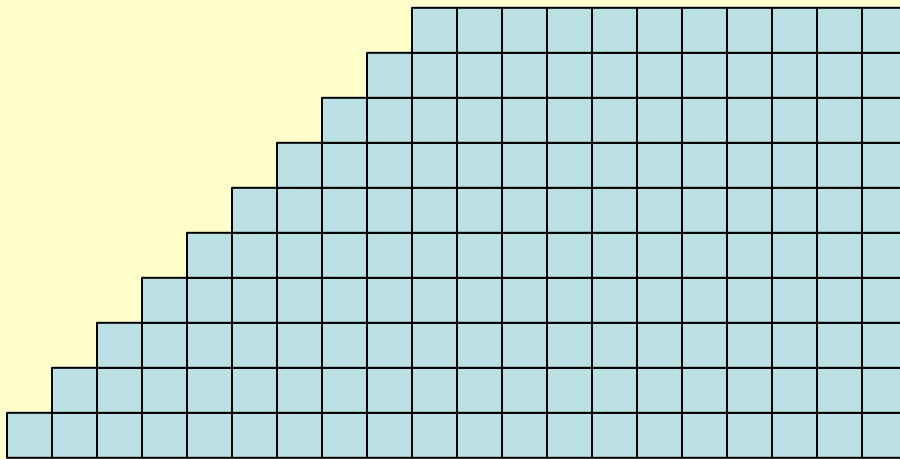# Genomics to Improve Livestock Farming

Dr Steven Morrison

Genetic improvement

- Long term strategic process
- Goal is to breed better animals for: particular traits or economically derived index of traits

Genetic Improvement
Permanent and Cumulative

If each increment of gain is valued at only £1000
Cumulative response £165,000

Examples of livestock genetic gain

1972

379 kg

100 kg

14.5% less feed

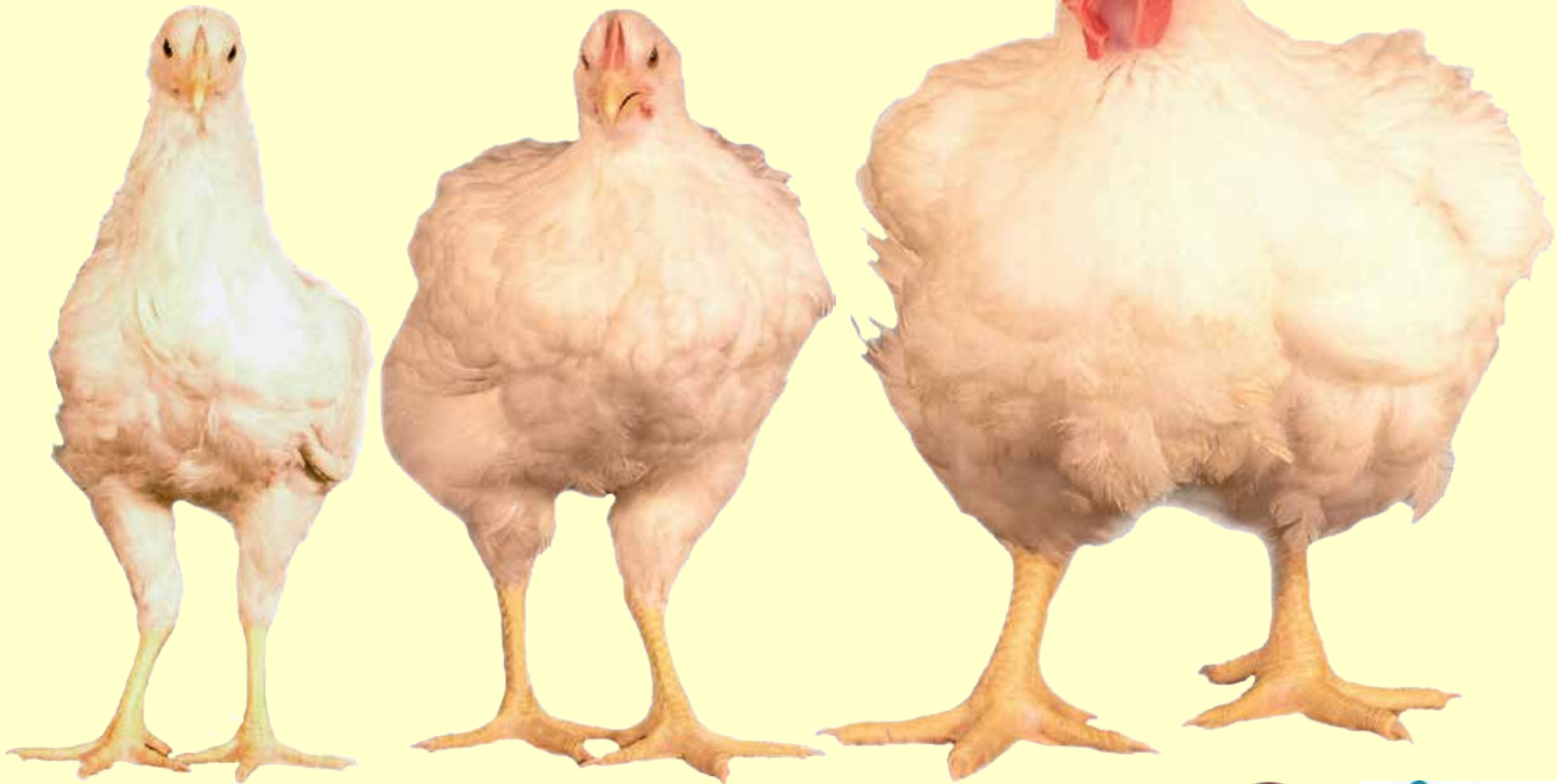**yet 25% heavier**

2007

324 kg

125 kg

Examples of livestock genetic gain

1957 broiler　　**1978 broiler**　　　　　　　　　**2005 broiler**

Source: The Poultry Research Centre, University of Alberta

Slide from Martin Zuidhof (*Poultry Science (2014) doi: 10.3382/ps.2014-04291*)
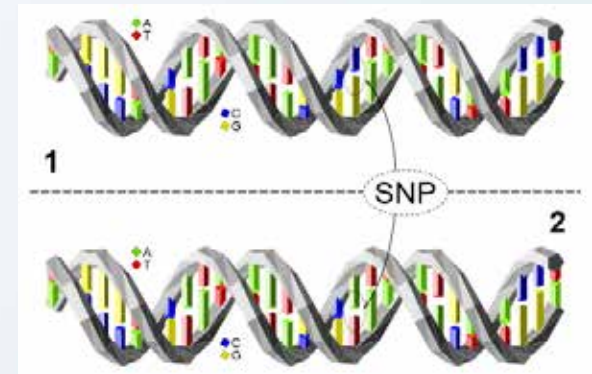
Route to genetic improvement

Requirements

- Genetic variation
- Selection intensity combined with heritability
- Accurately identify superior animals
  - Traditional
    - Ancestry, own performance, progeny performance
  - Genomic selection
    - Relate patterns in DNA to those in proven animals
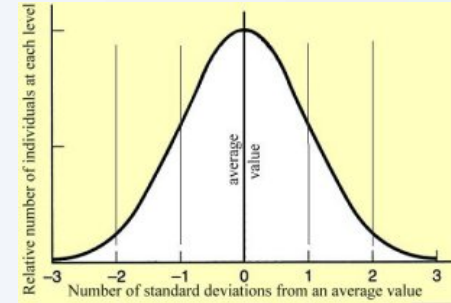
Technological advancements

- Human Genome Project (1990) ~$3 Billion & 13 years ($1M)
- Bovine Genome Project (2009) – $50 million & 4 years ($100k)
- Currently full sequence ~ £900 & 1 week
- Development of rapid low cost tests e.g. Single Nucleotide polymorphism (SNP)

- Variation in a single nucleotide at a specific position on the genome

- Variations have been mapped in livestock against susceptibility to diseases, performance traits, fertility traits etc

By SNP model by David Eccles (gringer), CC BY 4.0,https://commons.wikimedia.org/w/index.php?curid=2355125

- Can also be used of parentage verification

- Cost ~£20-70 / animal depending on density

How many base pairs in the Bovine genome?

37%

26%

24%

13%

~3 Million ~30 Million ~300 Million ~3 Billion
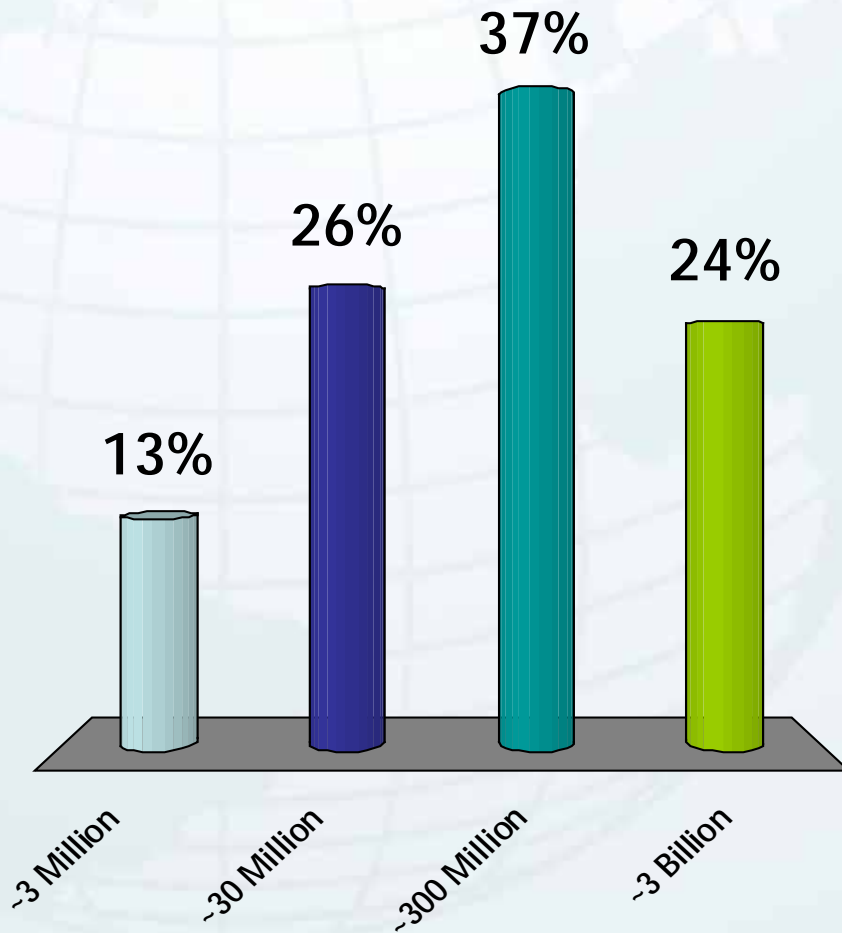
A. ~3 Million

B. ~30 Million

C. ~300 Million

D. ~3 Billion

Correct Answer: D

Almost 3 billion base pairs

What proportion of cattle genes are shared with humans?

47%

A. 20%

B. 40%

C. 60%

D. 80%

22%

18%

14%
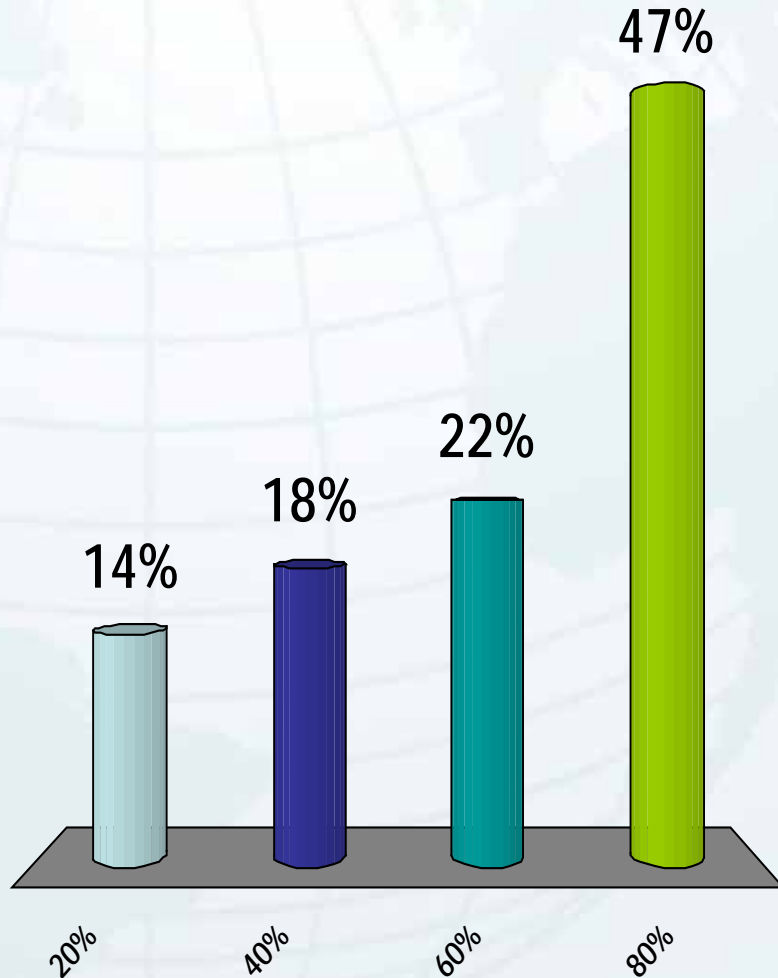
20%   40%   60%   80%

Correct Answer: D

80%

AFBI's role in livestock genetic advancement

- High quality and robust phenotype records
- Capture of difficult to measure traits
- Cross country research programmes
- Better understanding of the G+E effects
- New marker discovery and validation
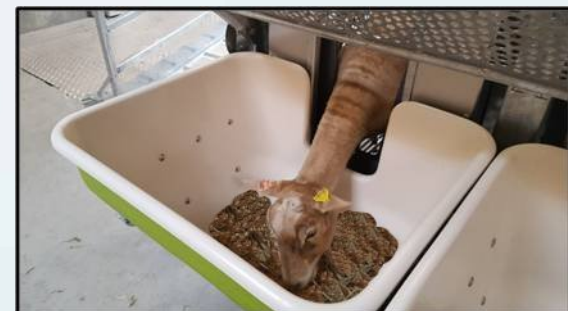
Monogastric example - ECO FCE

- Collaboration between AFBI, FBN Germany and Aahrus Denmark

- Identify and validate genomic markers of residual feed intake (RFI)

- Incorporate into international breeding programmes to increase rate of gain

- Tools Developed by FCE - valued at ~£100m

Dairy Examples - **Gplus**E and SOLID

SOLID – 25 member consortium (FP7)

- **t** Evaluation of adapted breeds
- **t** Analysing samples from AFBI herd for biomarkers

GplusE - 15 member consortium (FP7)

- **t** Collect difficult to record phenotypes - 60 AFBI cows & high density (HD) SNP
- **t** Phenotype and low density genotype 500 cows and impute to HD
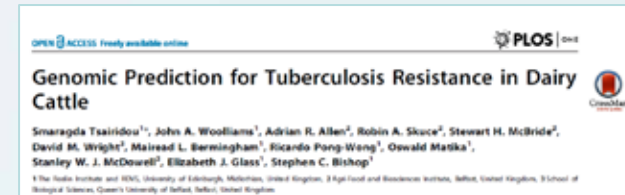- **t** Correlate milk and serum traits to validate milk components as key phenotype markers

Animal health genomics – host genetic resistance to bovine TB

- _**TB Advantage**_: new genetic selection trait (Holstein-based) launched January 2016 – a world first

- AFBI NI-based studies (in collaboration with the Roslin Institute and SRUC)

  - Confirmed heritable genetic variation in risk and genome-wide (case-control) genetic association study - heritability of ~0.23

  - Fine mapping identified genetic variants significantly associated with TB disease trait

  - Demonstrated that **genomic prediction/selection** was feasible for the TB resistance trait

OPEN ACCESS Freely available online — PLOS | One

Genomic Prediction for Tuberculosis Resistance in Dairy Cattle

Smaragda Tsairidou[1*], John A. Woolliams[1], Adrian R. Allen[2], Robin A. Skuce[2], Stewart H. McBride[2], David M. Wright[3], Mairead L. Bermingham[1], Ricardo Pong-Wong[1], Oswald Matika[1], Stanley W. J. McDowell[2], Elizabeth J. Glass[1], Stephen C. Bishop[1]

PROCEEDINGS OF THE ROYAL SOCIETY B | BIOLOGICAL SCIENCES

Bovine tuberculosis: the genetic basis of host susceptibility
A. R. Allen, G. Minozzi, E. J. Glass, R. A. Skuce, S. W. J. McDowell, J. A. Woolliams and S. C. Bishop
Proc. R. Soc. B 2010 277, 2737-2745 first published online 2 June 2010
doi: 10.1098/rspb.2010.0830

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ORIGINAL ARTICLE
Genome-wide association study identifies novel loci associated with resistance to bovine tuberculosis

ML Bermingham[1], SC Bishop[1], JA Woolliams[1], R Pong-Wong[1], AR Allen[2], SH McBride[2], JJ Ryder[3,4], DM Wright[3,5], RA Skuce[2,3], SWJ McDowell[2] and EJ Glass[1]

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Importance of phenotype

- Development of a 'purpose built' future proofed database
- Over 9 million phenotypic records uploaded
  - Over 20 years of data e.g. Intakes, milk records, health records, fertility, blood analysis
- Centre for Innovation Excellence in Livestock (CIEL) investment will increase the quantity of detailed phenotype recording in sheep, beef and dairy cattle

DNA Biobank and genotypes

- All AFBI dairy cows 'genotyped' since 2011 – 660 cows (IDB SNP chip)
- Exploring methods to ensure continued DNA sampling of AFBI livestock
- AFBI Genomics strategy group formed to:
  - Investigate strategic investment in next generation sequencing technology
  - Developing in-house sequencing/bioinformatics 'expertise'
  - Assessing future requirements across research disciplines

Genomics in the future at AFBI

- High quality and robust phenotype records

- Capture of difficult to measure traits only possible on highly controlled research farms

- Increased partnership in global research programmes to:
  - Better understand G by E effects
  - New marker discovery and validation
  - Genotype specific livestock nutrition and health plans
  - Validate & increase adoption rate of genetic breeding values on commercial farms

- Apply the technology to advance the sustainability and profitability of livestock farming