

Genomic Selection

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January 2009



Introduction

- ▶ Dairy cattle breeding
 - 1940s-1950s Dam-daughter comparisons ~ genetic gain = 0 kg fat/year
 - 1960s Artificial breeding progeny testing ~ genetic gain 0.3 kg fat/year
 - 1970s Contemporary comparisons ~ genetic gain 0.7 kg fat/year
 - 1970s-80s Dedicated sire proving scheme

Introduction

▶ Dairy cattle breeding

- 1980s Breed for fat, protein and volume ~ genetic gain 1.1 kg MS/year
- 1990s Animal model and Breeding Worth ~ genetic gain 1.8 kg MS/year
- 2000 Inclusion of crossbred sires “KiwiCross” in the sire progeny scheme
- 2000s Selection for fertility and somatic cell and test day model ~ genetic gain 1.8 kg MS/year

Introduction

▶ Molecular genetics

- 1944 DNA isolated as the “genetic material”
- 1953 DNA structure discovered
- 1977 DNA sequenced for the first in time
- 1985 DNA finger printing discovered
- 2001 First draft of human genome
- 2001 methods for genomic selection outlined

Introduction

▶ Molecular genetics

- 2001 First quantitative milk production gene discovered by LIC and Holland Genetics
- 2003 Second quantitative milk production gene discovered by LIC and Holland Genetics
- 2006 First draft of Bovine genome
- 2006 Affymetrix 15,000 SNP chip available for Bovine
- 2008 Illumina 50,000 SNP chip available for Bovine

Introduction

▶ Molecular genetics

- The process of information use and discovery in dairy cattle breeding
 - Determining if major genes exist
 - Estimating genetic marker effects within family
 - Estimating genetic marker effects within and across families
 - Finding causative mutations (DGAT1)
 - *Processing DNA information in routine genetic evaluations*

Genomic Selection

*breeding incorporating DNA information as new source information
we are at the beginning of journey*

Why do we progeny test?

Sire 90% Rel

Dam 50% Rel



Young Bull 35% Rel

Sire 100% Rel

Dam 100% Rel

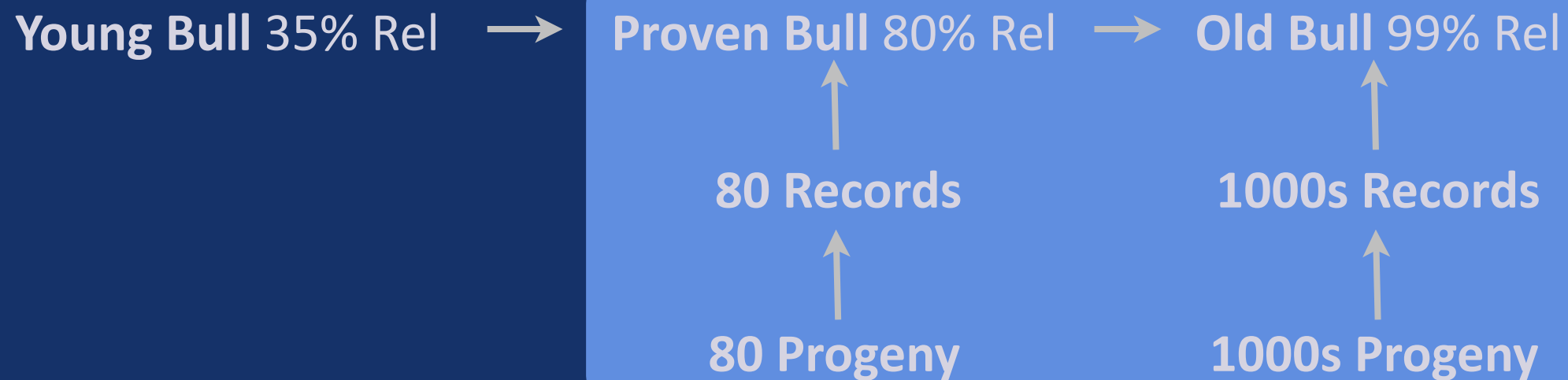


Young Bull 50% Rel

We only know that the young bull inherited 1/2 of his genes from the sire and dam, we don't know the actual genes that were inherited from each parent

Why do we progeny test?

50 years of technical improvement

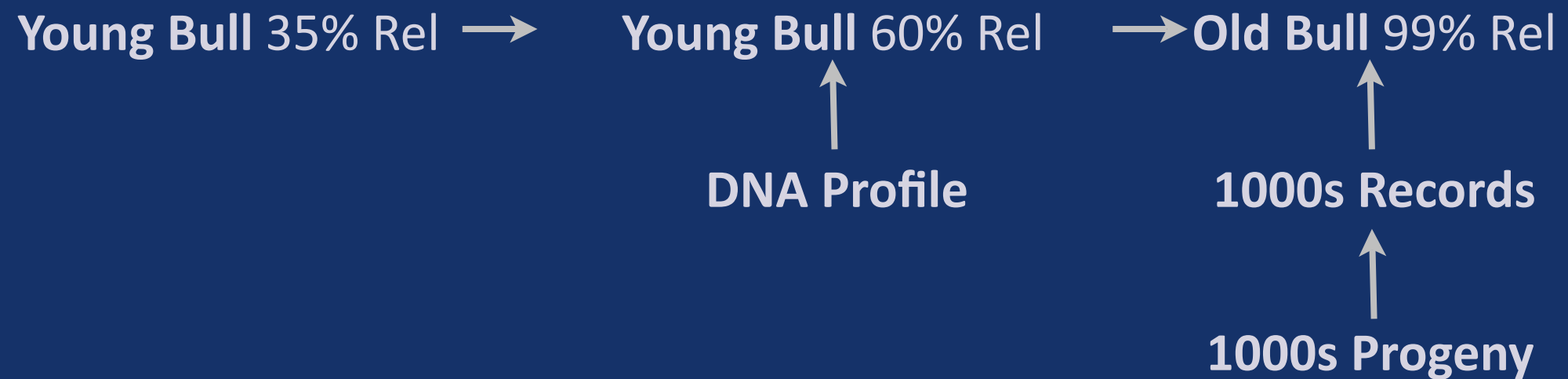


It is only progeny information that can indicate which genes were actually inherited

Genomic Selection

- ▶ Select bulls for widespread use based on their DNA profile rather than using progeny testing based on their the performance of their daughters
- ▶ DNA profile enables us to work out which parts of DNA were inherited from each parent
- ▶ Increased information relative to pedigree associations

Genomic Selection



Genomic Selection: Results LIC, CRV and USDA

- ▶ LIC genotyped 4,500 sires born in the 1980s to the present using the Illumina BovineSNP50 BeadChip (50,000 SNP)
- The data included approximately 2,400 Holstein Friesian, 1,500 Jersey and 650 Holstein Friesian–Jersey crossbred sires

Genomic Selection: Results LIC, CRV and USDA

- ▶ CRV genotyped 4,000 NLD and 1300 NZ sires born using the custom chip (57,000 SNP)

Genomic Selection: Results LIC, CRV and USDA

- ▶ USDA genotyped 7,000 sires born in the using the Illumina BovineSNP50 BeadChip (50,000 SNP)
- The data included approximately 5,300 Holstein Friesian, 1,300 Jersey and 350 Brown Swiss sires

Genomic Selection: Results LIC

- Increase in reliability of the young sires (over parent average)

Trait	HF	JR	KX
Protein	+23	+15	+29
Somatic Cell	+21	+22	+21
Liveweight	+18	+19	+33
Fertility	+30	+14	+14

- Predicting an increase in the rate of genetic trend $\geq 50\%$

Genomic Selection: Results CRV

- Increase in reliability of the young sires (over parent average)
- Protein yield +17%
overall conformation +14%
somatic cell count +11%
- Predicting an increase in the rate of genetic trend 30-40%

Genomic Selection: Results USDA

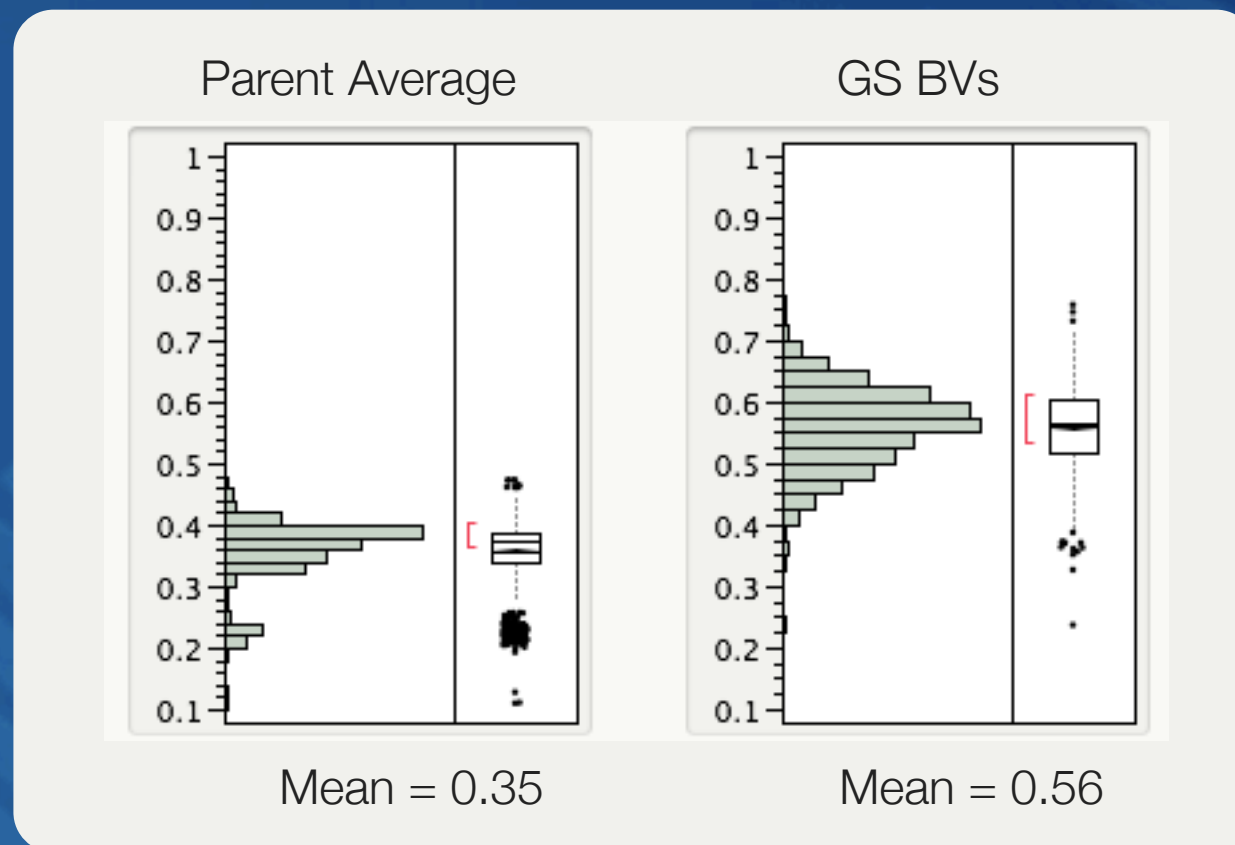
- Increase in reliability of the young sires (over parent average)

Trait	HF	JR	BS
Protein	+22	+4	+1
Somatic Cell	+21	+1	--
Stature	+26	+9	+3
Fertility	+16	+5	--

- Predicting an increase in the rate of genetic trend >50%

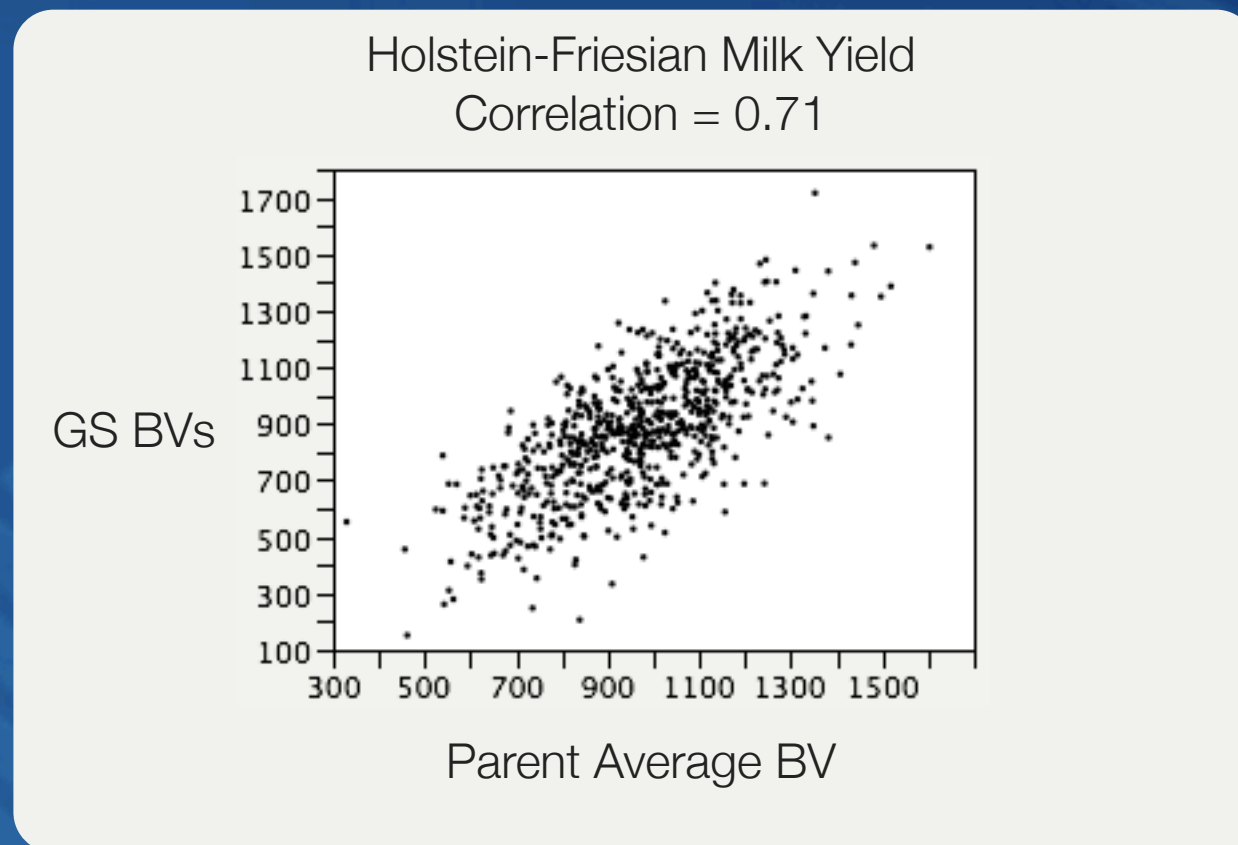
Genomic Selection: Results NZ

- Increase in reliability of the young sires (over parent average)
Protein Yield (n=1585)



Genomic Selection: Results NZ

- Genomic breeding values versus parent average (n=720)



Genomic Selection

- Ireland
 - 1000 genotyped Holstein sires on the BovineSNP50 BeadChip
 - Collaborating with New Zealand by exchanging Holstein phenotypes and genotypes
 - Joint analysis accounting for a genetic correlation between Ireland and New Zealand of < 1

Genomic Selection

- Ireland
 - Effective way to increase the training data size for both countries
Improves the accuracy of genomic selection in both countries
 - Provides a mechanism to select sires from foreign countries that perform in Ireland and vice-versa
 - Ireland can provide Irish genomic BVs for young sires from foreign countries rather than parent average

Genomic Selection

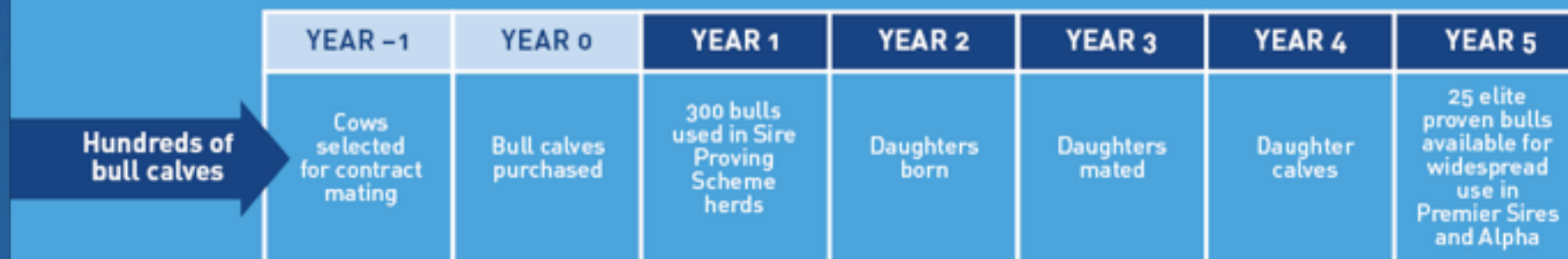
- Countries selecting bulls based on genomic information
Production HOL: DNK, FIN, SWE, NZL, USA, AUS, CAN, FRA, DEU, NLD
JER: DNK, FIN, SWE, NZL, USA, AUS
- Fertility HOL: DNK, FIN, SWE, NZL, USA, AUS, CAN, FRA, DEU, NLD
JER: DNK, FIN, SWE, NZL, USA, AUS
- Countries planning on having genomic information included in their official breeding values in 2009
NZL, ISR, FRA, IRL, CAN, DEU, USA, AUT, POL, ESP, AUS

Progeny testing program redesign

DNA PROVEN – 4 years



DAUGHTER PROVEN – 7 years



Genomic Selection and National Genetic Evaluation

- Include genomic data as the fourth source of information in the breeding value
- Methods to work in an across breed genetic evaluation in New Zealand

Genomic Selection and National Genetic Evaluation

- A method has been proposed that incorporates the SNP information as genomic relationships
- Genomic relationships replace the pedigree relationships
- Explains some of the Mendelian sampling which is not explained by the parent average breeding value
- Requires dense SNP chip

Genomic Selection

- Future Research (Short term)
 - Genomic Selection model refinement
 - Joint IRL and NZ analysis
 - Building a time series of validation data sets
- Future Research (Long term)
 - 300k bovine SNP chip
 - Full sequencing of sires DNA

Genomic Selection

- There will be better analytical methods and better DNA information in the future
- Considerable research will be undertaken to optimise the use of the new information over the next 10 years



Questions