Application of genomics in breeding schemes for the genetic improvement of sheep and goats

Learning from our experience in Australia

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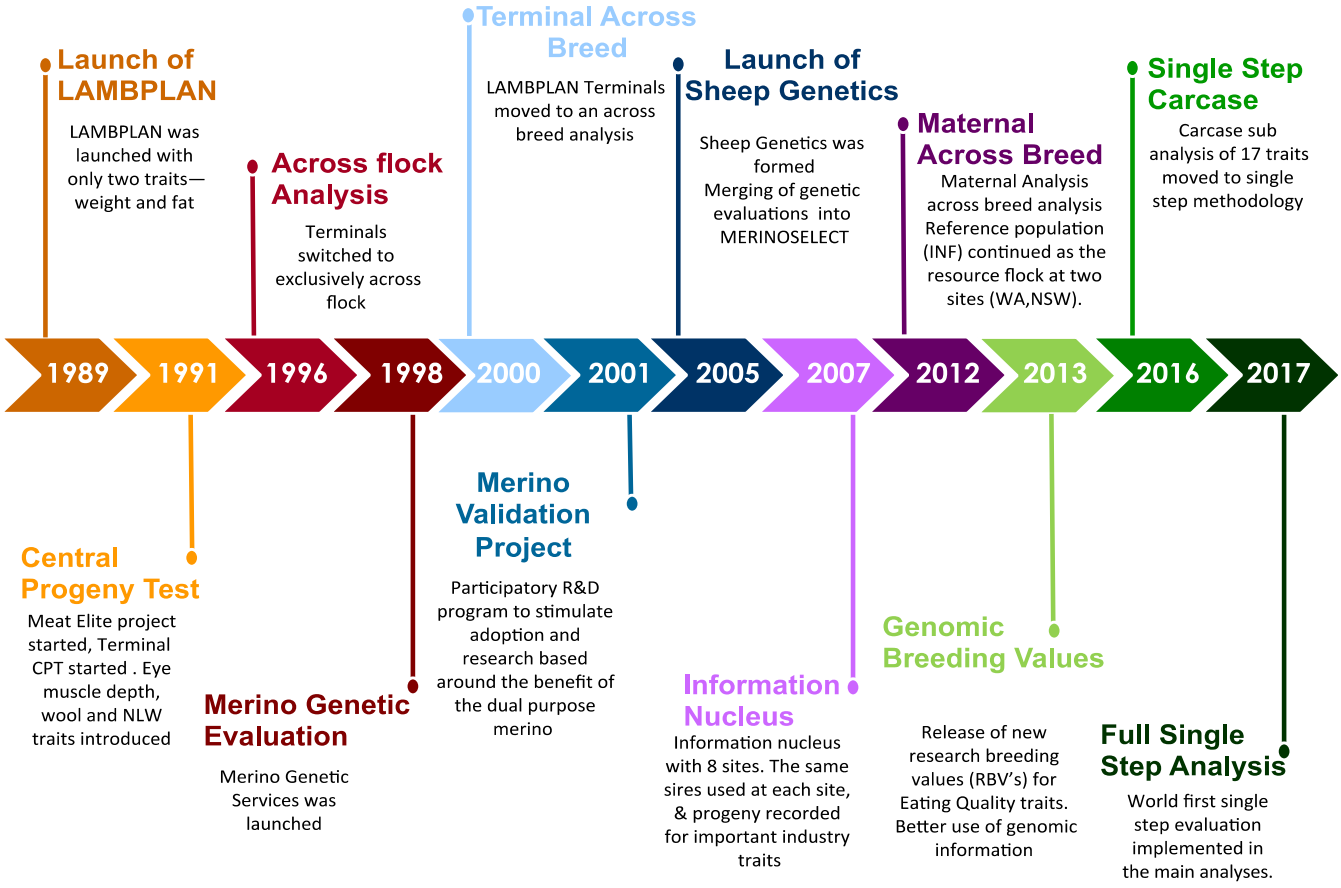
Outline

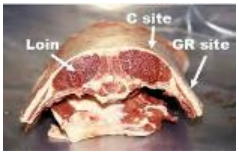
- Evolution of breeding values in Australia
- Genomic reference population
- Linkage
- Value of information sources
- Key technical challenges
- Validation of benefits
- Breeding tools

Evolution of Sheep Genetics genetic evaluation



Single Step Australian Sheep Breeding Values (ASBVs)

Animal performance



Carcass measurements

Consumer eating quality

Genomic testing

Resource flocks and ram breeders

LAMBPLAN ASBV

The multi-breed nature of Australian sheep

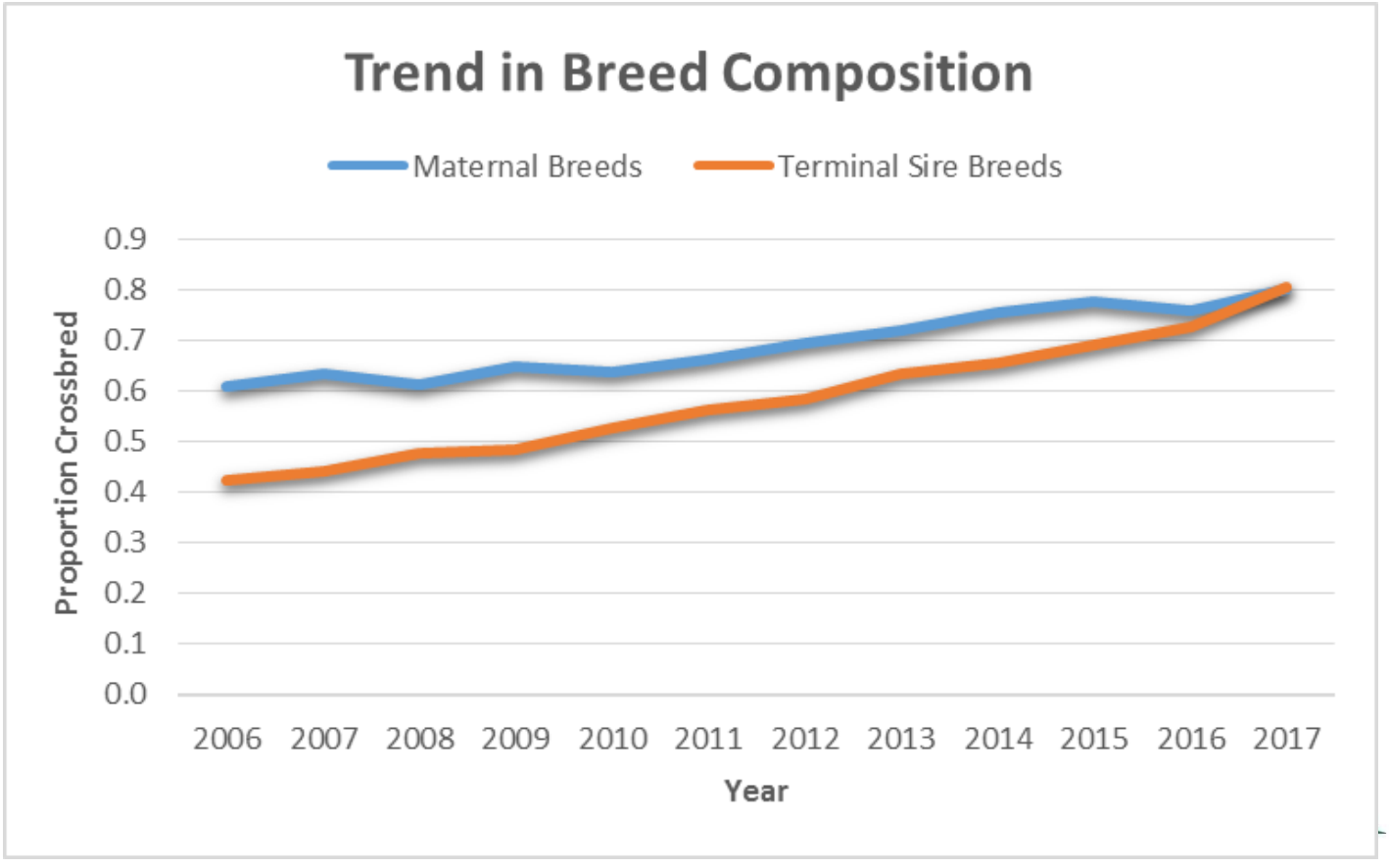
Three “breed groups” each with separate genetic evaluations (2M+ animals)

- Fine wool
- Medium wool
- Strong wool

- Border Leicester
- Coopworth
- Composites

- Poll Dorset
- White Suffolk
- Texel, …

Composite breeding is increasing



Scale of our Sheep Genetics evaluations (Aug 2018)

	Merino	Maternal	Terminal
Pedigree	2.5M	2.1M	2.9M
Records	13.6M	5.1M	8.8M
Flocks	510	324	929
Av Flock size	460	358	210
Traits	76	46	45
Genetic groups	558	104	94
Genotypes	24K	7K	22K
% current drop	1.1%	0.5%	1.5%
Solver time (hrs)	13.2	3.5	6

Number of genotyped sheep in the genetic evaluation

Animal Group	Breed Analysis			
	Maternal	Merino	Terminal	Total
Industry progeny	5,014	15,175	10,782	30,971
Industry sires	612	2,120	2,642	5,374
Resource flock progeny	4,875	13,407	11,671	29,953
Total	10,501	30,702	25,095	66,298

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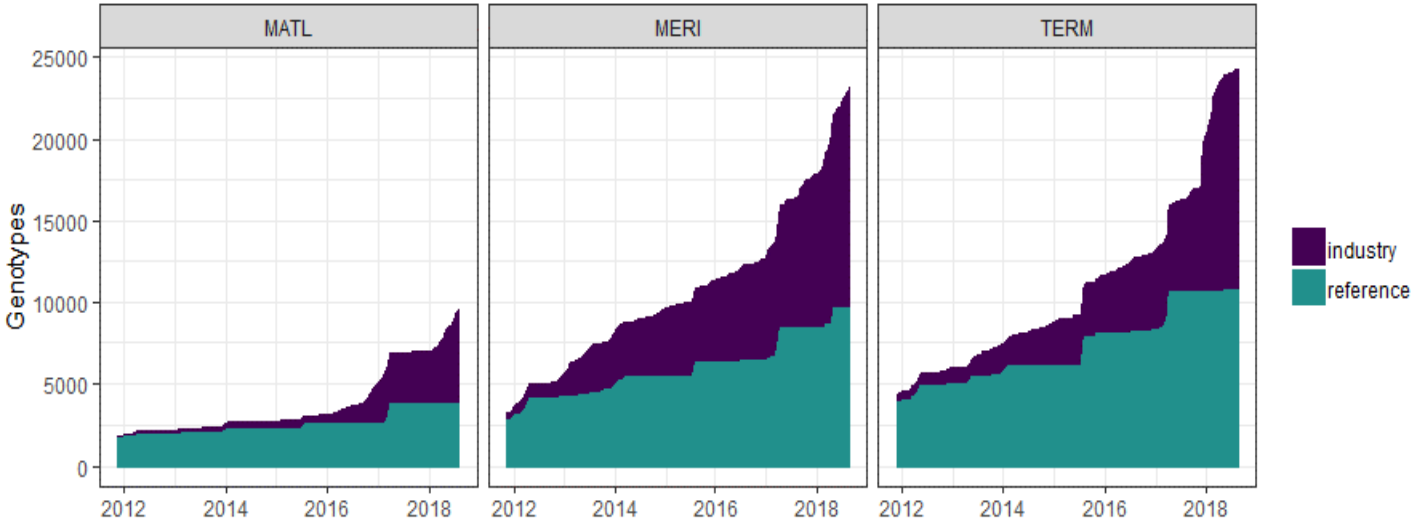
Trends in genotyping



The Genomic Reference Population

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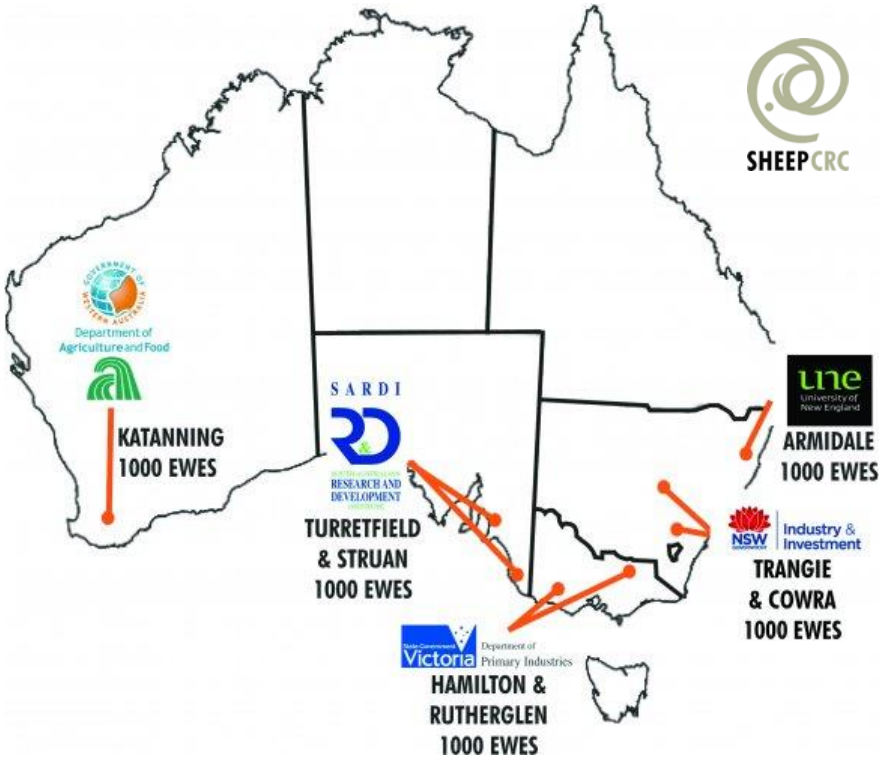
Reference population design (INF 2007 – 2012)

- Eight sites across Australia
- Mostly Merino ewe base
- 100 sires mated annually
  - 40 Merino
  - 40 Terminal
  - 20 Maternal
- Comprehensive phenotyping of progeny
- 50K SNP genotypes

  + (15K, HD, Seq)



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Reference population post 2012 (MLA Resource Flock)

- Two of the eight original sites (Armidale and Katanning)
- Focus on carcass and eating quality traits

- Of the other trait groups, reproduction is our biggest limitation:
  - Commenced genotyping recorded ewes in industry flocks to boost the repro reference → still need to boost numbers
- Exploring alternate structures to work with industry based flocks

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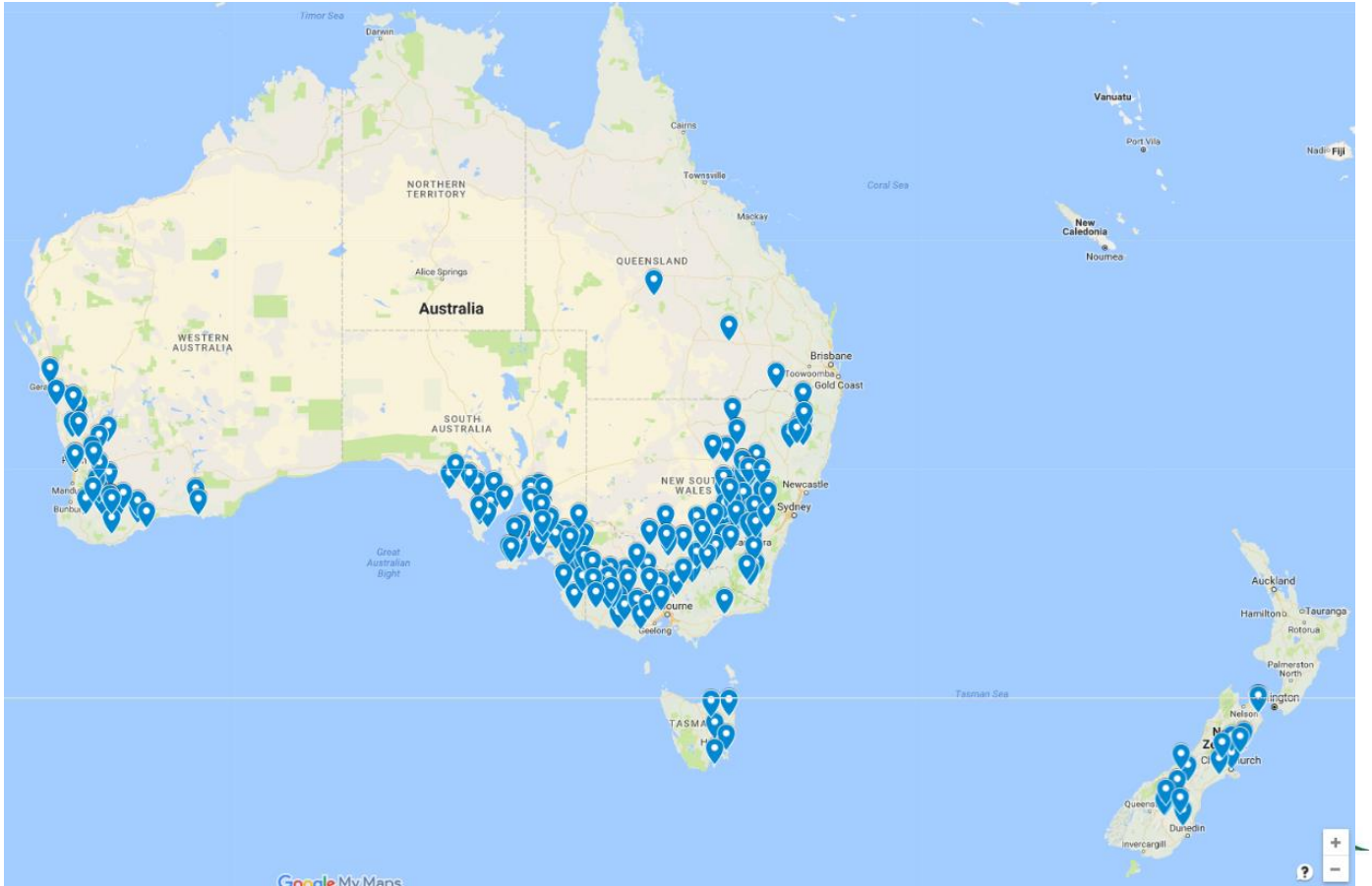
Genetic linkage between flocks

Strategies for generating linkage

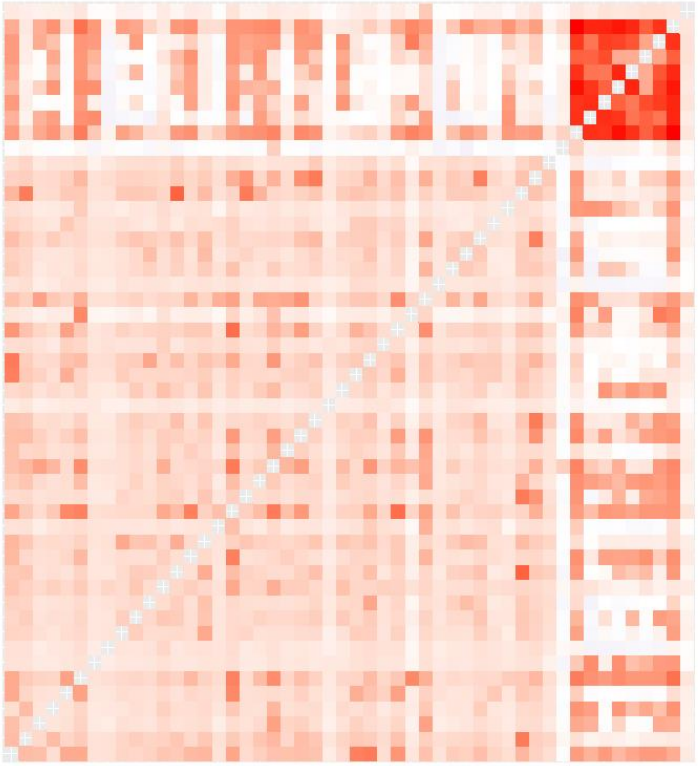
- Using sires from other flocks
- Entering sires into;
  - Resource flock
  - Sire evaluations
- Young sire programs / performance groups
- Dams and decedents or link sires help
- Need to be performance recorded for key traits
- Linkage need for all breeds, flock, years and groups
- Genomic testing will help

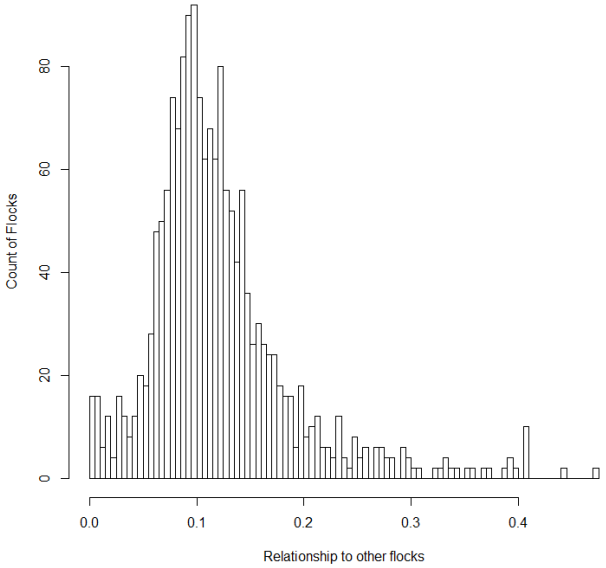
Flock x Flock genetic linkage

Dispersed Flocks



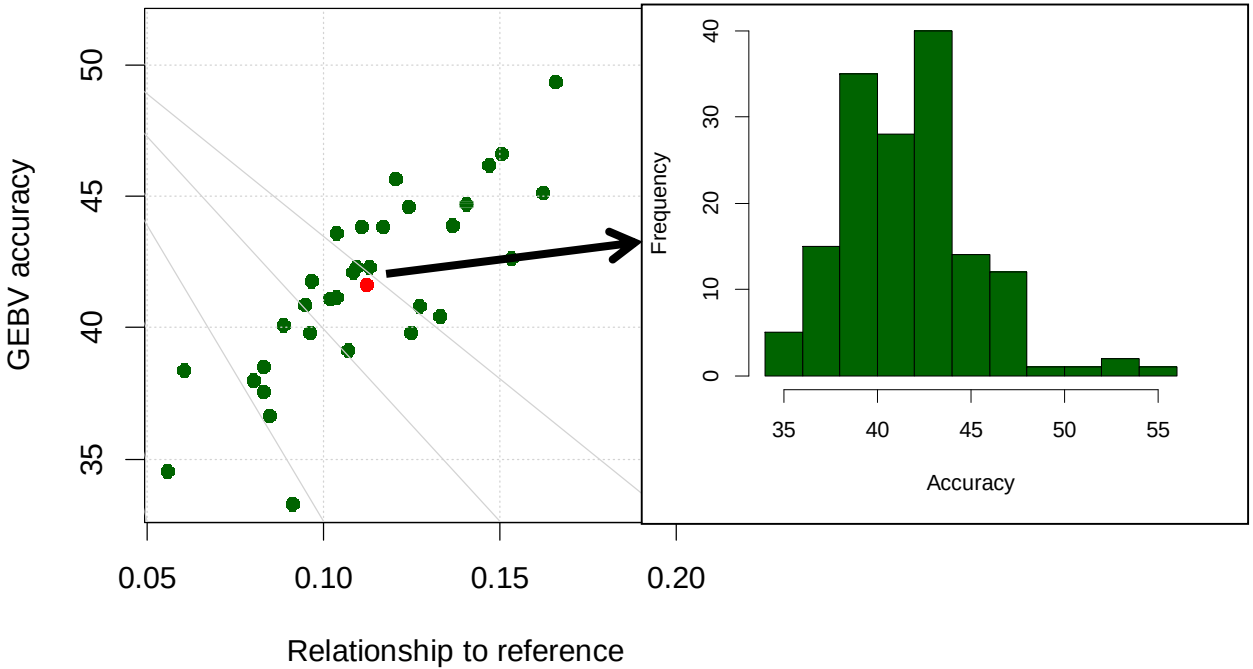
Genomic Linkage





Accuracy increase with relationship to reference

Average accuracy of yearling fibre diameter for pilot animals by flock



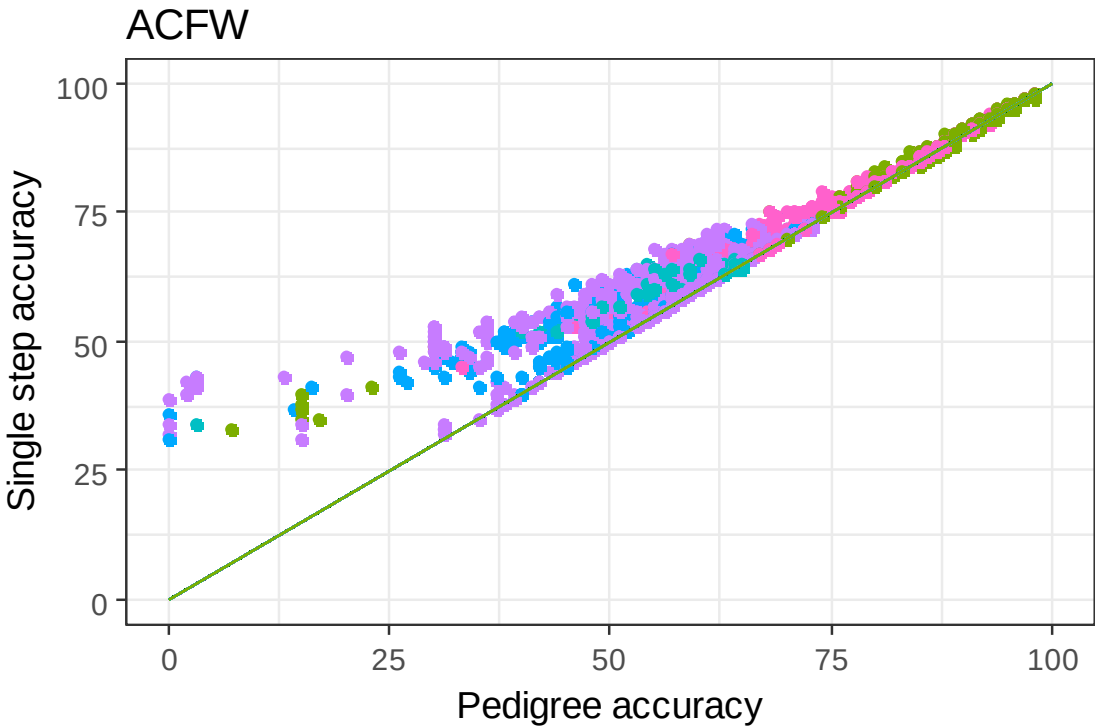
Value of information

Phenotype is still king

- Breeders seeing more value in;
  - Pedigree
  - Good quality phenotypes
  - Genomic tests

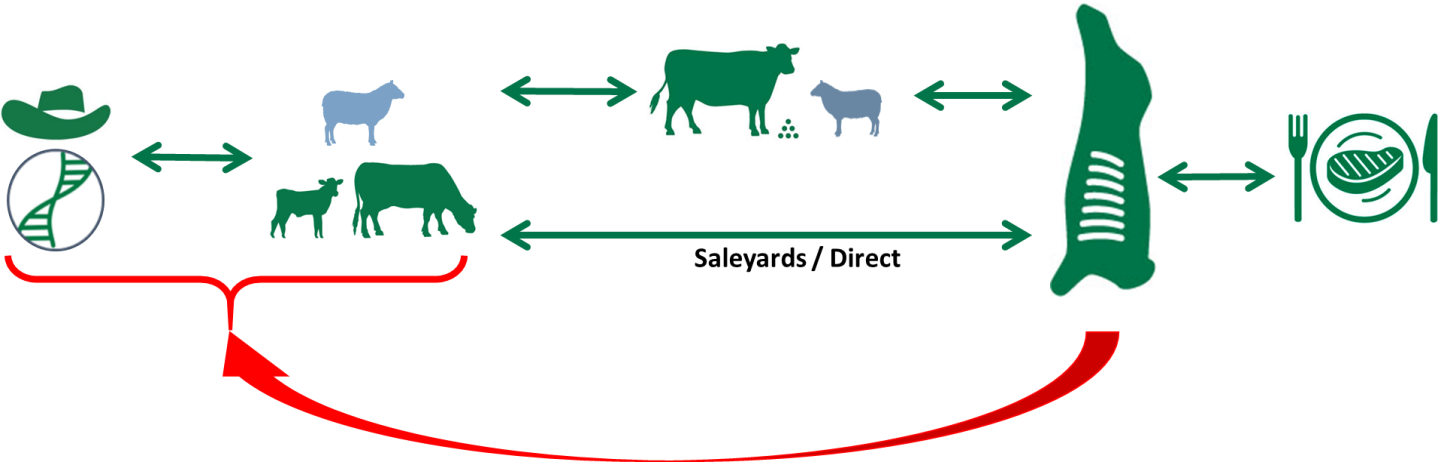
- Value of slaughter info from surplus ram breeding animals and progeny tests

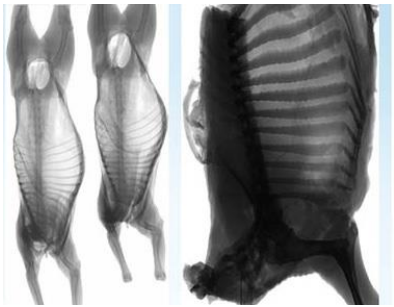
Value of genotyping



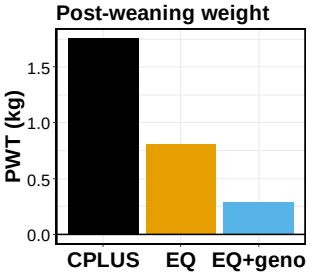
Genomic selection most beneficial when EBV accuracy is low

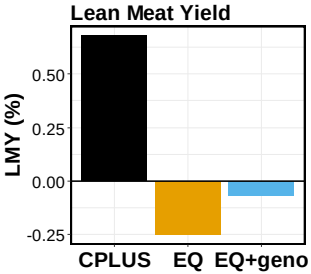
ALMTech: Advanced Livestock Measurement Technologies

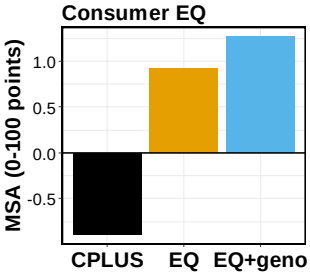


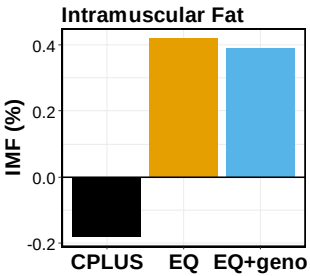


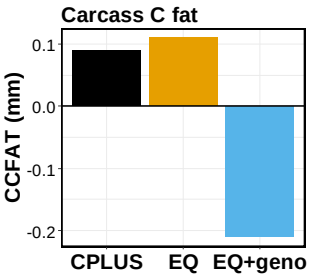
Superiority of top 10% selected on Carcass+ and EQ

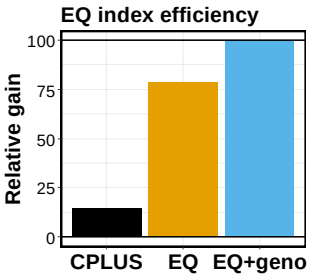












Merino example: Relative responses

Relative to Basic scenario

Scenario	Pheno	+Geno	+Short GL
WWT	35	66	76
Basic	**100**	111	**125**
Plus	111	119	135
NLW	126	133	151

Relative to NLW scenario

Scenario	Pheno	+Geno	+Short GL
WWT	27	52	60
Basic	79	88	99
Plus	88	95	107
NLW	**100**	106	**120**

- Massive improvement in gains by recording key Breeding Objective traits
- 5-10% increase in gain from genotyping alone
- 20-25% increase in gain if genotyping is combined with earlier joining
- 60% of gain from just a wwt, genotype and shorter GL
- Cost:benefit?

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Technical Challenges

SS-GBLUP model

- H-1 matrix with G calculated ala Yang
  - allele frequencies across all genotypes within breed group

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{pmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1} - \mathbf{A}^{-1}_{22} \end{pmatrix}$$

- Genetic groups fitted explicitly

- Lambda

$$G = \lambda G_m + (1 - \lambda) A_{22}$$

- Accuracies as per Li *et al* (2017) AAABG

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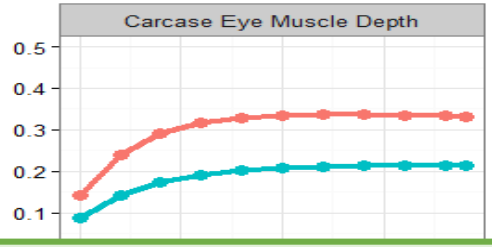
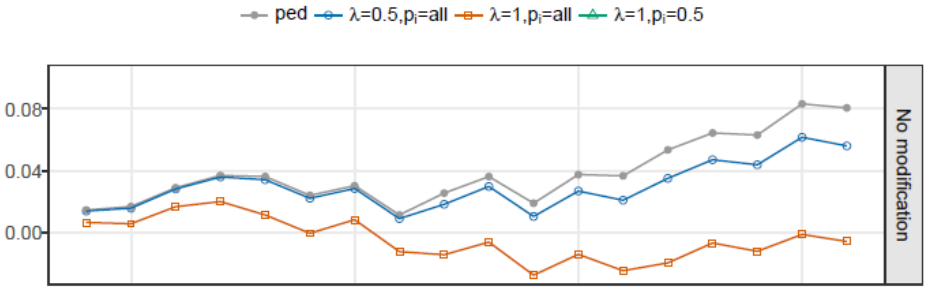
Lamba influences many aspects of EBVs

- Accuracy
  - Average correlation between adjusted phenotype and SS-EBV

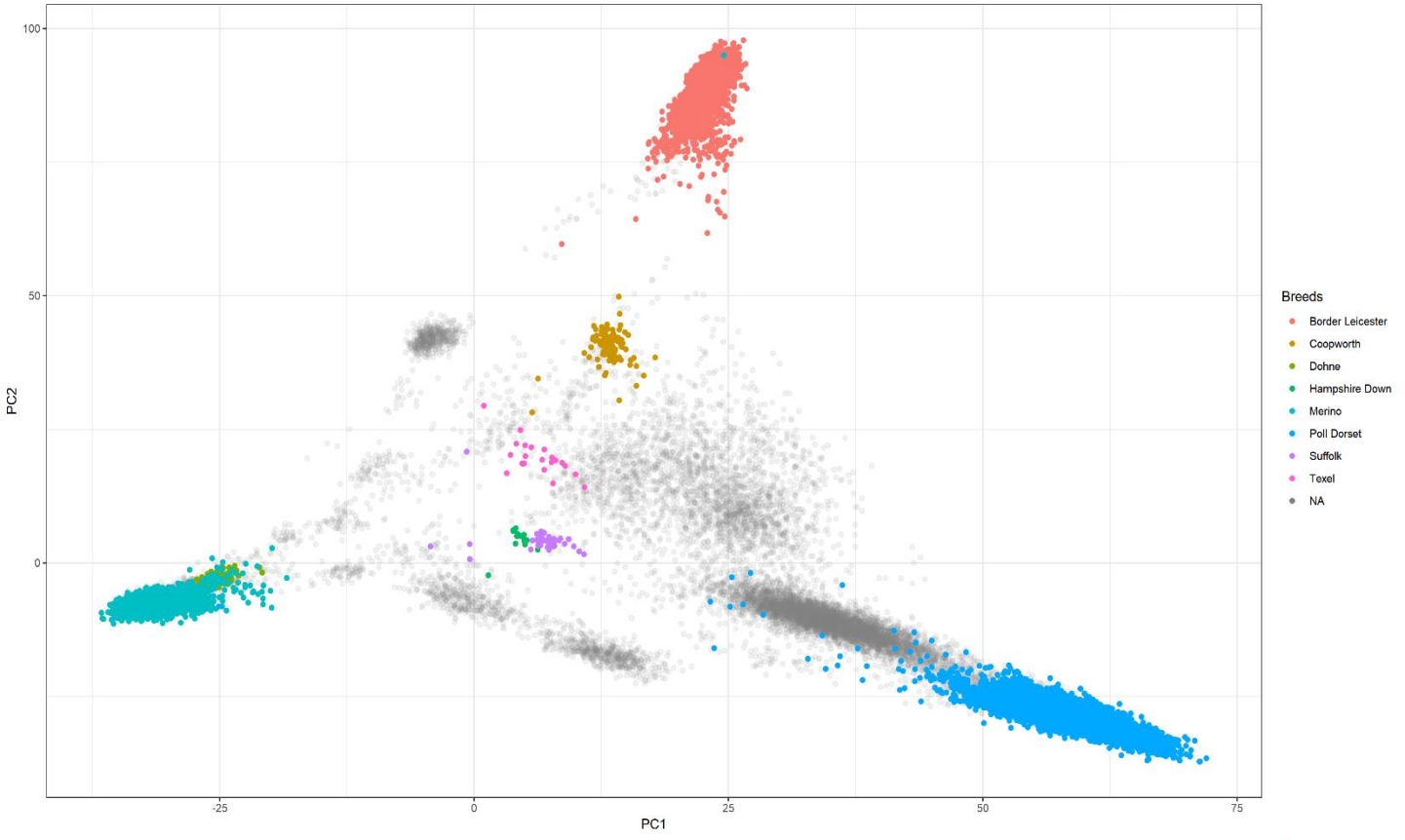


A weight of 0.5 is being used in genomic evaluations for sheep as a compromise between accuracy and bias across traits and breeds.

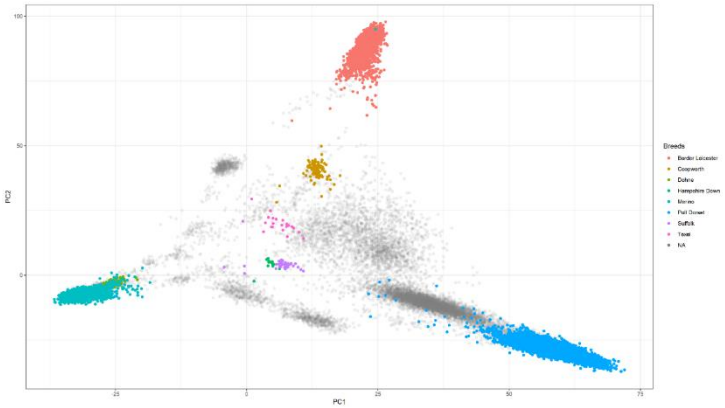
- Genetic Trends



Breeds via GRM

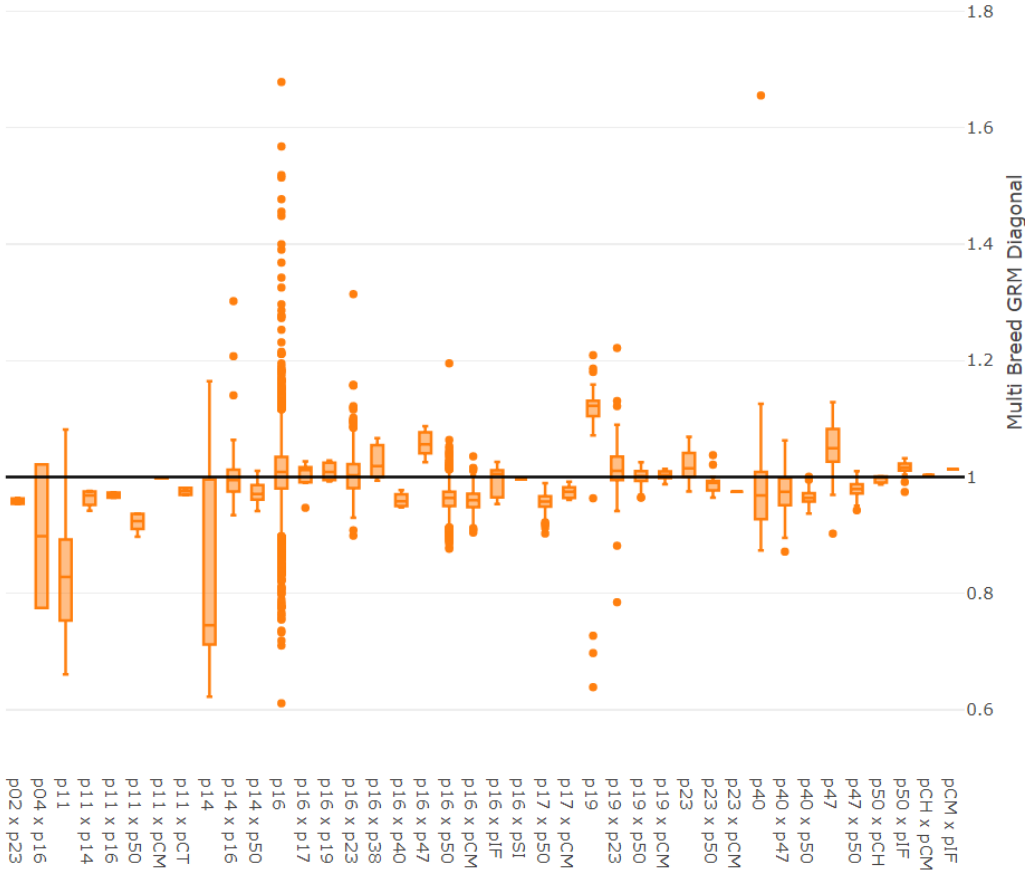


Genotypes show breed structure



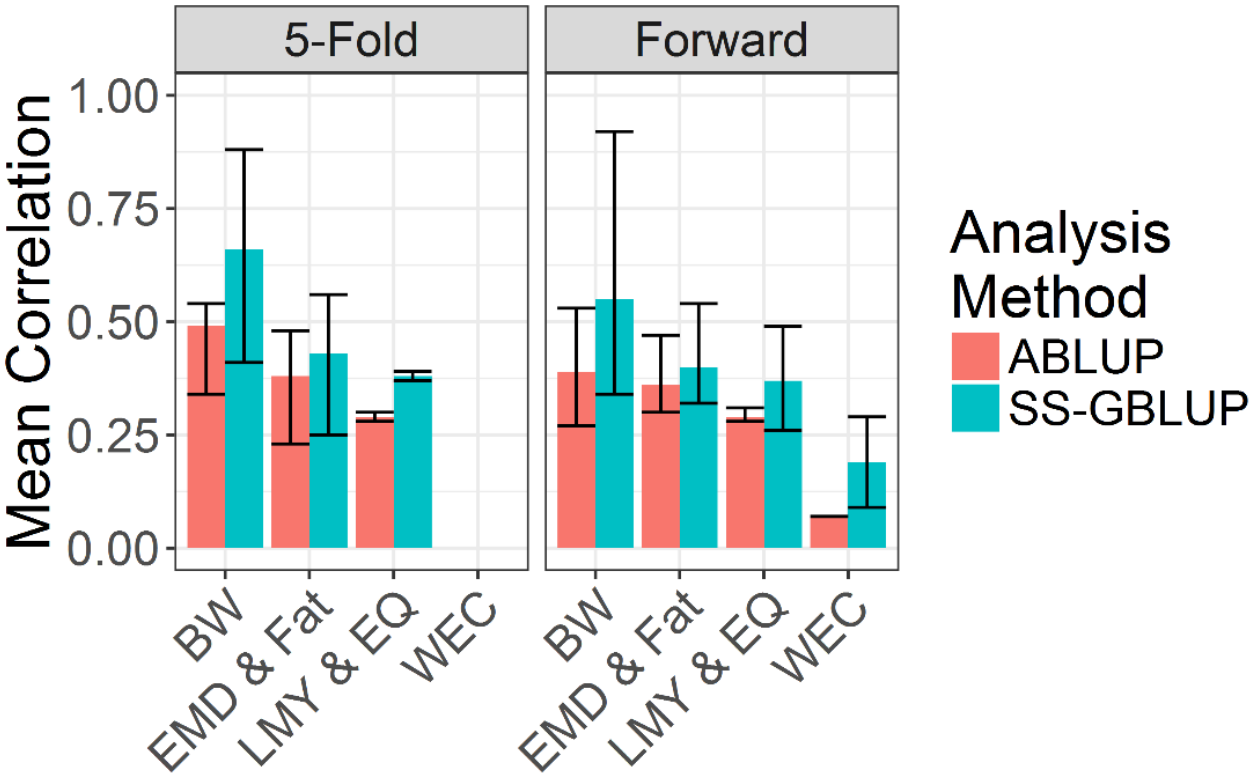
- Account for breed structure in H^{-1}:
  - Breed specific frequencies versus meta-founders?
- Obtaining sufficient genotypes to define a breed is a challenge
- Composites with missing parent breeds

Building the Multi-breed GRM



Validation

SS-GBLUP provides increased predictive ability compared to ABLUP



Gurman *et al.* 2018

Genomic predictions for small breeds

- Little or no benefit from across-breed genomic prediction
- Need a relevant reference population for breeds of choice
- Progressive breeders with specialist breeds or composites would like to use genomic information
- But breeders not genotyping because they are not included
- And we don't include them because there are not enough!

Small breed validations

- Including genotypes from small breeds improves empirical prediction accuracy by small amounts
- Accuracy improvements of SS versus pedigree EBVs are less than observed for the major breeds
- No impact on EBVs of animals from the main genotyping breeds (min r = 0.99)
- More impact from multi-breed G (min r = 0.97), but good reasons to use it

Inclusion of genotypes from small breeds needs qualification of benefits and advice on investment in reference populations

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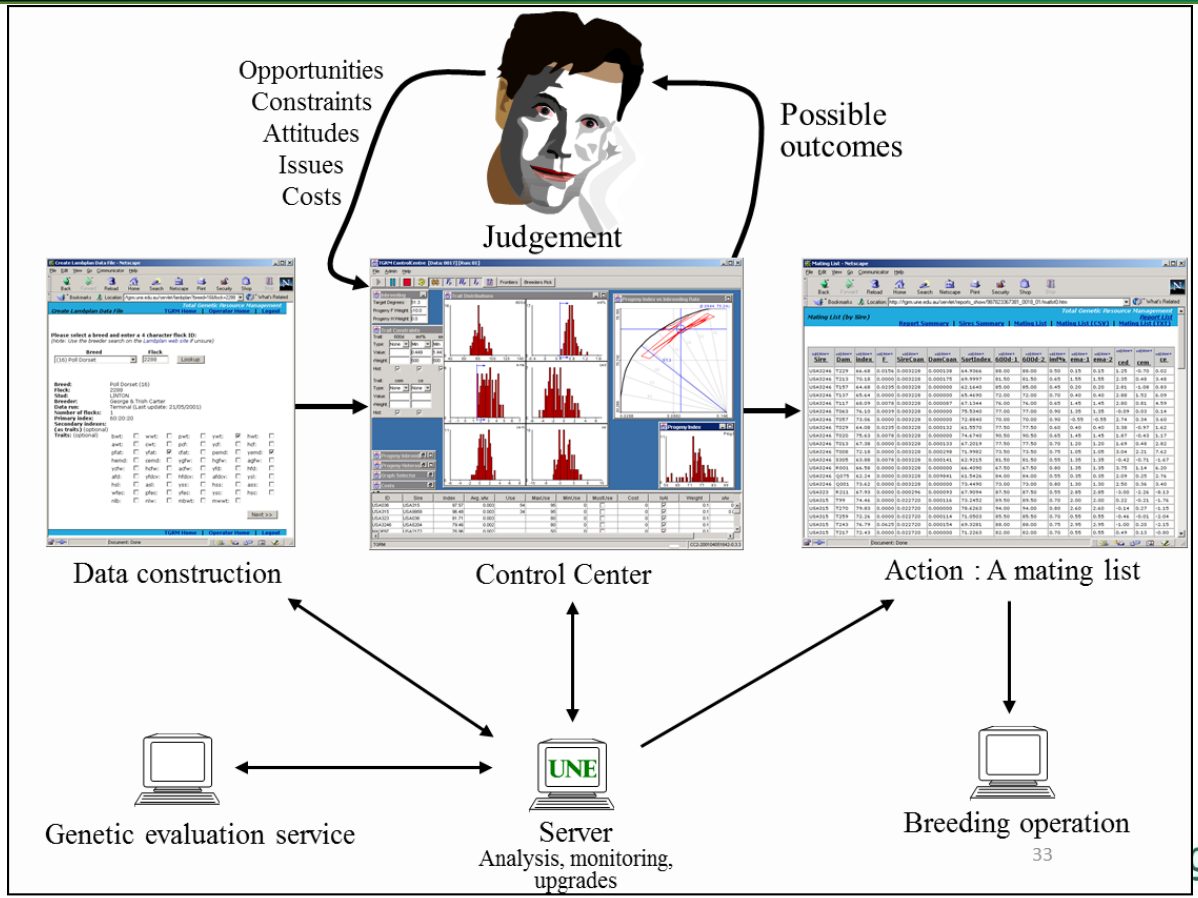
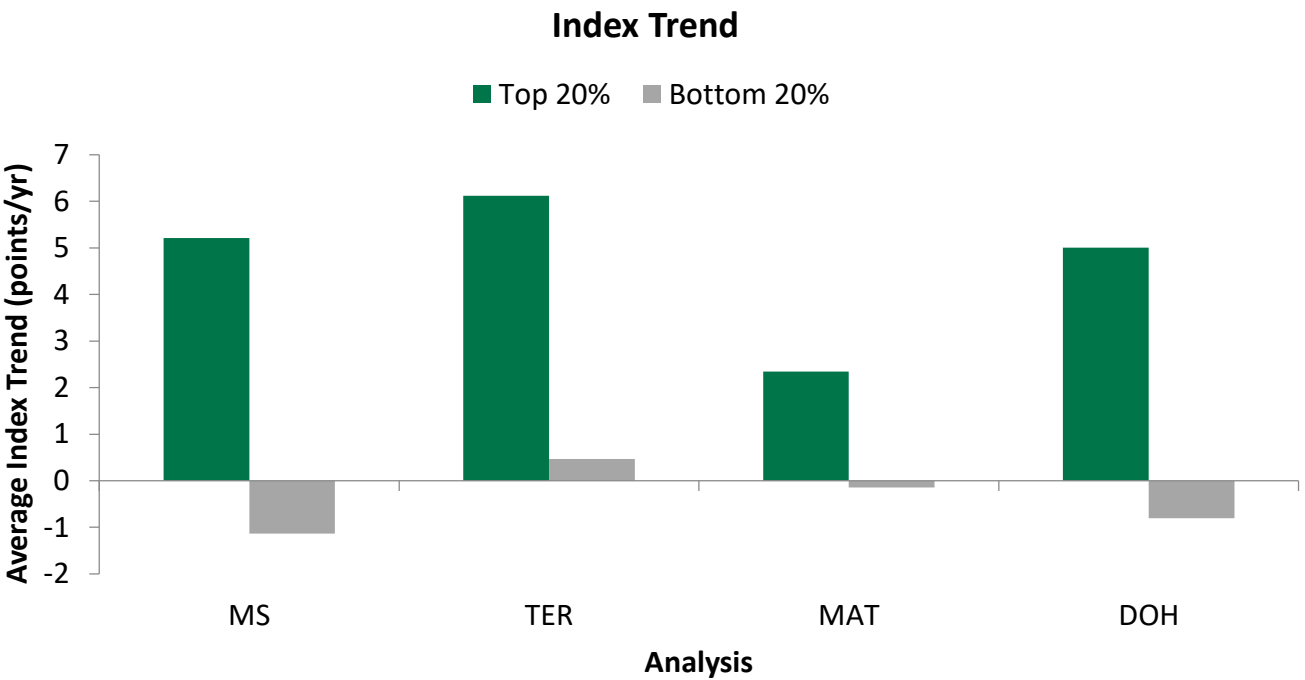
Breeding Program Tools

MateSel


Opportunities
Constraints
Attitudes
Issues
Costs
Judgement
Possible outcomes
Data construction
Control Center
Action : A mating list
Genetic evaluation service
UNE
Server
Analysis, monitoring, upgrades
Breeding operation

RAMping Up Genetic Gain

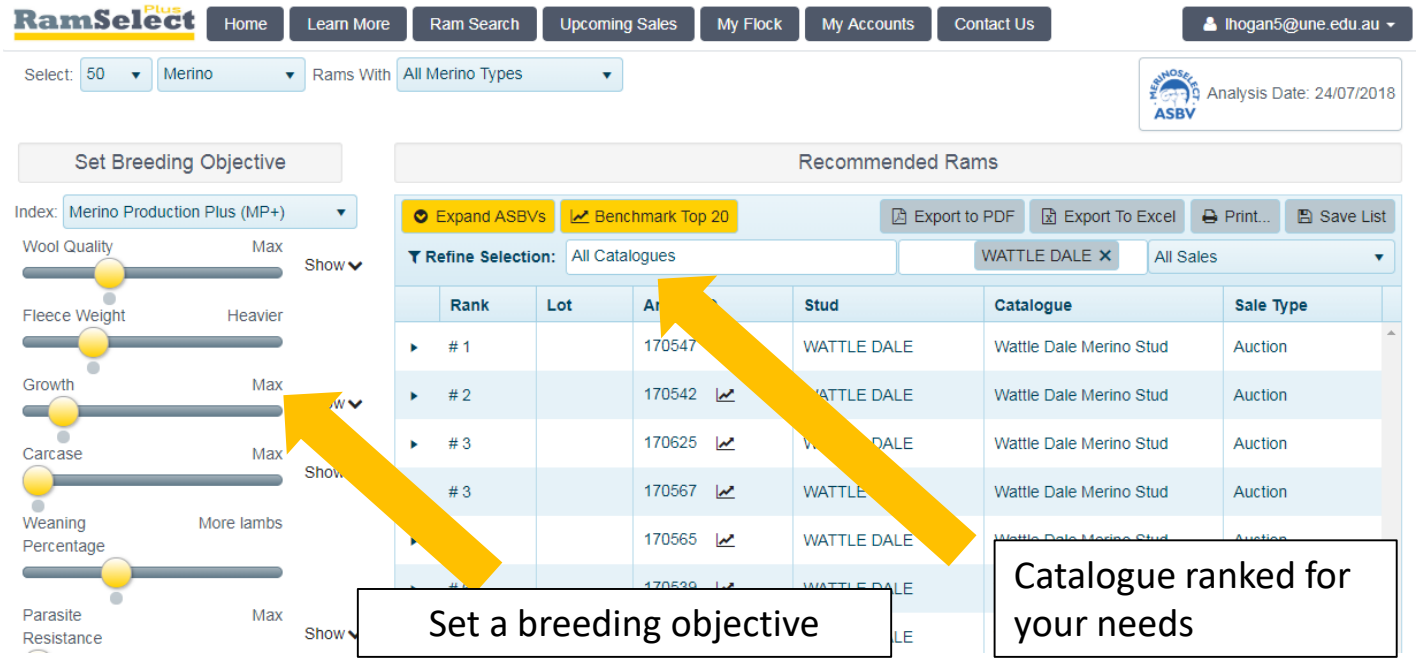


RAMping Up Genetic Gain

Flock based reports on three broad categories;

- Data Quality
  - Influences accuracy of selection
- Average sire & dam age
  - Indication of generation interval
- How well ASBVs are used to make selection decisions
  - As close as we can get to selection intensity

RamSelect

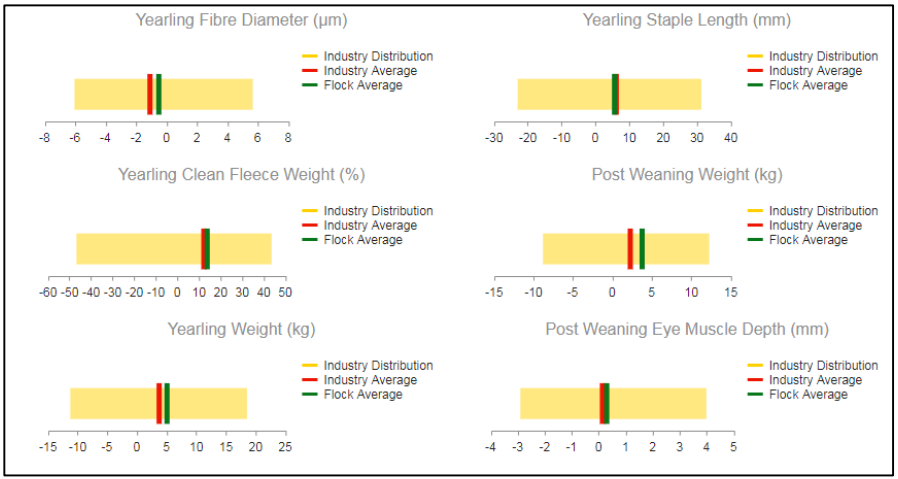

RamSelect Plus
Home
Learn More
Ram Search
Upcoming Sales
My Flock
My Accounts
Contact Us
lhogan5@une.edu.au
Select: 50
Merino
Rams With
All Merino Types
Analysis Date: 24/07/2018
Set Breeding Objective
Index: Merino Production Plus (MP+)
Wool Quality
Max
Show
Fleece Weight
Heavier
Growth
Max
Carcase
Max
Weaning Percentage
More lambs
Parasite Resistance
Max
Show
Recommended Rams
Expand ASBVs
Benchmark Top 20
Export to PDF
Export To Excel
Print...
Save List
Refine Selection:
All Catalogues
WATTLE DALE
All Sales
Rank
Lot
Stud
Catalogue
Sale Type
1
170547
WATTLE DALE
Wattle Dale Merino Stud
Auction
2
170542
Wattle Dale Merino Stud
Auction
3
170625
Wattle Dale Merino Stud
Auction
3
170567
Wattle Dale Merino Stud
Auction
170565
WATTLE DALE
Set a breeding objective
Catalogue ranked for your needs

What's my benchmark? Flock Profile Test

Flock Profile Genomic Test

- 20 randomly selected ewes
- Flock average estimates
- CFW, FD, SL, EMD, WT, CV, FAT, Curv, indices

SHEEPDNA



RamSelect.com.au

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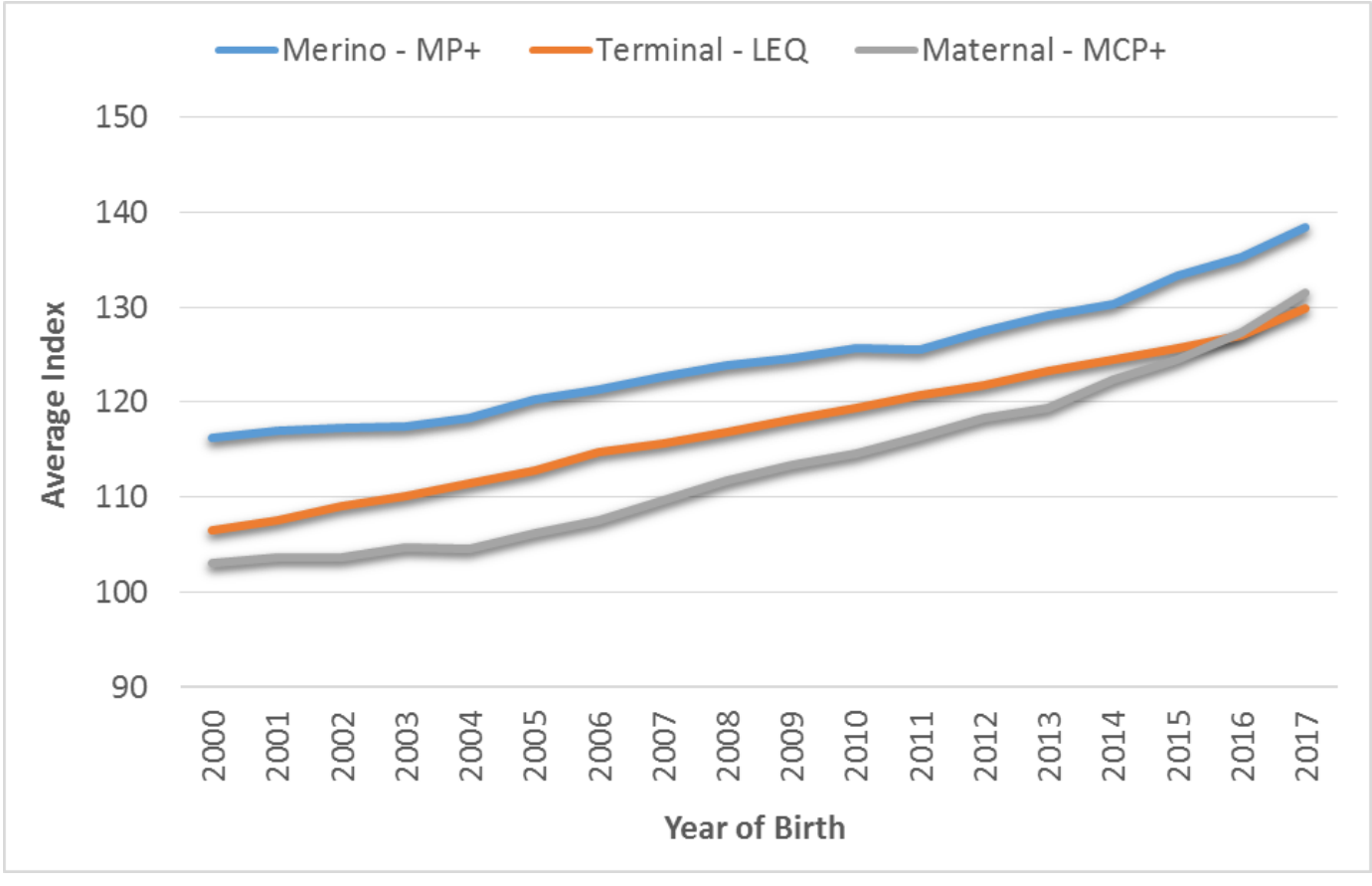
Genetic Progress



Impact on industry (genetic gain - index points/year)

- Summary of genetic progress since 2011
- 33 Terminal flocks with significant numbers of genotypes over last 5 years

	2000-2010	2011-2017	
Terminals (LEQ)	1.36	2.00	+47%
Terminals (C+)	3.85	4.29	+11%
Merinos (MP+)	1.57	2.19	+39%

Confounded with;

- Index development
- Genetic parameters (r_g)
- Industry awareness
- Reference population

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Conclusions

- Single step analysis fully implemented
- Process of continual improvement
  - Traits
  - Models
  - Computational capacity
- Working with industry on breeding program design

Acknowledgements

- Special thanks to;
  - Andrew Swan
  - Phillip Gurman
  - Nasir Moghaddar
  - Sam Clark