

Genomics in beef breeding in Australia - 2014

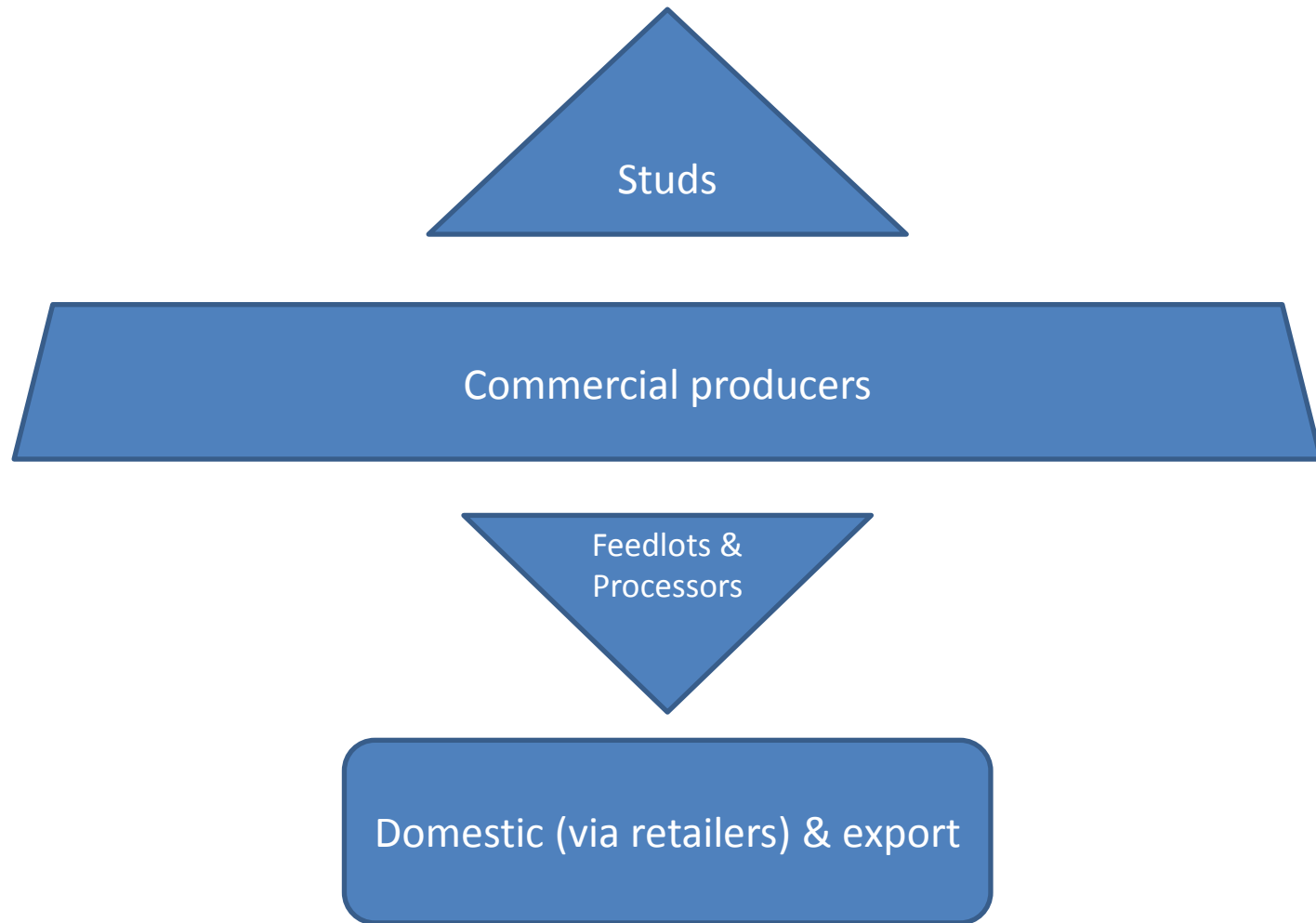
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AGBU

Questions:

- What are the breeding units?
- What have people done to create reference populations, or what do they use as ref pop'ns?
- Are there any plan or visions on what to do next?
- Are there breeding groups (or AI companies) that have implemented new strategies, e.g scanning lots of young bulls, or doing more JIVET or MOET?

Beef production & breeding in Australia I



Beef production & breeding in Australia II

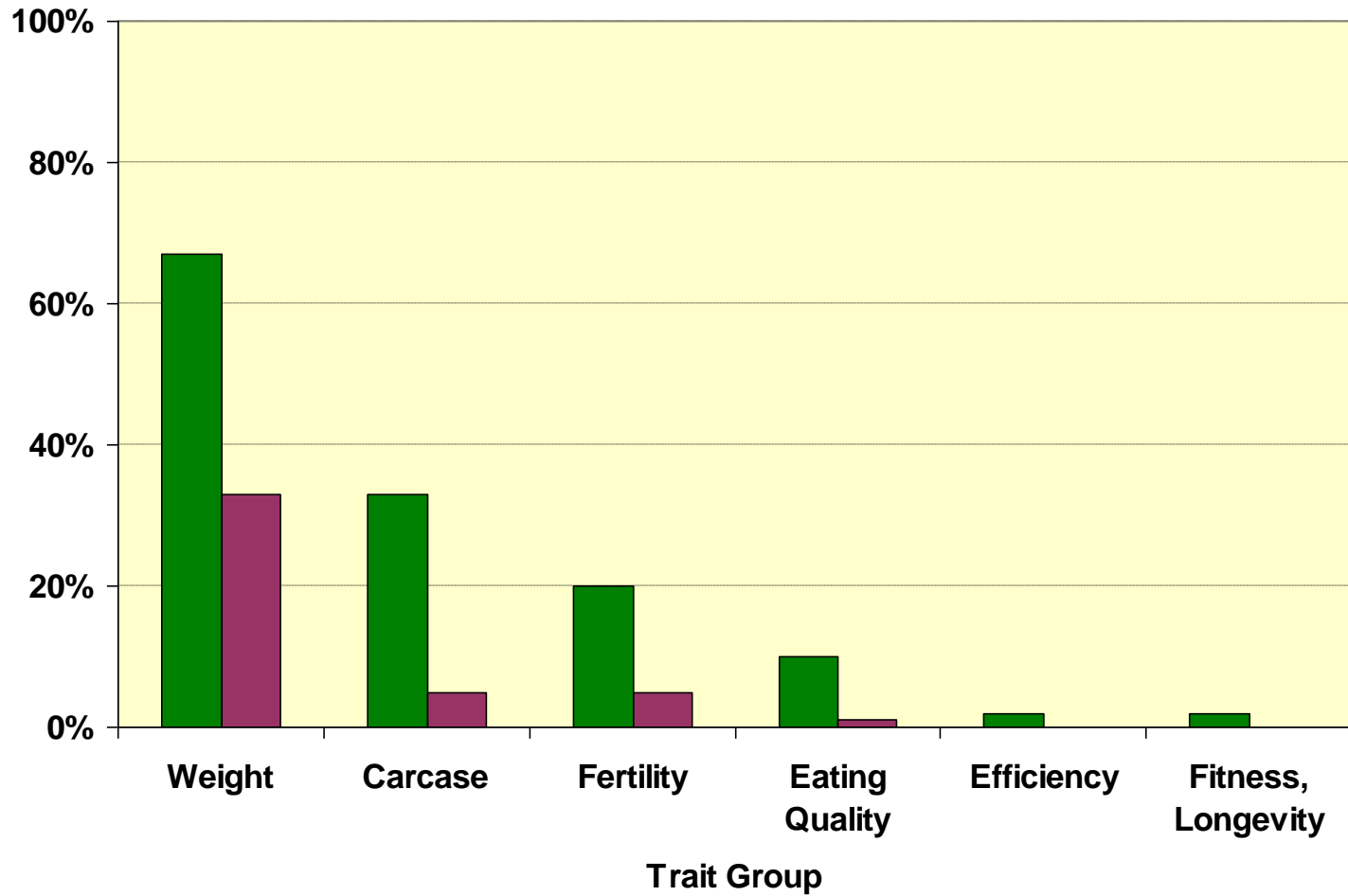
Sector	# Cows	# Businesses	Typical turnover per business	Comment
Stud (nucleus)	0.25m	1,500	<< \$0.25m	8 main breeds Average herd ~ 165 cows Recording \$25 per cow (up to \$00's)
Commercial	10m	50,000	< \$0.25m	60,000 bulls intake pa
Processing/ Feedlots		5-10 processors 5-10 feedlots	Several million	Very small margins
Retail		2 main domestic with 80% market share; 67% exported		Limited brand differentiation to date

Genetic evaluation

- All major breeds use BREEDPLAN
- Across-herd multi-trait evaluation
- Importation significant in Angus, less so in other main breeds
- Genetic trend average \$2.5-3 per cow joined per year (c. 3% of profit pa)
- gaps

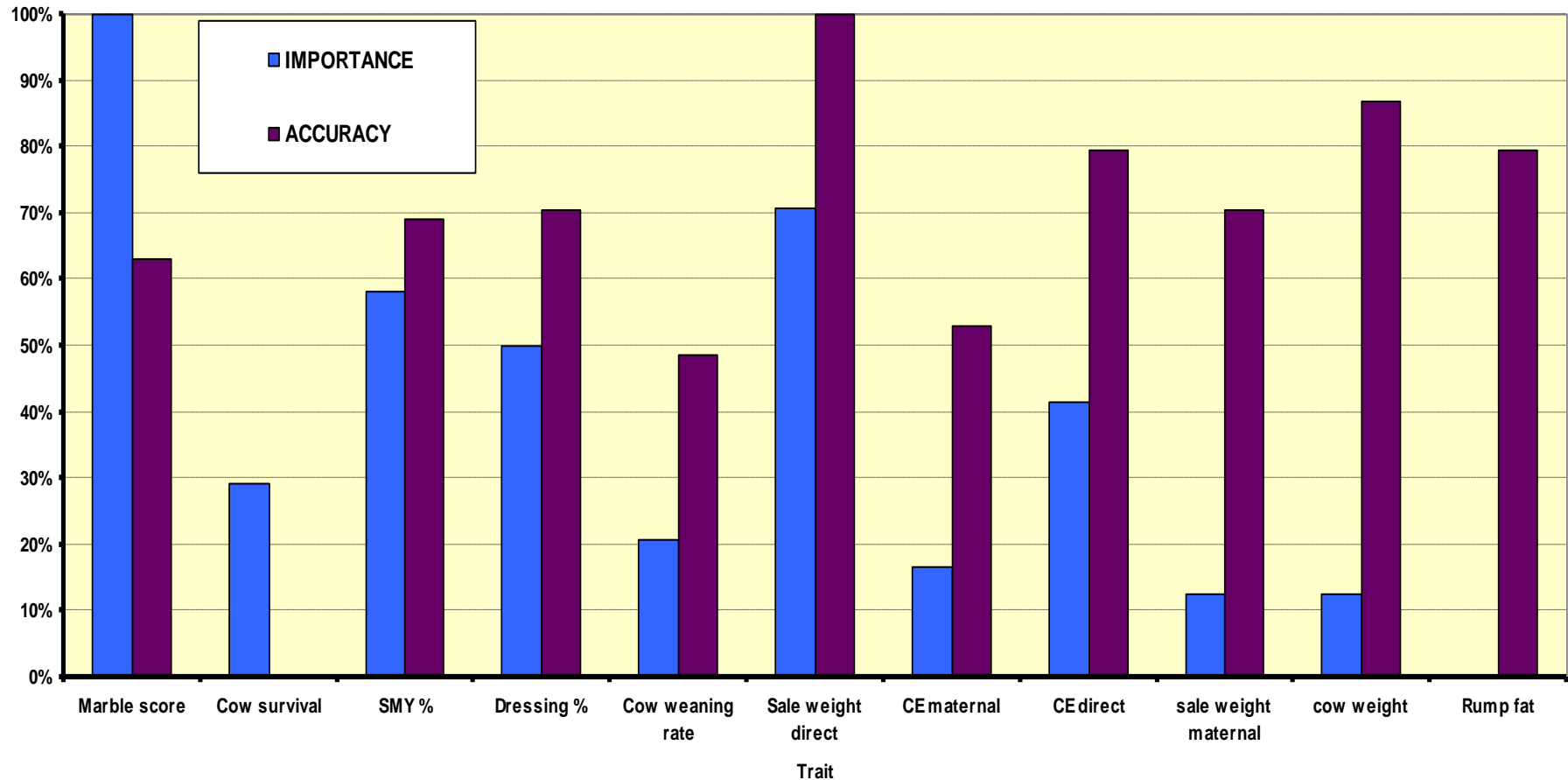
Current recording effectiveness:

Recording effectiveness

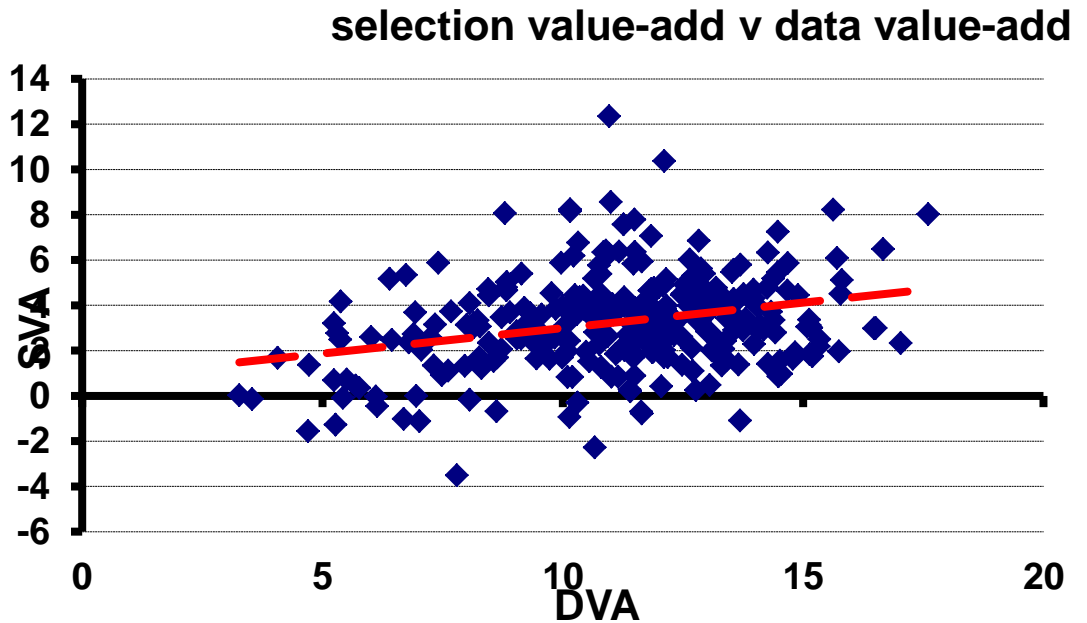
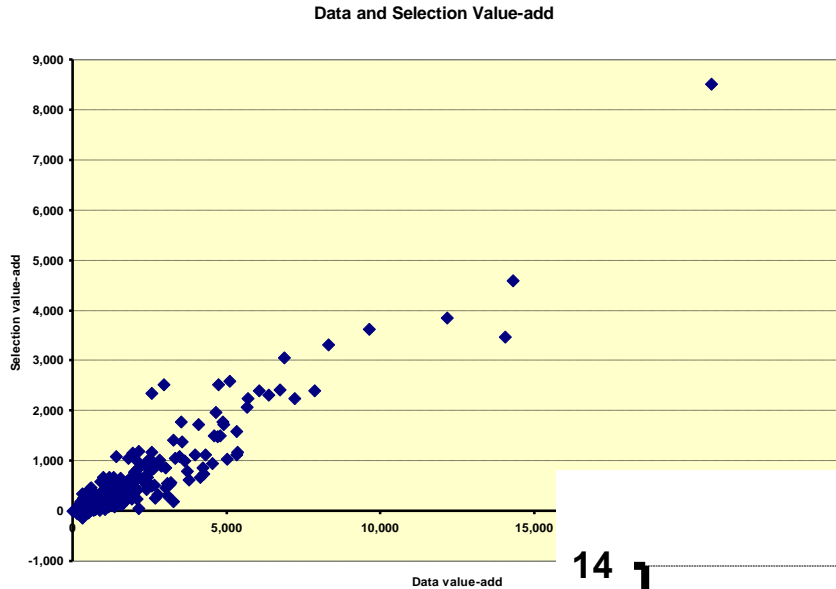


Current recording effectiveness:

Relative Importance and Accuracy



Value-adding in a beef breed:



Genomics to date - I

- CRC 1 and 2 (pre-2005):
 - Focussed more on QTL or small number of markers
 - Lead to GeneStar products
 - Tenderness based on Calpain/Calpastatin
 - Other traits based on very small number of markers
 - Very limited market uptake

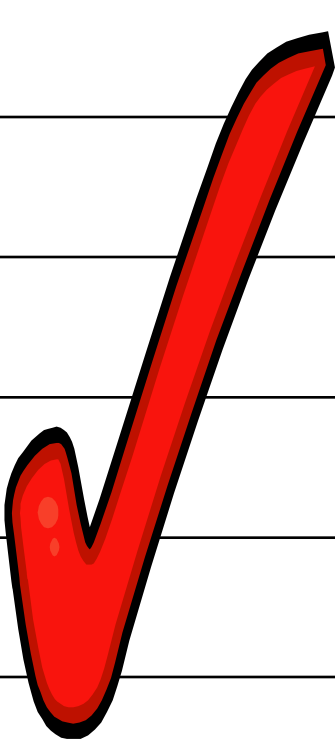
Genomics to date - II

- CRC 3 (2005-2012):
 - Aim to explain X% of variation for key traits
 - Applied GWAS to a number of projects based broadly around progeny tests
 - Multiple breeds
 - Developed strategy for implementation based around prediction equations
 - Moved to snp-based analysis in final stages – developed prediction equations (see later)

Genomics to date - II

- 2010 onwards:
 - In parallel, MLA and breeds developed Information Nucleus projects
 - Progeny test including hard-to-measure traits:
 - Individual feed intake
 - Some eating quality traits
 - Better measures of female fertility
 - Sires (and in some, progeny) genotyping

Information Nucleus projects

Trait group	Progeny per cohort	Sires per cohort	Growth, carcass and EQ Traits	Female Traits
Angus	1,000	>40		
Hereford	400	15		
Brahman	600	15		
				No
Charolais	360	12-15		
Limousin	360	12-15		

Other related R&D projects

- Te Mania
 - Collecting data on commercial progeny of known high merit Angus sires (approximately 1,300 progeny) through feedlot and MSA traits, plus sire genotypes
- Wagyu
 - Collecting data on commercial cattle in feedlot plus genotypes
 - Aiming for 2,000 animals in 1st phase
- Northern Fertility
 - Collecting new fertility traits plus genotyping sires and grand-sires (2-3,000 animals over 5 years)

All data into respective BREEDPLAN analyses, plus GBLUP and single step when available

As $f(p) = \frac{k}{2p(1-p)}$ we have $\int \frac{[2p(1-p)]^2}{2p(1-p) + \lambda_\beta/n_R} \cdot \frac{k}{2p(1-p)} dp = k \int \frac{2p(1-p)}{2p(1-p) + \lambda_\beta/n_R} dp$

$$\int \frac{2p(1-p)}{2p(1-p) + \lambda_\beta/n_R} dp = \int \frac{2p(1-p) + \lambda_\beta/n_R - \lambda_\beta/n_R}{2p(1-p) + \lambda_\beta/n_R} dp = 1 - \frac{\lambda_\beta}{n_R} \int \frac{1}{2p(1-p) + \lambda_\beta/n_R} dp$$

$$2p(1-p) + \lambda_\beta/n_R = -\{2p^2 - 2p - \lambda_\beta/n_R\} = -\left\{2\left(p - \frac{1}{4}\left(2 + \sqrt{4 + 8\frac{\lambda_\beta}{n_R}}\right)\right)\left(p - \frac{1}{4}\left(2 - \sqrt{4 + 8\frac{\lambda_\beta}{n_R}}\right)\right)\right\}$$

Let $a = 1 + 2\frac{\lambda_\beta}{n_R}$ then $2p(1-p) + \frac{\lambda_\beta}{n_R} = -\left\{2\left(p - \frac{1+\sqrt{a}}{2}\right)\left(p - \frac{1-\sqrt{a}}{2}\right)\right\}$ thus $\frac{1}{2p(1-p) + \frac{\lambda_\beta}{n_R}} =$

$$\frac{1}{2\sqrt{a}} \left[\frac{1}{\left(p - \frac{1+\sqrt{a}}{2}\right)} - \frac{1}{\left(p - \frac{1-\sqrt{a}}{2}\right)} \right]$$

$$\int \frac{dp}{p - \frac{1+\sqrt{a}}{2}} = \left[\log\left(p - \frac{1+\sqrt{a}}{2}\right) \right]_0^1 = \log\left(-\frac{1-\sqrt{a}}{1+\sqrt{a}}\right) \quad \text{and} \quad \int \frac{dp}{p - \frac{1-\sqrt{a}}{2}} = \left[\log\left(p - \frac{1-\sqrt{a}}{2}\right) \right]_0^1 =$$

$$\log\left(-\frac{1+\sqrt{a}}{1-\sqrt{a}}\right)$$

$$\int \frac{1}{2p(1-p) + \frac{\lambda_\beta}{n_R}} dp = \frac{1}{2\sqrt{a}} \log\left(\left(-\frac{1-\sqrt{a}}{1+\sqrt{a}}\right) / \left(-\frac{1+\sqrt{a}}{1-\sqrt{a}}\right)\right) = \frac{1}{2\sqrt{a}} \log\left(\frac{1-2\sqrt{a}+a}{1+2\sqrt{a}+a}\right)$$

Finally $\frac{1}{n_Q} \sum_{q=1}^{n_Q} \frac{n_R \sigma_{XS(q)}^4}{n_R \sigma_{XS(q)}^2 + \lambda_\beta} \sim k \left[1 - \frac{\lambda_\beta}{n_R} \int \frac{1}{2p(1-p) + \lambda_\beta/n_R} dp \right] = k \left[1 - \frac{\lambda_\beta}{n_R} \frac{1}{2\sqrt{a}} \log\left(\frac{1-2\sqrt{a}+a}{1+2\sqrt{a}+a}\right) \right]$

Outcomes and questions I:

- Horn/poll test – UQ testing

	2010	2011	2012	2013	2014	Total
BRAHMAN	135	248	705	701	10	1,799
SANTA	161	177	427	294		1,059
DROUGHTMASTER	2	70	174	273		519
LIMOUSIN	192	219	209	218	27	865
HEREFORD	35	108	336	361	11	851
CHAROLAIS	2	3	124	143	14	286
SIMMENTAL		25	22	16	4	67
XB	13	17	200	136		366
OTHER	166	656	679	293		1,794
TOTAL	706	1,523	2,876	2,435	66	7,606

Outcomes and questions I:

- Genetic defects testing (Teseling and Parnell, AAABG, 2013)
- Link with analytical tools (in this case, GeneProb)

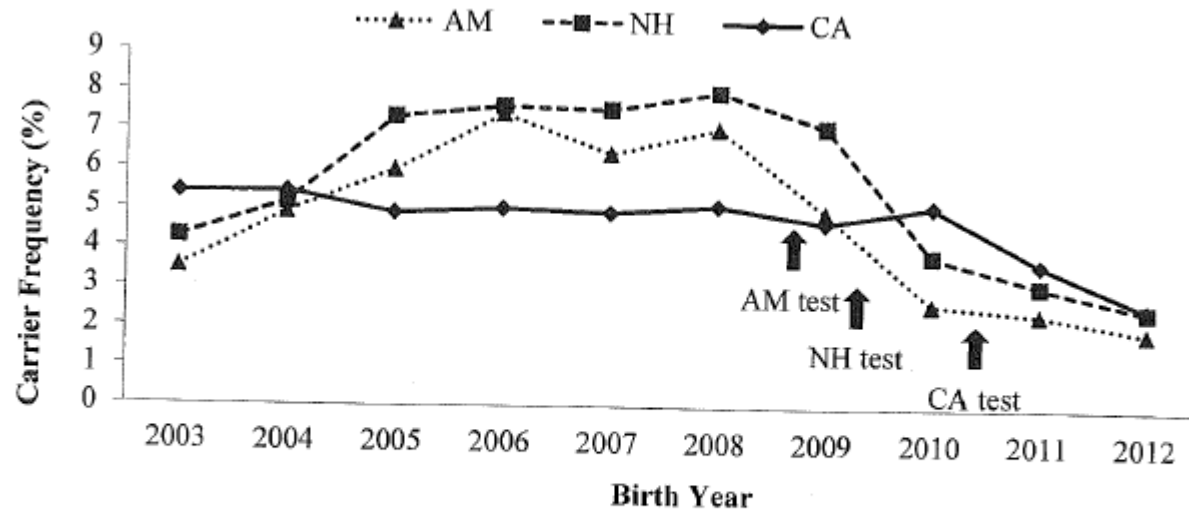


Figure 1. Frequency of carrier calves relative to birth years and the reductions in carrier frequency when DNA tests were made commercially available.

Outcomes and questions II:

- Calibration of CRC Prediction Equations:
 - Equations developed using CRC data and phenotypes (Bolormaa et al J Anim Sci 2013 91)
 - Calibrated against BREEDPLAN trait data, for inclusion of DGV into BREEDPLAN, where appropriate data exist
 - Calibration = correlation between prediction and observed adjusted phenotypes (Boerner and Johnston, AAABG 2013)

Outcomes and questions III:

- Calibration results:
 - c. 10 traits in Angus with accuracy > 0.2
 - Accuracy range of useful results 0.2-0.4
 - Some fertility traits in Brahman with accuracy > 0.2
 - Limited traits in other breeds
- Implementation:
 - 50k genotype, imputed up to 800k, apply prediction equation to produce DGV
 - Blend DGV with BREEDPLAN EBV

Outcomes and questions IV:

- How will genomics work for small breeds?
 - If < 1500 recorded animals per year, what is the benefit of genotyping – better control of inbreeding?
- How will it work for larger breeds?
 - How to handle different inputs – pedigree + phenotype, P + P + G, genotype alone
 - Phenotypes from outside stud sector? Genotypes to non-stud customers?
 - Pay for phenotypes, sell EBVs?
 - How to preserve public information
- What about international links?
 - Needs reference data in each country
- Investment model in Australia – RDC role, studs, breed associations?

Role of beef breed associations must evolve radically

Questions:

- What are the breeding units?
 - *Breeds? No (and never have been).*
 - *Motivated breeders? (Yes)*
 - *Alliances of motivated breeders plus data partners? (The future).*
- What have people done to create reference populations, or what do they use as ref pop'ns?
 - *BREEDPLAN data for calibration of prediction equations*
 - *Building BIN data to provide reference data for HTM traits. Industry data for other traits.*
- Are there any plan or visions on what to do next?
 - *Blending DGVs now available*
 - *Develop and implement single step for large-scale implementation (ie multiple herd or even breed)*
 - *Discussions starting around valuing data*
 - *R&D underway into tools to optimise recording and genotyping*
- Are there breeding groups (or AI companies) that have implemented new strategies, e.g scanning lots of young bulls, or doing more JIVET or MOET?
 - *Leading breeders already doing MOET ... JIVET, full scanning, capturing data from down the value chain, applying mate selection, some genotyping (likely already influencing ET programs)*

I'm not very good with Excel, but I'm great at spreading sheets.



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What beds are getting made?

