07 348 1111

Super Shuttle                         0800 748885

**Airlines**

Air New Zealand                       0800 737 000

**General**

Rotorua i-SITE                        07 348 5179

**Airport transfers**
The staff at the registration desk will be happy to assist you.

**Luggage storage**
Guests are able to store luggage at their hotel, please see the concierge to arrange for luggage storage. Storage will also be available near the registration desk at Rotorua Energy Events Centre on Friday.

**Mobile phones**
Please ensure your mobile phone is switched off or on silent mode during all conference sessions.

**Name badges and lanyards**
Please wear your conference name badge when attending conference sessions and within the conference venue.

**Smoking**
is not permitted in the conference venues.

# Abstracts

# NZGL
## NEW ZEALAND GENOMICS LIMITED

## CUSTOMISED GENOMICS SOLUTIONS FOR NEW ZEALAND SCIENTISTS

*Since 2012 **NZGL** has serviced genomics projects from all types of species and environments. Many of our projects are unique to New Zealand's special environment and include areas of economic importance such as silviculture, agriculture and horticulture.*

**www.nzgenomics.co.nz**

# WHOLE GENOME SEQUENCING OF PINUS RADIATA

In forestry we are proud to support the research programme of Scion through the examination of the transcriptome of Pinus radiata and investigating the transcriptome of major pathogens including novel gene discovery. Projects included sequencing transcriptomes for discovery of DNA sequence differences between genotypes and the generation of a whole genome sequence data for the first ever assembly of the Pinus radiata genome.

# FINDING ANSWERS AROUND RED-BAND NEEDLE BLIGHT

Massey University molecular plant pathologist Rosie Bradshaw is studying the genetic details of a fungal pathogen of pine trees, to determine if the timing and nature of its gene expression hold answers to help control dothistroma needle blight.

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**KEYNOTE**

## GENOMICS IN FORESTRY: WHERE ARE WE AND WHERE ARE WE HEADING TO?

**Antoine Kremer**

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What kind of applications can be foreseen in forestry given the recent advances and results obtained in the field of genomics? I will review some of the major achievements in genomics and address their potential applications in three major forestry areas: breeding; conservation; and adaptation. The repetitive confirmation that the genetic architecture of most traits of economic value is highly polygenic has indeed redirected the potential use and application of the genomic variation observed in breeding or natural populations of trees. In the same time the possibility to reconstruct genetic and genomic relatedness in structured and unstructured populations has open new perspectives for conservation and forest management. Beyond the development of genomic selection in breeding programmes, other reasonable applications can be foreseen in forest stands that are renewed by natural regeneration. These include estimation of selection gradients, heritability in situ and consequently evolutionary change triggered by ongoing environmental change.

**KEYNOTE**

**FOREST INDUSTRY PRIORITIES VISION AND PRIORITIES FOR FOREST GENETICS**

**Robert Banks**

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Genetic improvement of forest tree species is founded on the same underlying theory and principles as genetic improvement in other species, but with some specific challenges reflecting the biology and production systems specific to forestry. These challenges can be daunting, but need to be overcome if the opportunity costs of sub-optimal genetic progress and hence economic returns are to be avoided. A worthwhile vision for forestry genetic improvement is simply to achieve rates of genetic progress that offset rising input prices and ensure that forestry is sustainable economically and environmentally. The paper explores what this might include in terms of goals, as well as reviewing the tools available to help achieve that vision, and a systematic approach to their implementation. Increasingly, forestry breeders will need to design data generation and utilisation systems that enable implementation of genomic selection, and retention of genetic diversity, to maximise ability to cope with medium-term uncertainty. This will require coordination at the national and likely international levels, across organisations and technologies. If this can be achieved, sustainability of forestry operations can be enhanced, for benefit of both forestry companies and the broader community.

## THE DEVELOPMENT PROGRAMME AND BUSINESS CASE FOR GENOMIC SELECTION IN RADIATA PINE BREEDING

**John Butcher**

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The Radiata Pine Breeding Company, working with Scion as major research provider, commenced its R&D programme on genomic selection in 2014. The R&D programme is highly targeted at implementing a commercially viable process for shortening the breeding and deployment timeline and for increasing genetic gain in the target traits of volume, density, and corewood stiffness. The development pathway for genomic selection, and its integration with other breeding and deployment technologies, is described.

RPBC is using exome-based GBS technologies for genotyping. Initial training populations comprised two clonal trials with existing phenotypic data. An expanded training population has been established based on newly selected Elites with trials established in 12 regional sites and in the breeding archive. When phenotypic information is available to align with genomic information, sufficient plant material will be available to allow rapid bulking up for deployment. This approach allows good balance between optimising the impacts of genomic selection whilst minimising risk.

New crosses for the next generation of elites will be selected from archived material based on GeBVs. Several deployment options are being examined, including embryogenesis, to optimise planting stock development. Detailed scenarios are being developed to identify the fastest breeding and deployment route and to characterise potential financial gains. The existing targets of the Business Plan, although significant, do not as yet fully exploit the potential of genomic selection. Shortening breeding and deployment timelines, and speeding turnover of generations, delivers more benefit than can be achieved by the pursuit of genetic gain alone.

# REALISED GENETIC GAIN FOR GROWTH AND WOOD DENSITY IN NEW ZEALAND RADIATA PINE

**John Moore**, Mark Kimberley, Heidi Dungey

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**Objectives**: To estimate realised genetic gain for growth and wood density in radiata pine to aid decisions around the deployment and management of genetically improved tree stocks.

**Methods**: Using data from a network of large-plot trials, realised genetic gain for growth was quantified using two measures of productivity: site index and 300 Index [1]. The relationship between these indices and the genetic rating for a seedlot (GF Plus growth rating) was determined. Realised gain for wood density was calculated using a model of the radial variation in radiata pine wood density [2]. The relationship between GF Plus density rating and wood density at age 20 years was estimated using data from 679 families.

**Results**: There was positive relationship between GF Plus growth rating and both productivity measures. Differences of 25% in total standing volume at age 30 years and of 5.6% in site index were found between unimproved and highly improved seedlots. Each unit increase in GF Plus rating was associated with a 1.51% increase in volume growth. There was a positive relationship between GF Plus density rating and predicted wood density at age 20 years. Each unit of GF Plus density rating was associated with a 1.85 kg m$^{-3}$ increase in wood density at age 20 years.

**Conclusions**: Realised genetic gain has resulted in large differences in standing volume and a consistent improvement in wood density. Quantification of genetic gain in this manner facilitates its incorporation into growth and yield simulators.

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## CORYMBIA SPECIES AND HYBRIDS: CHALLENGES AND POTENTIAL

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*Corymbia* species and their hybrids are of increasing importance to world's plantation forestry sector for many reasons: suitability across a wide range of environments, relatively high productivity in environments that are marginal for either intensive agricultural production or other plantation species, tolerance to a range of pests and diseases and the high quality durable timber products that can be produced from the trees (Lee, 2007; Lee et al., 2010; Carvalho et al., 2010; Nichols et al., 2010). They are also known for their high pulp productivity in China, South Africa, and Australia (Phillips 1989, Gardner et al., 2007; Brawner et al., 2012) and are becoming important species for charcoal production in Brazil (e.g. Aperam; pers comm Eduardo Henriques, 2011).

Across Australia over 20,000 hectares of *Corymbia spp*. plantations have been established since the late 1990s (Barbour et al., 2008) primarily using *C. citriodora* subsp. *variegata* in the subtropics and *C. maculata* in temperate climates. This presentation reports on the taxonomy of the spotted gum group and our current knowledge of *Corymbia* species and hybrids when grown under plantations conditions focussing on: the productivity across different regions of the Australia's subtropics, genetic improvement of *Corymbia* species and hybrids, advantages of the *Corymbia* hybrids relative to the pure species and characterisation of *Corymbia* species and hybrids wood properties.

## SAMPLING STRATEGIES FOR WOOD PROPERTIES OF EUCALYPTUS BOSISTOANA ACCOUNTING FOR SPATIAL PATTERNS

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The New Zealand Dryland Forests Initiative (http://nzdfi.org.nz) has established breeding population trials for several eucalypt species, including *Eucalyptus bosistoana*. The breeding objective for this species is to produce high-value, durable wood with low growth stresses.

Early evaluations of *E. bosistoana* multiple environment trials have shown substantial variability for growth traits and survival both between- and within-site. Furthermore, there are strong spatial patterns reflecting, for example, position in the slope and aspect.

While growth traits are easy and cheap to assess, the wood properties of interest (e.g. heartwood content and quality, and growth stresses) are expensive and time consuming, so sampling is required. Common sampling approaches in tree breeding are truncation sampling (assessing wood properties only on best trees for growth) and random sampling (aiming to include trees from all families). This research also tests the use of ranked set and balanced acceptance sampling, which can consider spatial trends, family structure and other available auxiliary information.

Multivariate simulations of the four sampling strategies considered the growth-traits spatial trends together with a range of potential values for the correlation between growth and wood durability. Truncation sampling badly bias the estimates of genetic parameters, while random sampling provides good estimates but it is inefficient, requiring too many samples. Ranked set sampling and balanced acceptance sampling achieved better efficiency than random sampling, with lower assessment cost.

# PRODUCTIVE POTENTIAL OF SELECTED NORWAY SPRUCE POPULATIONS FROM NORTHERN POLAND (PRELIMINARY STUDY FROM TESTING PROGRAM)

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In 2006, State Forestry in Poland began the Program for Testing Forest Reproductive Material. The tests are conducted in order to select populations with the best adaptation, qualitative and quantitative properties. After five years of growing of the progenies of Norway spruce, selected seed stands the height stability determining were done. The study covered the progenies of 35 selected seed stands of Norway spruce from northern Poland and it was carried out in 4 sites (common garden) in randomised complete block designs. The analysis of variance for a linear mixed model with populations (genotypes) as fixed effect and environments and population (genotype) ˣ environment interaction (GEI) as random effects was performed. The GGE biplot graphic method was used to identify stable populations in relation to height. Based upon the mean height estimators, the "average environment" was defined. It allows to define the representativeness of growth conditions for sites, as well as the discriminating ability.

The results of growth height allowed for the identification of populations characterised by the above-the-average height stability. There were also identified populations which are equally stable, yet considerably lower than the average height of all tested genotypes. Finding populations which are the most similar to the theoretical "ideal population" allowed determining best population in terms of high stability and well mean performance. Those result should, however, be treated as preliminary and requiring further verification in the course of planned measurements in the following five-year cycles.

## INVESTIGATING EFFICIENCY OF SELECTION USING UNIVARIATE AND MULTIVARIATE BEST LINEAR UNBIASED PREDICTORS

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Over the last 16 years the Southern Tree Breeding Association (STBA) has developed a dedicated genetic evaluation system (TREEPLAN) for use in forest genetics. It was designed to be useable by operational breeders, tailored for use in rolling front breeding programs, and most importantly, have a massive multivariate capability for integrating all available data generated by a national breeding program. In this study an analysis based on simulated data was run in order to evaluate the benefit of integrated analysis to STBA members and clients. The breeding plan and the quantitative genetic architecture of the simulated species were based on *Pinus radiata*. The 27 traits in the analysis comprised 19 growth traits (growth for three age classes within seven site types), three branch traits, wood density for two age classes, one wood stiffness trait and one disease trait). Several genetic evaluation scenarios were considered: a multi-trait analysis of the 27 traits (MULTI); 27 single-trait analyses (SINGLE); and a multi-trait analysis of the 19 growth traits combined with single-trait analyses for the remaining traits (MULTI/SINGLE). In each case trait EBVs were combined into a $NPV index score for the objective of improving profitability in an integrated forest growing and structural timber production system. We compared the true $NPV index score for the top 5% of the population after three generations of breeding and selecting on the basis of the estimated $NPV score, under each scenario. The main finding is that the gain in $NPV under the MULTI scenario is significantly greater than in other scenarios.

## WHEN IS FAST GROWTH COSTLY? INSECT HERBIVORY SHIFTS SELECTION PATTERNS IN A FOREST TREE

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Why natural populations of forest trees exhibit wide genetic variation in growth rates while facing strong selective pressures has long captivated evolutionary biologists and forest geneticists. Conflicting fitness effects among traits and fluctuating selection pressures over time are thought to contribute to genetic diversity. However, empirical evidence of such conflicts is scant, particularly for long-lived organisms such as trees. We used a 40-year-old *Pinus ponderosa* common garden genetic experiment that experienced extreme herbivory pressure due to a mountain pine beetle outbreak (MPB; *Dendrochtonus ponderosae*) at approximately 35 years of age, to test such conflicts. We show that the relative fitness contribution of fast growth depends on time- and stage-specific selective pressures. Faster growing genotypes were more likely to survive during early establishment and stand development, but less likely to survive the MPB outbreak, which caused a change in selection patterns. Our results further suggest that the growth-survival trade-off during the outbreak was not solely driven by the beetle preference for larger trees. We provide much needed empirical evidence of the mechanisms underlying the maintenance of genetic variation in long-lived organisms in nature, which have ecological, evolutionary and management implications. Future: varying abiotic stress could also be a cause of fluctuating selection pressures and trade-offs among life history traits, particularly under current climate change and associated drought. Currently at the University of Alberta we are addressing the topic of potential trade-offs between growth and resilience to drought in other widespread pine species from western North America, e.g. *Pinus contorta*.

# IMPROVEMENT OF NON-KEY TRAITS IN RADIATA PINE BREEDING PROGRAMME WHEN LONG-TERM ECONOMIC IMPORTANCE IS UNCERTAIN

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Diameter at breast height, wood density and stiffness are the key traits chosen to improve radiata pine in the New Zealand radiata pine breeding programme. Any other traits which are of interest to radiata pine breeders are called non-key traits. External resin bleeding, internal checking, number of heartwood rings are three such non-key traits which affect wood quality of radiata pine timber and are currently used as culling traits in radiata pine breeding programme. Economic importance of these key traits and non-key traits is, however, difficult to define due to the long rotation period of up to 30 years.

In this paper we combined two methods: robust selection [1]; and desired-gain selection [2]. We investigated the best way to incorporate non-key traits into the breeding programme in a manner that dealt with the uncertainty of their economic importance. Desired-gain selection is a method that selects candidates based on the targeted genetic gains in the selected traits. Robust selection is a method that excludes candidates sensitive to the changes in economic weights.

We found that the expected genetic gains of traits in the proposed robust desired-gain index were all in a favourable direction. When the non-key traits were not measured and selected, the incidence of internal checking was always reduced but that of external resin bleeding and number of heartwood rings was increased. We concluded that robust desired gain index is an efficient way for selecting the key and non-key traits in radiata pine breeding programmes when long-term economic importance is uncertain.

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**KEYNOTE**

## GENOTYPE X ENVIRONMENT INTERACTION IN A LARGE MET ANALYSIS OF *PINUS RADIATA*

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The development of efficient plant breeding strategies requires a knowledge of the magnitude and structure of genotype by environment interaction. This information can be obtained from appropriate linear mixed model analyses of phenotypic data from multi-environment trials. The use of factor analytic models for genotype by environment effects is known to provide a reliable, parsimonious and holistic approach for obtaining estimates of genetic correlations between all pairs of trials. When breeding for outcrossing species the focus is on estimating additive genetic correlations and effects which is achieved by including pedigree information in the analysis. The use of factor analytic models in this setting may be computationally prohibitive when the number of environments is moderate to large. In this talk we present an approach that uses an approximate reduced animal model to overcome the computational issues associated with factor analytic models for additive genotype by environment effects. The approach is illustrated using two key traits from the RPBC *Pinus radiata* breeding program. Using this approach, we demonstrate the existence of substantial additive genotype by environment interaction for these traits and demonstrate how we have implemented this information in a decision support tool.

# IDENTIFYING SITE TYPES FOR PINUS RADIATA GENETIC EVALUATION IN AUSTRALIA

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In "rolling front" breeding programs there is often low genetic connection between sites planted more than a few years apart. For program wide genetic evaluation, there is probably enough connectedness between sites to estimate unbiased genetic values for different site-types, if the site-types are well defined and the correlation between the site-types can be estimated. Genotype by environment interaction (GxE) analysis methods which rely on (nearly) balanced treatment representation across sites are difficult to use when connection is low and may unnecessarily restrict the sampling of the different environments that the sites represent. Use of all possible sites with sufficient pair-wise connection ensures a broader sampling of environments and may allow better site-type definition. A database of site-site, trait-trait and age-age genetic correlations was created from single site and paired site analyses of over 60 trials. Additive correlations for DBH at ages up to 10 years were modelled with terms to account for age-age and site-type correlations. Error were weighted by the standard errors of the estimates, the number of estimates per site, and the last eigenvalue of the site-type correlation matrix to ensure positive definiteness, where needed. Site-types were identified by checking all possible cut off values of continuous variables (or groups of categorical variable levels) of long term environmental (mostly climatic) values which minimised the weighted error sum of squares of the model. Site-types based on additive correlations were identified from minimum temperature, and then rainfall within cool sites, and such a classification was better than the current a priori regional site-type grouping. Genetic values less confounded by poor groupings of sites should result.

# RELATIVE IMPACT OF MECHANICAL SITE PREPARATION AND STOCK IDEOTYPE ON SURVIVAL AND GROWTH OF SOUTHERN PINE HYBRIDS AGED 15 YEARS

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Changes to genetic material, site preparation equipment and expectations around water and soil management continue to drive changes in stock production and plant establishment for forest plantations internationally. In Queensland, Australia, this has particularly been the case for wet sites in the subtropical pine estate where changes to debris retention prescriptions substantially altered site preparation options at the same time as plant production moved from a traditional bare root seedling system to hybrid container cuttings.

During January – June 2000, a large field experiment, 23 ha in extent, was established on a typical wet site near Maryborough, Queensland, in order to determine the relative merits (in terms of survival and growth) of five mechanical site preparation techniques and six stock ideotypes (incorporating taxon and production system) on a site where the recent debris retention guidelines had been implemented. The site preparation treatments were imposed in a split-split plot design with the stock ideotypes using measurement plots of 10 rows x 16 trees.

Analysis of recent 15-year growth data (ANOVA) returned no significant differences between site preparation treatments or interactions between site preparation and stock ideotype. However differences between stock ideotypes were significant. F1 hydrid clones grown in containers outperformed all other stock ideotypes. Whilst site preparation treatment did not significantly influence volume at age 15 it was an important determinant of survival at age 1 and again age 5, and thus has implications for the economics of the plantation production system.

## INCREASED EFFICIENCY OF BREEDING VALUE PREDICTION OF SWEDISH NORWAY SPRUCE BREEDING PROGRAM BY SPATIAL ANALYSIS AND DISSECTING GENOTYPE BY ENVIRONMENT INTERACTIONS

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**Aims**: To increase efficiency of breeding value prediction of Swedish Norway spruce breeding program by using spatial analysis of multiple sites and by dissecting patterns of genotype by environment (GxE) interactions.

**Methods**: Factor analytical, reduced animal model, and spatial analysis were used to improve estimation of variance and covariance components, heritability, and accuracy of breeding value prediction. A total of 138 field trials of Swedish-wide with 457 variables were used in this meta-data analyses of Norway spruce.

**Results and Conclusion**: Large trials with big block variance tends to have more improvement from base to spatial model. Growth traits and pilodyn measurement of wood quality trait showed higher improvement in likelihood than form traits. Spatial model was more efficient than traditional method of post-blocking for growth traits. Heritabilities of diameter and height improved 26% and 34.2% using spatial model, respectively. However, no significant competition effects in single tree plots could be detected for height and diameter. Substantial additive GxE interactions for tree height were found across-Sweden and their patterns were analysed with geographical and climate parameter.

# GENOTYPE X SITE X SILVICULTURE INTERACTIONS IN RADIATA PINE: KNOWLEDGE, WORKING HYPOTHESES AND POINTERS FOR RESEARCH

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Favourable interactions between genotype, site and silviculture are desired for growing radiata pine, site and silviculture being components of environment. Our challenge is to characterise the interactions so they can be exploited to advantage. Four classes of interaction are involved: three first-order interactions between the different pairs of factors, and the second-order interaction involving all three factors. Also, these interactions belong to two types, involving: rank changes of genotypes (RC interaction), and differing levels of expression of genotypic differences (LoE interaction), among environments.

Tree breeders' immediate concern is with how interactions and main effects of environment affect genotype performance, yet the underlying interest for research and policy decisions lies in how environments and specific environmental factors generate interactions. Between the two main types of interaction, RC is seen as tending to be more important for breeding operations with LoE seen as tending to be more important for deployment decisions.

Existing knowledge and expectations of interactions are reviewed, mostly qualitatively, in terms of the comparative importance of RC and varying LoE. This is done for the first-order interactions, for different traits. Second-order interactions are still mainly conjectural. A framework is offered for progressively incorporating both input from others and new research findings.

In radiata pine, growth traits, especially stem diameter, have shown marked RC interaction with site. For tree-form traits, and especially disease resistance, LoE interaction can predominate. Among wood properties the picture is mixed and often unclear, some showing very little interaction, with others showing both RC and LoE interaction.

## SIMULATING REALIZED GAIN TRIALS BY INCORPORATING HERITABLE MORPHOLOGICAL TRAITS FROM DOUGLAS-FIR PROGENY TESTS INTO GROWTH MODELS

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Progeny tests worldwide have been designed to identify families that perform best on given site with respect to early growth, form, and wood quality. Random interspersion of seedlings from individual families in these progeny tests limits their utility for forecasting per-ha yield gain at rotation age. Regardless, genetic tree improvement has been represented in growth models by adjusting site indices or applying genetic gain multipliers to growth equations based on this information. Because seedlots deployed operationally include a small subset of the best families, forecasting stand dynamics, growth, and yield resulting from interactions of these untested family mixes is fraught with uncertainty. Realised gain trials have been established to help fill this information gap. The objective of our study was to simulate realised gain trials by identifying key mechanisms explaining differential performance of families and incorporating them into growth models. Growth equations were developed from a detailed study of a Douglas-fir progeny test [1] by identifying morphological traits that were highly heritable and strongly correlated with stem growth. Potential predictor categories included initial tree size, dry weight partitioning, foliage mass and area, growth efficiency, foliage attributes, branch characters, crown structure, crown size, stem form and wood quality. Growth models containing a few basic mechanisms allowed accelerated exploration of a wide variety of realised gain trials, provided early estimates of expected yield gains, and helped prioritise family mixes for field testing, all as part of a strategy to dynamically integrate genetic tree improvement with silviculture for yield improvement.

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# INFLUENCE OF SITE FACTORS ON GROWTH AND PHYSIOLOGY OF PINUS RADIATA GENOTYPES, AND THE IMPLICATIONS OF SILVICULTURE ON TREE BREEDING TRIALS

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Tree productivity at any given site is determined by fixed factors (e.g. soils), variable inputs (e.g. weather), the genotype planted, and silviculture applied. Forestry management practices have traditionally focused on how a species grows at a site, the realised yield which is the resultant of genetic material, inputs, and the growing conditions during that particular rotation. However, these practices do not evaluate the potential site yield, nor what can be done to close the gap between the potential and realised yield. Scion's Growing Confidence in Forestry's Future research program seeks to understand the productivity drivers for *Pinus radiata* (D.Don) and define this gap between realised and potential productivity and then explore how it can be closed. The process-based model CABALA was used to map the productivity gap for *P. radiata* throughout New Zealand and explore the implication of realised yield of different silvicultural practices and stocking.

The results show that the productivity gap typically ranged between 5%–30%. Crucially, the drivers of *P. radiata* productivity are complex and vary with location. Both experimental data, and modelling scenarios, showed that the physiological response to a productivity driver varies with genotype. The selection of the wrong genotype can lead to a poor site performance. Closing the productivity gap requires more than genetic improvement alone. Capture of the genotype by environment component of the gap can be facilitated through a mechanistic understanding of site productivity drivers leading to the selection of the right combination of the genotypes and targeted silviculture for maximum productivity.

# SILVICULTURAL VALUE OF PROGENY OF EUROPEAN BEECH PROVENANCES UNDER THE HABITAT CONDITIONS OF SOUTHERN POLAND

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In 2006 State Forests in Poland began the Program for Testing Forest Reproductive Material. The tests are conducted in order to select families and populations with the best adaptation, qualitative and quantitative properties. The first tested species was the European beech. After ten years of growing of the progenies of selected seed stands, we made an attempt to analyse the silvicultural value of European beech provenances under the habitat conditions of the Beskid Żywiecki Mountains. The experimental site belong to one out of four sites that were established in 2006 was established in randomized complete block design. The aim of this study was to analyse the adaptive trait (survival), growth parameters and morphological features progenies of 30 selected seed stands of European beech from southern Poland.

Research includes the following traits: survival rate; height growth; a diameter at breast height; a canopy shape; straightness of stem; apical dominance of leading sprout; and type of fork. The analysis of variance for a linear model was used to determine variability of examined traits between populations. Furthermore, correlation between qualitative and quantitative traits, assessment of silvicultural value and dependence of examined characteristics on the geographic coordinates were carried out.

## PROGRESS WITH THE ROLLING FRONT IN RADIATA PINE

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Breeding of radiata pine in Australia began in the 1950s with plus tree selection and the establishment of seed orchards by various companies and state and federal agencies. The STBA breeding cooperative, established in 1983 in South Australia, continues to expand, consolidating genetic resources on a national basis, providing cost efficiencies and enhancing the rate of genetic gain. The breeding program moved to a rolling front in 2000, where activities are done on an annual basis. Each year, parents are crossed, new progeny trials established, some existing trials measured, new data incorporated into genetic evaluations, and new parents selected on the basis of the updated genetic values. Prior to this, discrete generation breeding was the norm, with breeding, testing and selection largely completed before the next cycle began. Implementation of a rolling front has not been without its challenges. Data are generated on trees for a range of traits assessed at different ages in different years and at different locations. The degree of genetic linkage across previously independent programs also varied depending on the number of parents exchanged and/or the amount of collaborative testing done over time. Assessment and measurement protocols also changed over time and varied among breeders. Data imbalance and imperfect information is the norm. Nevertheless the rolling front has resulted in efficiencies and the authors will share some of their experiences of the past 15 years. Technical challenges and solutions for management of co-ancestry will be discussed, the operational benefits identified, and improvements in the rate of genetic gain and return on investment highlighted.

# SLASH × CARIBBEAN PINE HYBRID GENETIC IMPROVEMENT IN QUEENSLAND

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The slash x Caribbean pine hybrid (*Pinus elliottii* var. *elliottii* × *Pinus caribaea* var. *hondurensis*) continues to grow in importance in Queensland forestry, demonstrating broad adaptability across coastal South East and Central Queensland. Forward selection and mating are underway to form a synthetic hybrid breeding population, supported by simulation and empirical studies, with initial F3 hybrid families now in trials. Multivariate BLUP is applied to data from cloned and seedling progeny trials, and an economic breeding objective including wood quality traits is used to maximise economic gain from selection subject to constraints on relatedness. In order of importance, key traits are: MAI; wood stiffness; stem straightness; wind-firmness; crown defect traits; and spiral grain. Standing-tree acoustic velocity at a young age is strongly related to corewood stiffness and is routinely assessed for breeding value prediction. Genetic relationships between acoustic velocity and measures of stem slenderness and straightness assist in predicting breeding values for wood quality and can reduce the expense of direct assessment. A Category 4/5 cyclone in February 2015 provided extensive genetic information about the genetic architecture of wind-firmness traits, which is being applied to selection. Molecular genetic tools have been used for pedigree reconstruction and other uses are being explored.

# GENETIC EVALUATION OF SWEDISH SCOTS PINE BREEDING PROGRAM

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Genetic evaluation of the Swedish Scots Pine breeding program uses a multivariate BLUP (Best Linear Unbiased Prediction) approach which integrates all available data by using inter-site type, inter-trait and inter-age correlations. This avoids biases in predicted values due to artificial or natural selection (mortality) on correlated traits. A database of genetic parameters is used to model correlations separately from the BLUP evaluation. The strong provenance cline in northern Sweden is accounted for by dividing sites on latitude and site harshness, and defining provenances based on country, latitude and selection history. Provenance and provenance-progeny trial survival and height data are included to overcome the narrow provenance representation in routine progeny trials. The growth traits (survival, health, height and diameter) have different additive correlations on the harsh and mild sites and inter-latitude correlations have an auto-regressive decay pattern. Estimation of variance components for survival data on the liability scale remains a challenge. Spatial analysis and data adjustment is used to deal with high within site environmental heterogeneity and to pseudo-normalise the data. High between-site variance and heritability heterogeneity is accounted for by standardising the data by the additive genetic variance for each trait in each trial, and allowing a separate error variance. Correlations between four growth and six form and branching traits, and Lambeth model age:age correlations allow integration of all data. The largest runs predict genetic values for 124 traits for 535,000 genotypes from 41 provenances. The results show reasonable congruence with externally developed transfer functions. Selections for different site types are derived from appropriate provenances and trials from appropriate regions and these show increased gain compared to historic selections from univariate analysis of groups of trials.

## OPTIMISING SELECTION IN TREE BREEDING WITH CONSTRAINTS ON RELATEDNESS AND OPERATIONAL FLEXIBILITY

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Tree breeders often face the challenge of conserving genetic diversity, while at the same time maximising response to selection. When assembling advanced-generation breeding populations and seed orchards, the selection candidates will the best breeding values are quite often be closely related and selecting them without consideration of their relatedness will very quickly erode genetic diversity. Optimal selection will not completely avoid kinship, but rather maximize gain while imposing a constraint on average relatedness. While this principle has long been recognised by breeders through "rule-of-thumb" approaches to selection, mathematical approaches to truly optimise selection only first appeared in breeding in the late 1990s. We have advanced the use of mathematical programming to optimise selection using state-of-the-art approaches such as Mixed-Integer Quadratically Constrained Optimization (MIQCO), Semidefinite Programming (SDP) and Second-Order Cone Programming (SOCP). These more advanced techniques can satisfy constraints on relatedness while finding the truly optimum selected population under a variety of operational constraints. A breeder-friendly tool known as OPSEL (www.skogforsk.se\opsel) is now publically available and makes it possible for tree breeders to apply these techniques in a way that is simple and flexible. Various examples are presented and the future of mathematical programming to optimise selection in operational breeding is discussed.

# BREEDING TO IMPROVE FOLIAR OIL YIELDS IN EUCALYPTUS POLYBRACTEA

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Aims: *Eucalyptus polybractea* (blue mallee) is the primary source of 1,8-cineole–rich, medicinal grade eucalyptus oil in Australia. West Wyalong, NSW is a key production centre. The company involved is transitioning from oil production from coppiced natural stands to plantations. To further improve production efficiencies from this notoriously phenotypically variable species, this company commenced a modest tree breeding program in 2009. Estimated genetic parameters informing selection and breeding strategy for this program are given here.

Methods: Tree height, leafiness score, concentration of 1,8-cineole and total oil and percentage of 1,8-cineole were assessed in a six-year-old provenance-progeny trial comprising 41 families from six provenances Thirty-eight families were phenotypic selections (oil yield and cineole%) from natural stands surrounding West Wyalong, while three families were from a clonal seed orchard established in the 1990s.

Results: While provenance variation was not significant, variation among families was observed for all traits. Narrow-sense heritabilities ranged from low for growth traits to moderate-high for oil traits. Adverse genetic trait-trait correlations between growth and oil traits were not found. Predicted genetic gain in oil concentration from initial culling of all trees with below average oil yields to create a seedling seed orchard was estimated to be 22%.

Conclusions: Moderate-high heritability of oil traits and apparent lack of adverse genetic correlations between growth and oil-related traits auger well for the genetic improvement of this species. Further work on the genetic variation of coppice survival and optimising interaction between silviculture and genetics increase the scope for ongoing efficiencies.

# GENETIC CONTROL OF GROWTH STRAIN IN EUCALYPTUS BOSISTONANA: VERY EARLY SCREENING OF A LEFT-CENSORED TRAIT

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Recently, breeding programmes for commercial timber have expanded their scope, including wood quality at the same, or higher, priority as growth. In eucalypts, growth strain is a major barrier to milling for high quality products. Assessing growth strain has been too time consuming and expensive to incorporate into breeding programmes until recently. Chauhan and Entwistle [1] developed the splitting test, a fast and cheap method for evaluating growth strain at an early age (~ 2 years).

The splitting test involves taking a straight clear-wood section of stem and splitting it along the pith, resulting in movement of the two halves. Testing assumes peripheral contraction resulting in the two halves moving apart. In practice, closing occurs where the true opening is negative; however, the test's detection limit is zero opening, causing a zero inflated (censored) data set.

Data analysis has to account for the left-censoring, otherwise parameters are poorly estimated. Removing censored data provides an observation bias in the remaining dataset so is undesirable. Bayesian frameworks allow for the treatment of censored data via simulation of the unknown data points coming from a prior distribution. By sampling these unknown data points a significant number of times the true distribution can be estimated, even below the detection limit.

Bayesian simulations applied to left-censored growth strain measurements of *Eucalyptus bosistonana* were used to estimate the heritability of growth strain as part of a breeding trial focusing on improving solid wood quality.

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## APPLYING EXPERIMENTAL DESIGN IN SWEDISH FOREST TREE GENETICS TRIALS

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Use of the completely randomised design is the current experimental design strategy used by Skogforsk and was developed in response to operational restrictions preventing more complex designs being used. It has been suggested that more complex designs should be used to reduce residual error and increase the accuracy of genetic evaluation. Simulation of progeny field trials has been used to investigate the validity of this proposition. In order to obtain a set of parameters for simulating realistic trial data, a survey of actual Skogforsk progeny trials was undertaken. The survey revealed that medium to strong local trends were generally evident when analysing traits such as diameter, height, vitality and survival. Local trends are defined by local patches of within-site, non-random variation and are fitted statistically using an AR1 process. Fitting an AR1 process generally led to all design effect variances shrinking to zero. The simulation confirmed that spatial analysis is able to adequately correct for non-random within-site variation typical for Swedish progeny trial sites, and even for variation more extreme than that typically observed in Sweden. Use of different experimental designs had minimal effect on whether prediction of breeding values and estimation of (co)variances could be made more accurate and precise. It is concluded that the current strategy used by Skogforsk is reasonable in the sense that more complex designs may not enhance genetic gain when spatial and individual tree models are used. However, the simulation tested only within-site, non-random variation that conformed to a spatial process. More research is warranted that extends the range and types of variation that could be observed in world forestry.

# SCREENING FOR RED NEEDLE CAST RESISTANCE IN RADIATA PINE

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*Phytophthora* species are recognised as causal agents for numerous forest and tree-crop diseases. In New Zealand, the most widely planted forest tree species, *Pinus radiata* D.Don (radiata pine), is affected by red needle cast (RNC) caused by the aerial pathogen *Phytophthora pluvialis* [1]. Recent work in radiata pine has indicated a genetic component for resistance to RNC [2]. However, environmental factors can impact the assessment of disease, with the presence/absence or even severity of disease varying within and among sites. Furthermore, the geographical distribution of established genetic trials does not always align with areas of high disease pressure. These limitations impede the accuracy and level of extrapolation permissible in phenotyping disease responses, thus a more systematic and reliable system for quantifying resistance is required for resistance screening. We describe an in vitro assay system, using detached needles, that has been developed to differentiate resistance responses between genotypes in a controlled environment, and report on estimated heritabilities for this trait in a structured radiata pine population.

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# PRODUCING FORESTS FOR THE FUTURE CLIMATE

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Simulations suggest that CO2 concentrations of 500 ppm and a mean temperature increase of 1 oC will be reached by 2049 in New Zealand, associated with increased frequencies of drought and strong storm events [1]. While these changes will directly impact on the planted forest estate, they will also affect the numerous biotic and abiotic processes that underpin productive forestry in New Zealand. Given the potential significance of these indirect effects on forest productivity and resilience, a review was undertaken to better understand how climate driven changes in these supporting processes could affect forest performance, and the opportunities to utilise tree breeding programmes to maximise any beneficial effects while reducing negative consequences. Key potential benefits identified were the potential for warmer conditions to stimulate nutrient availability by enhancing rates of soil microbial activity, and greater access to soil resources due to the response of mycorrhizal symbionts to elevated CO2 concentrations [2]. Negative effects included more periodic reductions in resource availability with more droughts and greater topsoil erosion with more frequent storms, reducing nutrient pools. Insect pests and pathogenic microbes will be more active, as increased temperature supports survival through winter, a longer active period, and the potential for changes in the effective geographic ranges of insect and pathogen, while any increased stress on plants will increase their susceptibility to attack. Given these risks, we suggest that breeding programmes which focus on flexibility – sacrificing some growth for the maintenance of nutrient reserves and increased health – should be strongly considered.

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**NOTES**

**KEYNOTE**

## GENOMIC SELECTION IN TROPICAL EUCALYPTUS BREEDING: ADVANCES AND CHALLENGES

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Twenty-five years of forest tree genomics research have gone by. Despite important advances, Marker Assisted Selection (MAS) has not made it yet into operational tree breeding. Reasons include the limitations of early genomic technologies, the genetic heterogeneity of undomesticated trees but mainly the overoptimistic view of the architecture of complex traits. The advent of high throughput genotyping technologies coupled to Genomic Selection (GS) provide a new paradigm to integrate genomics into breeding. By fitting thousands of genome-wide markers concurrently in predictive models, GS captures most of the genome-wide effects that linkage and association mapping classically fail to detect. The publication of the *Eucalyptus* genome allowed us to develop a multi-species SNP genotyping chip that provides high density genotyping for all 'Big Ten' *Eucalyptus* species. Using this genotyping platform in a number of breeding programs in Brazil, we have shown that GS accuracies can match or surpass phenotypic selection for growth and wood quality traits. GS may significantly reduce the length of a breeding cycle by ultra-early selection of genomically multi-trait ranked seedlings, precluding progeny trials. Nevertheless, since predictive abilities are impacted by GxE and driven mainly by relatedness between 'training' and 'validation' populations, population-specific predictive models will be needed. GS brings a new perspective to the understanding of quantitative trait variation in forest trees and shall make genomics finally find its way into applied breeding. Strategic and logistics aspects for the adoption of GS are now the challenges faced to fully integrate this new breeding technology into routine tree improvement.

# FIRST EVALUATION OF GENOMIC SELECTION FOR RADIATA PINE

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The New Zealand Radiata Pine Breeding Company is testing genomic selection for the potential to rapidly increase the delivery of genetic gain. Recent deployment scenario analyses suggest potential increases in genetic gain could be 80% or higher. In this paper we describe the development of the genotyping assay and training populations, the first genomic estimated breeding values (GeBVs) and lessons learned so far.

The program chose an exome capture genotype-by-sequencing (GBS) [1] assay platform that has been developed in collaboration with Rapid Genomics LLC. The first training population being tested is based on two clonal trial series established across multiple sites. From this initial population, we expect the first GeBVs with associated accuracies for growth, wood density, stiffness and form traits will be available in 2016. We report progress in the estimation of GeBVs using methods developed specifically for alternative GBS datasets [2], [3] and compare accuracy with more commonly used methodologies [4]. We also report on pipelines used to filter and clean exome capture GBS datasets. Finally, we describe plans to expand the training population, assess new traits in radiata pine and strategies to apply genomic selection in radiata pine breeding and deployment.

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**KEYNOTE**

## PHENOTYPING PLANTS IN VARIABLE AND HETEROGENEOUS ENVIRONMENT - INTEGRATED APPROACHES TO MECHANISTIC, HIGH-THROUGHPUT AND FIELD PHENOTYPING

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Plant phenotyping develops rapidly into a bottleneck for progress in basic and applied research. Lack of adequate solutions for quantitative analysis of plant architecture and function as well as their interaction with the dynamic and heterogeneous environment hampers progress in basic sciences as well as in breeding-related research. In recent years significant interdisciplinary approaches have been started to overcome this "phenotyping bottleneck". Techniques were developed to quantify the dynamics and the heterogeneity of plant structure and function as well as of environmental cues. These mostly non-invasive technologies are developed and implemented into biological concepts that allow novel insights in the dynamic characteristics of plants above- as well as belowground. The technologies include high-resolution analysis for mechanistic understanding (like MRI and PET for structure, growth and activity of roots and shoots), the high-throughput approach for analysis of large numbers of genotypes and environmental conditions as well as field approaches, which are the reference to indicate the relevance. The talk will provide an overview on recent developments in technologies as well as conceptual approaches as the basis for a quantitative understanding of plant-environment-dynamics and its application for plant breeding and plant management. The talk will also present recent developments in infrastructure platforms that have been and will be established in Germany, in Europe and globally.

**KEYNOTE**

**THE USE OF LIDAR FOR PHENOTYPING**

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Remote sensing methods to characterise individual trees could allow cost-effective phenotyping of genetics trials and even whole forests [1]. We aimed to develop and evaluate novel methods for using airborne laser scanning (ALS) data to phenotype individual trees in terms of key traits: tree size, stem form, wood quality and disease resistance.

Discrete return ALS data were acquired over a radiata pine (*Pinus radiata*) genetics trial in the North Island of New Zealand. Conventional intensive ground-based phenotyping of trial trees included the following variables: tree height, DBH, straightness, malformation, branch cluster frequency, basic density, stiffness, and degree of Dothistroma infection.

Individual trees were detected in the ALS using recently developed methods [2]. A set of crown metrics were derived from the ALS for use in estimating tree traits. Variance components estimated by ASReml-R were used to determine narrow sense heritabilities, breeding values, and genetic gains for all traits. We then compared the ground-based and remote sensing phenotyping methodologies.

Heritabilities and genetic gains were consistently higher from on-ground measurements. Errors on estimates of genetic parameters and genetic gains from remote sensing were acceptable for operational use for the tree size traits: height, diameter and stem volume. Results support the use of ALS data for phenotyping tree size traits and indicate potential to quantify disease expression. Further research is suggested to quantify the cost effectiveness of using ALS for phenotyping, and to develop methods to phenotype stem form and wood quality traits, including the use of emerging forms of remote sensing.

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## LIDAR UPDATE: IMPROVEMENTS AND OPPORTUNITIES IN USING DATA-RICH POINT CLOUDS FOR FOREST MONITORING

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Conventional forest inventory and monitoring methods involve the installation of sufficient ground based sample plots, on a random or systematic basis, to estimate required stand variables within predefined error limits. This same method has been applied to forest breeding and productivity trials. These methods are labour intensive, costly, and limited in their wide scale application.

Airborne laser scanning (ALS) has been widely applied to improve inventory precision. ALS systems are active remote sensing systems that make use of light detection and ranging (LiDAR) technology to generate dense point clouds that represent three dimensional forest canopy structure. Recent changes in sensor technology is clearly evident from wide scale data capture over forested areas throughout 2015 in both New Zealand and Australia. These datasets have resulted in data rich point clouds where individual trees are far greater defined. This enhanced detail could open the possibility for development of novel LiDAR metrics that can more accurately characterise features such as branching patterns and the percentage of structural grade, that were not possible in the past. The richer level of detail available from newer sensors combined with the ability to store the full LiDAR waveform warrants a re-examination of how much could be gained through analyses using the full waveform and individual tree data, and looks to improve the way we monitor forest productivity for analysis in breeding productive and resilient forests.

**KEYNOTE**

**GENOMICS IN ACTION IN SHEEP FOR ACCELERATED GAINS**

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Use of molecular information in New Zealand sheep breeding became widespread 15 years ago with adoption of DNA "mix and match" parentage testing coupled with single gene tests including those affecting fertility and carcass muscling. An international effort to sequence the genome and create high density SNP chips suitable for genomic selection then commenced a decade ago and resulted in the introduction of genomic selection in New Zealand five years ago. This has expanded into a monthly across flock and breed national genomic evaluation for more than 20 traits in selected maternal breeds and crosses. A similar development programme is underway in terminal breeds and includes meat quality traits. Research is also underway into using genomics to select animals that emit less methane and this has renewed focus on key input traits such as feed efficiency. While a significant fraction of the industry uses this technology, the cost currently limits its use to elite ram lambs via two stage selection and also depends on imputation from lower density chips. Current research is now focussed on reducing the cost of genotyping via the use of genotyping by sequencing. The target outcome is parentage, breed prediction, co-ancestry and genomic selection for the equivalent of the current cost of DNA parentage so that it will becomes a routine measurement for all animals in ram breeding flocks.

## ADVANCED GENERATION TREE BREEDING: CHALENGES AND OPPORTUNITES

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Many tree breeding programs worldwide have entered into second and third generation (cycle) with radiata and loblolly pine in the fourth generation (cycle). There are many challenges to further advance these programs in a scientifically optimal way. Managing inbreeding depression and genetic gain, and coping with adverse genetic correlation between growth and wood quality traits are among the two major scientific challenges.

We have conducted several empirical and simulation studies to develop optimal breeding strategy to manage these challenges. Empirical studies include: (1) a long-term inbreeding experiment; and (2) a quantitative genetic survey of genetic correlation between growth and wood quality traits in radiata, Scots and lodgepole pines, and Norway spruce. Genomic allelic models were established to examine optimal breeding methods to manage inbreeding depression and genetic gain, and to cope with adverse genetic correlation.

Results indicate that: (1) medium to high adverse genetic correlation from -0.3 to -0.7 were observed among pines and spruce; (2) a single breeding population was more favorable than multiple breeding populations in coping with adverse genetic correlation; (3) inbreeding-crossbreeding was only effective in short-term; (4) single breeding population of mass selection and nucleus breeding strategies were favorable for long-term tree breeding in balancing inbreeding depression and genetic gain; and (5) genomic information from GWAS in pine and spruce are enhancing our understanding of genetic architecture of quantitative traits and our study of optimal breeding strategy.

# TOWARDS GENOMIC SELECTION FOR WOOD PROPERTIES IN EUCALYPTUS NITENS

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The aim of this study was to investigate possibilities to improve wood properties for solid wood products in the New Zealand breeding programme of *Eucalyptus nitens* using both phenotypic and genotypic information. A secondary objective was to make forward selection and establish a seed-orchard specifically for solid wood production.

Previous studies showed moderate heritability estimates for growth stress, shrinkage and density indicating that considerable genetic gains might be achieved through genetic improvement of these traits. We assessed 750 trees from a third generation open-pollinated progeny trial in the South Island of New Zealand for growth stress, wood shrinkage, collapse measurement, internal checking and wood density at age seven. Leaf samples for DNA extraction were also collected at the same time. The progeny trial, comprising 3600 trees was phenotyped for growth and form at age six. Genetic parameters and breeding values were estimated using spatial individual tree models using models appropriate for open-pollinated progeny with ASReml –R (Butler et al. 2009). Individual trees phenotyped for wood properties were also genotyped using the EuCHIP60K (Silva Junior et al. 2015). The marker based relationship matrix was constructed and used to estimate genomic breeding values (GEBVs) with individual tree mixed model implemented in the ASReml-R package.

Marker data from the 60k Euc SNPchip was used to compare the accuracy of pedigree-based estimations of breeding values and genomic breeding values. We discuss the implications for the E. nitens breeding programme and the use of marker-based technologies for use in similar discrete open-pollinated breeding populations.

**KEYNOTE**

## GENE DISCOVERY THROUGH GENOME-WIDE ASSOCIATION STUDIES

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Genome-wide association studies (GWAS) are designed to statistically link phenotypes to genes and ultimately genes to functions. Stated in a more quixotic manner, GWAS connects "sequence to consequence". There are multiple phases in this process, each with their own set of requirements and approaches, which then each vary based on the biology [i.e., life history, genome complexity, evolutionary history, etc.] of the candidate organism. The three main phases in the "sequence to consequence" paradigm are: Discovery, Validation and Deployment. During Discovery decisions regarding: 1) selection of a test population/panel; 2) genotyping platform/technology; 3) targeted phenotypes; and 4) association methods/tactics have to be made based on known or assumed biology of the candidate organism. The potential test population/panel can vary in its inherited genetic structure, degree of relatedness and reproductive history. The choice of resequencing, genotype-by-sequencing or chip-based genotyping each create advantages and disadvantages in the implementation of GWAS approaches and interpretation. The initial identification of the targeted, economically important phenotypes also affects the final interpretation and deployment of the GWAS results. High-throughput versus high-precession versus high-accuracy measurements generate tangible tradeoffs in the discovery of initial GWAS associations. Finally, during Discovery phase decisions of alternate association approaches, adjustments for kinship, adjustments for population structure and methods for controlling type II error impact the interpretation of GWAS results. After Discovery rational decisions on Validation approaches need to be made, including the choice of independent population/panel versus transient assays, heterologous transgenics and/or stable transgenics. If Validation is approached through independent GWAS testing in an alternate population/panel then the validation population's genetic structure, reproductive biology and evolutionary history need to be considered. For some phenotypes, Validation can occur through transient expression assays, but this is dependent on the phenotype and availability of informative reporter genes. Heterologous and/or stable transgenics can be used to Validate GWAS results, though these are limited to analogous phenotypes and known [or unknown] epistatic and pleiotropic effects in the case of heterologous transgenes, and availability of reliable transformation systems in the candidate organism and phenotypic ontology in the case of stable transgenes. As validated results are obtained, translational Deployment can occur via propagation of stable transgenics in single or stacked gene lines and/or via marker-based breeding integrated into traditional progeny testing. Examples of each of the above phases and "sequence to consequence" outcomes will be presented based on results from a six-year-old *Populus trichocarpa* range-wide, multi-year, multiple test site GWAS analyses.

## INTEGRATED PHENOTYPING: BRINGING TOGETHER QUANTITATIVE DATA FROM ACROSS DISCIPLINES FOR MORE INFORMED PLANT BREEDING

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*Phytophthora* pathogens have the potential to devastate entire industries with new incursions through increasing globalisation. In New Zealand, our conservation, forestry and horticultural tree estates are all impacted by *Phytophthora* species. Of particular note are *Phytophthora pluvialis*, causal agent of red needle cast in *Pinus radiata* (radiata pine), *Phytophthora agathadicida* which is causing severe disease in a native tree species, *Agathis australis* (kauri), and *Phytophthora cactorum* which has long caused collar rot in *Malus domestica* (apple). Quantitative methods of assessing disease impacts usually rely on the presence of the disease in established field trials. However, as disease expression is the result of host, pathogen and environmental factors field based phenotypic data is often confounded which impeedes our ability to accurately phenotype disease responses. Furthermore, the geographical distribution of established trials does not always reflect that of the disease.

To get around these limitations, we are applying a modern 'omics' based systems biology approach to phenotype trees. This is enabling quantitative assessments at the genetic, metabolic and physiological levels to be integrated with traditional pathology, histological and field based disease quantification. Bringing each of these disciplines together is providing a powerful platform for better understanding host-pathogen interactions, plant resistance and the mechanisms underlying resistance observed in the field. The multidisciplinary nature of our approach has been a key challenge but it is enabling us to develop a robust phenomic platform for identifying broad resistance to an ever increasing number of *Phytophthora* biosecurity threats. Our integration model and phenomic platform will be presented and discussed in reference to progress in identifying resistance to *Phytophthora* pathogens in radiata pine, kauri and apple.

## SUCCESSFUL CLONAL FORESTRY WITH RADIATA PINE IN NEW ZEALAND

**Michael Carson**, Susan Carson

*Forest Genetics Ltd, Rotorua, New Zealand*

We manage one of the few successful clonal programmes with pines, built on 60 years of R&D in breeding and propagation. It requires clear strategic vision, rigorous prioritisation of goals, and attention to risk and cost management. Since clones represent a new paradigm, we needed to confront new technical challenges, and some entrenched views. Successful marketing of clonal treestocks requires an intimate understanding of client objectives, site and silvicultural interactions, and the ability to demonstrate and validate gains on the client's estate. Closer integration with clients provides additional opportunities for realising gain, through:

- tracking clonal performance into plantations
- matching genotypes to site conditions and economic objectives, and
- responding much more rapidly to feedback, compared to seed-based programmes.

Trial designs, assessment and analysis methods have been refined to maximise cost-efficiency without sacrificing effectiveness of selection. Development of 'breeder-friendly' cloud-based software (Gemview) assists decision-making and accelerates the testing and selection process. Our focus on developing small numbers of elite clones for deployment places greater emphasis on the importance of selecting stable high performers and multi-trait 'correlation-breakers' for managing both inter-trait correlations and G X E.

Propagation methods have been extended to improve yields and plant quality for field-proven genotypes, providing cost-efficient commercial production that enables business growth, with small staff, and low capital requirements.

New applications of genomic selection, may be ineffective unless designed in conjunction with clonal deployment processes. Cloning of the breeding population offers new options for realising genetic gains and represents the next stage of improvement of radiata pine.

# GENETIC DIVERSITY, CONSERVATION AND BREEDING OF *EUCALYPTUS BENTHAMII*

**David Bush**[1], Nigel England[1], Linda Broadhurst[2]

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**Aims:** *Eucalyptus benthamii* is amongst the most cold tolerant of fast-growing, subtropical eucalypts. It is generally planted in warm parts of the world that are subject to sudden low temperature events including southern China, parts of South America and southern USA. The species is listed as threatened in the wild, with very few trees remaining in some populations. Though genetic improvement programs are underway in various countries, the genetic base of all programs is likely narrow. The challenge of broadening the genetic base may involve accessing highly vulnerable and fragmented populations and/or introgression of genes from putatively close relatives such as *E. dorrigoensis*.

**Methods:**
1. Dispatch records from the Australian Tree Seed Centre were analysed to ascertain the likely diversity of the species exported outside of Australia.
2. Grafting of isolated trees in relict subpopulations of *E. benthamii* has commenced to form a clonal seed orchard (CSO)
3. DNA from wild trees, field trials and the grafted trees of *E. benthamii* and E. dorrigoensis was analysed to assess the diversity within and between populations and the two species (formerly considered to be subspecies of *E. benthamii*).

**Results and Conclusions:** Analysis of historical records indicates that the global breeding base of *E. benthamii* is very narrow. Grafting of isolated, wild trees into a CSO is a slow but successful process that holds some promise. Analysis of DNA from *E. benthamii* and *E. dorrigoensis* is helping to reveal the relationship between the two species and inform options for breeding and conservation population management.

## TRANSLATIONAL RESEARCH ACTIVITIES IN THE POST-GENOMIC ERA: SPRUCE AS A CASE STUDY

**Nathalie Isabel[1]**, Julie Godbout[1], Claude Bomal[1], Patrick Lenz[1], Jean Beaulieu[1,3], John Mackay[2], Jean Bousquet[3]

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Natural forests dominate the Canadian landscape almost everywhere. They yield most of the wood used by the forest industry and provide numerous ecosystem services. Changing environments, pressure to conserve forest lands, and society's demand for sustainable forest management call for new approaches and practices to increase forest productivity and adaptability.

At the beginning of new millennium, genomic science was seen as a means of developing tools to characterise and help preserve the natural genetic diversity of trees, and of more rapidly developing new varieties for reforestation. This vision became particularly compelling in the context of environmental change and the adoption of better sustainable forest management practices. Over the last decade, we have witnessed the development of extensive genomic resources (including the know-how) for many tree species. In some cases (growth or wood quality improvement, climate change adaptation, forest certification, etc.), these newly available data are being used to create tools for the translation of results to be used by end-users from across Canada. Here, we will present different examples of applications (a traceability method, genomic selection, etc.) that may or will spring up from large-scale genomic projects conducted using spruce, a species of economic importance in Canada, as a case study.

## MOLECULAR GENETIC MARKERS TO ACHIEVE PRODUCTIVE AND RESILIENT FORESTS

**Valerie Hipkins**

*National Forest Genetic Electrophoresis Laboratory, United States Forest Service, Placerville, CA, USA*

The United States Forest Service has been committed to using molecular genetic markers to achieve productive and resilient forests for over a quarter of a century. The National Forest Genetics Laboratory (NFGEL) was established in 1988 with the purpose of providing genetic testing and information for integrated solutions to on-the-ground problems faced by natural resource managers and policy makers. NFGEL uses state-of-the-art technology to address genetic conservation and management of all plant species using various laboratory techniques including advanced DNA technologies. We use genetic markers to investigate genetic diversity and structure for a variety of purposes, from questions of individualization (addressing timber theft, and providing information to support breeding programs) to assessing differences among populations and species (maintaining species and genetic diversity in reforestation programs, and identifying genetic variation in climatic tolerances of restoration species). Because genetic and genomic tools are constantly changing and evolving, we use the technique that is the most appropriate to resolve the genetic question asked, whether that is allozymes, microsatellites, or 'next-generation' sequencing platforms.

# Posters

**Poster Board 1**

## THE NEW ZEALAND CYPRESS BREEDING PROGRAM

**Charlie Low[1]**, Heidi Dungey[1], John Russell[2], Mark Miller[1]

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The New Zealand cypress breeding program started in 1982 with the selection of *Cupressus macrocarpa* and *C. lusitanica* to form separate breeding populations. These two species grow faster than other cypress species in New Zealand, but their timber is not as durable as that of *Chamaecyparis nootkatensis* and they are troubled by cypress canker. The breeding populations are now in their second generation and seed orchards have been developed.

Cypresses form hybrids between species more readily than most forest trees and some accidental hybrids have shown promise. Recent advances in pollen storage techniques made by scientists in British Columbia have been used to make new hybrids to introduce better timber durability and resistance to cypress canker.

Selected clones have been multiplied by grafting and crossing archives have been planted. The first hybrid seed was produced in 2007 and early results show heterosis with the hybrids growing as fast as the most vigorous parent. Some crosses involving *C. guadalupensis* for improved resistance to cypress canker produced as much viable seed as within species crossing. However, crosses between *Chamaecyparis nootkatensis* and trees from the *Cupressus* genus produced few viable seeds. Vegetative multiplication by cuttings may be crucial to producing commercial quantities of cypress hybrid plants and trials of block plantings of cloned cypress hybrids were planted out in 2014.

Hybrid cypresses therefore appear to be a better planting option than pure species and will continue to be pursued to provide healthier plants that perform more consistently across a wider range of sites.

**Poster Board 2**

## GENETIC VARIATION IN BARK STRIPPING OF PINUS RADIATA

**Julianne O'Reilly-Wapstra[1]**, Heidi Dungey[2], Brad Potts[1], Alison Miller[1], Hugh Fitzgerald[1], Don Aurik[3], Stephen Elms[4], Paul Jefferson[5] and Noel Davies[6]

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The conifer plantation estate forms a major component of Australia's forestry industry, with more than a million hectares of *Pinus radiata* trees. Bark stripping by mammalian herbivores in *Pinus spp*. plantations is a major threat to productivity and a large economic burden for forestry companies. The industry needs a cost-effective, socially acceptable and environmentally sustainable alternative. One such approach is to use the plant's natural, genetic-based variation in traits (e.g. defensive chemicals in the phloem and bark) to select genotypes that are more resistant to attack and deter herbivores from targeting trees. Here we looked at multiple field trials across multiple sites containing a wide genetic complement of *P. radiata* deployment stock (open-pollinated or full-sib families). Trials were assessed for animal damage and tree characteristics. We found evidence of genetic-based field variation in bark stripping by mammals on several sites with one site exhibiting a range of 11- 53% variation in bark damage between genotypes. Some variation was also explained by tree size where smaller trees received more damage than larger ones, and trees with smooth bark received more damage than those with rough bark. Future work will further elucidate genetic-based variation in the mechanisms driving variation in damage.

**Poster Board 3**

## GENETIC VARIATION IN NEEDLE δ13C IS POSITIVELY ASSOCIATED WITH RADIATA PINE GROWTH UNDER DRY CONDITIONS

**Jianming Xue[1]**, Heidi Dungey[2], Peter Clinton[1], Sylvie Niollet[3], Yong Li[2]

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The potential of using carbon isotopic composition (δ13C) (a surrogate index of water use efficiency, WUE) as selection criteria for drought tolerance has not been rigorously tested in radiata pine species. This study was to investigate the genetic variation in needle δ13C and determine genetic correlations between needle δ13C and growth traits. This study was mainly based on a Radiata Pine Breeding Company breeding trial established at a dry site in Christchurch but validated using other three trials across New Zealand. The RPBC trial is a sets-in-replicates design, with 30 replications of 122 open-pollinated (OP) families from the New Zealand radiata pine breeding programme. The mature current-year needles from 20 individual trees of 122 OP families were sampled for δ13C analysis, and tree height and DBH were also measured for 2440 individual trees at age 8 years.

At age 8 years, the narrow-sense heritability was low for tree height (0.12 ± 0.03) and DBH (0.20 ± 0.04), but moderate for needle δ13C (0.40 ± 0.08). This indicates that needle δ13C was a heritable trait for radiata pine. The genetic correlations between needle δ13C and tree height (rg = 0.22 ± 0.17)) or DBH (rg = 0.43 ± 0.13) were moderate and positive. This indicates the genotypic differences of needle δ13C among individual trees in this breeding population were mainly determined by differences in photosynthetic capacity. Our results highlight the potential use of needle δ13C as a useful trait for indirectly selecting radiata pine genotypes with improved WUE and growth performance under dry conditions.

**Poster Board 4**

## GENETIC PARAMETERS ESTIMATION AND BREEDING VALUES PREDICTION FOR GROWTH AND WOOD QUALITY TRAITS IN THE FRENCH MARITIME PINE BREEDING PROGRAMME.

**Gregory Dutkowski[2]**, Laurent Bouffier[1], Annie Raffin[1]

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Maritime pine (*Pinus pinaster Ait*.) represents one million hectares of cultivated forest in southwestern France. A breeding programme has been implemented since the early 1960s following a recurrent scheme from a base population selected in unimproved plantations. Today, it has reached its third generation with genetics gains of 30% for the improved growth and stem straightness varieties. The aim of this study was to carry out a joint-analysis of 44 main progeny trials (i.e. more than 450,000 trees) with advanced statistical methods in order to accurately estimate genetic parameters and predict breeding values. Twelve traits related to growth, stem straightness, branching, wind damage and wood density in up to four age classes were considered, making a total of 33 selection criteria for the breeding value prediction.

Genetic parameters were first calculated within each trial after adjustment for spatial heterogeneity (spatial autocorrelation models) and tabulated into a database. This genetic parameter database allowed estimation of inter-traits and age - age genetic correlations at the population level. Then, multivariate analyses with derived fixed population genetic correlations were carried out on adjusted data in order to estimate additive variances, residual variances and residual correlations for each trait in each trial. Finally, these parameters were used to run the BLUP solver TREEPLAN, and predict breeding values and their associated accuracies.

This study represents the first wide scale use of spatial analyses in Maritime pine trials and first joint multivariate analysis of all trials. The large data set analysed here allows the estimation of accurate genetic parameters for various traits related to wood production. The genetic evaluation with the TREEPLAN system demonstrates the possibility if integration of all available information from the successive breeding generations to increase the accuracy of breeding values and maximise gain from selection.

**Poster Board 5**

## PRODUCTIVITY OF POPLAR CULTIVARS (POPULUS SPP.) SELECTED IN DIFFERENT COUNTRIES IN SHORT ROTATION FORESTRY IN POLAND

**Marzena Niemczyk**, Tomasz Wojda

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The use of renewable energy sources such as biomass is an important aspect of European Union policy. In light of the restriction concerning the use of the "full-value wood" from forests for energy purposes, short-rotation forestry may become an alternative source of woody biomass. In this context, the most promising species in Polish conditions is poplar (*Populus spp.*), the productivity of which depends on various aspects such as: plant spacing, cutting cycles, fertilization and cultivar characteristics. The aim of this study was to analyse the productivity of 10 poplar clones: 4 from Italy: 'AF2', 'AF6', 'AF8', 'Monviso'='MON', 4 introduced from the Dutch breeding program: 'Degrosso', 'Albelo', 'Polargo', 'Koster', and two poplar clones 'Hybrida 275' and 'Fritzi Pauley', recommended by Polish Forest Research Institute for use in long- and medium rotation forestry.

An experiment was set up in the north-eastern part of Poland. Survival, tree stocking, and biomass yield were compared. Productivity of clones was examined in a five-year cutting cycle. The highest yield of 7.8 Dt ha-1 yr-1 was achieved by the clone *Populus 'Hybrida* 275'. In comparison to that, the biomass yield of the worst clone 'AF-8' amounted to 2 t ha-1 yr-1. Some other Italian clones, such as 'AF-6' and 'MON' could not adapt to the local climatic conditions at all, even though they are characterized by high productivity in their homeland. Overall, the results indicate the need to test clones in the local climatic condition, before they will be used in commercial scale.

**Poster Board 6**

## WESTERN HEMLOCK REALISED GAIN TRIALS: RESULTS ARE GOOD – WHY DOES PLANTING CONTINUE TO DECLINE IN BRITISH COLUMBIA?

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Western hemlock is the most important commercial timber species in coastal British Columbia (BC). It is the largest volume producer (close to 4 million cu m per year) and is second only to red cedar in value to the provincial treasury for coastal logging – with close to $50 million a year revenues. Natural regeneration of hemlock stands can at times be prolific, and in recent years there has been a steady decline in seedlings planted from over 9 million hemlock seedlings planted annually to only a million – a nearly 10 scale reduction. This is despite evidence that high gains can be delivered from current seed orchard seed and the faster green-up and more even-spaced stocking associated with artificial regeneration more than compensates for the additional costs of planting stock.

The decline in hemlock planting in BC is in sharp contrast to increased planting in the US Pacific Northwest i.e. Washington (WA) and Oregon (OR) –going from under 4 million to over 8.5 million within the past 5 years and largely driven by increasing incidence of Swiss Needle Cast disease on coastal Douglas-fir. Interest in hemlock breeding in OR and WA has been sufficiently high to support a third cycle breeding program.
Hemlock tree improvement began in the 1970's, with the establishment of OP trials. In 1991, an international cooperative tree improvement program (the Western Hemlock Tree Improvement Cooperative, Hemtic) was established with private and governmental organisations from across the coastal regions of BC, Washington, and Oregon. Co-operators included the BC Forest Service (BCFS) of the Ministry of Forests (MoF), the US Bureau of Land Management (BLM), the Oregon Department of Forestry (ODF), the Quinault Indian Nation (QIN), and 9 forest industry members. The Hemtic program set up F-1 crosses of selections from five first-generation testing programs. Hemlock tree improvement has been summarized for the US in [1]; and the value for a potentially valuable pulp and paper species in [2].

At the same time realised gain trials were established in BC that could compare "woods run" – wild seed to "elite crosses" from the OP trials – equivalent to new seed orchards that were being set up. 20 year results, approximately half-rotation, show 65% volume gain of elite crosses ("A" class seed) to "woods run". Even more impressive are the potential gains of a plantation program compared to natural regeneration. – estimates are many hundreds of % of increased yield. New area plot trials to thoroughly investigate even higher levels of genetic gain and compare to natural regeneration are being planned in BC and implemented in OR and WA.

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**Poster Board 7**

## FOREST TREE BREEDING AND MAJOR ACHIEVEMENT IN KOREA

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Korea forests were highly rich, productive and had good formed, big trees before Japanese colonial regime and Korean War. During the Japanese occupation, a large part of forest was destroyed by over-cutting indiscriminately. In addition, the Korean War broke out and lasted for three years. After that, social disorder was so serious that everyone went to the forests and cut the trees without any permit from the authority. Thus, almost all mountains except remote areas were denuded so severely that the mountains looked red. Korea needed urgently a good tree species for the devastated land. Early 1990s, Korea met a great scholar and research advisor whose name was Dr. Sin Kyu Hyun. It is very hard to talk about tree breeding history without mentioning him in Korea. In fact, the late Dr. Hyun was a founder of tree breeding work in Korea, establishing the Forest Genetics Research Institute (now Department of Forest Genetic Resources) in Suwon in 1956. First, the Institute has done much of hybrid breeding such as hybrid pines and hybrid poplars. *Pinus regitaed*a, hybrid between *P. rigida* and *P. taeda*, shows better cold tolerance and superior timber quality compared to the mother and also superior straightness as like as the father tree. At age of 20, the hybrid pine showed 12.5 m height and 20 cm DBH, while the mother tree showed 8.8 m height and 15.5 cm DBH. This work was cited on cover page of FAO report and context of US congressional report as Wonder pine. Korea needed also the poplar that was suitable for slope and mountain area. After much hybridization among poplar varieties, *Populus alba x P. glandulosa* was found to be suitable one at dry and mountainous areas. It showed 40 cm DBH and straight stems at age of 20. Recently this hybrid poplar used to research on phytoremediation, riparian buffer forest (SRC) and biotechnology (genomics). Second, we have been doing introduction breeding. In the first phase, a total of 376 species was introduced from 30 foreign countries and tested adaptation ability at 388 different sites. After that, *Pinus rigida, Robinia pseudoacacia, Alnus inokumai* and *Larix leptplepis* were selected, but the adaptation data were destroyed during the Korean War. In the second phase, 415 species from 38 countries were introduced again and 8 species including *Liriodendron tulipifera, Quercus rubra* and *Prunus serotina* were selected and released base on the adaptation test. In the third phase (1996-present), continuous adaptation test and selection have been doing. Third, plus trees have been selected from wild forests since 1959 and used for establishing seed orchards. So far, a total of 2,724 plus trees from 29 tree species (1,582 plus trees from 11 conifers including red pine and 1,142 plus trees from 18 deciduous species including oaks) have been selected. Since 1968, seed orchards have been established with the selected plus trees. Up to now, we have established 620.5 ha of seed orchards for 15 conifer species. As there has been an increasing demand for deciduous trees, we need to secure seed sources for these species. Deciduous stands occupy about 1.7 million ha (26%) of 6.5 million ha forests in Korea. More conifer stands are being converted to deciduous forests. To meet the social demand, we have established 160.5 ha seed orchards with 47 deciduous species. The seed orchards began to produce genetically improved seeds in 1976 about 10 years after their establishment. As the seed orchards mature, they are expected to produce enough improved seeds of many conifers including red pine, black pine and hybrid pine. During the over last 38 years, the seed orchards have produced genetically improved seeds of around 252.4 tons, which are sufficient for conifer reforestation but lack for broadleaves in our forest land. Lastly, special purpose tree breeding program has been doing and developed many new varieties of chestnut, walnut, native kiwi, national flower, etc.

**Poster Board 8**

## THE INHERITANCE OF THE ANNUAL PATTERN OF HEIGHT GROWTH IN CRYPTOMERIA JAPONICA

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The in-depth understanding of phenotypes and appropriate determination of selection trait are important for the improvement of efficiency of the early selection in forest tree breeding. To pursue efficient early selection for growth performance, we examined the clonal differences in seasonal growth pattern in juvenile stage, and its correlation with the clonal growth performance in adult stage in *Cryptomeria japonica*, one of the major forestry species in Japan. We measured height growth of totally about 300 juvenile ramets (1 to 3 years after planting) of 12 clones with one to two weeks interval for three years. Maximum diurnal growths were observed at the late May, with relatively higher heritabilities. The clonal growth in mature stage showed the highest correlation with the early June diurnal growth of juvenile stage. We discuss the efficiency of the decomposition of height growth into periodic growths in a year for the early selection of height growth in *C. japonica*.

**Poster Board 9**

## GENOME-WIDE ASSOCIATION STUDY AND GENOMIC PREDICTION FOR CRYPTOMERIA JAPONICA PLUS TREES

**Yuichiro Hiraoka[1]**, Tomonori Hirao[2], Kentaro Mishima[1], Miho Tamura[3], Eitaro Fukatsu[4], Taiichi Iki[5], Miyoko Tsubomura[1], Mine Nose[1], Mineko Ohira[1], So Hanaoka[1], Makoto Takahashi[1], Hiroshi Hoshi[1], Atsushi Watanabe[3]

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*Cryptomeria japonica* is one of the most important species for forestry in Japan. With the ultimate aim of molecular breeding for *C. japonica*, we performed a genome-wide association study (GWAS) for identifying specific single nucleotide polymorphisms (SNPs) for various traits (growth, wood quality, and pollen productivity) based on the first-generation plus tree clones of the species. Additionally, we verified the capabilities of genomic prediction for each trait. SNP discovery was carried out based on >30,000 isotigs, which were integrated sequences of the expressed sequence tags (ESTs) obtained from various organs. Axiom 70K SNP array was designed and was used for genotyping a panel population consisted of 514 clones. Phenotype data of the genotyped clones were obtained from clonal tests. We detected >33,000 SNPs that were polymorphic and informative for the following analyses. As a result of GWAS for each trait, a number of SNPs were significant and were scattered all over the genome. The accuracies of genomic prediction were different among traits and/or prediction models. The prediction of pollen productivity showed higher accuracy than that of the other traits. We discussed the possibility and future subject of molecular breeding for *C. japonica*.

**Poster Board 10**

## HYBRID ASPEN CLONES OF SOUTHERN ORIGIN ARE MORE PRODUCTIVE THAN CURRENTLY USED NORTHERN CLONES IN HEMIBOREAL CONDITIONS AFFECTED BY CLIMATE CHANGE

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Short-rotation forestry (SRF) with hybrid aspen (*Populus tremula L. × P. tremuloides Michx*.) is a new silvicultural concept in Northern Europe. In hemiboreal Estonia the first hybrid aspen plantations for the production of pulpwood were established in 1999 on abandoned agricultural lands with clonal plants produced from crossings having one or both parents of northern origin. However, considering climate change and elongated growing season, there is lack of knowledge about suitability of hybrid aspen clones selected from crossings of parents from southern regions.

Comparison trial of 22 hybrid aspen clones with parental material representing different latitudes was established to evaluate their growth, biomass characteristics and suitability to Estonian climate conditions. Data were collected in six consecutive years. Biomass model trees were analysed destructively after the 5th growing year to test clonal effect on biomass and wood characteristics. Phenological surveys were carried out during the 3rd and 6th growth year.

Clonal effect was significant on all studied characteristics (height, stem diameter, above-ground biomass, wood density, share of stembark and branches). The length of the growing season was in a strong positive correlation with current annual growth increment. Fastest growing clones were of southern origin, while the poorest were currently commercially used clones of northern origin.

Under the changing climate and elongating growing season in higher latitudes, hybrid aspen clones of more southerly origin that are adapted to longer growing season could be successfully grown in the hemiboreal region where they are more productive than currently used clones of northern origin.

**Poster Board 11**

## PARTICIPATORY EVALUATION OF CALYCOPHYLLUM SPRUCEANUM BENTH. PROVENANCES IN AGUAYTIA BASIN, UCAYALI REGION, PERU

**Leoncio Ugarte-Guerra[1,2]**

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The objective was to evaluate the effect of provenance in the productivity of 12 *Calycophyllum spruceanum* Benth. in small holder forest plantations (replications) of 48 months old in a total area of 5.72 has. Seeds was collected from 11 provenance, seedling were produce and distributed into 3 blocks in the Aguaytía River, located in the Ucayali Region. Researcher and farmers work together for maintenance and evaluation. Direct measurements were used to evaluate state of the plantations and the relationship with soil and climate factors in order to identify potential places for the establishment of successful plantations. Site Index (SI), was defined as the average of the total height in meters of the higher quintile. Site Index was highly correlated to basal area, and total bark volume.

Noteworthy differences were found in the plots evaluated. This allows the generation of a classification based in the Site Index. This classification is consistent with the blocks and the altitude throughout the basin in most of the cases. Growth average in the best replication resulted in a volumetric increment of up to 13.349 $m^3$ $ha^{-1}year^{-1}$. Local provenance shows the highest increase of volume.

**Poster Board 12**

## QUANTITATIVE GENETIC SURVEY OF LODGEPOLE PINE

**Haleh Hayatgheibi**

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Lodgepole pine (*Pinus contorta ssp. latifolia*) was introduced from western Canada to Sweden during 1970s for new plantation establishment to supplement local species due to its faster growth rate (35% faster than local Scots pine). So far, 600 000 hectares of forest has been established using lodgepole pine. However, high mortality, lack of wind-stability and low snow pressure tolerance due to low wood density is a challenge for the expansion of plantation.

In order to enhance the quality of commercial plantation of lodgepole pine, we started a quantitative genetic project to: (1) estimate genetic parameters of growth (height and diameter) and wood quality traits (modulus of elasticity (MOE), microfiber angle (MFA), wood density, spiral grain angle and fiber, and cell wall traits) and their genetic correlations; (2) explore the importance of genotype by environment interactions among sites; and (3) incorporate wood quality traits into selective breeding program.

Six 36-year-old progeny trials with 200 half-sib families were selected for the project, and 1200 standing trees were measured using acoustic tool and 800 increment cores were examined by SilviScan.

The genetic variance and covariance matrices for solid wood and pulp and paper production traits are estimated and will be used to develop optimal economic selection index for breeding and deployment selection of lodgepole pine in Sweden.

**Poster Board 13**

## UAPACA GUINEENSIS [1]. REFORESTATION BY UAPACA GUINEENSIS: AN INNOVATIVE STRATEGY FOR THE FIGHT AGAINST GLOBAL WARMING, A SOLUTION TO ENERGY AND THE FIGHT AGAINST HUNGER IN THE NORTH BATÉKÉ CHIEFDOM IN DEMOCRATIC REPUBLIC OF CONGO

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In order to fight against global warming and solve the thorny problem of fuelwood, several solutions are being considered including reforestation. This reforestation is done with well-chosen plants according to the use that will make local communities. For the communities of the North Batéké leadership in the Democratic Republic of Congo, they have chosen *Uapaca guineensis.*

*Uapaca guineensis* promotes the repopulation of gallery forests can recreate the ecosystem [2] that grows mushrooms. These fruits are an appropriate diet of wildlife and birds. The ecosystem that creates is suitable for animals of the antelope family. It provides a natural reforestation that replenish the forest galleries. Which will also gallery forests sequester carbon and thus offers the opportunity to sell carbon credits in the future. There are two methods for its planting. It is put on earth mature seeds that produce seedlings in six months and is carried out the transplantation. A second procedure is to pique the natural seedlings and plant them immediately. Five years are enough for starting seedlings in the forest. The method used by local NGOs in partnership with WWF is to reforest the forest edges to protect existing ones and create new ones in the savannas.

It is therefore a question of the 2020 emission reduction estimates will reach a total of 29 mt $CO_2$ [3]. The World Bank [4] through the Forest Carbon Partnership Facility (FCPF) has awarded the province of May-ndombe $80 million (USD) for its efforts in protecting its forests.

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**Poster Board 14**

## GENETIC DIVERSITY AND STRUCTURE OF DWARF STONE PINE IN MT. SEORAK, SOUTH KOREA

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Dwarf stone pine (*Pinus pumila*) is a five-needle pine occurring in north-eastern Asia. In South Korea, it grows only in the Daecheongbong area (1550-1700 m above sea level) of Mt. Seorak. We studied the genetic diversity and spatial structure of a dwarf pine stand on Mt. Seorak using six nuclear microsatellite (nSSR) markers. The population was divided into three parts based on the genetical bandwidth mapping (GBM) analysis. The genetic diversity ($H_e$=0.608) was relatively low compared to the other *Pinus* species (Mean $H_e$=0.700), which might be resulted from the reproduction of progenies among genetically related kinship individuals. The analysis of the spatial autocorrelation showed a positive spatial autocorrelation (genetic structure) at spatial scales of up to 24 m. Based on the results of genetic structure, we provided baseline information of sampling strategies for the ex situ conservation of *P. pumila* in Mt. Seorak.

**Poster Board 15**

## EVALUATION OF FIELD RESISTANCE TO WHITE PINE BLISTER RUST IN COASTAL BRITISH COLUMBIA

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White pine blister rust, caused by *Cronartium ribicola* J.C. Fischer, has been a major problem in white pine plantations across North American forests. Although this exotic disease has been devastating to native white pine species since its introduction a century ago, significant genetic resistance has been found [1]. King et al. [2] reviewed the different approaches in breeding for resistance to blister rust in North American white pines. In our poster we review long term "field resistance" that demonstrates the progress that has been made to date and establishes guidelines for the re-introduction of western white pine (*Pinus monticola* Dougl. ex D. Don) to Coastal British Columbia. We investigated block plot trials that are now 15 years some of which are very heavily infected. Up to 100% of wild unimproved blocks are now dead of rust. Seedlots representing the 1st & 2nd stage of improvement have only 15% clean or un-infected trees on these heavily infected sites. Seedlots representing the current state of selection for partial resistance (3rd stage impovement) show 35% clean trees. Seedlots with the major gene (Cr2) provides total resistance but is susceptible to breakdown – showed 80% clean trees - so far no break down has been noted in Cr2 deployed stock in B.C. Most current orchard seedlots combine the top partial resistance (35%) with MGR (Cr2) applied through supplemental mass polination (SMP). This combination provides an opportunity for western white pine to once again become part of the regenerated forests of Coastal B.C..We recommend planting pure white pine with MGR just in small blocks or as mixtures (with just partial resistance) with Douglas-fir and/or western red cedar.

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**Poster Board 16**

## SYMPTOMLESS AND HYPERSENSITIVE RESISTANCE OF EUCALYPTUS GLOBULUS TO THE RUST PATHOGEN PUCCINIA PSIDII: EVIDENCE FOR DIFFERENT QTL UNDERLYING EACH RESPONSE

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The rust *Puccinia psidii* infects plant species of the family *Myrtaceae*. Native to South America, the pathogen has recently entered Australia which has a rich *Myrtaceous* flora, including trees of the ecologically and economically important genus Eucalyptus. We studied the genetic basis of variation in rust resistance in *Eucalyptus globulus*, the main plantation eucalypt in Australia. Quantitative trait loci (QTL) analysis was undertaken using 220 trees of an outcross F2 mapping family and a previously published linkage map. Mapped individuals were phenotyped by growing their open pollinated progeny in a screening facility where seedlings were inoculated with the strain of P. psidii found in Australia. QTL analyses were conducted using a binary classification of individuals with no symptoms (immune) versus those with disease symptoms, and in a separate analysis dividing plants with disease symptoms into those exhibiting the hypersensitive response versus those with more severe symptoms.

Four QTL were identified using this method; two underlying the segregation of the phenotype exhibiting no symptoms (*Ppr2* and *Ppr3*), and two underlying the segregation of the phenotype exhibiting a hypersensitive reaction (*Ppr4* and *Ppr5*). These QTL mapped to 4 regions on different linkage groups, and do not overlap previously identified loci for rust resistance in eucalypts, including *Ppr1*. The independent genetic control of these phenotypic classes provides evidence that at least two mechanisms contribute to rust resistance in *E. globulus*. Together with past findings, our results suggest that *P. psidii* resistance is likely to be quantitative in nature and influenced by the complex interaction of multiple loci of variable effect in this naïve host genus.

**Poster Board 17**

## STRUCTURAL DIFFERENCES BETWEEN THE GENOMES OF THE MAJOR EUCALYPT LINEAGES

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The plant family *Myrtacea*e includes many taxa of economic importance, including the closely related genera *Eucalyptus* and *Corymbia*. The recent release of the *Eucalyptus grandis* reference genome, now provides unprecedented opportunities for comparative genomic analyses. To this end, two mapping crosses of *Corymbia torelliana* (CT) x *Corymbia citriodora subsp. variegata* (CCV) were established, both sharing the CCV pollen parent. Parental linkage maps were constructed using 115 and 245 offspring from each cross. DArTseq markers, a marker binning process, and a strict iterative approach were employed to create three robust high-density linkage maps, each with 11 linkage groups and ranging from 4,616 – 6,055 markers. The genetic position of each marker in the CCV map was compared to its physical position in the *E. grandis* reference genome to explore any gross changes in chromosome structure. 1441 CCV markers could be located on the E. grandis genome using a stringent BLAST threshold. Of these, 29% were non-syntenic (on different chromosomes) or non-collinear (in different order within a chromosome), with 13% involved in major intra-chromosomal rearrangements relative to the *E. grandis* genome. Large terminal inversions were detected on chromosomes 4, 9, 10 and 11 in CCV, and complex translocations on chromosomes 2 and 6. These rearrangements (excluding the translocation on chromosome 2) were verified in both CT maps by similar analyses. Before this study it was widely assumed that the eucalypt genomes were largely syntenic and collinear. We now have strong evidence that this is not the case.

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