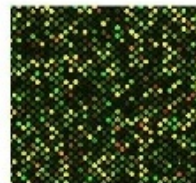
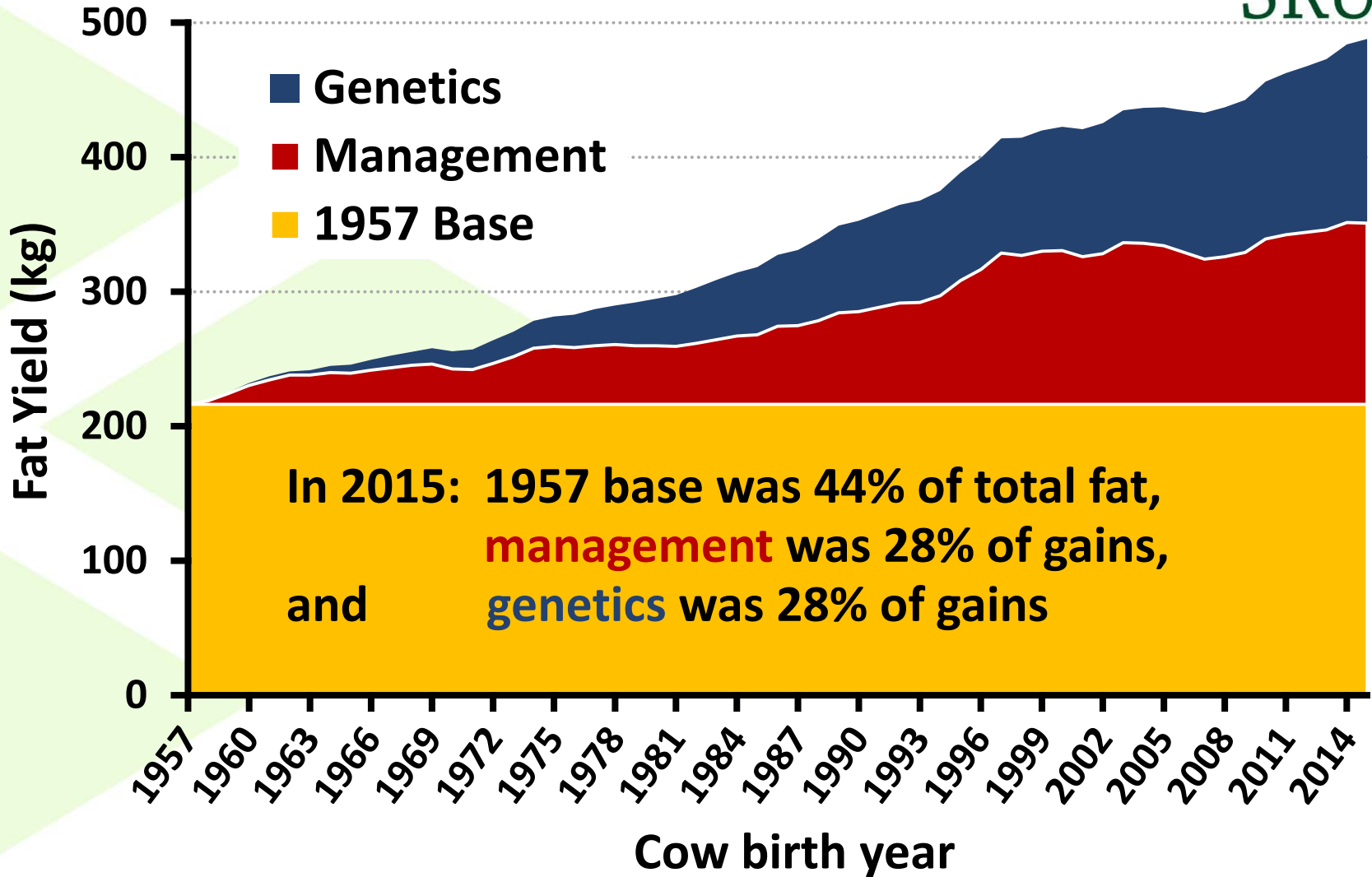


# InnovationL improving beef efficiency

Step change in genetic (and genomic)  
improvement in Scottish beef industry.

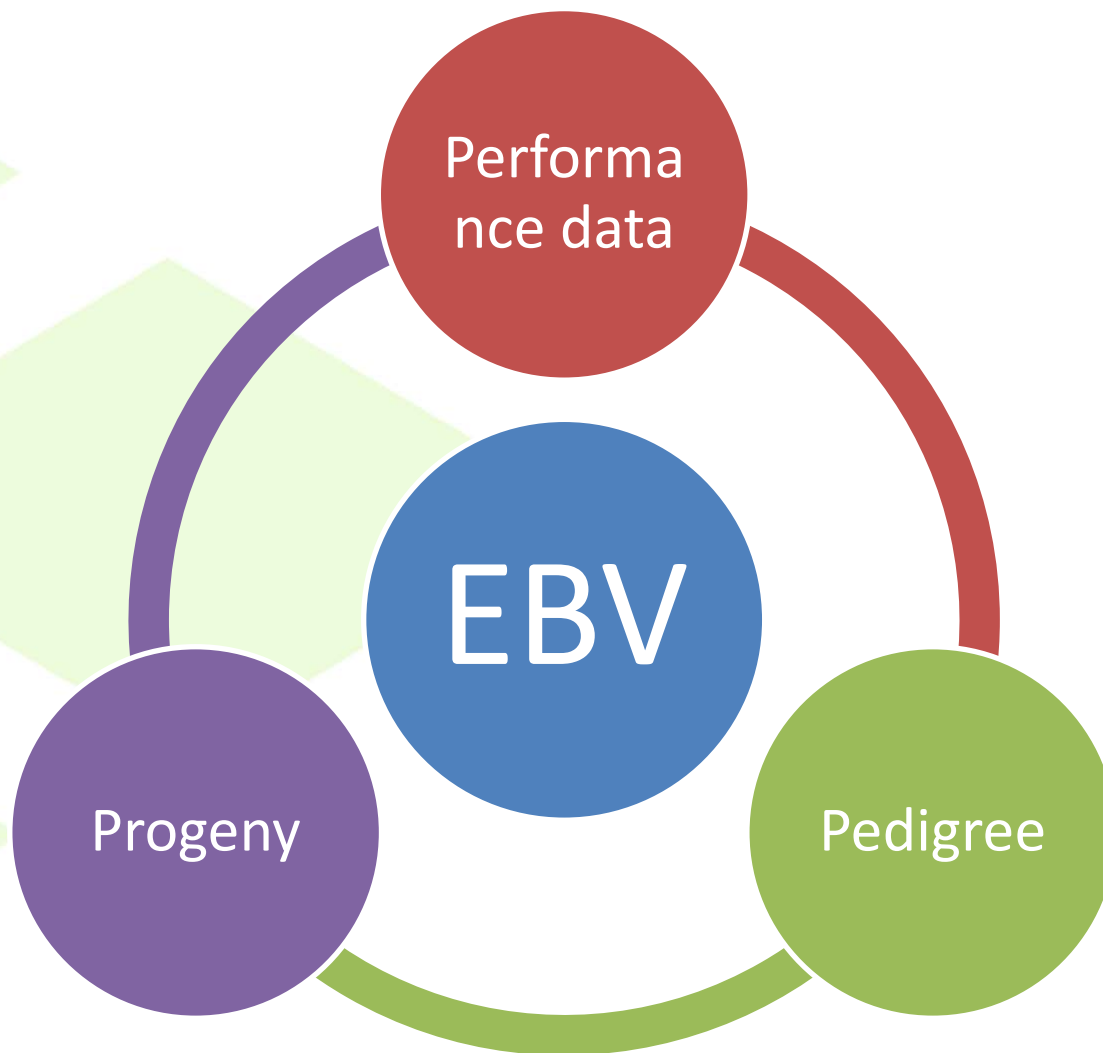


# What is the value of genetic selection? (US dairy cows)

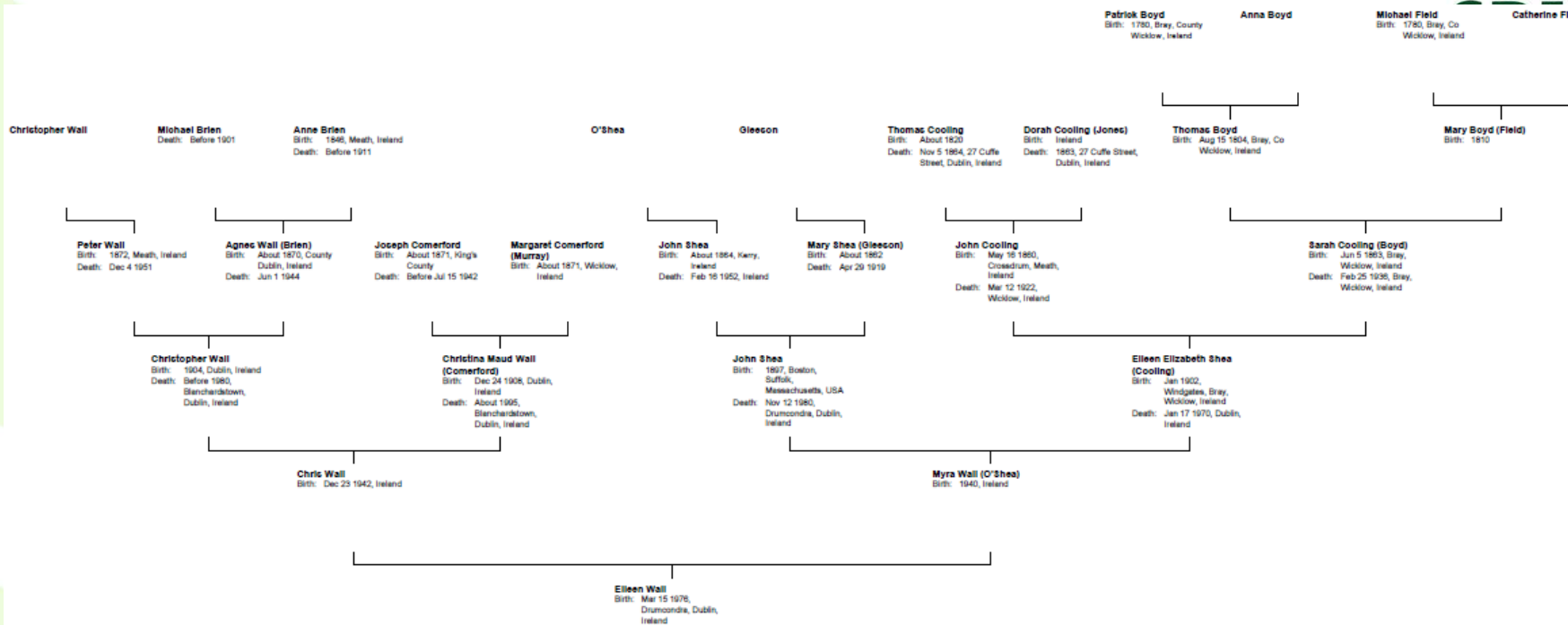


# Current information in breeding values

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# Tracing genes through pedigree



# Tracing genes through pedigree vs genome



Patrik Boyd  
Birth: 1780, Bray, County Wicklow, Ireland

Anna Boyd

Michael Field  
Birth: 1780, Bray, Co Wicklow, Ireland

Catherine Field



Ancestry Composition tells you what percent of your DNA comes from each of 31 populations worldwide. This analysis includes DNA you received from all of your recent ancestors, on both sides of your family. The results reflect where your ancestors lived before the widespread migrations of the past few hundred years.



This lab estimates your genome-wide percentage of Neanderthal ancestry

## Got Neanderthal DNA?

An estimated **2.9%** of your DNA is from Neanderthals.

Eileen Wall (you)



2.9%

87th percentile

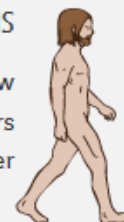
Average European user



2.7%

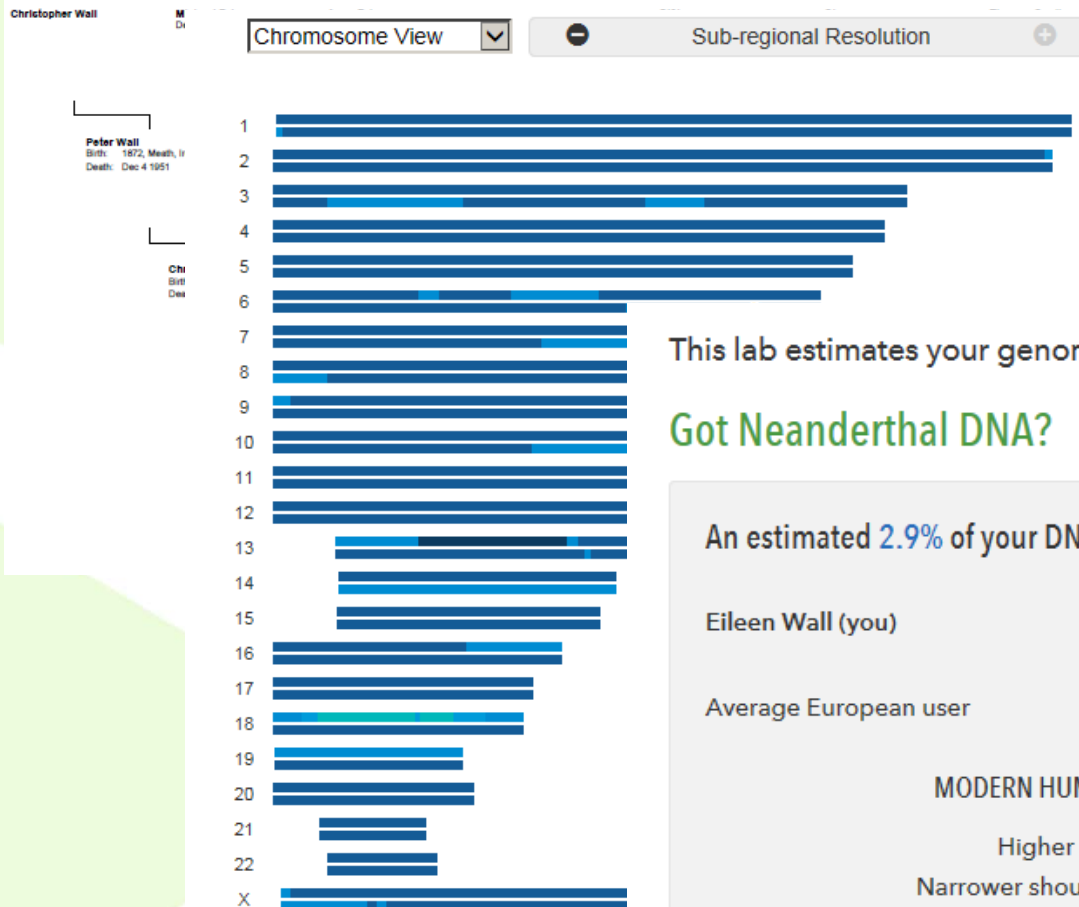
MODERN HUMANS

Higher brow  
Narrower shoulders  
Slightly taller



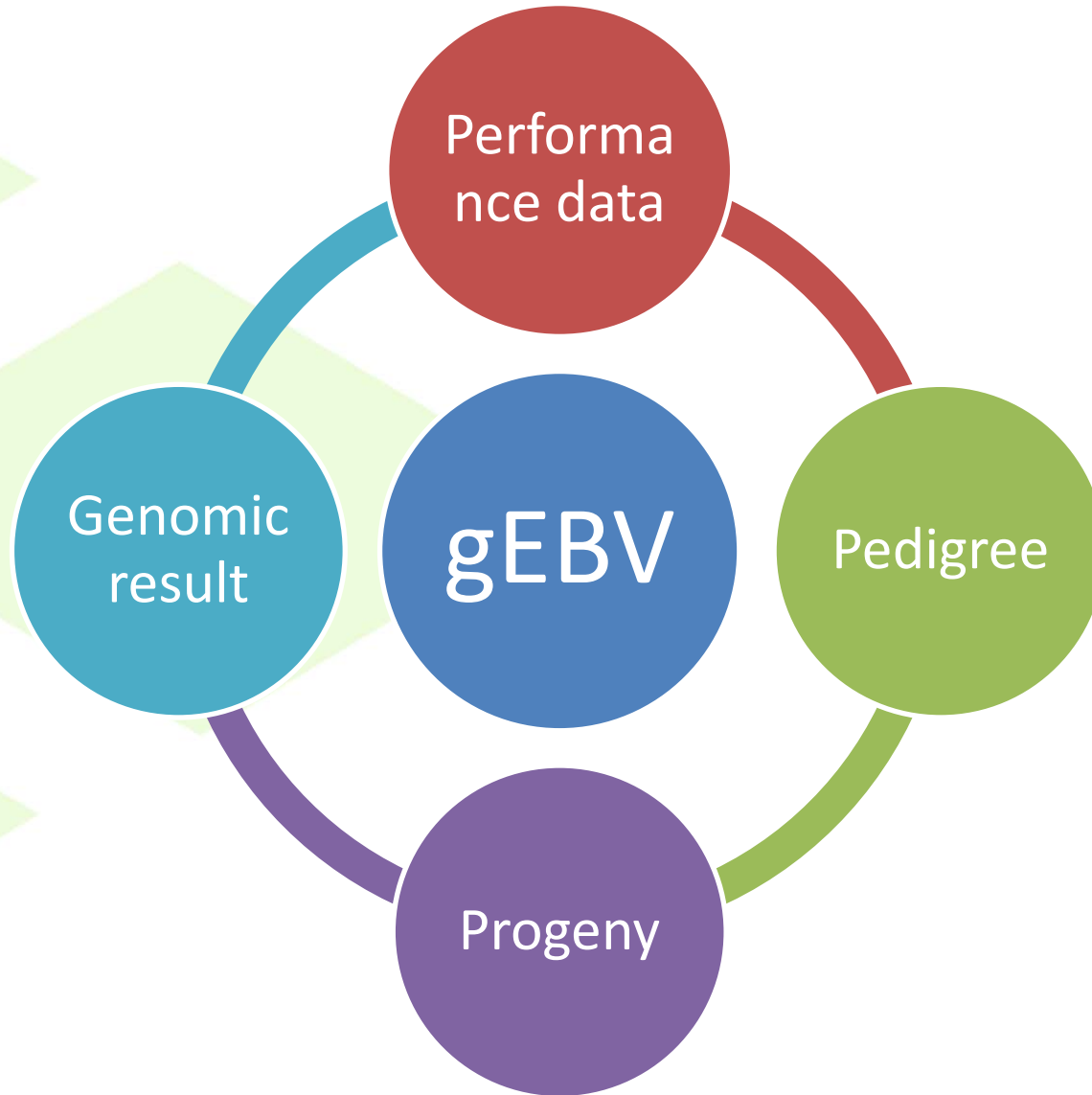
NEANDERTHALS

Heavy eyebrow ridge  
Long, low, bigger skull  
Prominent nose with developed nasal chambers for cold-air protection



# Current information in breeding values

## - DNA add genomic prediction



# Genomic selection impacts genetic gain



$$\Delta G_{\text{year}} = \frac{\sqrt{\text{reliability}} \times \text{selection intensity} \times \sqrt{\text{genetic variance}}}{\text{generation interval}}$$

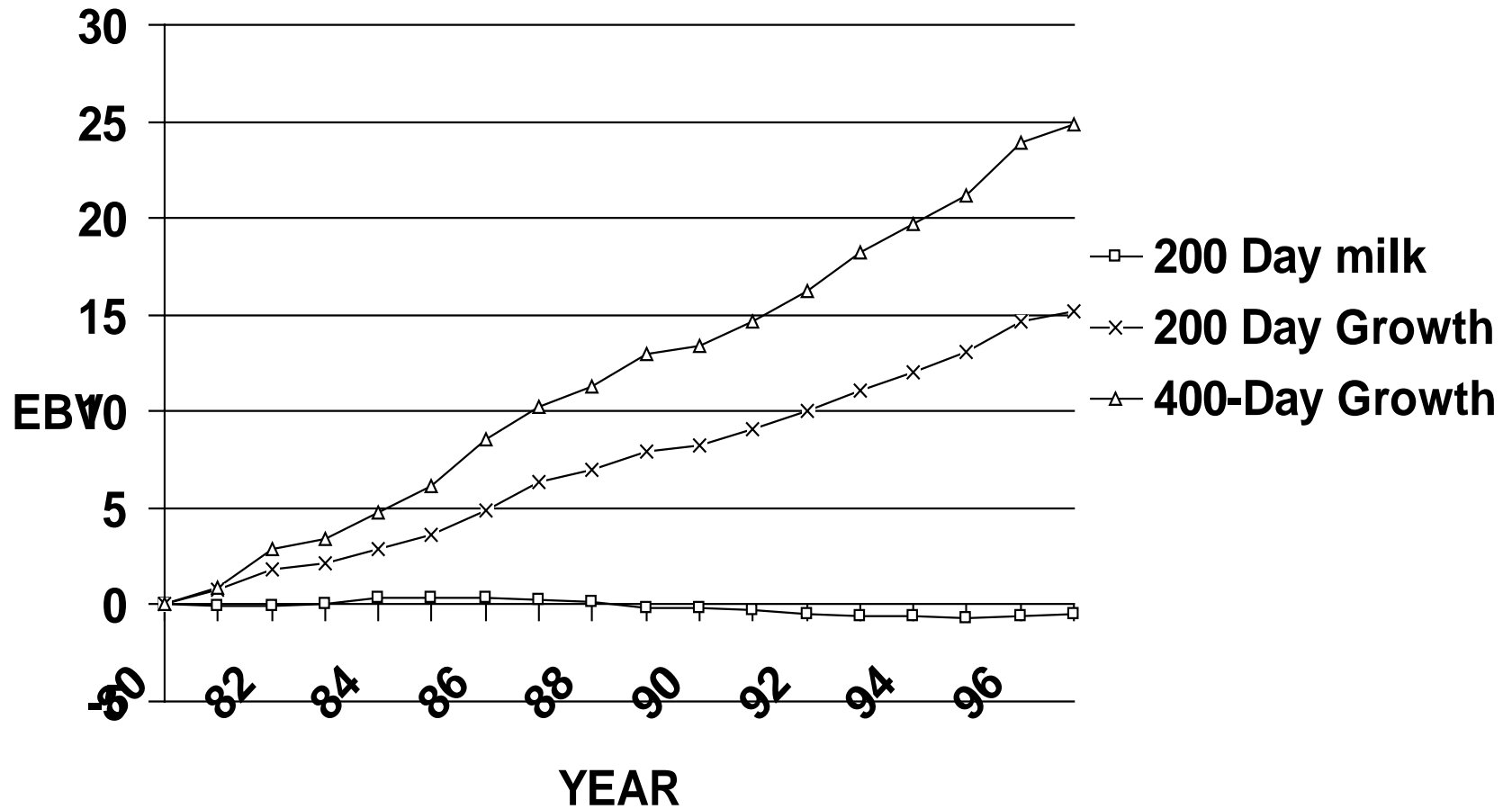
- $\Delta G$  = genetic gain each year
- reliability = how certain we are about our estimate of an animal's genetic merit (**genomics** ↑)
- selection intensity = how selective we are when making mating decisions (management can ↑)
- genetic variance = variation in the population due to genetics
- generation interval = time between generations (**genomics** ↓)

# Beef Genomics



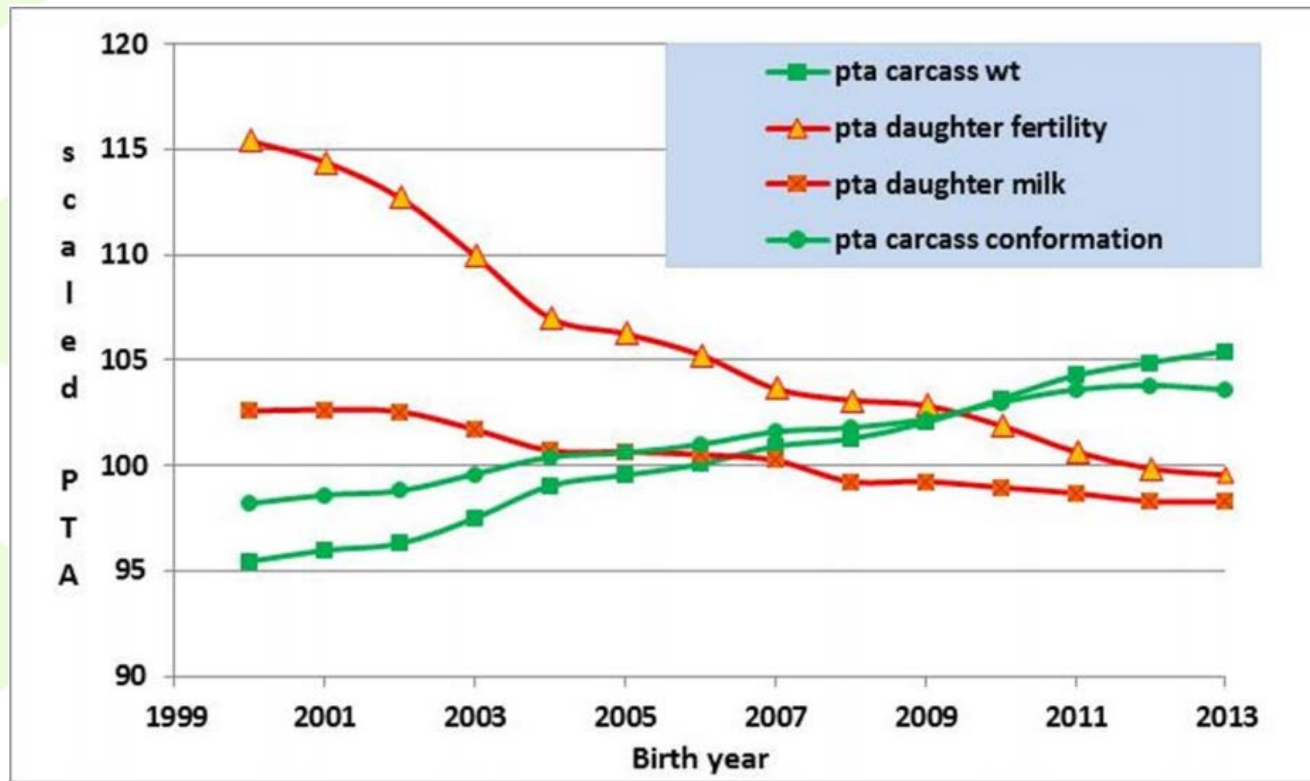


# Genetic trends in Charolais

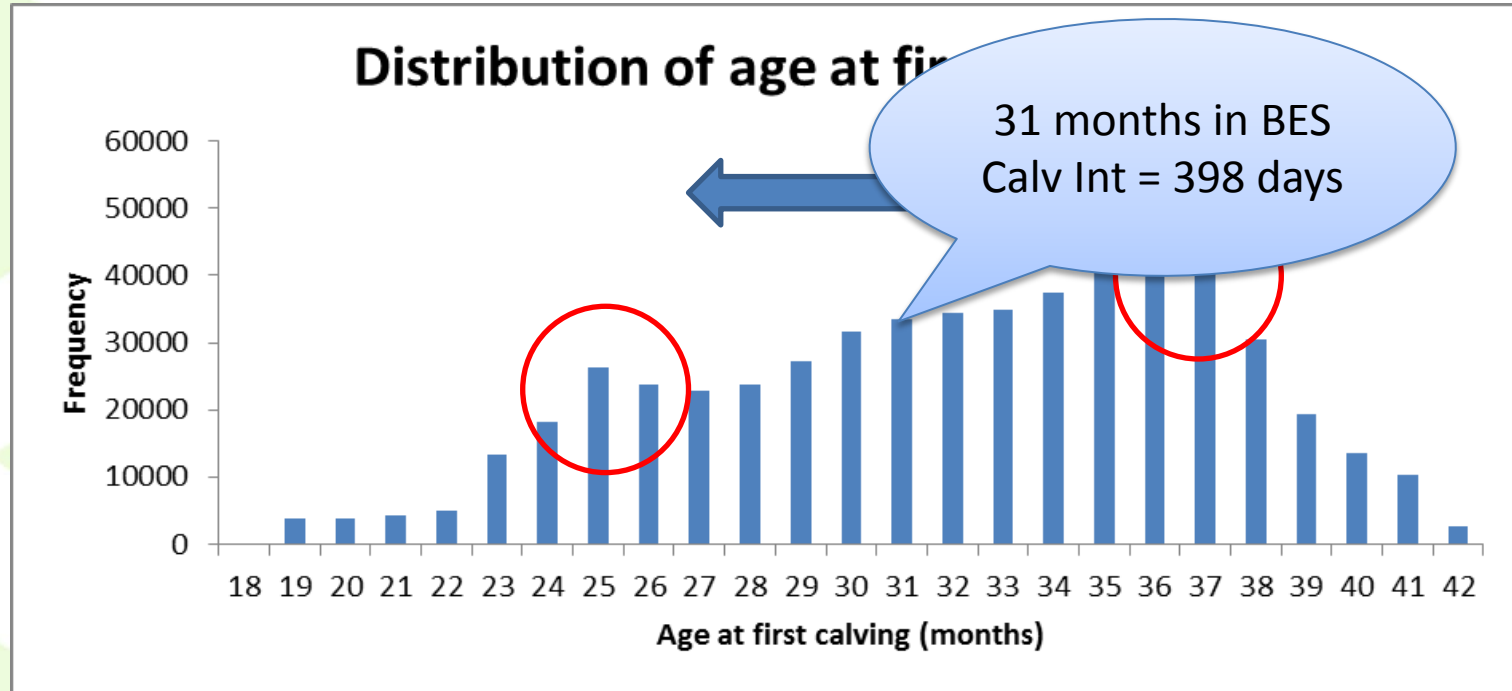


# .... And over in Ireland

- Genetic progress focused on terminal traits, with little progress attained in maternal traits

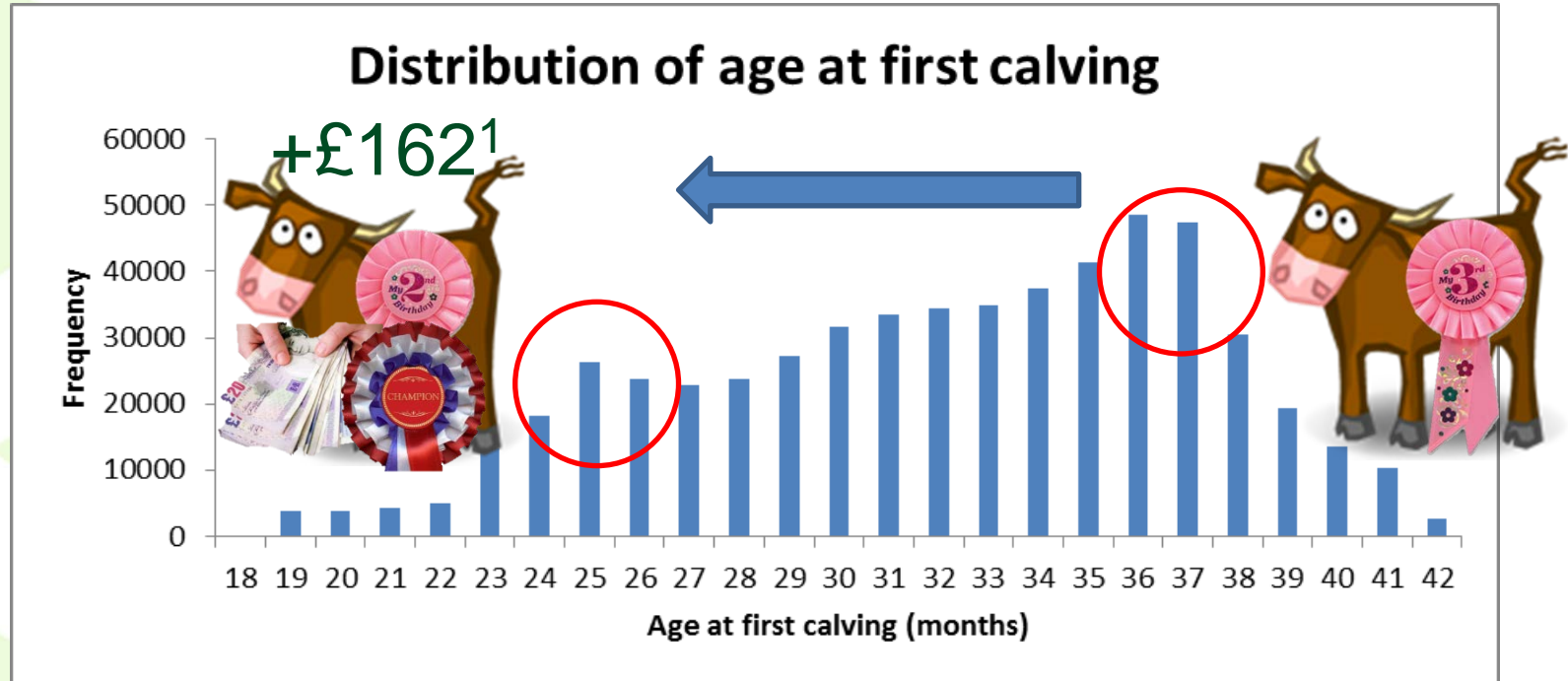


# Why maternal and calf traits?



- Most cows are 36 months when they have their first calf
- Huge potential to reduce to 24 months (where appropriate)

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# Improving Maternal Beef traits

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- Selection focused on beef growth and carcass traits has neglected many maternal traits
- Initiatives to improve maternal beef herds through increased use of improved maternal genotypes and genomic selection
  - Scotland Beef Efficiency Scheme (BES)
    - Improve herd profitability
    - Reduce greenhouse gas (GHG) emissions

# BES impact prediction



- Predict effects of farmer sourcing elite maternal genotypes to breed herd replacements

## Maternal Dual Purpose Index

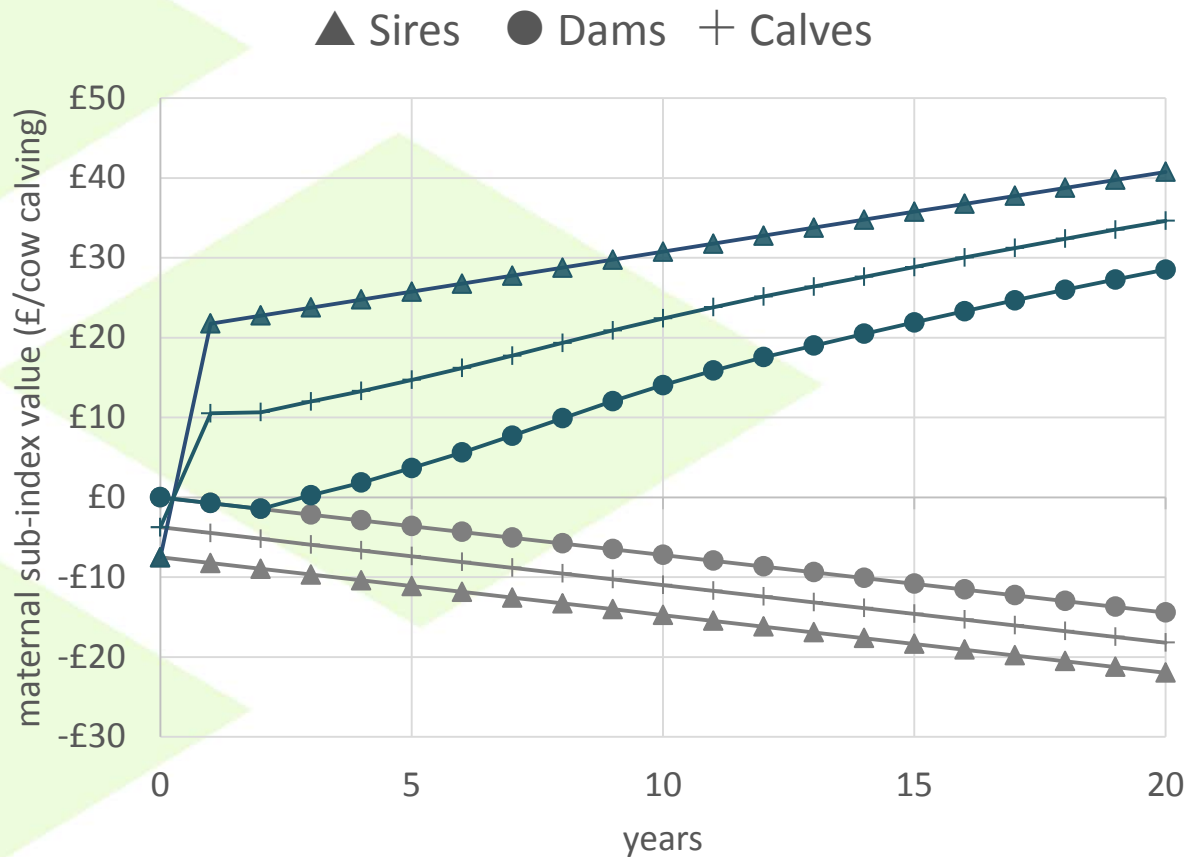
### Maternal Sub-index

- Mature weight (heifer, cow, cull cow)
- Calving interval
- Age at first calving
- Longevity
- Gestation length
- Calving ease

### Terminal Sub-index

- Beef value

# Genetic effect of Elite Maternal sires



Elite maternal  
+£30 sires used  
for 20y

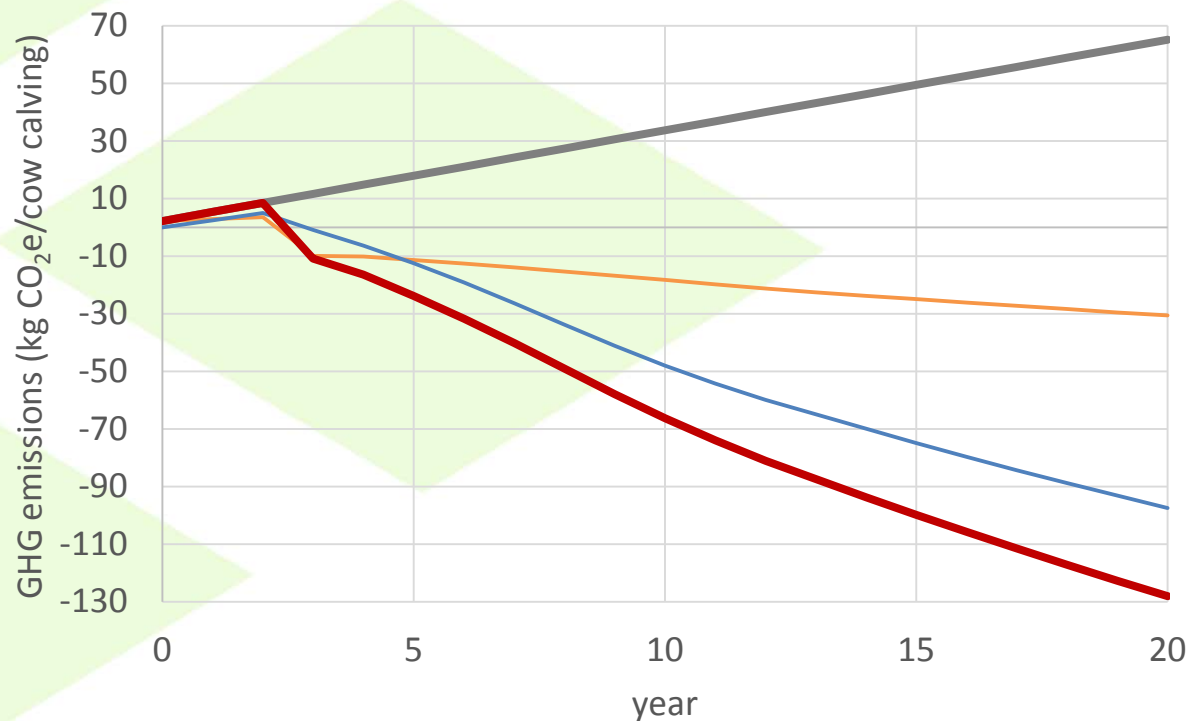
Current trend =  $-\text{£}0.722/\text{y}$

- ↑ Weight
- ↑ Calving interval
- ↓ Calving ease

# Expressed GHG with Elite Maternal sires



+£30 Elite maternal sires mated to herd for 20 years



Current Total maternal GHG trend

Replacement heifers

Breeding cows

Total maternal GHG



# BES – potential benefits

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- Genetic improvement value
  - £3.50/cow/year maternal traits
  - £4.11/cow/year efficiency/terminal traits
  - Permanent and cumulative
- 10 years = 270,000 t of CO<sub>2</sub>e and ~ £22m

# BES – Data benefits

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- Better data, and using it (!). Help farmers make the best breeding and management choices.
  - better rates of breeding
- A more sustainable beef sector – environmentally

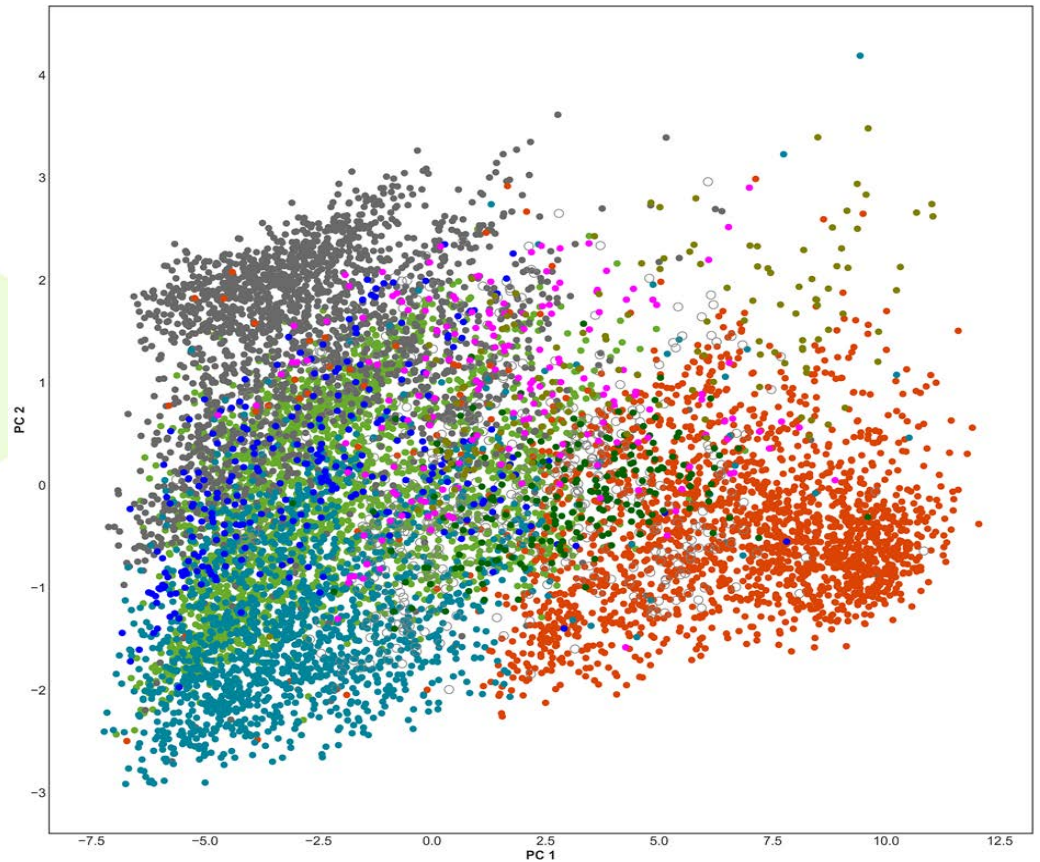
350,000 calvings  
55,000 animals selected for  
genotyping

# Highlights



- Sub-clustered by breed but linkages

- Charolais
- Limousin
- Aber. Angus
- Simmental
- Other
- Salers
- Stabiliser
- B. Blue
- Hereford

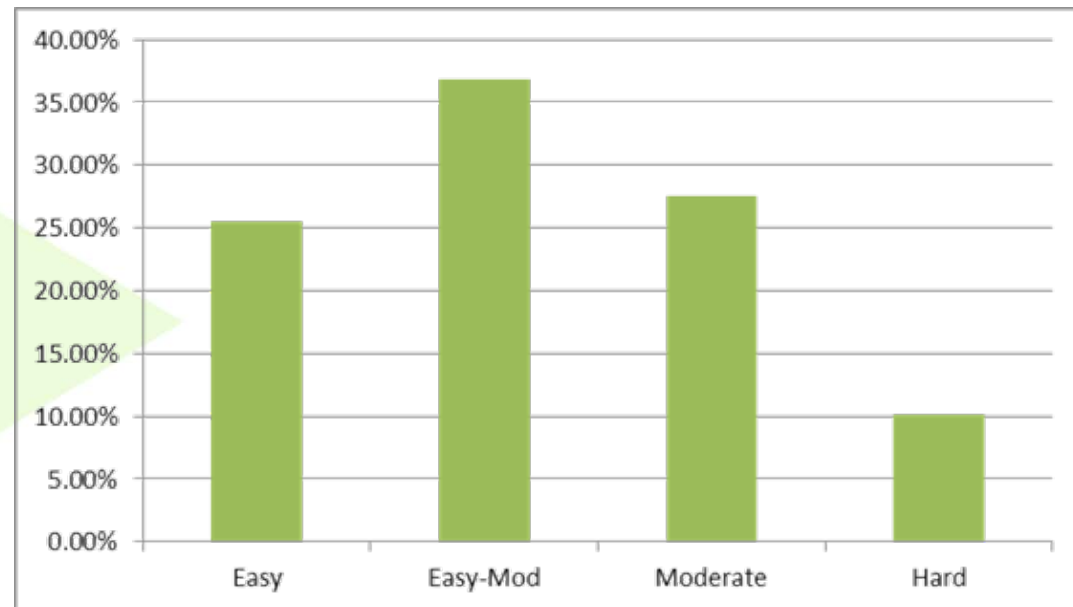


\* "Other" represents breeds with less than 100 cows and included: Blonde D'Aquitaine; Galloway; Luining; South Devon; Highland Cattle; and other breeds with numerically small numbers of genotypes

# Highlights



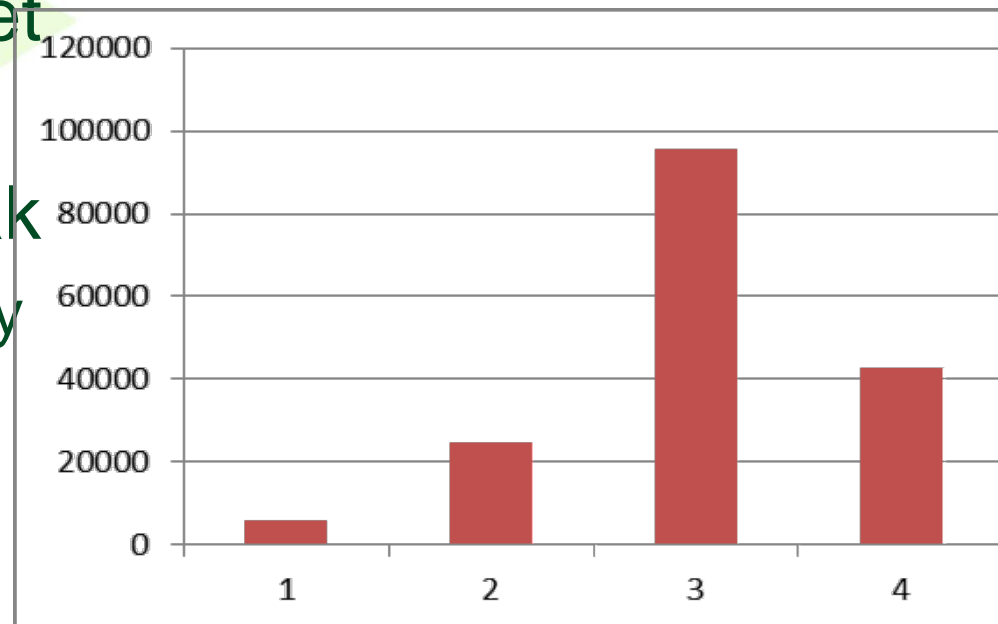
- Sub-clustered by breed but linkages
- 85% self calved
  - 2.2% vet assistances



# Highlights



- Sub-clustered by breed but linkages
- 85% self calved
  - 2.2% vet assistances
- 73% of dams docile/quiet
  - 2.5% aggressive
- 3.5% of calves lazy/weak
  - 5X more likely to die early



# Highlights



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- 85% self calved
  - 2.2% vet assistances
- 73% of dams docile/quiet
  - 2.5% aggressive
- 3.5% of calves lazy/weak
  - 5X more likely to die early
- Traits from historic data
  - $h^2$  age @ slghtr = 17%
  - $h^2$  age @ 1<sup>st</sup> calf = 39%

parity	CalvInt (days)	stdev	count
1	405	104.0	158,691
2	388	88.2	130,220
3	383	81.4	104,879
4	382	78.1	82,728
5	382	76.3	63,255

Sire Breed	Age @ 1 <sup>st</sup> Calf	Count
Angus	30.2	22,743
Simmental	30.4	16,663
Limousin	32.9	15,634
Stabiliser	26.3	6,641
Hereford	32.2	5,068

# Summary

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- Beef behind dairy in terms of genetic improvement
  - Lots of low hanging fruit
- tep changes in the coming years
- Genetic evaluations developed for novel traits, e.g,
  - feed efficiency – industry trait collection ongoing
  - disease resistance if large enough populations can be amassed and data shared - top 5 disposal reasons where old age, **infertility**, **born dead**, **pneumonia** and general health
- Integration of data across farm types and industry for gEBVs for all
- Good baseline data helps implement and realise potential of innovations – genomics and wider

THANK YOU!

