

October 2013



Australia's genomic information nucleus (Ginfo)

Jennie Pryce

Genomic information nucleus (Ginfo)

Intro....



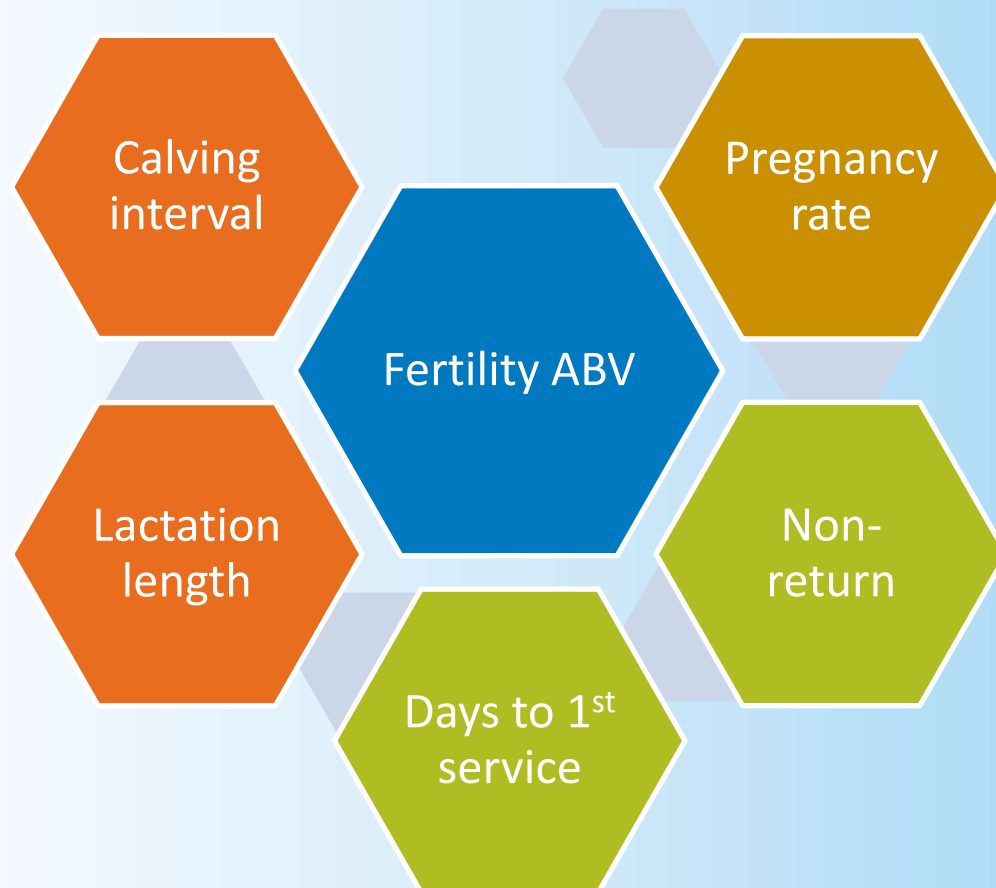
Outline

DFCRC research to improve fertility using genetics

1. New fertility ABV
2. More data
3. Ginfo

Multi-trait fertility model

Launched in April 2013



Bulls born since 2000: Fertility breeding values



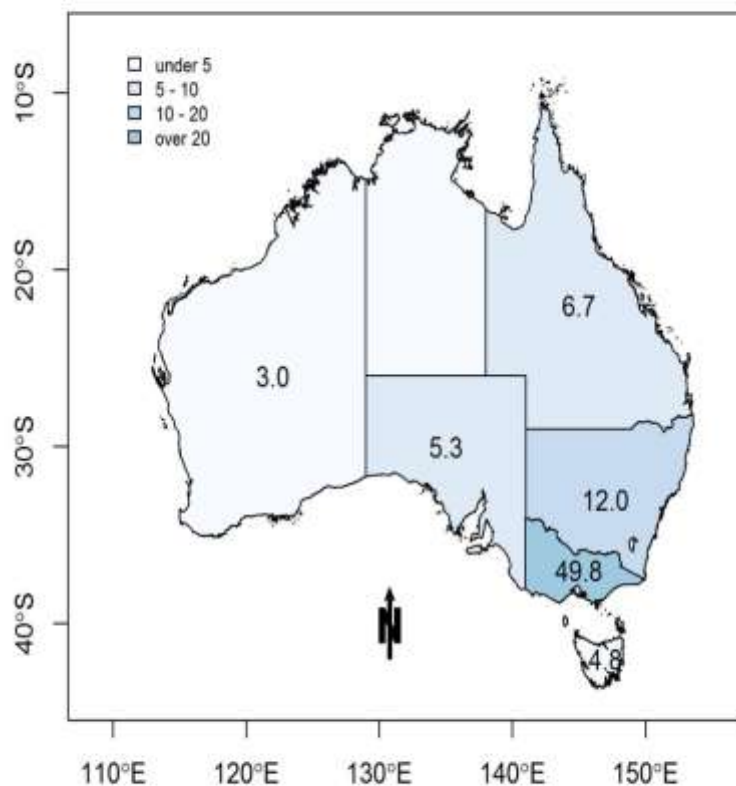
Breed	Number	Reliability OLD	Reliability NEW	Change
Holstein	2421	61.9	68.3	6.5
Jersey	498	62.4	70.0	7.6

Number of bulls with publishable proofs



	Holstein		Jersey	
	Old ABV	New ABV	Old ABV	New ABV
Domestic	3,711	7,038	746	1,350
Interbull	0	55,362	0	2,466
Total	3,711	62,400	746	3,816

Percentage of herds that have insemination data that qualifies for fertility breeding values



- Project underway to increase the amount of fertility data that is captured
- Increase of 18% cows with fertility data that qualifies for ABV calculation in the same period for data extracted in August 2012 and March 2013
 - Increased awareness milk recording companies
 - Actively going out and getting the data



Potential impact of extra data

Fertility breeding values

Breed	Number	Reliability NEW	Reliability + 10% extra data	Reliability + 20% extra data
Holstein	2421	68.3	72	75
Jersey	498	70.0	74	77

Benefits larger for bulls with lower numbers of daughters

Genomic information nucleus (Ginfo)

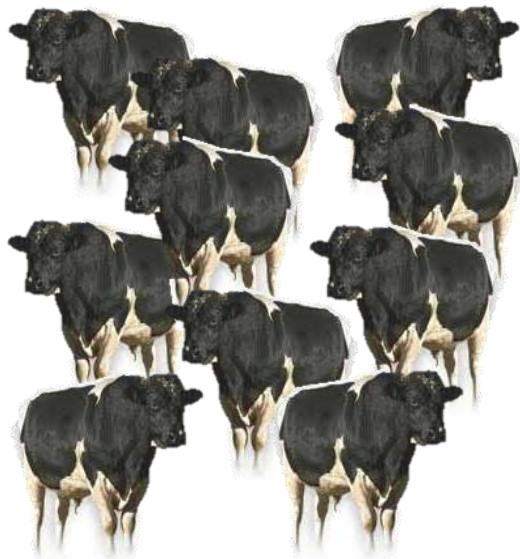


Ginfo

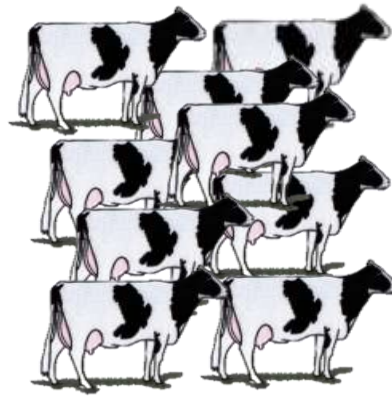
Herds contributing most data to ABVs

Genetic diversity

Holsteins and Jerseys



3719 bulls with
Australian daughters

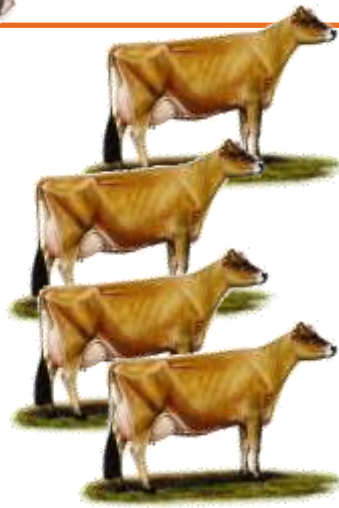


9630 cows
deliberately selected

10,000 cow

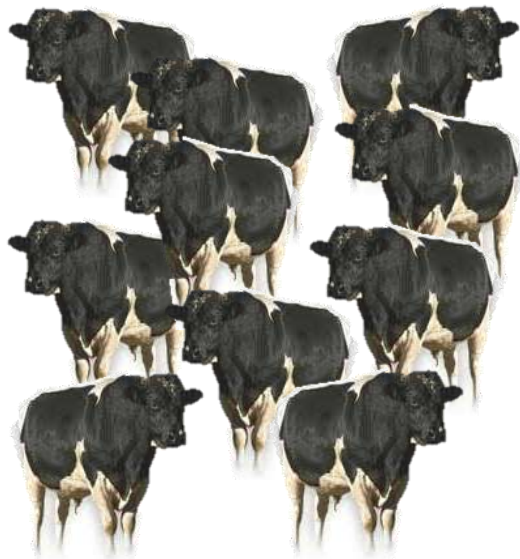


1017 bulls with
Australian daughters

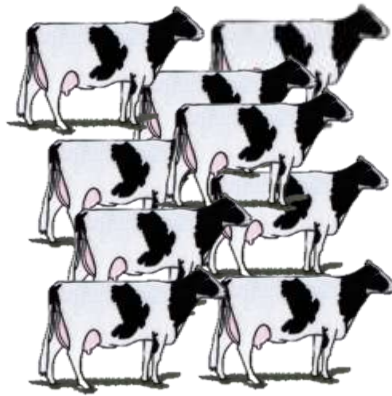


JERNOMICS
4249 cows
deliberately selected

**Australian
National
DNA
Reference
population**



3719 bulls with
Australian daughters

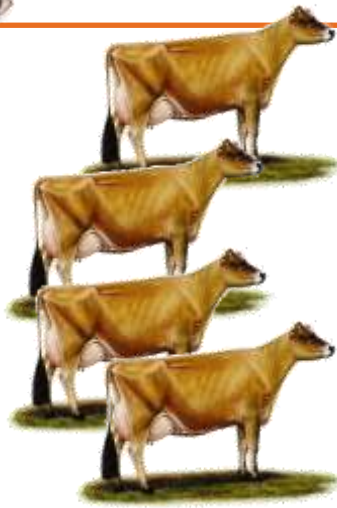


9630 cows
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1017 bulls with
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JERNOMICS
4249 cows
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Ginfo

Genomic information nucleus

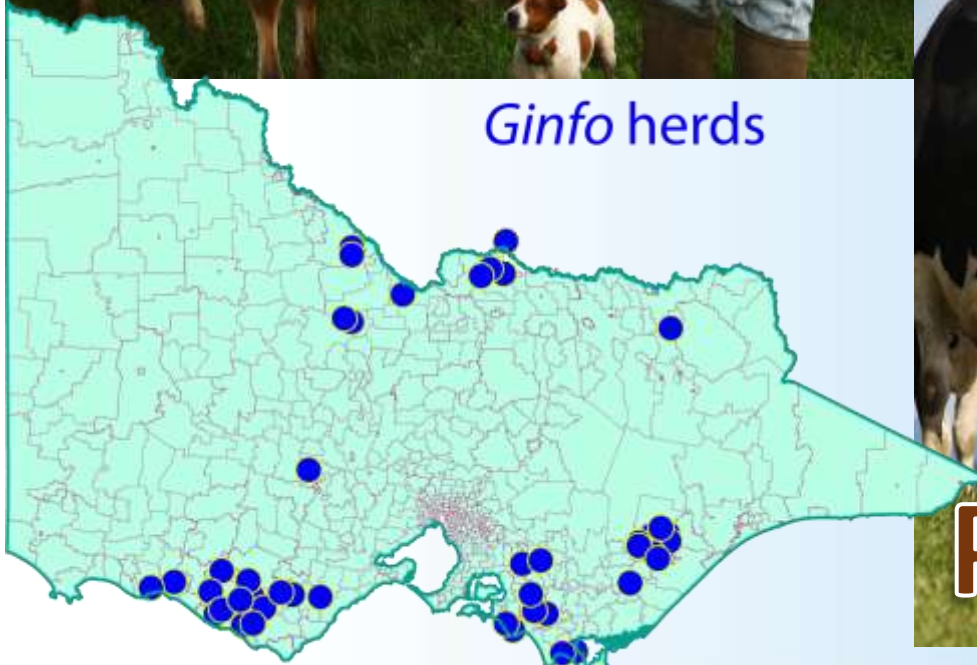
- 10,000 Holstein genomes and Jernomics captured 1 time-point, *Ginfo* is designed to be on-going
- Work with herds with great data, rather than cows with great data
- The reference population needs updating, predictions of genomic breeding values deteriorate as the reference population differentiates from the general population
- Scoring system to identify cows with excellent records

Ginfo ambassadors

Con Glennen



Ginfo herds



Patrick Glass

Ginfo

Better genomics using your herd records

Contact

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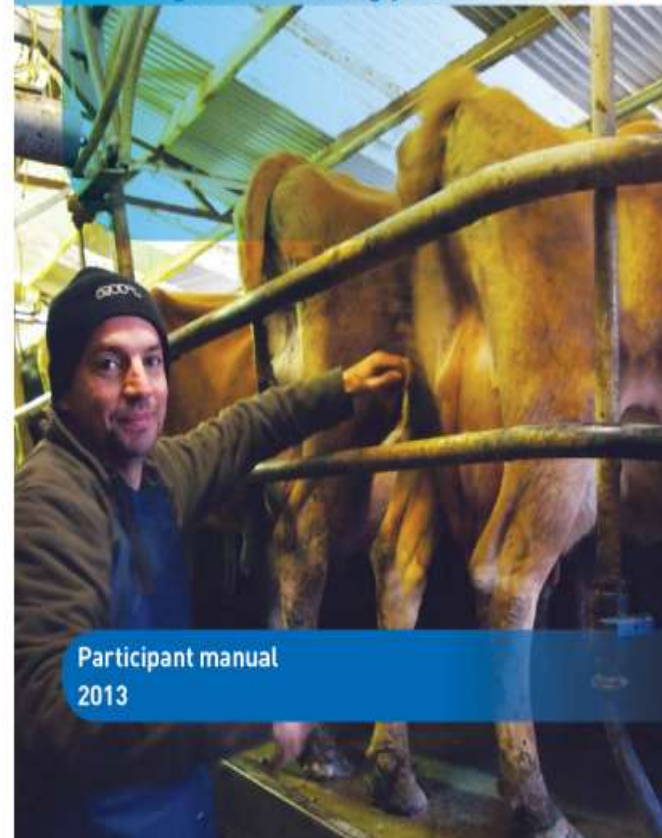
Further Information

Brochure: Collecting tail hair
Youtube video: Tail hair collection for genotyping



August 2013

www.dairyfuturescrc.com.au



Participant manual
2013



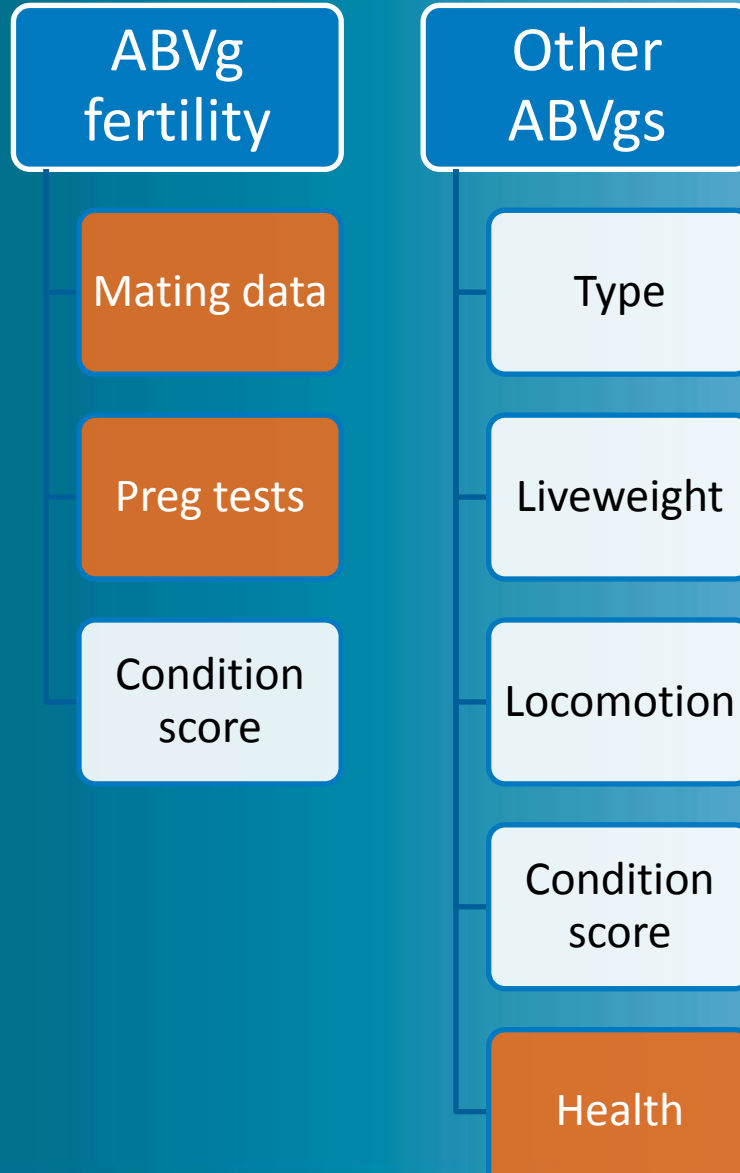
How Ginfo will contribute to ABVgs

Data

30,000+ cows

Great recorders of
herd data

Extra phenotypes
collected by Holstein
Australia



Novel phenotypes (not part of current project)

- Some possibilities...
 - Pregnancy-testing using milk
 - Most cows have preg-test results
 - Pedometers or GPS monitors
 - Fatty acids from blood (some herds) NEFAs etc
 - MIR (mid-infrared technology)

- Free genotyping of lactating cows
- ABVgs for all cows
- Parentage verification
- Two year olds classified
- Reduced cost genotyping of heifers
 - Selection of replacements
- Advance on new reports (to be developed)
- Open days and information sharing

The next 50 Ginfo herds

Search for herds that have great phenotypes

Upgrade
EasyDairy

Best 50 herds selected

All States
included

Invitations
from
January

Ginfo 100 herds
established

Genomic evaluations
enhanced

ABVgs to farmers

Summary

ABVgs will have higher reliabilities because of Ginfo

Ginfo is part of the DFCRC strategy for continuous improvement of genomic predictions and fertility phenotypes for Australia

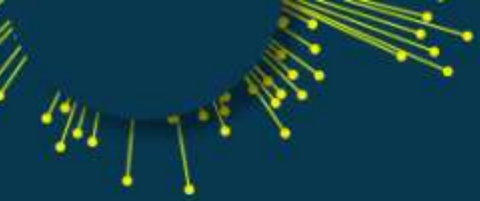
Ginfo will help to improve fertility through genetics



Acknowledgements

- Ginfo farmers
- Dairy Futures CRC
- DEPI
- ADHIS
- Holstein Australia
- Jersey Australia

- Matt Reynolds, Coralie Reich, Thuy Nguyen, Ben Hayes, Rohan Butler, Phil Bowman, Pete Williams, Mekonnen Haile-Mariam, Oscar Gonzalez-Recio



Questions?

www.dairyfuturescrc.com.au



In the age of the genotype.....



PHENOTYPE IS KING!



Prof Mike Coffey (SRUC, Edinburgh)



Reliability of fertility with genomics

Group	Pre-genomics	Post-genomics	Change
Young sires	0.16	0.38	0.22
Progeny test	0.44	0.55	0.10
2 nd crop	0.79	0.80	0.01

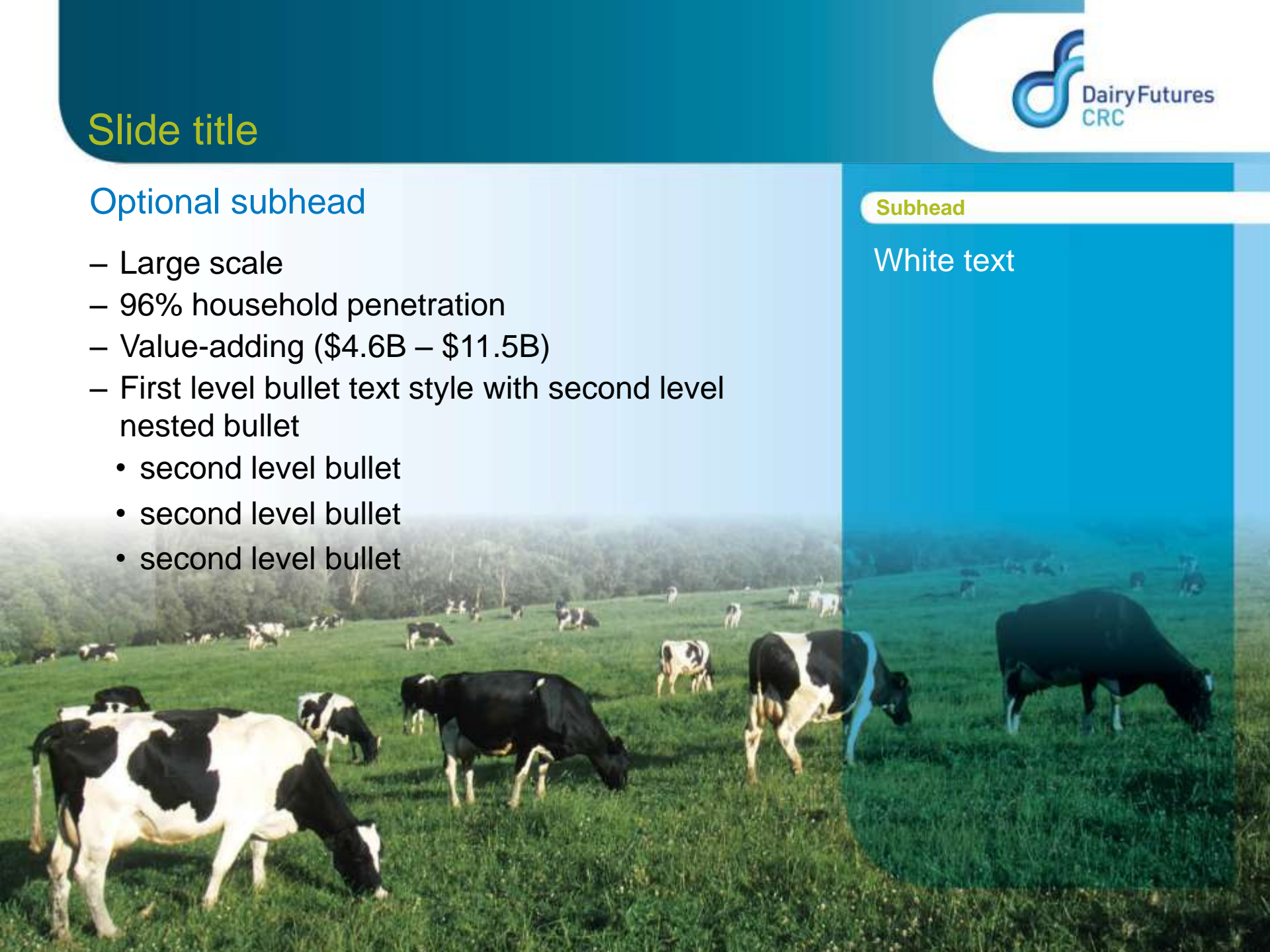
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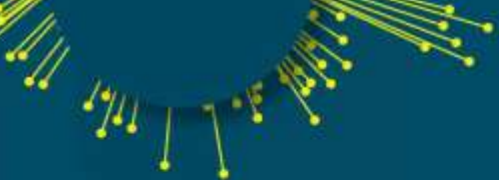
Optional subhead

- Large scale
- 96% household penetration
- Value-adding (\$4.6B – \$11.5B)
- First level bullet text style with second level nested bullet
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Subhead

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Slide title

Genomics making a difference to fertility

A new genomic information nucleus (Ginfo) established

A new multi-trait fertility ABV has just been released

We are working towards getting more mating and pregnancy test data to get the most out of this model!

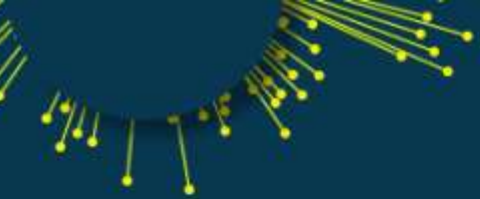


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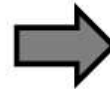
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Use of MIR spectra

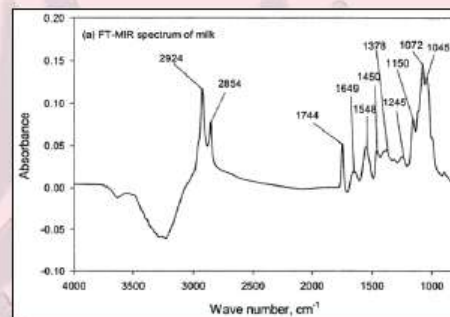
Milk recording



Mid infra-red spectrometry



MIR spectra



Calibration
equations

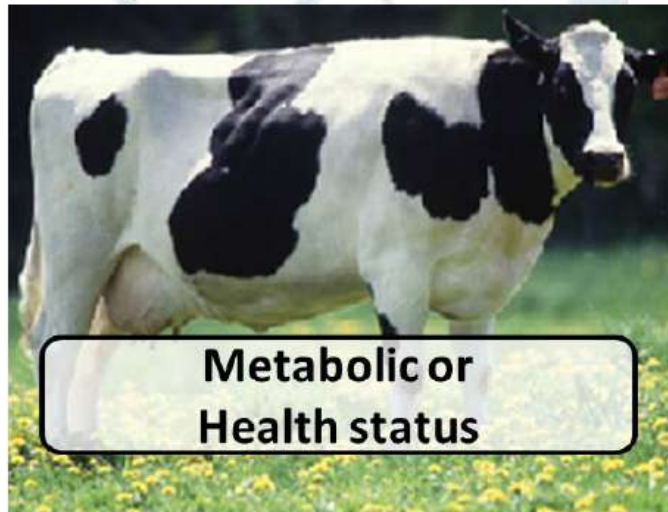
Reference
data

Milk components

Fat
Protein
Urea
...



First predict milk composition ... Then predict status of the cow



Reference
data

Prediction
equations

Milk components
Fat
Protein
Urea

+
Fatty acids
Minerals
Lactoferrin
....



Presenter's name

www.dairyfuturescrc.com.au

