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The next generation of genetic technologies

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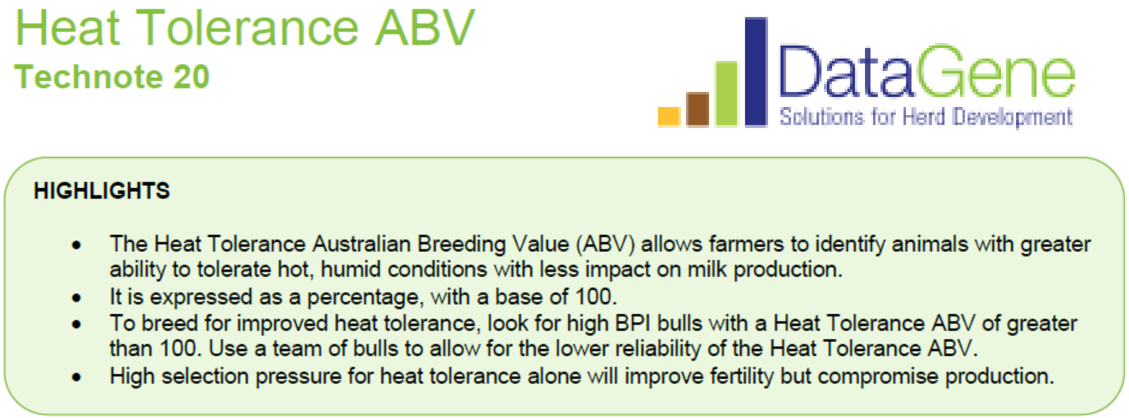
Australian Genomics Highlights

Genomic breeding values for lamb eating quality traits

SHEEP CRC



Heat Tolerance ABV

Technote 20

DataGene
Solutions for Herd Development

HIGHLIGHTS

- The Heat Tolerance Australian Breeding Value (ABV) allows farmers to identify animals with greater ability to tolerate hot, humid conditions with less impact on milk production.
- It is expressed as a percentage, with a base of 100.
- To breed for improved heat tolerance, look for high BPI bulls with a Heat Tolerance ABV of greater than 100. Use a team of bulls to allow for the lower reliability of the Heat Tolerance ABV.
- High selection pressure for heat tolerance alone will improve fertility but compromise production.

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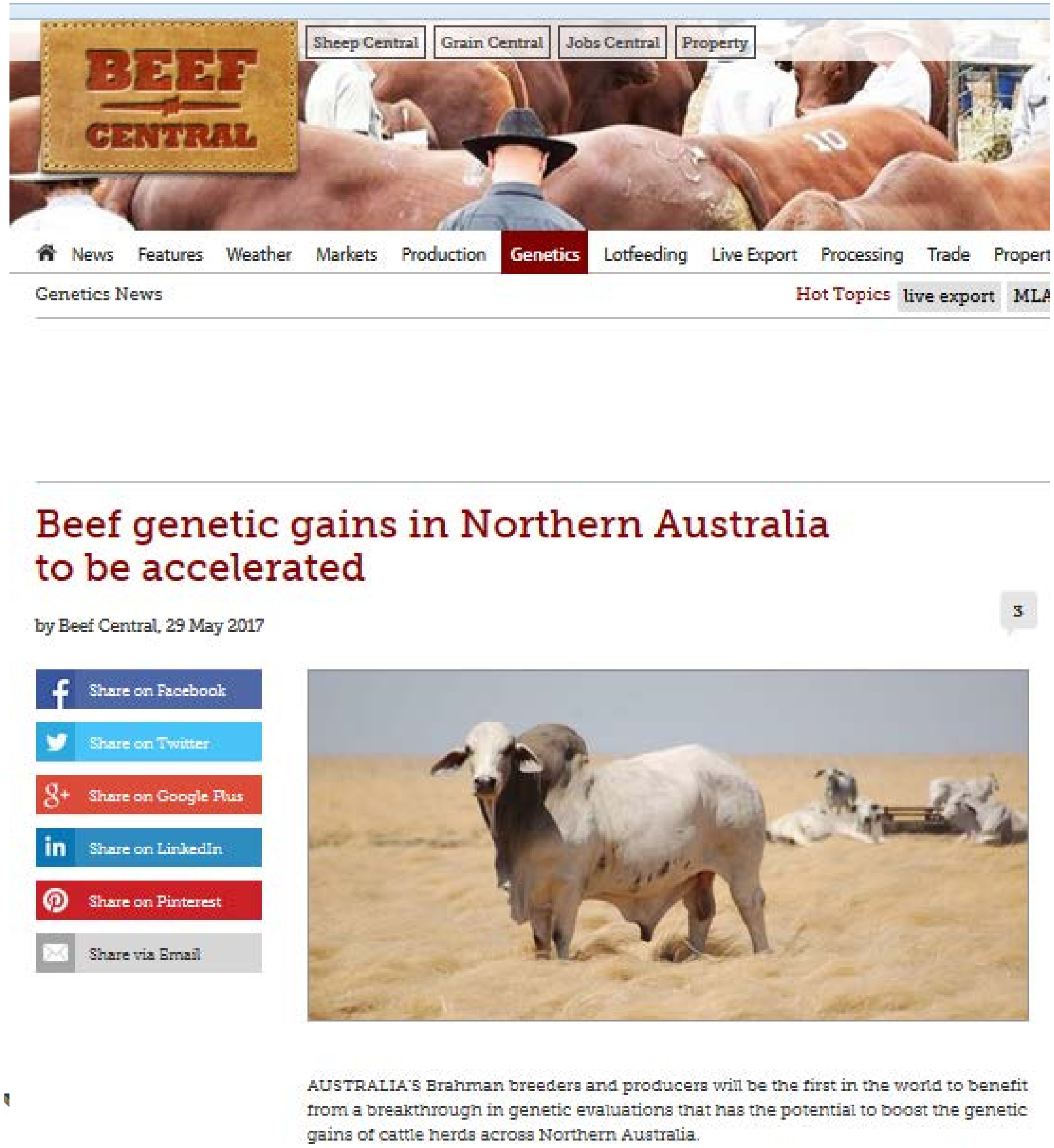

Beef genetic gains in Northern Australia to be accelerated

by Beef Central, 29 May 2017

AUSTRALIA'S Brahman breeders and producers will be the first in the world to benefit from a breakthrough in genetic evaluations that has the potential to boost the genetic gains of cattle herds across Northern Australia.

Brahman single step for days to calving

AGBU, BREEDPLAN

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Where to next?

- More accurate -> faster gains
- Works in any breed/crossbred/composite
- For traits that have been hard to breed for (fertility/feed efficiency)
- Genomics -> management

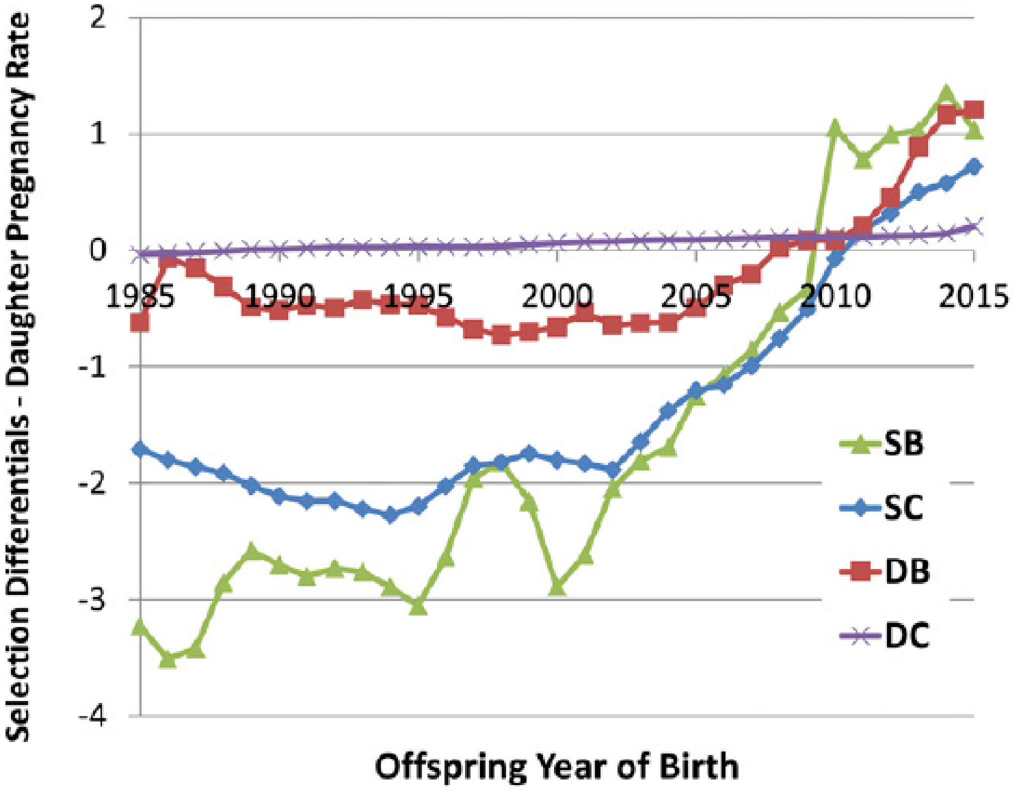
Learnings from Dairy

- Ginfo project – genotype 30,000 cows in commercial dairy herds (main emphasis good fertility records)
- Accuracies genomic breeding values for young genomic bulls now quite high
- Every young bull genotyped, >50% use of "young genomic sires"

Trait	Accuracy
BPI	79
Production	87
Survival	69
Fertility	69
Feed efficiency	54

It works

- Double rate of genetic gain



García-Ruiz et al. Proc Natl Acad Sci U S A. 2016 113(28):E3995-4004

Where to next?

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Multi-breed genomic evaluations

- Structured populations
- Commercial data

Repronomics

- David Johnston (AGBU)
- Industry sires
  - Brahman, Droughtmaster, Santa
- Heifers evaluated for fertility 3 sites
  - Brian Pastures, Spyglass, Douglas Daly
- All genotyped
- Great data coming in

Northern Genomics Project

- 33 Herds with
  - large management groups
  - Multiple breeds/crosses/composites in same group
  - Range of environments
- Record
  - cycled or not at 15/18 months (heifers), wet rebreed (pregnant or not for lactating cows)
  - Temperament scores, udder and teat scores
- 30,000 cows in herds across the North
- Environment: Pasture monitoring, faecal NIR

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Multi-breed genomic evaluations

- Structured populations

- Commercial data

- Will it work?

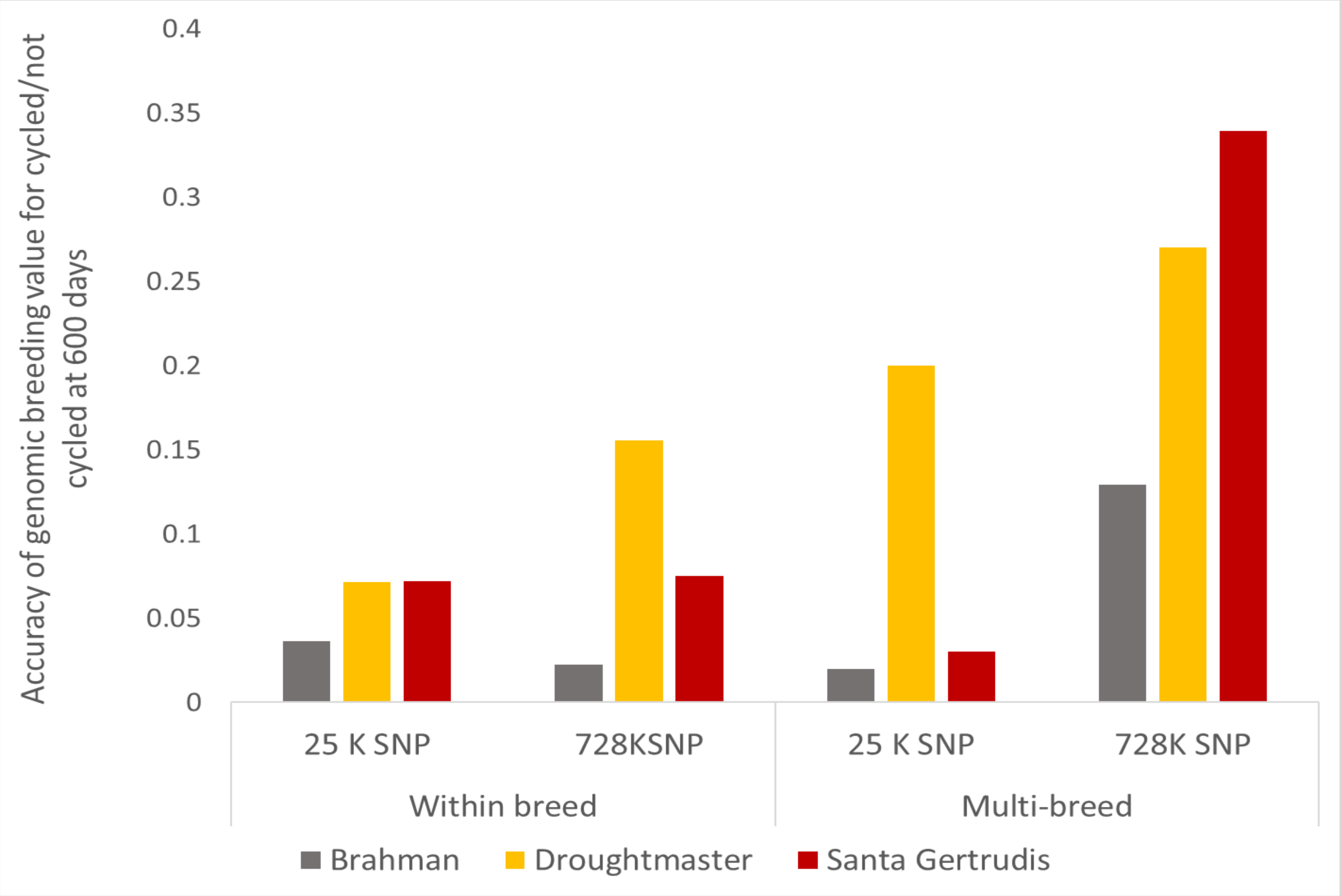
Multi-breed genomic evaluations

- Smart Futures Project (Brian Burns)
- 7 Collaborating herds with 979 Brahman, 1803 Santa Gertrudis, 914 Droughtmasters
- Scanned for presence/absence corpus luteum at 600 days -> age at puberty
- Genotyped for 24K SNP

Multi-breed genomic evaluations

- Does information from other breeds help accuracy of genomic breeding values for target breed?

Multi-breed genomic evaluations



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Crush side genotyping

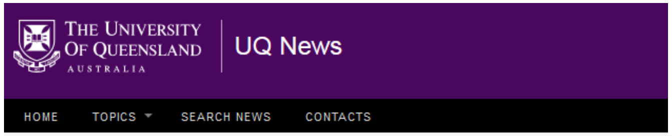
Portable DNA sequencers help African farmers fight crop disease

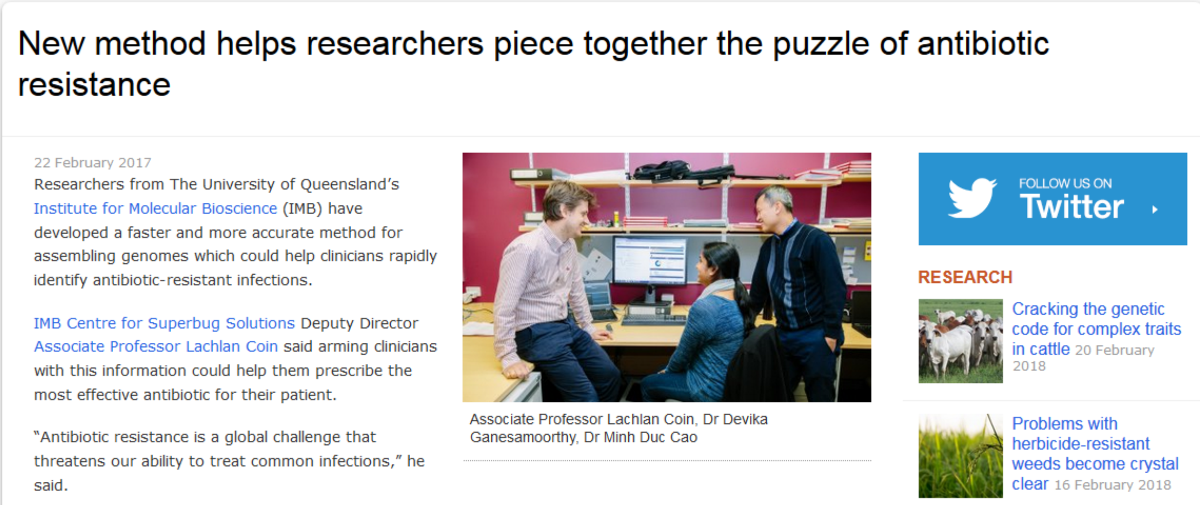
September 18, 2017 by David Stacey, University of Western Australia

Scientists at The University of Western Australia are using new portable DNA sequencing technology for the first time in East Africa to help farmers fight the devastating impact of crop disease.

Farmers struggling with diseased cassava crops can take immediate action to save their livelihoods based on information about the health of their plants, using the portable, real-time DNA analysis device.

The DNA handheld sequencer, called the MinION, was developed by British company Oxford Nanopore. It is being used to identify which strain of virus is destroying the cassava crops of farmers in Tanzania and Uganda as part of a collaboration of scientists and farmers, known as the Cassava Virus Action Project (CVAP).





New method helps researchers piece together the puzzle of antibiotic resistance

22 February 2017

Researchers from The University of Queensland's Institute for Molecular Bioscience (IMB) have developed a faster and more accurate method for assembling genomes which could help clinicians rapidly identify antibiotic-resistant infections.

IMB Centre for Superbug Solutions Deputy Director Associate Professor Lachlan Coin said arming clinicians with this information could help them prescribe the most effective antibiotic for their patient.

"Antibiotic resistance is a global challenge that threatens our ability to treat common infections," he said.

Associate Professor Lachlan Coin, Dr Devika Ganesamoorthy, Dr Minh Duc Cao

Cracking the genetic code for complex traits in cattle 20 February 2018

Problems with herbicide-resistant weeds become crystal clear 16 February 2018

The Economist

AUGUST 18TH–24TH 2012

Economist.com

Paul Ryan: the man with the plan

The rot in India's banks

Generation Xhausted

China, victim of the Olympics?

On the origin of specie

Microbes maketh man

How 90% of the cells in your body are bacteria, the benefits of faecal transplants and other things you would rather not know before breakfast

The future - Feedlot pre-screening

- Can now profile rumen of cattle with sequencing -> which organisms, abundance
- Can we use this to predict performance of cattle for feed efficiency?

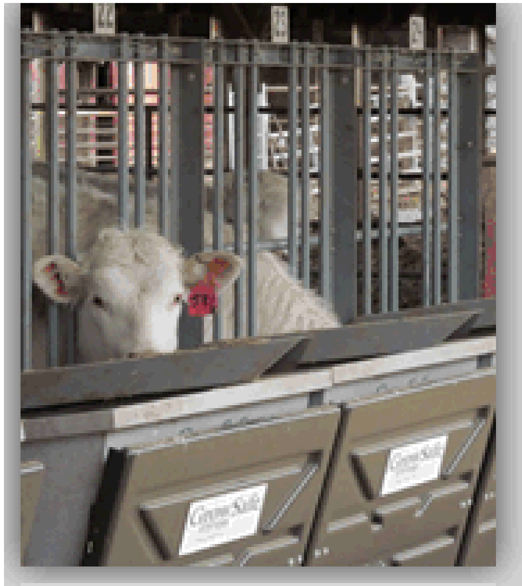


Photo taken at the University of Alberta beef ranch, Kinsella, AB

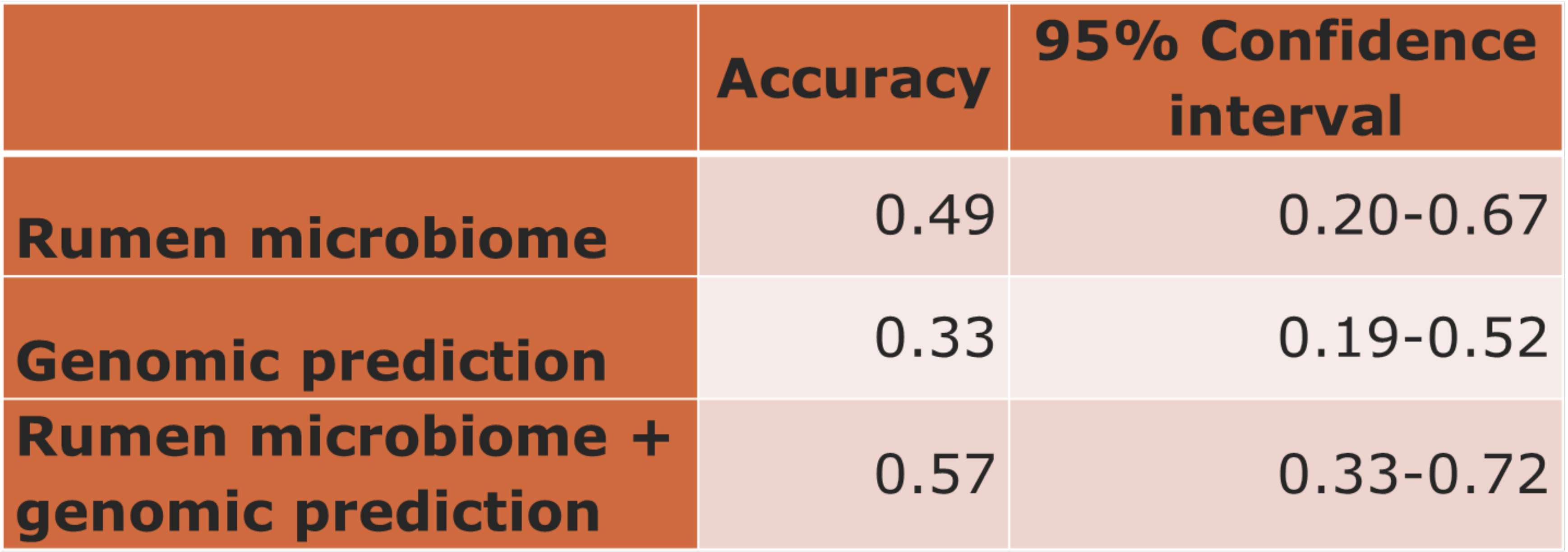
The future - Feedlot pre-screening

- 28 heifers measured for feed efficiency, rumen microbiome profiled

- Accuracy of predicting feed efficiency from rumen microbiome sample?

- Accuracy of predicting feed efficiency from rumen microbiome + genomic prediction

The future - Feedlot pre-screening



	Accuracy	95% Confidence interval
Rumen microbiome	0.49	0.20-0.67
Genomic prediction	0.33	0.19-0.52
Rumen microbiome + genomic prediction	0.57	0.33-0.72

Conclusion

- More accurate genomic breeding values for traits like fertility as reference sets grow -> **balanced breeding**

- Multi-breed genomic breeding values from combination of structured and commercial data -> genomics that works in any breed/cross/composite

- Potential for crush side genotyping, feed lot performance predictions from microbiome + genotype in near future

With thanks

Smart Futures
Brian Burns, Nick Corbet, Jack Allen, Alan Laing, Geoffry Fordyce, Michael McGowan, *Collaborating herds*

Northern Genomics Project
Shannon Landmark, Geoffry Fordyce, Dave Smith, Elizabeth Ross, *Collaborating herds*

DEDJTR Victoria
Min Wang, Jennie Pryce, Hans Daetwyler, Josie Garner, Bill Wales, Thuy Nyguen

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