Sheep Genetics
2016 Analysis Upgrades Webinar

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Agenda

1. Sheep Genetics Introduction
2. Analysis Changes
3. Impact of changes to ASBVs
4. RAMping Up Genetic Gain
5. Regional Forum Dates

We will stop for questions after the main sections
Sheep Genetics Introduction

• David Rubie is back full time

• Welcome to Clara Collison – LAMBPLAN

• Management Agreement and business plan is in planning process
Changes to OVIS and Routine Analyses
Summary

- **New traits added**
  - PSS and PSL
  - A5 and A6

- **Reproduction analysis**
  - Pregnancy scans now utilised
  - Grouping improved

- **New carcass analysis**
  - Single step multiple trait
  - Maternal effect for cwt

- **Visual traits**
  - Exclusions
  - Reporting more ASBVs (Col, Frot, Char, Wth)

- **New Indexes**
  - Maternal and Terminal
New traits

• Post weaning SS and SL
  – Merino and Dohne
  – In MERINOSELECT
    • 45,423 records for psl and 12,543 for pss

• Additional repeat adult weight and wool traits
  – 5 and 6 year old
  – Adult weights for all analyses
### Additional adult records available in MS

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Changes to reproduction analysis
Changes to the reproduction analysis

• Now using pregnancy scan data
• adding nlb records for ewes which do not have lambing records
• Only through mating module
• Grouping
  – Merging lambing groups with pregnancy scan groups
  – Changed OVIS to have different CG for nlb and nlw

• Must supply
  – Mate date, conception method and groups
  – Scan date and result
  – Service sire
  – Joining weight and condition score desirable
Additional reproduction data

• Merino: 16,737 preg scans which will be used from 17 flocks and 60 flock-years.

• Maternal: 9,453 preg scans which will be from 9 flocks and 27 flock-years

• Preg scans change the amount of data used
  – Flock – drop filters
  – Service sire cleaning
  – Eg Merino additional records
    • Approx 35k nlb
    • Approx 13k nlw
New carcase Analysis
Carcase and E.Q. ASBVs

- RBVs have been available since 2011:
  - Lean meat yield and dressing%
  - Carcase eye muscle and fat
  - Intra-muscular fat and shear force

- Single trait analyses

- Including genomic information via “single step”

- Limited in scope:
  - Resource population animals with measurements and genotypes
  - Animals genotyped by breeders in pilot projects etc
  - Some animals via pedigree

In 2016 we make the transition from RBV to ASBV
The new analysis for carcass and E.Q. ASBVs

- Full multi-trait single step genomic analysis:
  - Body weight and scan traits
  - Carcase and eating quality traits

- Data from all LAMBPLAN animals from 2000 year of birth

- All animals will have breeding values for all traits → reporting still subject to accuracy thresholds

- ASBVs for eating quality traits now available for many more animals

- ASBVs from this analysis used to build eating quality indexes
How to get ASBVs for carcass and E.Q.

- Need linkages to the genomic resource population
- Use sires who have been genotyped and progeny tested
- Enter sires for progeny testing
- Genotype your ram selection candidates
The move to Single Step analyses
SS increases accuracy via better relationships

- **Half sibs:**
  - From pedigree only we expect half sibs to have 25% of genes in common
  - From genomic tests we observe that this ranges from 15 to 40%

- **Full sibs with genomic information we can separate:**
  - Identical twins (100% common genes)
  - Full sibs (40 to 60%)
  - Half sibs by different sires in syndicate matings

- **Animals unrelated through the pedigree:**
  - Genomic information can show 2 – 10% genes in common between many animals
  - These relationships underpin genomic reference populations
Increased complexity with SS analysis

• Need to be able to efficiently reconcile differences between pedigree and genomic information:
  – What do we do when pedigree says two animals are related but genomics says they are not?

• Diagnosing changes in ASBVs will be more complicated with genomics because there are many more potential relationships between animals to investigate

• Accounting for the impact of genomic information on multi-breed sheep data has not been fully resolved

Single Step research is ongoing, and the goal is to increase ASBV accuracy
Changes to Visual Analysis
Visual trait analysis changes

• Visual trait exclusions

• Reporting ASBVs for additional visual traits
  – There are visual traits currently analysed which will now be reported
    • wool colour
    • fleece rot
    • Character
    • staple weathering (although there is limited data being collected for staple weathering in industry flocks)
New Indexes
Index changes

• Index Development Webinars
  – Maternal  [www.youtube.com/watch?v=JQX0N2RxWNQ](https://www.youtube.com/watch?v=JQX0N2RxWNQ)
  – EQ  [www.youtube.com/watch?v=0P7_c14VAkg](https://www.youtube.com/watch?v=0P7_c14VAkg)

• Maternals
  – BLX  = Border Leicester crossing system
  – MatC  = Commercial Maternal carcase
  – MatC+  = Commercial Maternal carcase + fleece and WEC

  – Need to measure important traits

• Terminals
  – CPLUS + Eating quality traits
  – LP2020 + Eating quality traits

  – Need to measure EQ - genomics
Impact on ASBVs

- Merino
- Dohne
- Maternal
- Terminal - RBVs
MERINOSELECT Analysis

- PSS and PSL
- Extra adult records
- Repro
  - Preg scans
  - Better Grouping
- Visual trait exclusion
MERINOSELECT Analysis

MPPtest_v10

\[ y = 1.0046x - 0.5478 \]

\[ R^2 = 0.8892 \]
Dohne Analysis

• Extra traits
  – PSS and PSL
  – Adult records

• Reproduction analysis upgraded to latest version of OVIS
  – Previously had own version of parameters without Yearling trait
  – Y now separate trait
    • More records being used
  – Can use pregnancy scans – no data as yet
  – Better grouping
Dohne Analysis

DOHNE_S05, Acc>0, n=176813, r=0.99

DOHNE_S05, Acc>25, n=174901, r=0.99

DOHNE_S05, Acc>50, n=87744, r=0.99

DOHNE_S05, Acc>75, n=128, r=0.98
Dohne Analysis

Top 150 on DOHNE index

\[ y = 0.987x + 3.0037 \]

\[ R^2 = 0.9337 \]
LAMBPLAN ~ Maternal

- Additional adult weights
- Repro
  - Preg scans
  - Better grouping
LAMBPLAN ~ Maternal

- Additional adult weights
- Repro~Preg scans
- Better grouping

MATDOLtest_v10

\[ y = 0.9734x + 3.4452 \]
\[ R^2 = 0.8812 \]
LAMBPLAN ~ Terminal

- Additional adult weights
- Repro
  - Preg scans
  - Grouping

- Single step RBV traits are the biggest issue
## INF Sires

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RBVs

IMF

- Acc 50 to 75%
- Acc > 75%
Summary

• New traits
  – PSS and PSL
  – A5 and A6
  – Visual wool traits
• Reproduction
  – Pregnancy scans and better grouping
• Single step carcass and eating quality trait analysis
  – RBVs > ASBVs
• New indexes
  – Maternal review
  – Terminal EQ
Conclusions

• All changes designed to improve ASBVs

• Small effects over whole analysis
  – Some significant changes within some flocks, esp those with
    • Pregnancy scans
    • Adult traits
    • Genotypes

• Get your data in
  – Adult weights and wool info
  – Joining details and pregnancy scans

• Ongoing R&D aimed at delivery of more accurate ASBVs for a wider range of traits
RAMping up genetic gain

Project Aims

• Improve Breeding Program Effectiveness and Genetic gain:
  – Develop series of on farm reports
  – Identify potential barriers to genetic gain through benchmarks
  – Develop clear recommendations

• Develop training package that accredited Service Providers can use

• Allow a more proactive approach
### RAMping up genetic gain

#### Stoplights Report: MERI index2

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Upcoming events for Sheep Genetics

• **Service Provider Workshop**
  - Melbourne, 10\textsuperscript{th} & 11\textsuperscript{th} May

• **Regional Forums**
  - NSW  Armidale, 17\textsuperscript{th} May  Young, 19\textsuperscript{th} May
  - VIC  Wodonga, 24\textsuperscript{th} May  Hamilton, 26\textsuperscript{th} May
  - TAS  Launceston, 9\textsuperscript{th} June
  - SA  Adelaide, 21\textsuperscript{st} June  Mount Gambier, 23\textsuperscript{rd} June
  - WA  Williams, 26\textsuperscript{th} July