



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

14-18 MARCH 2016 | ROTORUA | NEW ZEALAND

Handbook



## 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 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 phenotyping 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.

## KEYNOTE

### FOREST INDUSTRY PRIORITIES VISION AND PRIORITIES FOR FOREST GENETICS


#### **Robert Banks**

*Animal Genetics and Breeding Unit, University of New England, NSW 2351, Australia*

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.

## Risks, opportunities and vision for Forestry Genetics

**Rob Banks**  
AGBU




### RB, AGBU:

RB:

- PhD in Genetics
- 25 yrs at Meat & Livestock Australia (LAMBPLAN, Genetics RDE, R&D Strategy)
- 3 yrs at AGBU


AGBU:

- Development and support of genetic evaluation systems for Australian and international breeders
- Development and support for TREEPLAN

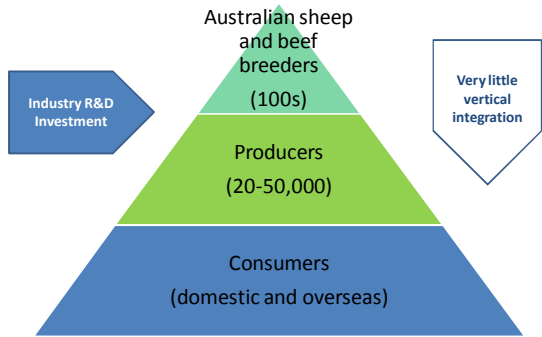


### Outline:


- Risks
- Opportunities
- An approach to genetic improvement
  - Implementation
  - Supporting, real-time R&D
  - Genomics
- Vision



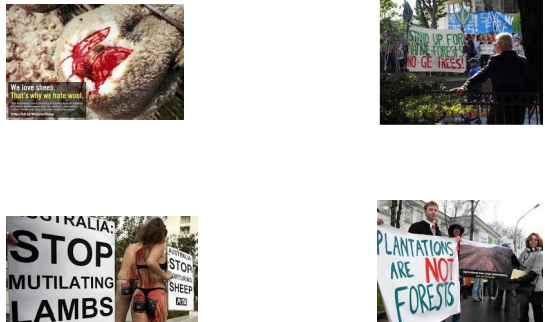
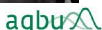
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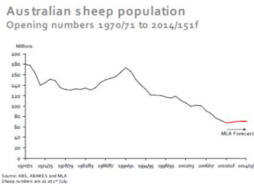
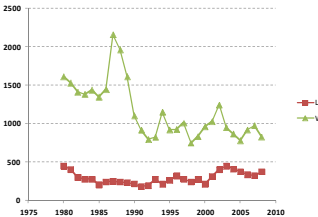
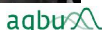
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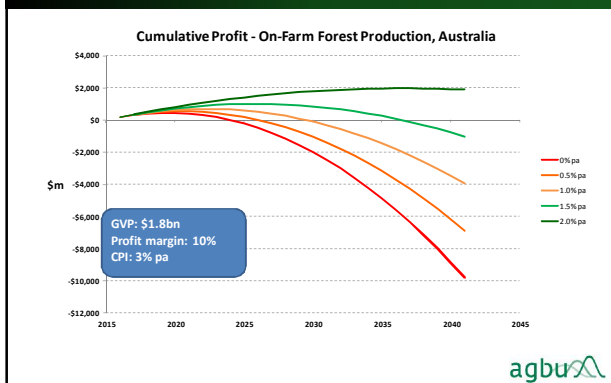
### Risks:

### Risks:

## Risk & opportunity:



## Systematic approach to genetic improvement:

1. Define breeding objective
  1. impact on profit
  2. Include all traits
2. Evaluate available stocks and use best one(s)
3. Estimate genetic parameters for criteria and objective traits
  1. Additive and non-additive effects
  2. GxE
4. Evaluate crossing and/or selection program
5. Implement recording and genetic evaluation
6. Implement selection, including mate allocation or selection; and/or crossing

## Breeding objectives:

- Marginal impact on income and cost
  - Rigorous economic basis
- Can incorporate desired gains, non-linearity, production system
- Care re range of objectives provides insurance value
- Treatment of time
  - An important question in the absence of vertical integration, and with long production cycles

## Indexes driven by objectives:

**TIPS & TOOLS**

**A Quick Guide to Angus Selection Indexes**

There are four selection indexes calculated for animals within the Angus BREEDPLAN analysis.

- Angus Breeding Index
- Domestic Index
- Heavy Grain Index
- Heavy Grass Index

The Angus Breeding Index is a general purpose selection index that is suitable for use in the majority of commercial beef operations, whereas the Domestic, Heavy Grain and Heavy Grass selection indexes are specific to beef operations targeting a defined production system and market endpoint.

Table 1 : Selection Index Descriptions	
Angus Breeding Index	<ul style="list-style-type: none"> <li>• Self-replacing herd</li> <li>• Daughters are retained for breeding</li> <li>• Identifies animals that will improve overall profitability in the majority of commercial grass and grain finishing production systems</li> </ul>
Domestic Index	<ul style="list-style-type: none"> <li>• Self-replacing herd</li> <li>• Daughters are retained for breeding</li> <li>• Steer progeny finished on either pasture, pasture supplemented with grain, or grain targeting the domestic supermarket trade</li> <li>• Steer progeny slaughtered at a carcass weight of 270 kg at 16 months of age</li> </ul>

10

<http://www.angusaustralia.com.au/breedplan-60460/1772-understanding-selection-indexes.html>

Index	Definition
Angus Breeding Index	<ul style="list-style-type: none"> <li>• Self-replacing herd, daughters retained</li> <li>• Overall balance of grass- and grain-fed finishing</li> </ul>
Domestic Index	<ul style="list-style-type: none"> <li>• Self-replacing herd, daughters retained</li> <li>• Steer progeny (grass or grain) slaughtered at 270kg at 16 months</li> <li>• MSA important</li> </ul>
Heavy Grass-fed Index	<ul style="list-style-type: none"> <li>• Self-replacing herd, daughters retained</li> <li>• Steer progeny grass finished</li> <li>• Slaughtered at 340 kg at 22 months</li> <li>• MSA important</li> </ul>
Heavy Grain-fed Index	<ul style="list-style-type: none"> <li>• Self-replacing herd, daughters retained</li> <li>• Steer progeny grain finished</li> <li>• Slaughtered at 420 kg at 24 months</li> <li>• MSA important, marbling premiums</li> </ul>

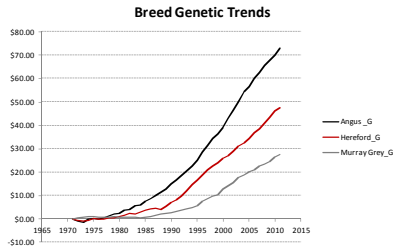
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## Genetic evaluation:

- eg BREEDPLAN, LAMBPLAN, MERINOSELECT
- Multi-trait BLUP ~ 25-65 traits, run monthly to fortnightly
  - International
- Genotypes:
  - Have been blending
  - Now implementing single step multi-trait analysis

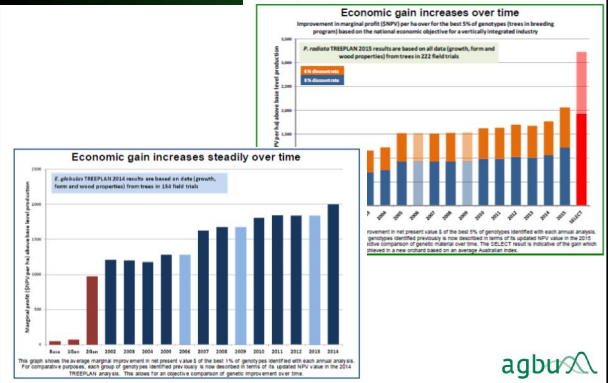
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### Genetic progress – examples:



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### Genetic progress – examples:



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Species	Sector	Rate of progress in \$ per female per year	Rate of progress in \$ per DSE per year	Rate as % of current average gross margin
Sheep	Terminals	\$2.00	\$1.00 (divided by 2)	5-10%
	Maternals	\$1.75	\$0.86	8-9%
	Merinos	\$0.85	\$0.50	5%
Beef	Southern	\$2.95	\$0.15 (divided by 20)	2.5%
	Northern	\$0.80	\$0.04	0.8%
Dairy cattle		\$8.50	\$0.34 (divided by 25)	Approx. 1%
Trees	c. \$100 per ha per year, corresponding to c. \$1 per DSE per year			

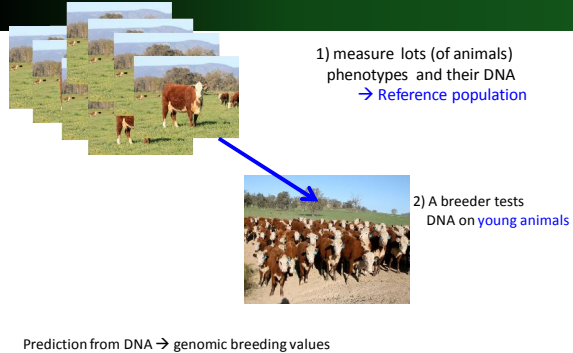
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### Genomics:

- The QTL & GWAS eras
  - Must aim to utilise all genetic variation
- Genomics
  - Real challenges in data storage and data checking, cost v accuracy equation
- Genomic selection
  - Beef and sheep now genotyping c. 10-15% of nucleus population each year, and this is rising
    - Expect c. 10-20% increase in rate of progress
  - Dairy cattle – switched almost entirely to genomic selection
    - Achieving 50%+ increase in rate of progress

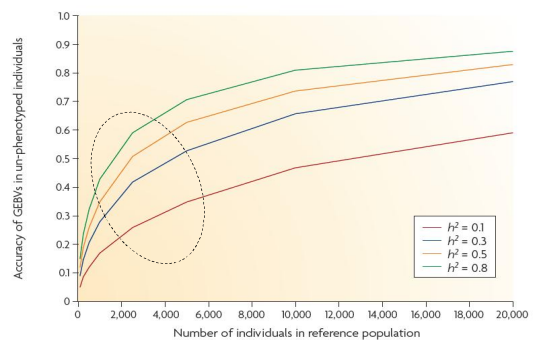
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### Genomic Prediction: basic idea

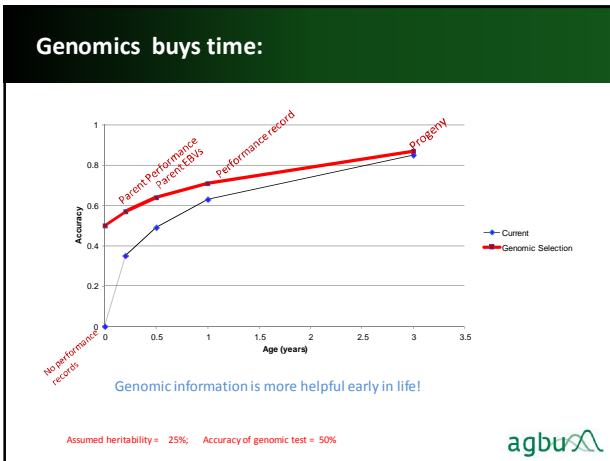


17 agbu

### Performance records are gold:



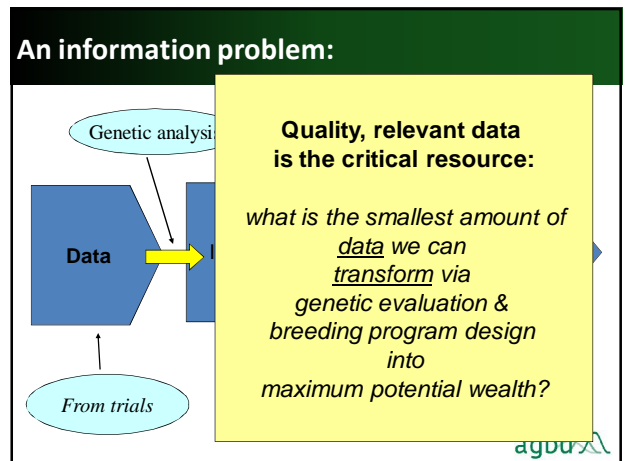
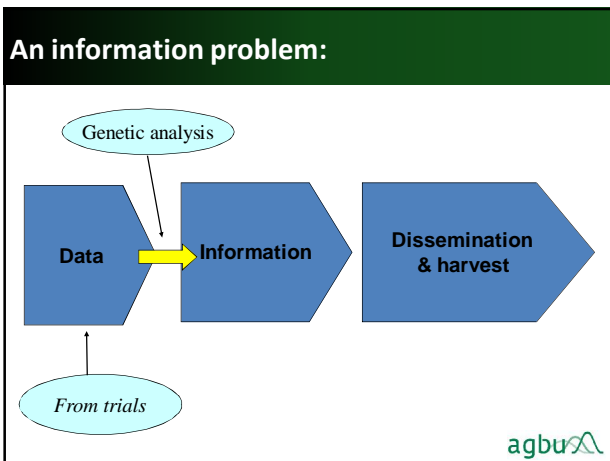
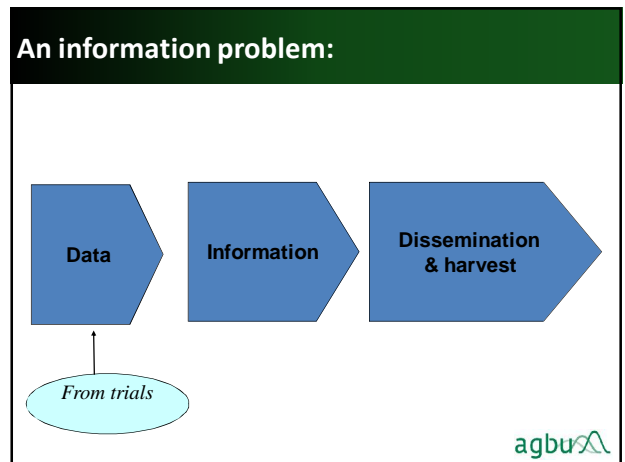
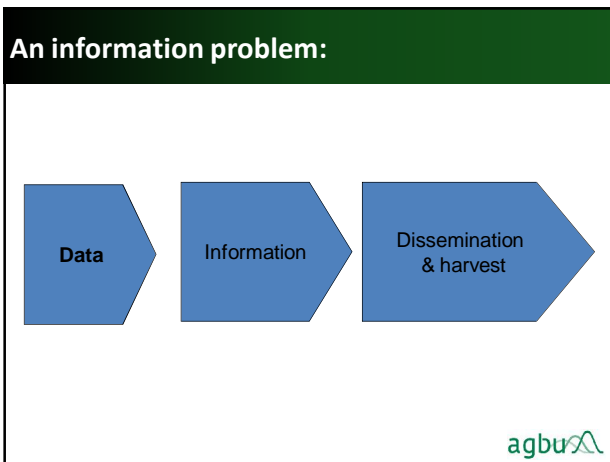
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### February 2016 Wagyu GROUP BREEDPLAN

Name/ID	Gestation Length (days)	Birth Wt. (kg)	200 Day Wt. (kg)	400 Day Wt. (kg)	600 Day Wt. (kg)	Carcass Wt. (kg)	Eye Muscle Area (sq.cm)	Rib Fat (mm)	Rump Fat (mm)	Retail Beef Yield (kg)	Marble Score	Marble Fineness (kg)	Fullblood Terminal Index
MACQUARIE WAGYU C1176	-1.4 56%	-1.2 69%	+4 75%	+7 86%	+8 86%	+17 87%	+3.1 84%	-0.6 72%	-2.0 84%	-0.3 72%	+3.1 88%	+0.52 71%	+5.735
RUMO CATTLE CO MICHIFUKU F126	+0.9 57%	+1.0 60%	+6 62%	+8 64%	+9 64%	+11 69%	+3.2 67%	+0.1 62%	+0.3 67%	+0.2 61%	+2.5 74%	-	+5.578
MACQUARIE WAGYU Y408	-1.6 54%	+1.6 69%	+13 77%	+22 82%	+27 81%	+22 84%	+2.3 80%	-2.5 72%	-4.5 80%	+1.0 71%	+2.2 83%	+0.41 69%	+5.567
MAYURA TOSHIGENAMI R18	+0.8 54%	0.0 67%	+5 70%	+10 80%	+13 77%	+11 92%	+7.2 91%	-0.2 75%	-0.1 91%	+1.7 74%	+2.4 94%	+0.44 92%	+5.557
HER ZURLUSHIGE 0119	-0.4 53%	+1.1 58%	+11 60%	+19 65%	+26 64%	+12 73%	+3.5 70%	+1.7 63%	+4.2 70%	-0.5 62%	+2.2 76%	+0.51 65%	+5.521
Breed Avg. EBVs for 2014 Born Cows	+0.1	+0.9	+9	+15	+19	+12	+0.7	+0.2	+0.6	-0.2	+0.1	+0.00	+116

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### Who benefits from genetic improvement?

- *depends on ...* what changes are made, which
- *depends on ...* what traits are recorded (and selected for), which
- *depends on ...* what traits are rewarded

generating a **design** choice


25 

### Who benefits from genetic improvement?

- Record and select for only those things where the rewards are clear:
  - *Easy but low value*

or

- Record and select for everything that someone might benefit from
  - *Hard but high value*



26 


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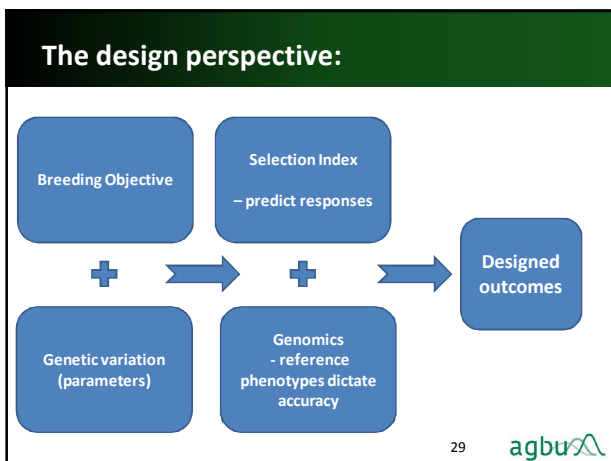
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### Who benefits from genetic improvement?

- **is not a helpful question**
  - Consumers must get some benefit, as well as everyone else in the value chain
- **More useful:**


*What benefits do you want to deliver?*

28 



### So, the real questions are

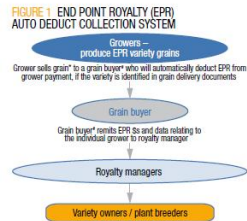
- What benefits do we want to deliver where in the value chain
- and
- How to fund phenotyping, especially for Hard-to-measure (HTM) traits:
  - zero disease = zero chemicals, less waste in processing, carbon cycling, water efficiency
  - Unclear signals, uncertain demand, costly

30 

## Funding the future ~ End-point Royalties:

Collects a royalty on seed sold  
Typically c. 2-3% of value of product  
Funds collected are allocated to breeding organisation to fund further breeding

This is separate from, and additional to, R&D levies



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## Vision:

- Forestry is a valued, respected and trusted activity within the community
  - long lead times dictate recording everything you can think of
- Forestry is economically sustainable because genetic improvement is continuous and at high rate, underpinned by:
  - continuous recording in the active population of every trait that matters to anyone in the value chain (real-time R&D)
  - multi-trait genetic evaluation that accounts for GxE, non-additive effects, moving to genomic selection asap
  - utilised via mate selection systems that maintain genetic variation
  - Some continuous funding mechanism (future perspective)

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## Vision: - genetic improvement for our future

Forest & Bird  
GIVING NATURE A VOICE

healthy forests beautiful world  
AVON

Trust  
Value  
Respect

Sustainable forestry refers to the use of forest lands in away and a rate that maintains their ecological diversity, regeneration capacity, vitality and their potential to fulfil now and in the future.

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## RW:

- Genetic trends and (absence of) selection plateaus in long-running selection programs
- Breeding objectives – how other industries go about it, how to accommodate uncertainty and appropriate discount rates
- Some benefit-cost estimates for genetic improvement programs (and how not to do it!)
- Enterprise vs industry gains – your “co-opetition” concept and related issues around who pays, who benefits and balancing competitive advantage with benefits of data sharing
- Relevance of above with both P and G selection
- Issues around genetic improvement pipeline and overcoming blockages
- Long-term vs short-term gains and genetic diversity
- The impact of BLUP and related technologies
- Quantifying and dealing with GxE
- Flirtations with transgenics
- Issues around parentage ascertainment, error rates, genomic tools and costs
- Potential of advanced reproductive technologies and novel applications thereof

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## Some challenges:

- Collecting enough of all the relevant phenotypes
- Who pays and how?
- Scope for data sharing in some spp?

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