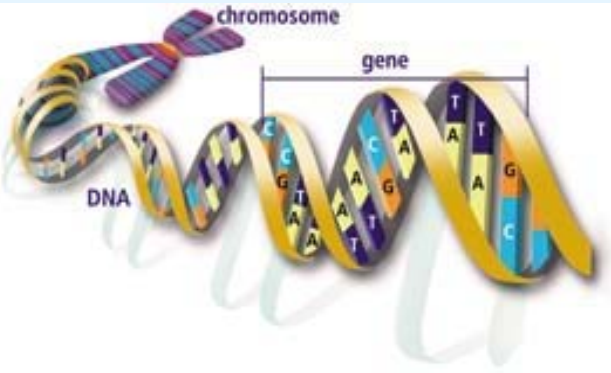
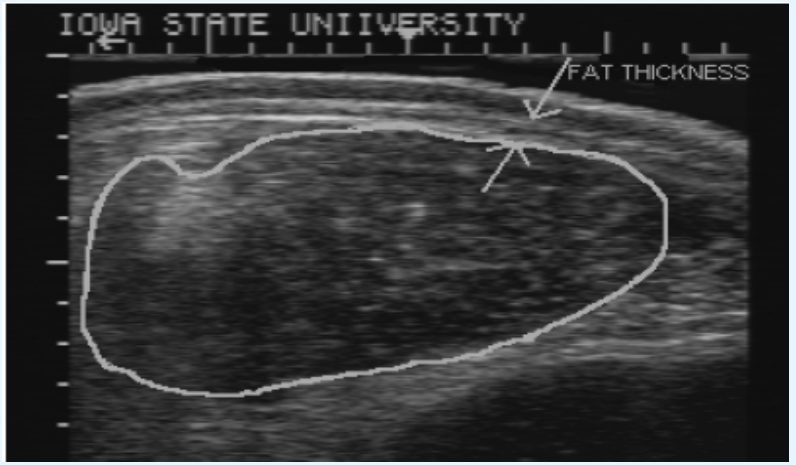
Utilising sequence data and genomics to improve novel carcass traits in beef cattle

Kirsty Moore and Mike Coffey



Carcass trait UK genetic evaluations ~ current

- Traditional BLUP EBVs for proxy traits
- Limousin Pedigree sector (~20,000/year)
  - 400 day weight (~5,000/year; 25%)
  - Ultrasound fat and muscle depth (~1,500/year; 7.5%)
- Commercial producers are paid based on EUROP system



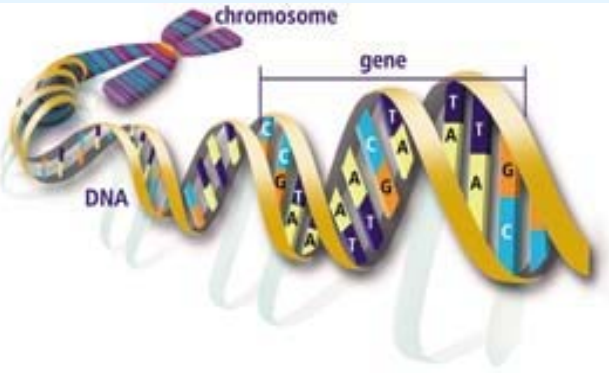
Carcass trait UK genetic evaluations ~ future

- Actual carcass traits
- More animals recorded
- New technologies
  - Genomic breeding values
- Improved market signals

- Collaboration required

Genomic breeding values for VIA carcass traits

- A 3 year project (November 2011 – October 2014)
- Anglo Beef Processers (ABP), British Limousin Cattle Society (BLCS) and SAC
  - Technology Strategy Board funding
- Deliver to the industry genomic breeding values for Video Image Analysis carcass traits
- Provide platform
  - for future genomics work
  - other breeds



VIA system

- E plus V
- Carcass position over a holding frame
- Cameras and lighting fixed into position
- Computer control unit
  - automated

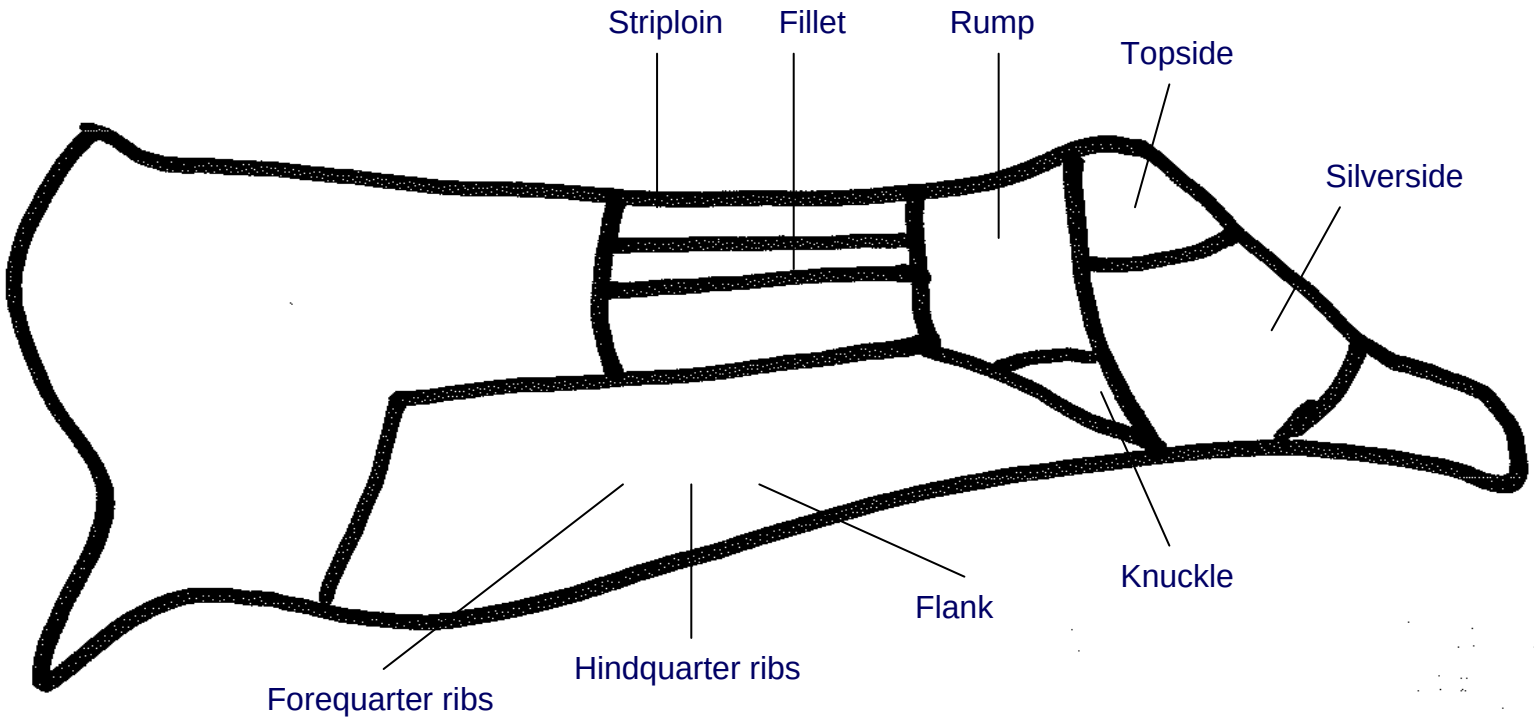
Image capture (2D & 3D)

- Calibrated images captured
- Mechanically grades carcass
  - fat (2D)
  - conformation (3D)
- Primal yields

Additional features

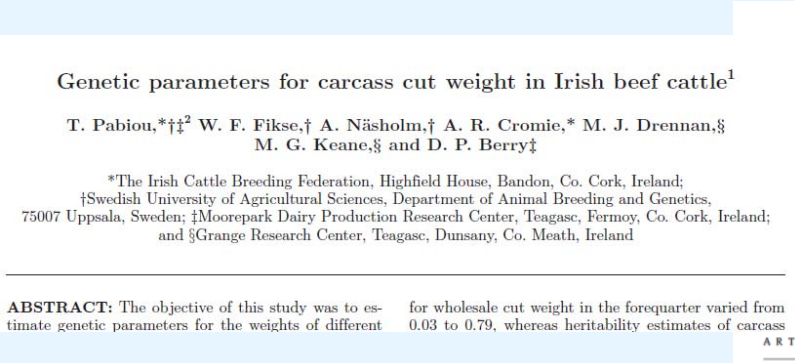
- Stop/start or moving carcass chain lines (<120/hr)
- Position triggered by sensors monitoring chain hook positions
- Needs carcass weight, sex and ID inputs for classification
- Provides classification outputs and estimates of lean yields

ABP VIA traits



VIA as selection criteria

- A lot of research
  - T. Pabious ICBF
- VIA is a good predictor of carcass cuts
- VIA carcass cuts
  - heritable
  - genetic variation



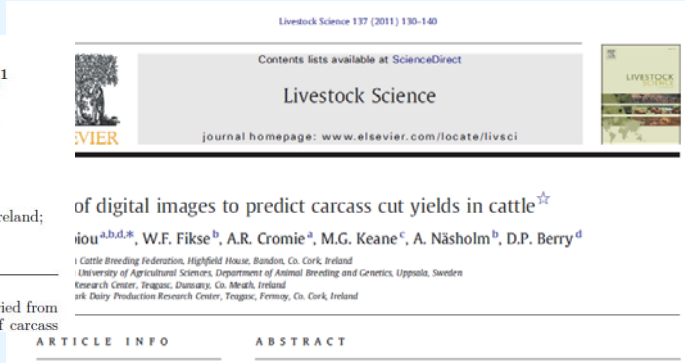
Genetic parameters for carcass cut weight in Irish beef cattle[1]

T. Pabiou,*†‡[2] W. F. Fikse,† A. Näsholm,† A. R. Cromie,* M. J. Drennan,§ M. G. Keane,§ and D. P. Berry‡

*The Irish Cattle Breeding Federation, Highfield House, Bandon, Co. Cork, Ireland; †Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics, 75007 Uppsala, Sweden; ‡Moorepark Dairy Production Research Center, Teagasc, Fermoy, Co. Cork, Ireland; and §Grange Research Center, Teagasc, Dunsany, Co. Meath, Ireland

ABSTRACT: The objective of this study was to estimate genetic parameters for the weights of different

for wholesale cut weight in the forequarter varied from 0.03 to 0.79, whereas heritability estimates of carcass



Livestock Science 137 (2011) 130–140

Contents lists available at ScienceDirect

Livestock Science

journal homepage: www.elsevier.com/locate/livsci

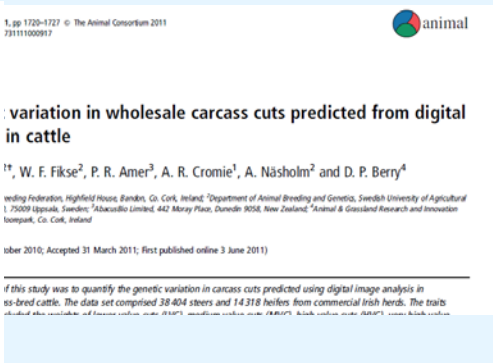
of digital images to predict carcass cut yields in cattle☆

iou[a,b,d,*], W.F. Fikse[b], A.R. Cromie[a], M.G. Keane[c], A. Näsholm[b], D.P. Berry[d]

Cattle Breeding Federation, Highfield House, Bandon, Co. Cork, Ireland
University of Agricultural Sciences, Department of Animal Breeding and Genetics, Uppsala, Sweden
Research Center, Teagasc, Dunsany, Co. Meath, Ireland
ark Dairy Production Research Center, Teagasc, Fermoy, Co. Cork, Ireland

ARTICLE INFO

ABSTRACT



animal

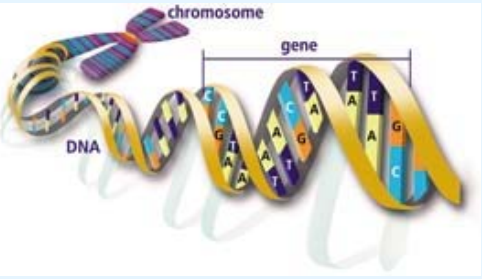
variation in wholesale carcass cuts predicted from digital in cattle

W. F. Fikse[2], P. R. Amer[3], A. R. Cromie[1], A. Näsholm[2] and D. P. Berry[4]

ober 2010; Accepted 31 March 2011; First published online 3 June 2011)

Sources of information

- VIA will be used to collect carcass information from animals processed by Anglo Beef Processors
- A large number of Limousin cattle will be genotyped by both the British Limousin Cattle Society and industry
- British Cattle Movement Service and performance recording data bases



SNP Key

ABP VIA data

BCMS database

Limousin pedigree and performance recording

Phenotypes, Fixed effects

Pedigree, fixed effects

Data set to produce de-regressed VIA EBVs

Genotypes from purebred Limousin sires

VIA SNP key produced

Data merging systems

ABP carcass data

1 site since 2008

N=65,000 annually

BCMS database

99.9% match rate

Large amounts of Data

Encourage farmers to record sire on BCMS passport

N=15,600

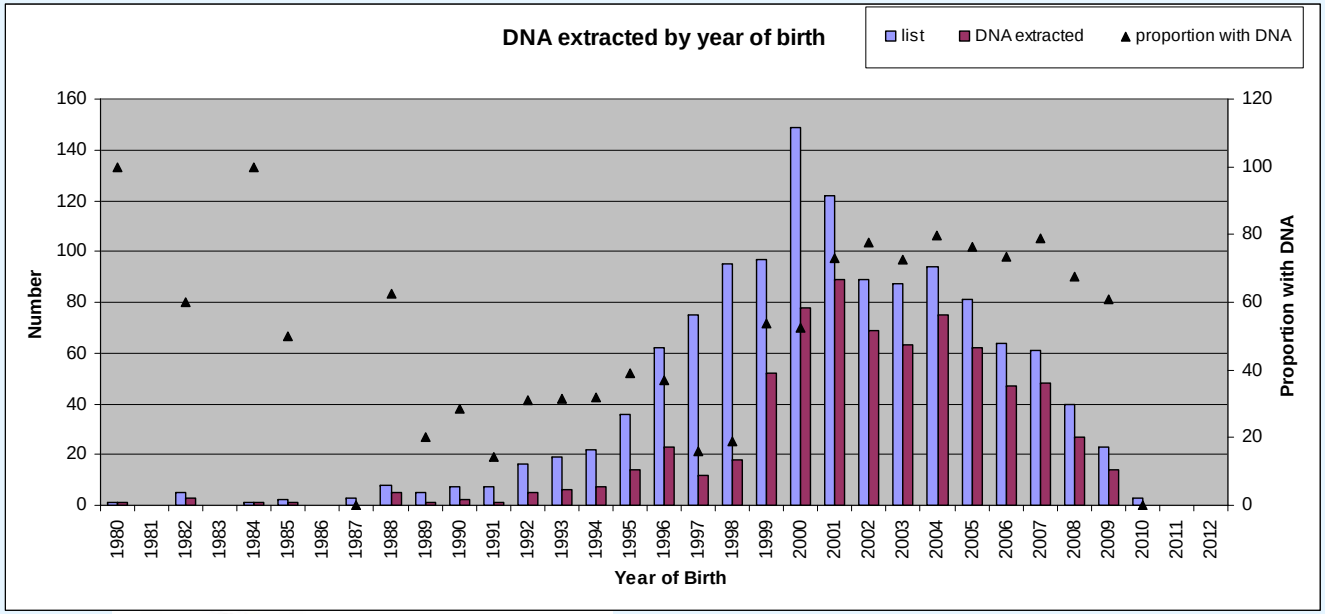
22,000 Limousin/LimousinX animals annually

5,200 with sire recorded

A third of the carcass data was from Limousin or Limousin cross animals

SNP Key

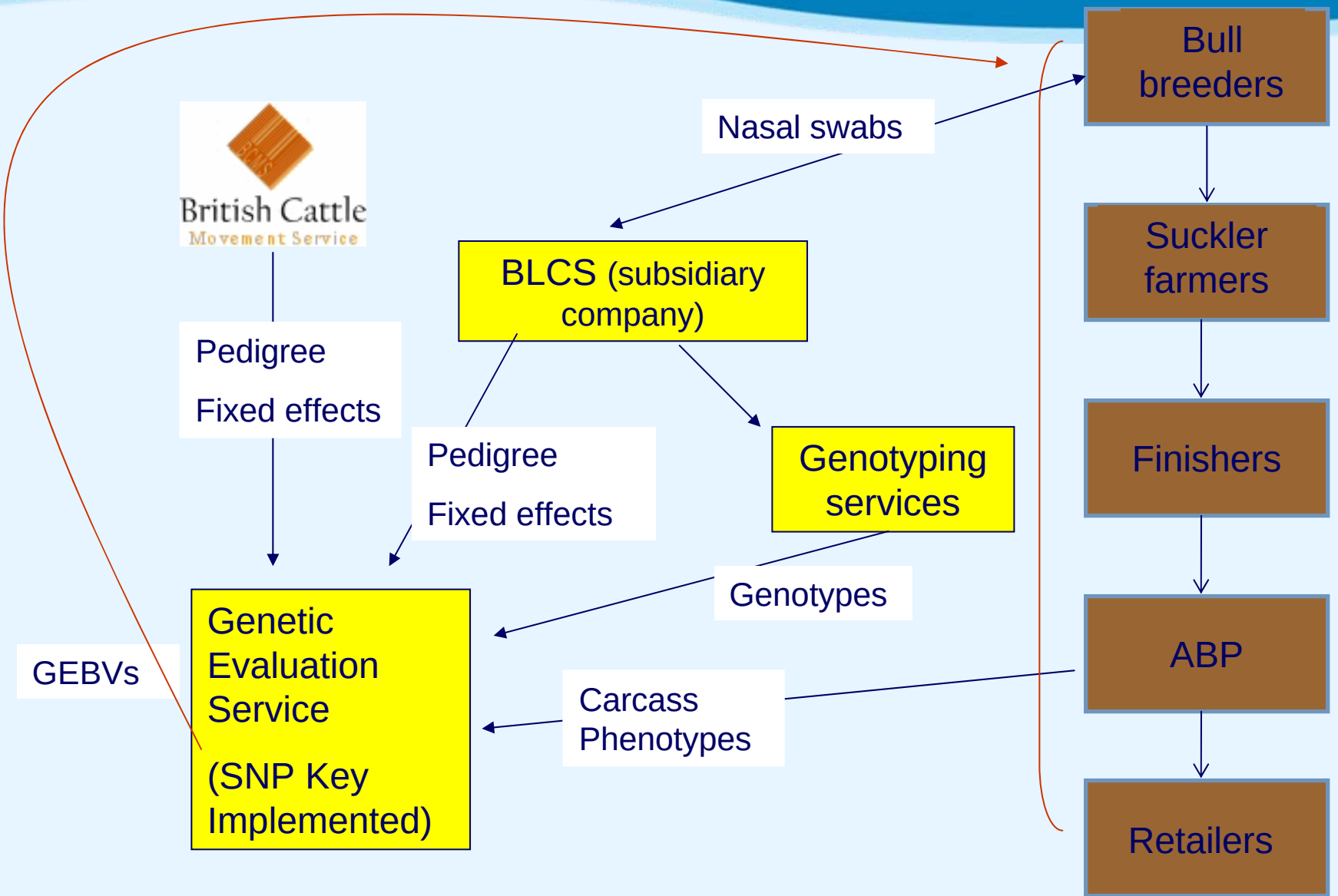
- SAC have 720 Illumina HD genotypes from influential Limousin males
- BLCS will genotype ~2000 more Limousin males



Genotypes from purebred Limousin sires

VIA SNP key produced

Flow of New Breeding Values



Benefits

- Accelerated genetic progress
  - GEBV at birth (generation interval)
  - Trait is actual abattoir trait (accuracy)
- Platform for future genomics
  - New technologies
  - New traits
- Places UK beef genetic evaluation with the world leaders
- Clear market signals
  - For the first time abattoir through to breeders are talking about the same trait

Project Collaborators and Acknowledgements

Stuart Roberts

James Draper

Iain Kerr

Simon Mead

Mike Coffey

Kirsty Moore

Tim Roughsedge

Tomas Krzyzelewski

Ian Archibald

Raphael Mrode