Genomics – *what does the future hold for dairy farmers?*

Jennie Pryce, Ben Hayes, Mike Goddard

Victoria
The Place To Be

DEPARTMENT OF PRIMARY INDUSTRIES | biosciences research

- Question: Is anything 300,000 times cheaper now than in 2000?

No. ~ 5 times cheaper (depending on what you buy)

- Question: Is anything 300,000 times cheaper now than in 2000?

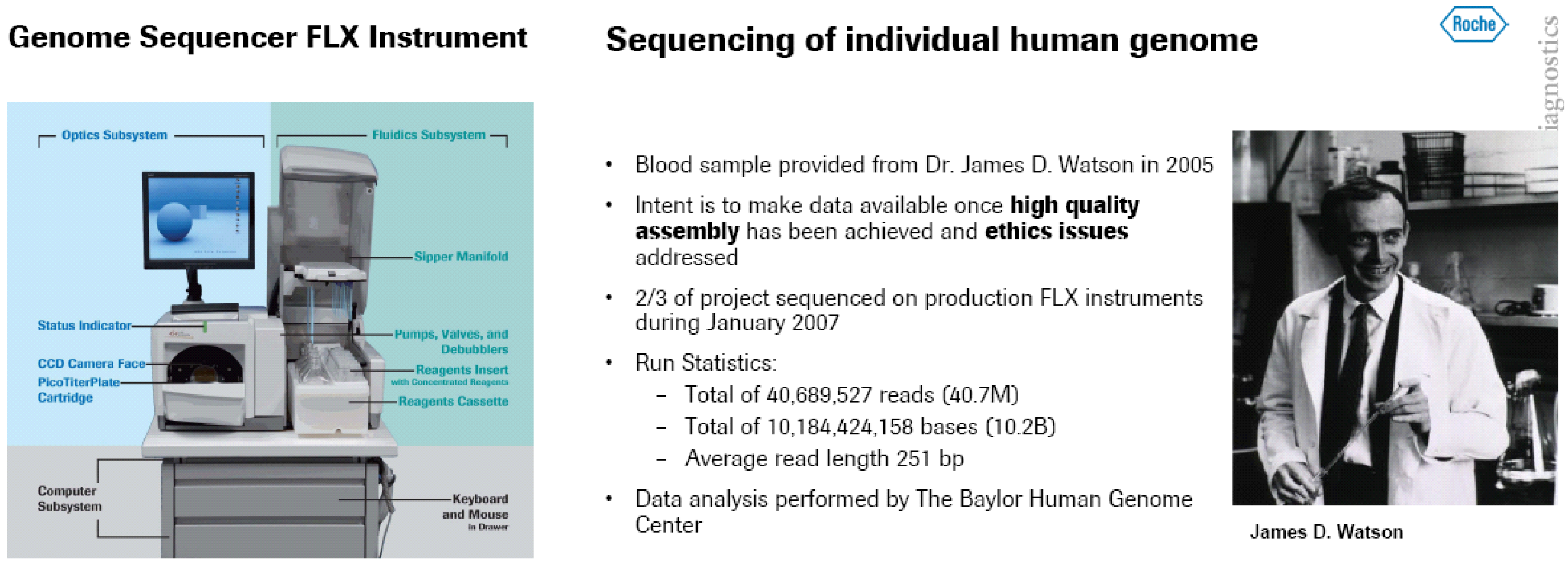
No. ~ 3 times cheaper

(if you're lucky)

Sadness as young woman is killed in crash

No. ~ 2000 times cheaper

Sequencing technology



Genome Sequencer FLX Instrument

Sequencing of individual human genome

- Blood sample provided from Dr. James D. Watson in 2005
- Intent is to make data available once **high quality assembly** has been achieved and **ethics issues** addressed
- 2/3 of project sequenced on production FLX instruments during January 2007
- Run Statistics:
  - Total of 40,689,527 reads (40.7M)
  - Total of 10,184,424,158 bases (10.2B)
  - Average read length 251 bp
- Data analysis performed by The Baylor Human Genome Center

James D. Watson

Cost of sequencing a genome ($)

2003	300,000,000
2007	1,000,000

2012 $1000

Scientific American (January, 2012)

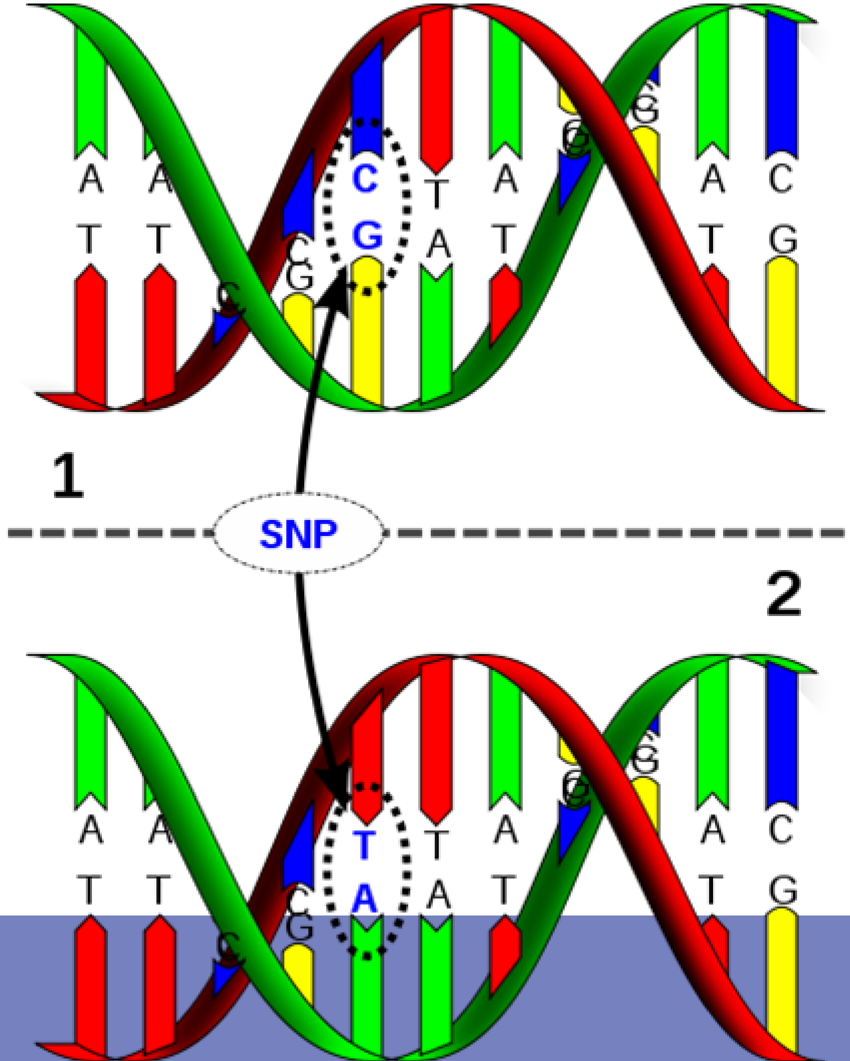
Capturing the benefits for the dairy industry

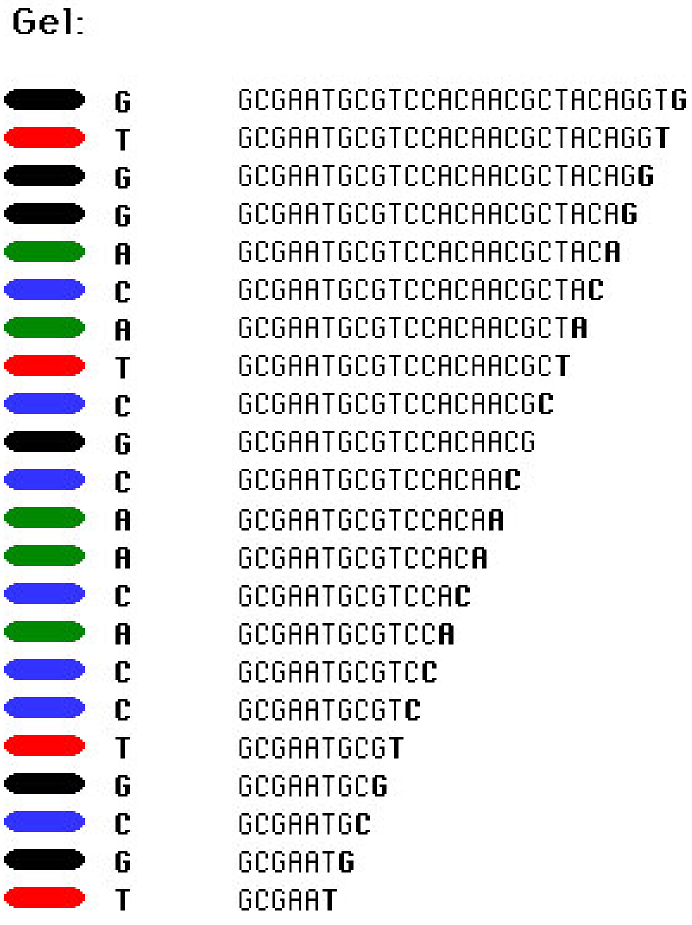
- Improve profitability of dairy cattle
  - Fertility
  - Production
  - Feed conversion efficiency
  - Survival
  - Disease resistance

- Decrease environmental impacts
  - Reduce methane emissions per litre milk

How?

- Find differences between animals in sequence (DNA code) which cause variation in these traits





Gel:

⬛	G	GCGAATGCGTCCACAACGCTACAGGTG
🟥	T	GCGAATGCGTCCACAACGCTACAGGT
⬛	G	GCGAATGCGTCCACAACGCTACAGG
⬛	G	GCGAATGCGTCCACAACGCTACAG
🟩	A	GCGAATGCGTCCACAACGCTACA
🟦	C	GCGAATGCGTCCACAACGCTAC
🟩	A	GCGAATGCGTCCACAACGCTA
🟥	T	GCGAATGCGTCCACAACGCT
🟦	C	GCGAATGCGTCCACAACGC
⬛	G	GCGAATGCGTCCACAACG
🟦	C	GCGAATGCGTCCACAAC
🟩	A	GCGAATGCGTCCACAA
🟩	A	GCGAATGCGTCCACA
🟦	C	GCGAATGCGTCCAC
🟩	A	GCGAATGCGTCCA
🟦	C	GCGAATGCGTCC
🟦	C	GCGAATGCGTC
🟥	T	GCGAATGCGT
⬛	G	GCGAATGCG
🟦	C	GCGAATGC
⬛	G	GCGAATG
🟥	T	GCGAAT

How?

- Find differences between animals in sequence (DNA code) which cause variation in these traits

- Use this to
  - ➢ predict breeding values for bulls and cows
  - ➢ select on these

- Potential to select bulls and cows for breeding early in life, accelerate genetic gain

- Sequence data will be used in the future, SNP chips are used now
  - Sequencing of key ancestors already happening

1,000 Bull Genomes Project

- Membership
  - Groups that have sequenced bulls or cows of any breed can add to sequence database

- 151 bulls + 1 cow to date
  - Holstein, Fleckvieh, Jersey, Reds, Angus

- 400 expected by end of year

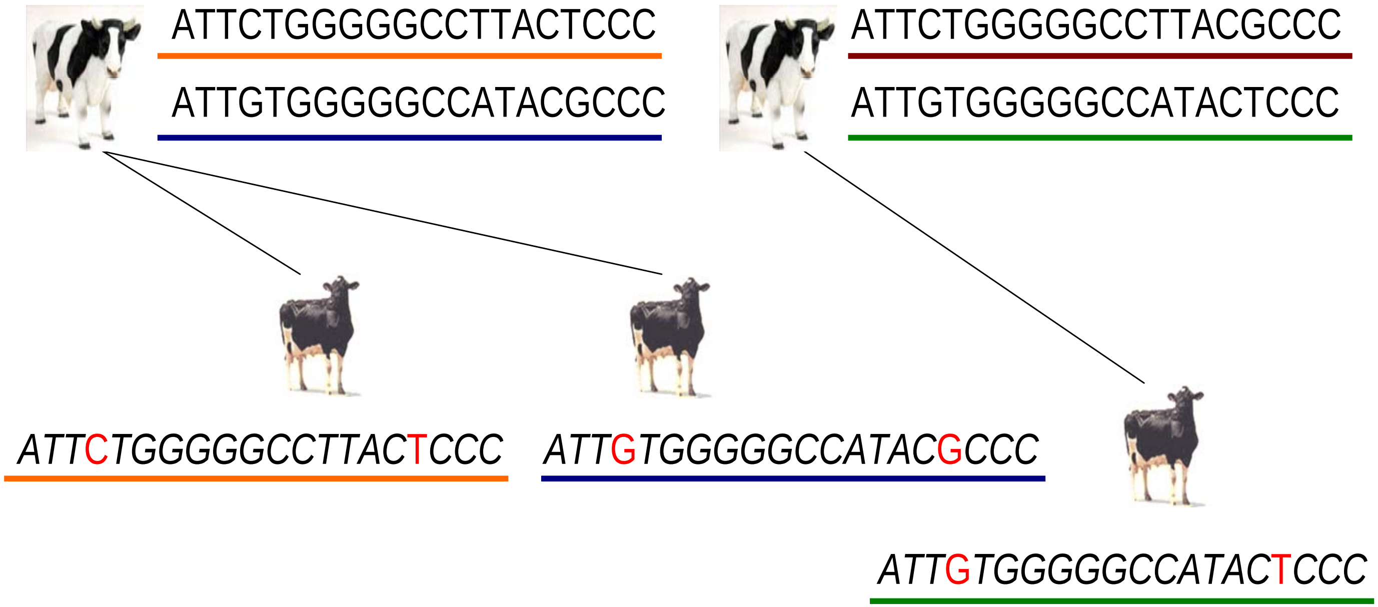
- Global effort!

Name	Fold coverage
Starlite	12.8
Shotime	11.9
Goldsmith	11.8
Gravita	15
Orana	9.5
Beau	12
OVGM	12.3
Goldwyn	22.7
Starbuck	30.3
Rameses	12.4
Donor	15.4
Donante	17.1
Mountain	18.9
Enhancer	16.8
Yukon	19
Gibbon	17
Jocko	15.1
Oman	14.7
Manhattan	17.9
Fatal	16.9
Cash	16.8
Boudewijn	18.5
Sabastian	26.2
Vickai	15.2

etc

Sequence key ancestors

Work out sequence of genotyped cows



ATTCTGGGGGCCTTACTCCC

ATTGTGGGGGCCATACGCCC

ATTCTGGGGGCCTTACGCCC

ATTGTGGGGGCCATACTCCC

ATTCTGGGGGCCTTACTCCC

ATTGTGGGGGCCATACGCCC

ATTGTGGGGGCCATACTCCC

Increasing the reliability of genomic selection

Using sequence:

  - Able to capture the differences in DNA that result in variation in a trait
  - Idea is to increase reliabilities to level of progeny-test

- Large reference populations
  - Needed for accurate EBVs
  - International collaboration
  - Across breed reference populations
  - Cows

Commercial livestock SNP chips

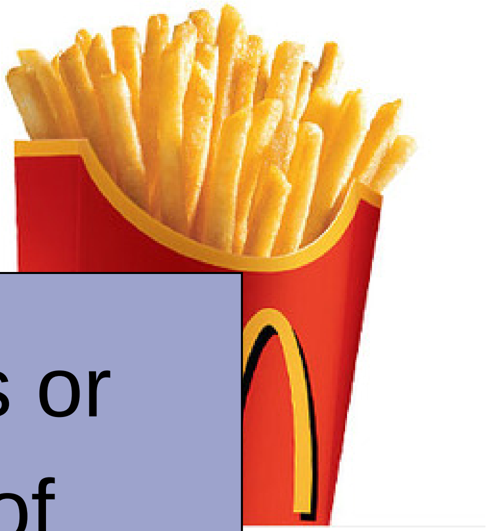
Bovine: 7,000, 50,000, 800,000

Ovine: 50,000

Porcine: 60,000

etc…

Commercial livestock SNP chips



Bovine: 7,000, 50,000, 800,000

Ovine: 50,000

Porc

etc..

There will be new SNP chips or perhaps even other ways of capturing genetic information

In the future: All cows and bulls in key dairy nations likely to be genotyped (or sequenced)

What will this enable us to do:

1) Identify and select the best males and females
   - Increase the rate of genetic gain
2) Unambiguously identify sire and dam of a calf
3) Select the best heifers as replacements
4) Control inbreeding (manage matings)

Advantage of Genomic Selection in Dairy Cattle

Australian Dairy Herd Improvement Scheme

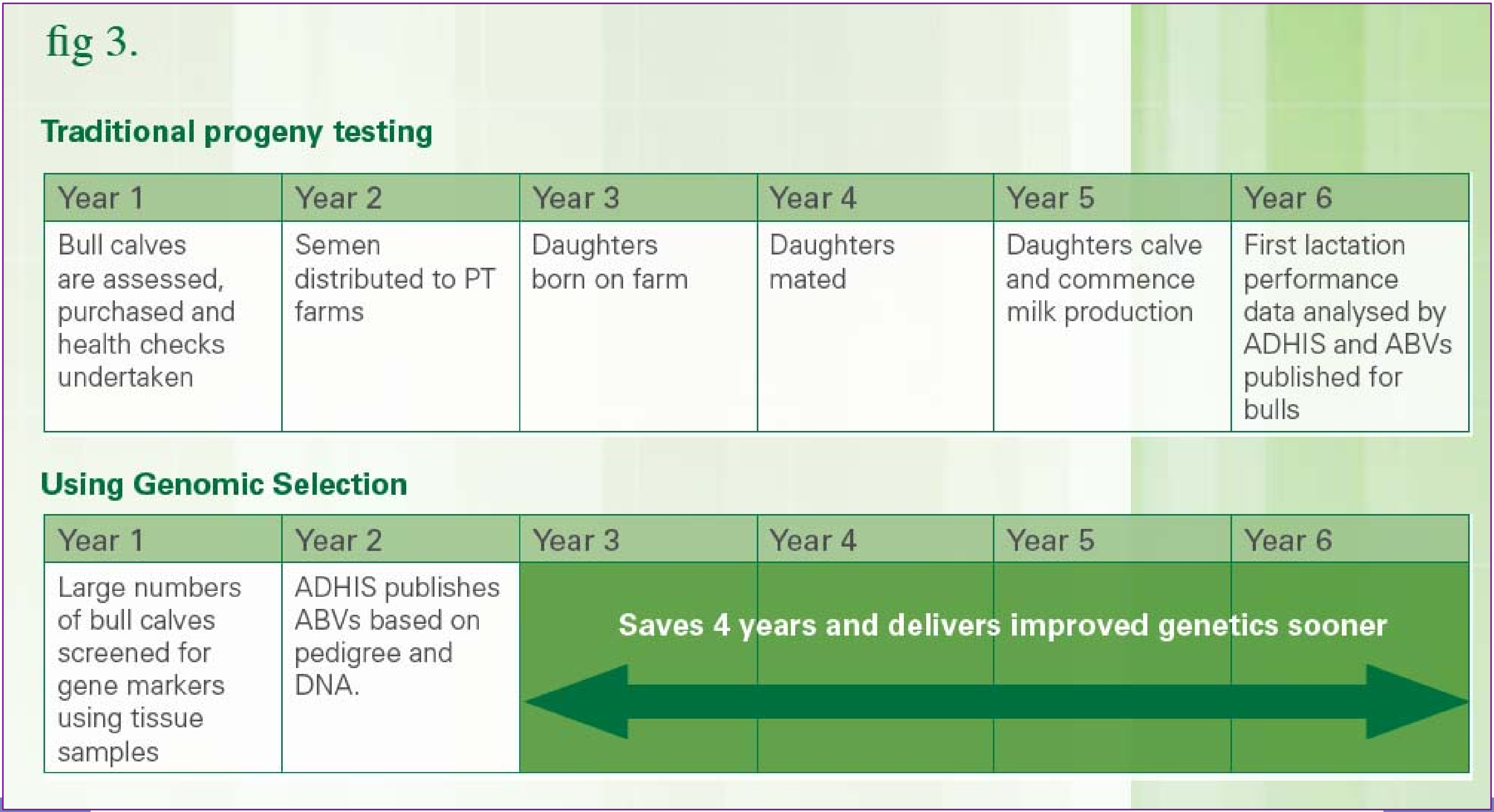


fig 3.

Traditional progeny testing

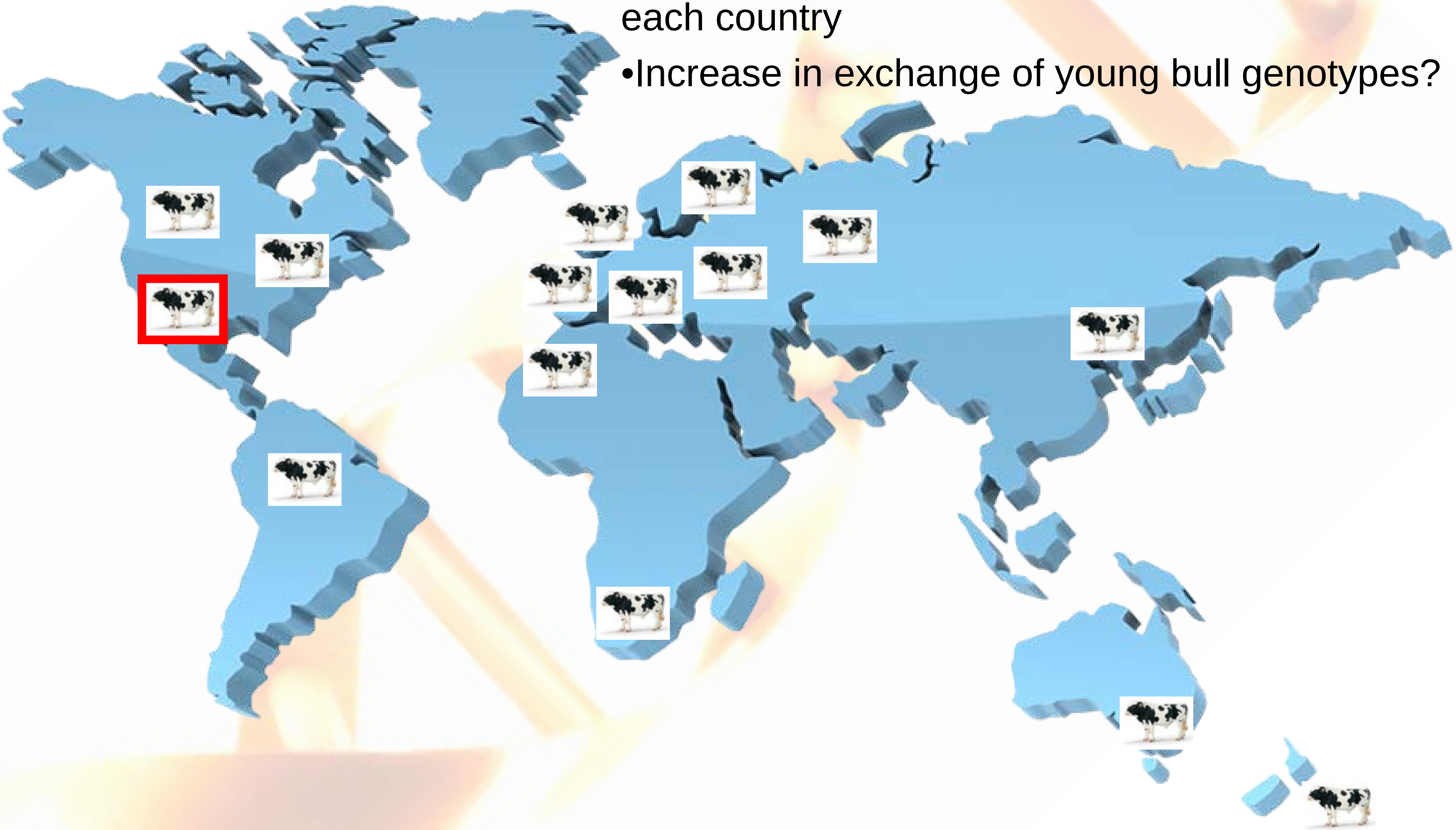
Year 1	Year 2	Year 3	Year 4	Year 5	Year 6
Bull calves are assessed, purchased and health checks undertaken	Semen distributed to PT farms	Daughters born on farm	Daughters mated	Daughters calve and commence milk production	First lactation performance data analysed by ADHIS and ABVs published for bulls

Using Genomic Selection

Year 1	Year 2	Year 3	Year 4	Year 5	Year 6
Large numbers of bull calves screened for gene markers using tissue samples	ADHIS publishes ABVs based on pedigree and DNA.	Saves 4 years and delivers improved genetics sooner			

Source: [ADHIS Genomics brochure final.pdf](http://www.adhis.com.au/v2/downv2.nsf/0/bac10774d74442b2ca25766b00207aa5?open)
http://www.adhis.com.au/v2/downv2.nsf/0/bac10774d74442b2ca25766b00207aa5?open

- Thousands of bull calves screened worldwide
- Reliability around 60% at birth
- DNA can help you choose best bull for each country
- Increase in exchange of young bull genotypes?



A shorter generation interval may mean generations turn over more rapidly

A bull may be high impact for a year or two

“Iconic” bulls may become less common?

Reduction in the number of bulls progeny tested, as confidence in genomic selection grows

Hanoverhill Starbuck

The dawn of the age of computerised mating plans

Computerised tools to work out the matings to reduce inbreeding (at the genomic level) while still making genetic progress in the breeding objective

- Calculate relationships between males and females (i.e. potential inbreeding in progeny) at the DNA level
- Select the best mating for each heifer

Five ET full sisters

Proportion of genome shared

	FCE0543	FCE0544	FCE0547	FCE0577	FCE0594	Rank on ASI(g)
FCE0543		0.51	0.52	0.47	0.44	4
FCE0544	0.51		0.51	0.46	0.50	1
FCE0547	0.52	0.51		0.46	0.48	3
FCE0577	0.47	0.46	0.46		0.48	5
FCE0594	0.44	0.50	0.48	0.48		2

Each square represents the degree of relationship

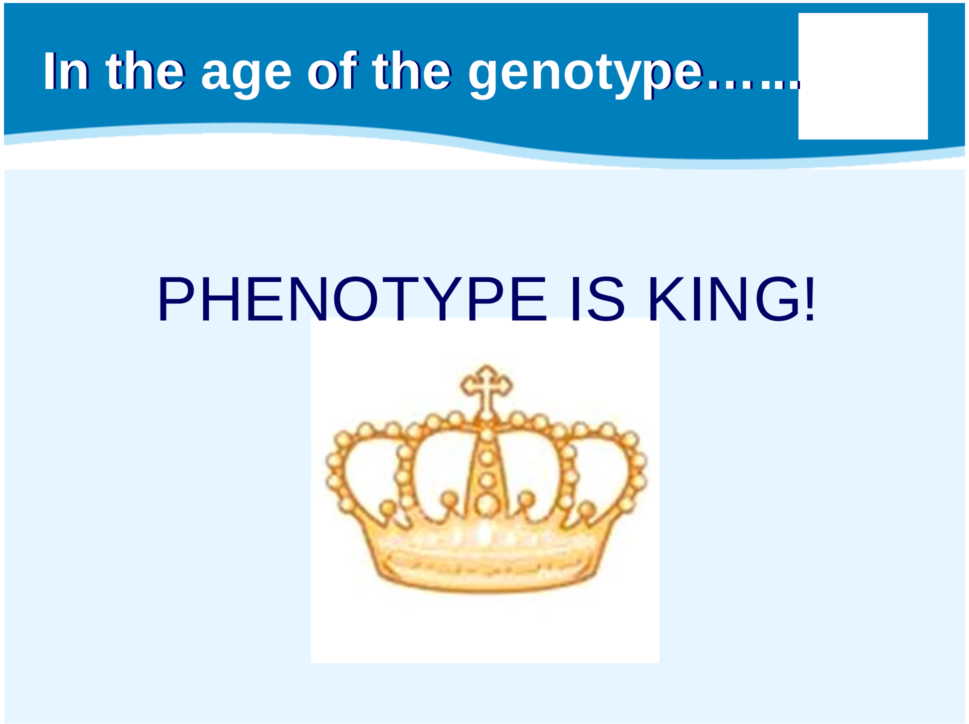
Darker orange/red indicates closer relationships

Impact of strategies on inbreeding and value/cow/year

Method of controlling inbreeding	Genomic inbreeding
Genomics	2.5% ($12.50)*
Pedigree	1.4% ($7)

$12.50*4 = $50 per lifetime or €39

Will we still need to record data?



In the age of the genotype……

PHENOTYPE IS KING!

Dr Mike Coffey (SAC, Edinburgh)

Will we still need to record data?

Yes - to make sure that the associations between the genetic markers and current population remains relevant

Genetic evaluations are still a by-product of data recorded for other purposes e.g. management

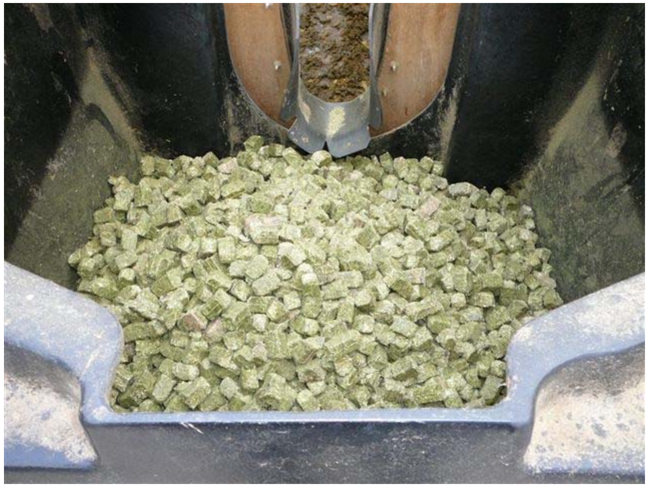
Challenges of capturing data from inline recording?

What will happen to data collected by breeding companies e.g. type data in some countries?

Is there a role for “*industry resource*” herds?

New traits

- Potential to include new traits in the breeding objective
  - Feed conversion efficiency/intake
  - Methane emissions
  - Better measures of fertility etc



Feed conversion efficiency

- 2,000 heifer calves (Australia and NZ)
- Measured (RFI) residual feed intake (predicted minus actual feed intake) in feeding trial
- Heritability of RFI was 0.25
- Genomic prediction accuracy 0.4
- International collaboration to improve the prediction

Summary

What does the future hold?

- Higher reliabilities
  - Use of more and more genetic markers (sequence)
  - Gradual reduction in progeny testing
  - Farm-recorded data still needed!
- Rapid turnover of sire of cows and bulls
  - Fewer breed “icons” i.e. more rapid turnover of bulls
  - Greater use of mating software to avoid inbreeding
- New traits
  - Feed efficiency
  - Better fertility measures etc

Acknowledgements

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GARDINER FOUNDATION