# Utilising sequence data and genomics to improve novel carcase traits in beef cattle

Overview of the project

AIM: improve carcase traits in beef by identifying animals with superior genetics for carcase traits.

To achieve this we are combining Video Imaging Analysis (VIA) of carcasses and genomic information to produce genomic breeding values for UK Limousin cattle.
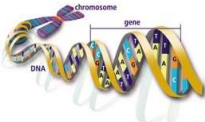
OUTCOME: a SNP Key for carcase traits will be created specific for UK Limousin cattle. Breeders can then genotype animals with no carcase records and use the genomic breeding values to select and breed from animals with superior carcase attributes.

DATA:
- A VIA machine has been installed in an abattoir to collect phenotypic records on commercial cattle
- For each carcase record we have - 9 VIA primal cuts
EUROP fat and conformation grades, and carcase weight
- Genetic marker data

SILVERSIDE
RUMP
STRIPLOIN
TOPSIDE
KNUCKLE
FLANK
FILLET
8 RIB HQ
5 RIB FQ
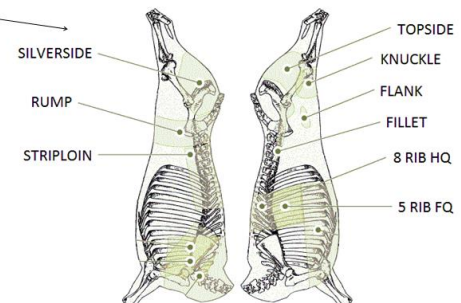
WORK ACHIEVED TO DATE:
- Heritabilities have been estimated for the carcase traits
- EBVs have been produced for the carcase traits
- Animals have been identified for genotyping and we are currently in the process of obtaining DNA samples for genotyping animals to include in the reference population

NEXT STAGE:
i)   we are collecting more DNA samples to increase the reference population
ii) more VIA machines are to be installed in abattoirs across the UK

        then the SNP key can be created to produce genomic breeding values for carcase traits for UK Limousin cattle

Setting Standards

Utilising sequence data and genomics to improve novel carcase traits in beef cattle

UK

Variation in the carcase traits

- VIA machines produce a large amount of data and show that there is large variation in the primal cuts of carcases produced in the UK
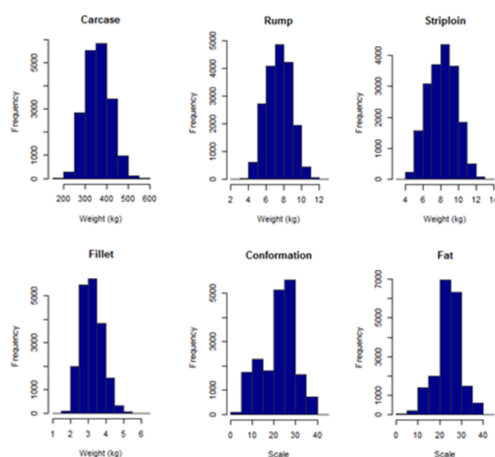

Figure 1 Variation observed for carcase weight and yields of certain primal cuts (20,000 prime slaughter steers)
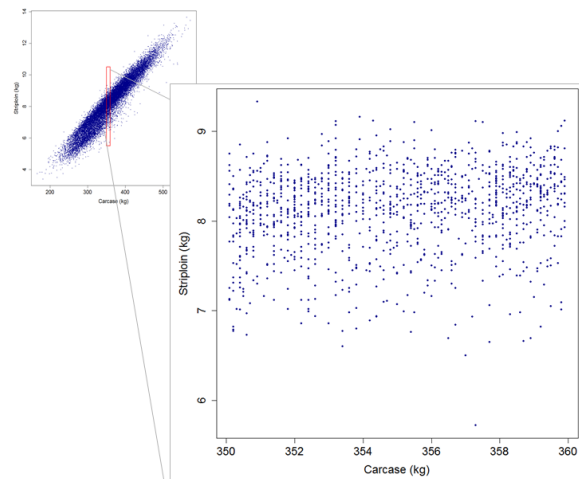

Figure 2 Striploin yield (20,000 prime slaughter steers)

- Substantial variation observed in carcase weight and primal cut yields across animals (Figure 1)
- Figure 2 focuses on the primal cut striploin and shows that
  i.   As carcase weight increases striploin yield also increases
  ii. But, if we zoom in on animals of a similar weight (350 – 360 Kg) we can see there is also a large amount of variation in striploin yield across animals of the same carcase weight
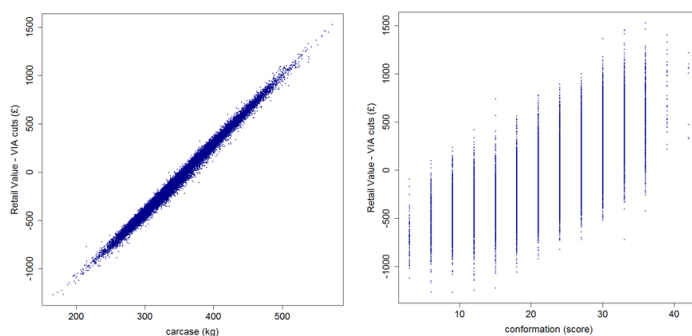

- The variation in primal cut yield also translates into financial differences
- Figure 3a,b shows a relationship of with increasing retail value of the primal cuts there is increasing carcase weight and conformation score
- However, both graphs also show that for a given carcase weight or conformation score there is large variation in retail value

Figure 3a,b Variation in retail prices of the primal cuts (primal cut prices taken from www.meatprices.co.uk; 20,000 prime slaughter steers)

Setting Standards

UK   SRUC   LIMOUSIN

Utilising sequence data and genomics to improve novel carcase traits in beef cattle

UK

Genetic analysis

With our VIA carcase traits, before we produce breeding values, we are interested in determining how much of the phenotypic variation observed in the traits can be attributed to genetic factors.

Analysis:
- To do this we need to partition the phenotypic variation into genetic and environmental components
- In statistical models we accounted for environmental effects, such as birth and finishing herds, date of slaughter, age of dam, animal sex, season of birth and breed
- In doing so we can calculate the heritability, which is a measure of how much of the trait's phenotype is controlled by the animal's genes
  - The higher the heritability, the more influence genetics has on the trait. However, genetic improvement has been shown to be beneficial even for traits low heritabilities

Results:
- As can be seen in the figure below, heritabilities of the VIA carcase traits are moderate to high
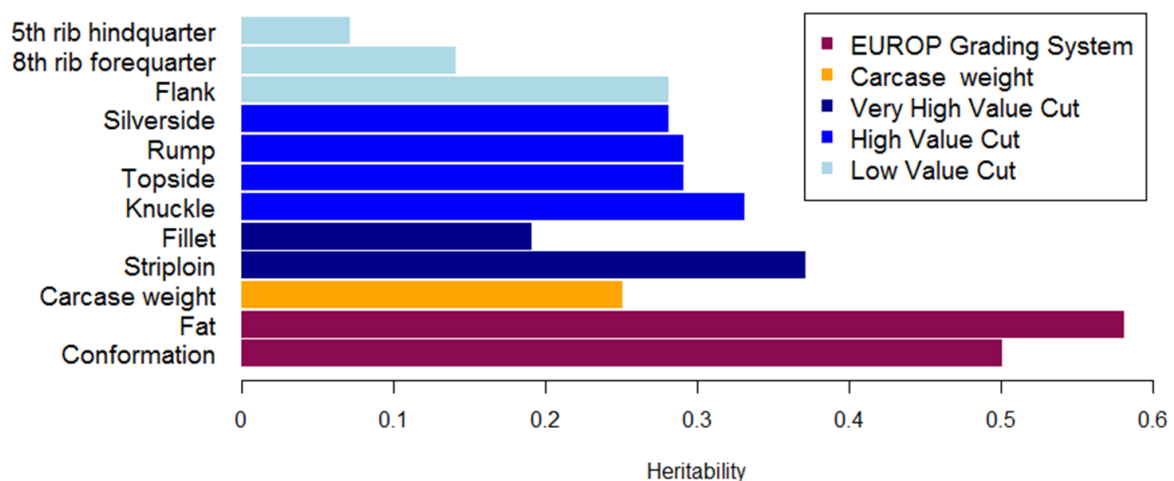

Figure 1 The heritabilities for the 12 carcase traits. All estimates had a standard error < 0.05.

Implications:
- The heritabilities show that an animals genetics has significant impact on the carcase traits
- This indicates that selection to improve these carcase traits is feasible and likely to be highly successful

Setting Standards

UK   SRUC   LIMOUSIN

Utilising sequence data and genomics to improve novel carcase traits in beef cattle

Limousin EBVs

VIA carcase trait EBVs were calculated for the prime slaughter population and the EBVs of 30 Limousin sires with 10 or more progeny with VIA traits recorded compared.

Figure 1 below ranks the sires based on the average retail value (based on 9 VIA primal cuts) of their progeny (blue dots). Compare the top and bottom 4 sires shows a difference of £350 for the retail value of the progeny produced. The VIA EBVs produced were weighted to derive a VIA retail value index (red dots). Comparing the VIA retail index values for the 4 top and bottom sires based on phenotypes show an average difference of 8.67. However, in a lot of cases the bulls that had high phenotypes did not have the better index value – meaning that the reason for the good phenotypes was environmental and not genetics. This illustrates the importance of selecting animals based on EBVs to ensure that genetically superior animals are selected
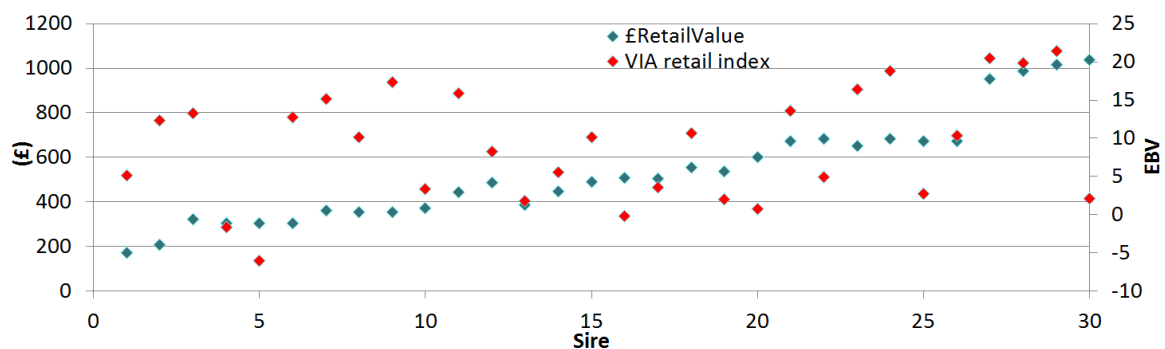

Figure 1 Plot of increasing retail value of Limousin sires and a weighted VIA retail index

The figure below ranks the animals based on their VIA retail index value; the difference between top and bottom sires is 27.50 and this translates to a £463 difference between the raw retail value of progeny
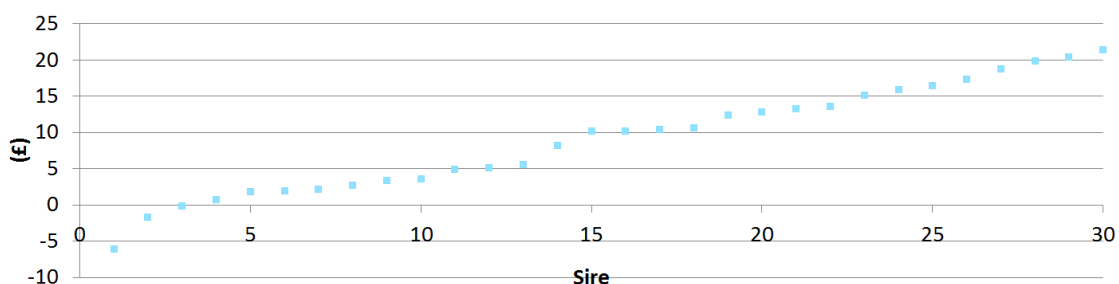

Figure 2 Plot of increasing weighted VIA retail index

Setting Standards