



The use of carcass traits collected in the abattoir using video image analysis to improve beef yield

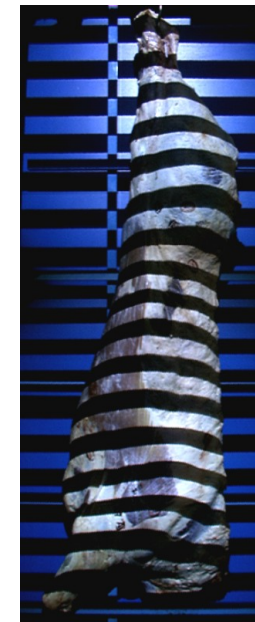
Dr Kirsty Moore, R Mrode & M Coffey

Leading the way in Agriculture and Rural Research, Education and Consulting

Overview



- Current Genetic evaluations
- UK beef genetic evaluation developments
 - EUROP carcass trait evaluations
 - Genomic evaluations for VIA carcass traits



Current carcass trait evaluations



- 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%)



In the age of the genotype.....



PHENOTYPE IS KING!



Why are we interested in abattoir records?



Answer: the quantity of extra information available

e.g. Limousin

- ~ **1,500** animals / year ultrasonically scanned
- In 2011 abattoir records on ~**93,000** animals
Limousin/Limousin cross
- Of these ~**20,000** had Limousin sire recorded
- The addition of this extra information should increase the accuracy (reliability) of genetic evaluations

Valuing carcasses



- Commercial farmers paid using EUROP grid
- Paid per kg deadweight
- + penalty/premium based on
 - Conformation class
 - Fat class
- VIA provides carcass component traits
 - Multiplied by retail value

Limousin Cross steers



Carcase weight = 279kg
Conformation = P-
Fat = 3+

Carcase weight = 370kg
Conformation = O-
Fat = 2+

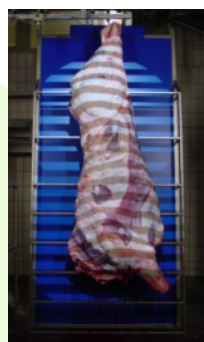
Carcase weight = 314kg
Conformation = R=
Fat = 1=

Carcase weight = 306kg
Conformation = R=
Fat = 3=

Carcase weight = 497kg
Conformation = E=
Fat = 2+



Utilising data from multiple sources



UK eartag
Carcase
traits
Dates of birth
& slaughter,
sex, breed



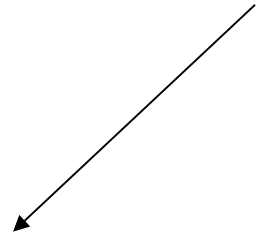
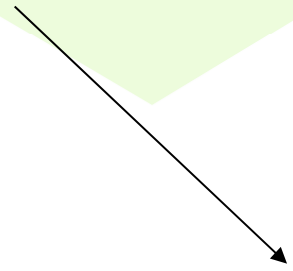
**British Cattle
Movement Service**

UK eartag
Dates of birth
& death, sex,
breed,
pedigree
(sire and
dam), full
movement
information



UK eartag
Dates of birth,
sex,
breed,
pedigree
(sire and
dam)

Carcase trait EBVs



Combined data – June 2014



- 3.5m carcass records
 - 6 processors, multiple sites
- 89 % carcass records matched to BCMS (3.1 million animal records)
- 23% had sire recorded in BCMS (~0.71 million animal records)
 - 28% for 2012+ born animals

Breeds



- **Dairy genetics** are a **major** component of beef carcasses
 - Holstein Friesian the most common dam breed of the slaughter generation (accounting for 46%)



Ten most common dam breed types

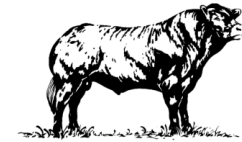
	Breed code	Progeny Count	%		Breed code	Progeny Count	%
1	Holstein Friesian	1,078,469	45.7	6	Belgian Blue	90,459	3.8
2	Limousin	341,457	14.5	7	Charolais	85,118	3.6
3	Aberdeen Angus	225,330	9.6	8	Blonde d'Aquitaine	31,778	1.4
4	Simmental	175,326	7.4	9	Shorthorn	29,526	1.3
5	Hereford	117,247	5.0	10	Saler	26,363	1.1

VIA genomic breeding values

- 4 year project (2012-2015)
- Limousin genomic breeding values for abattoir VIA carcass traits
 - Available 2015
- First UK genomic breeding values



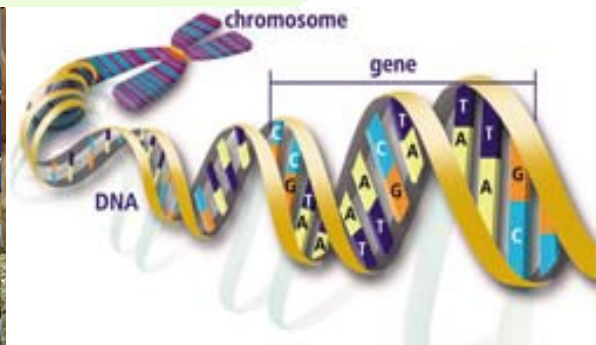
SRUC



LIMOUSIN



Food Group



Technology Strategy Board
Driving Innovation



Video Image Analysis (VIA)



- VBS2000
 - E+V
- Calibrated images (2D and 3D)
- Carcase weight and sex
- Mechanically grades the carcase
 - EUROP conformation and fat classes
 - 7 primal cut yields



• Heritability of carcass cuts

Forequarter

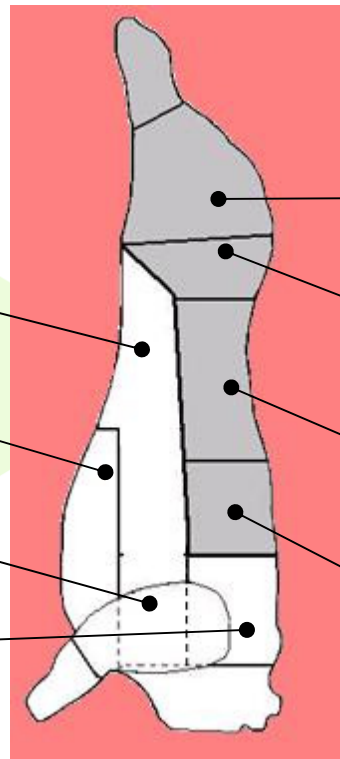
Ribs & Flank : 0.03

Brisket : 0.25

Shoulder : 0.79

Chuck : 0.83

[0.15 ≤ s.e. ≤ 0.24]



Hindquarter

Round : 0.86

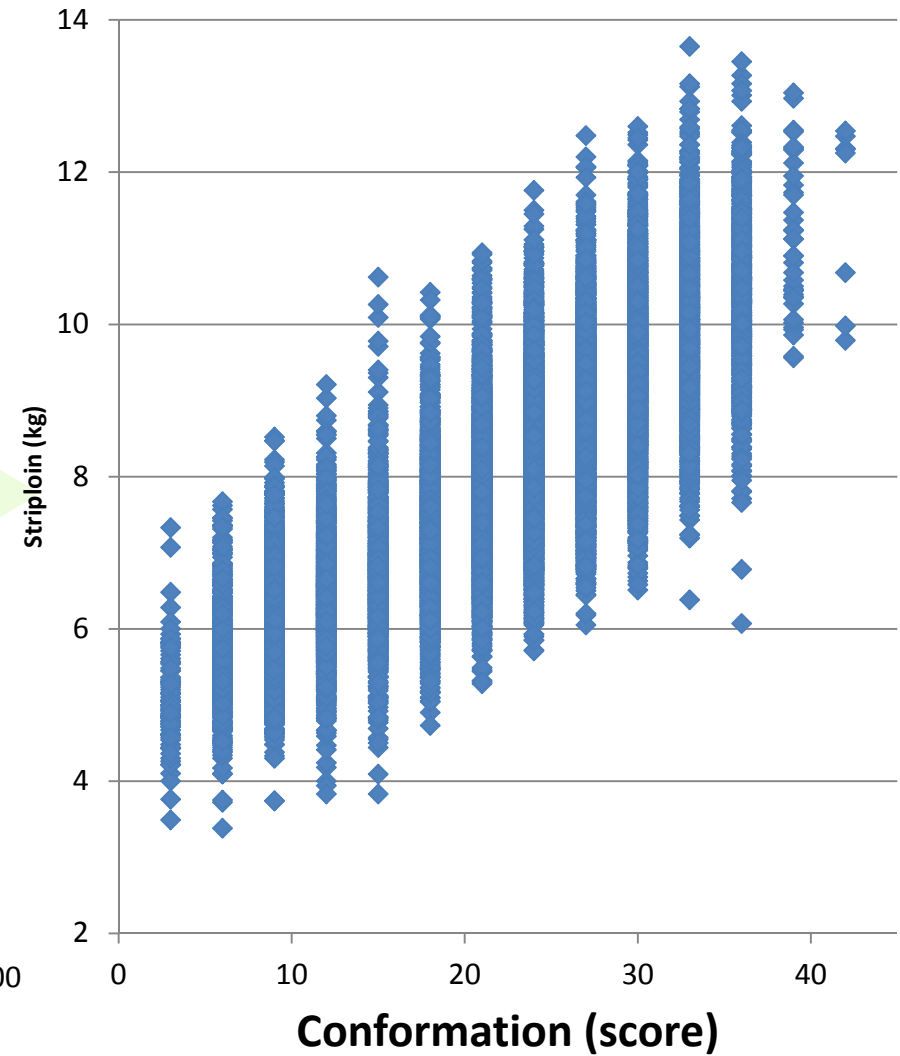
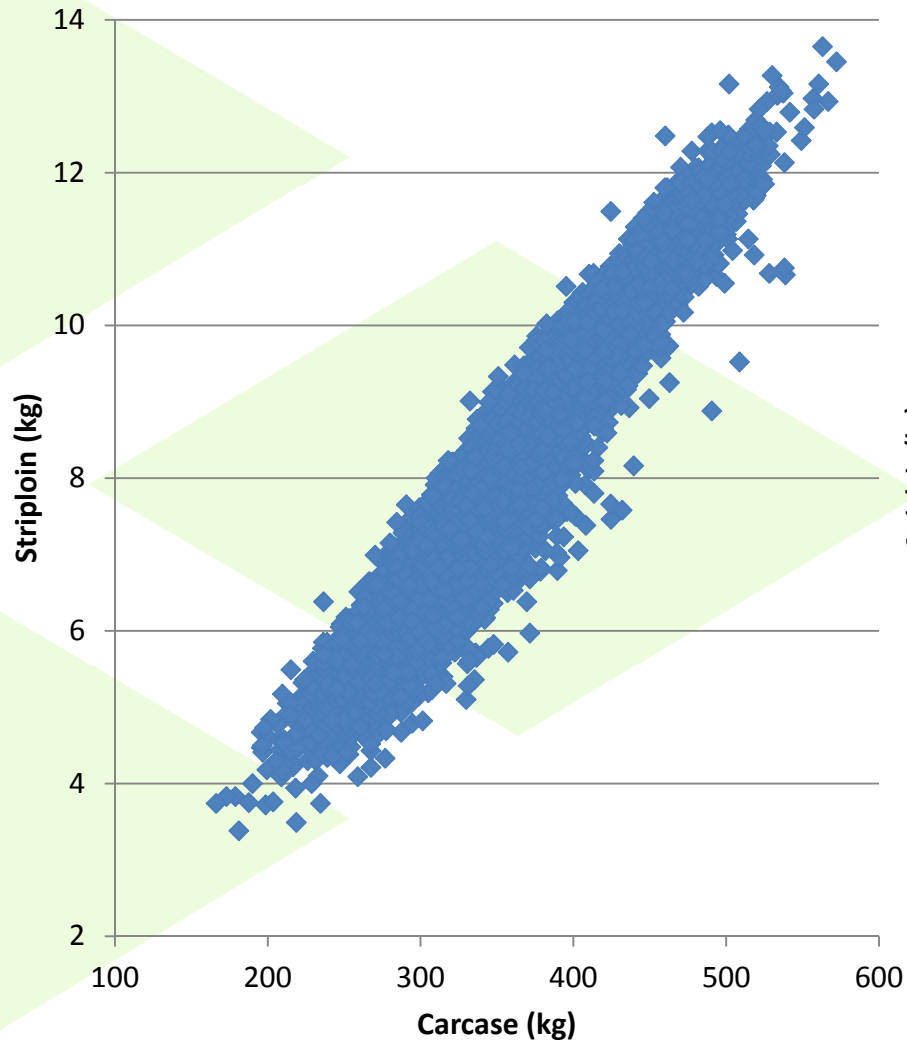
Sirloin : 0.67

Strip-Loin : 0.49

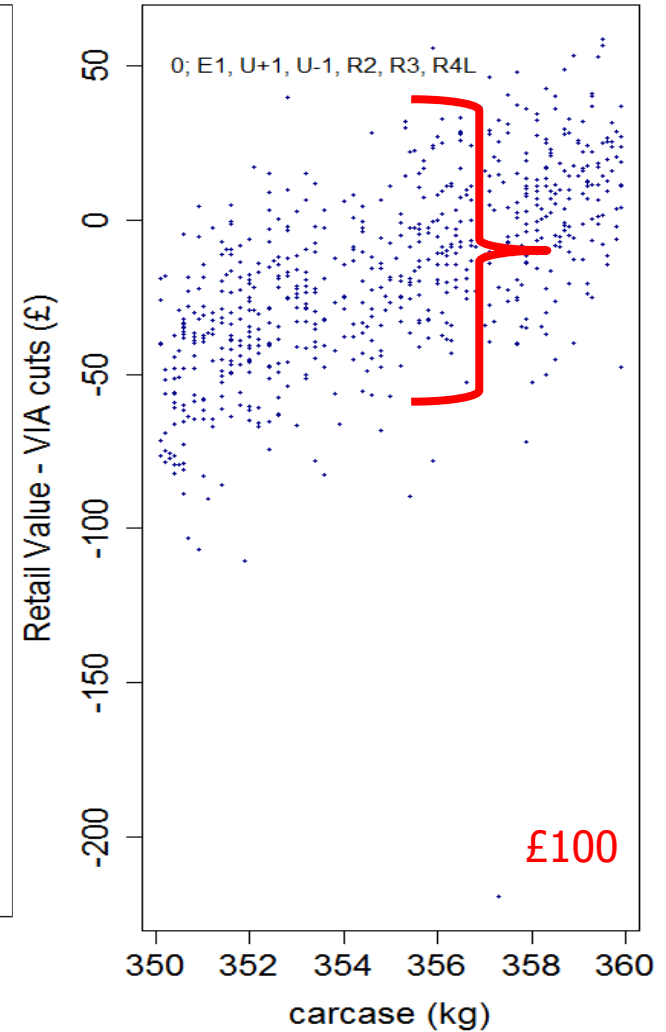
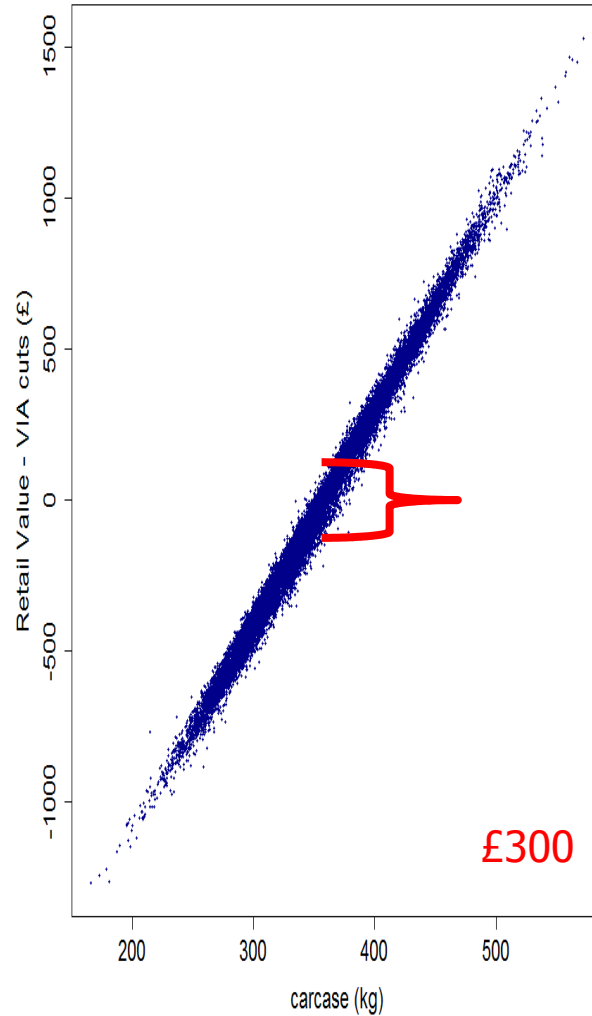
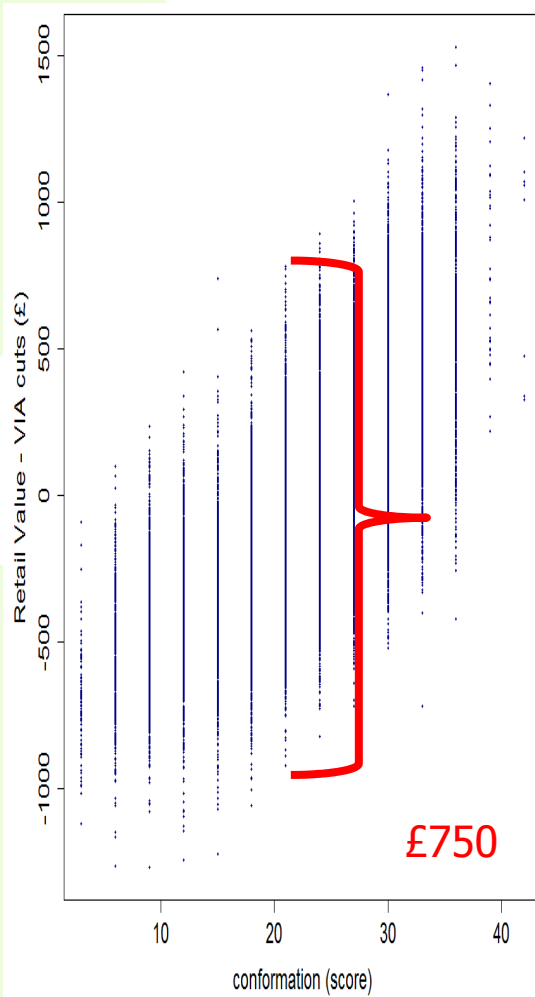
Rib-Roast : 0.14

[0.16 ≤ s.e. ≤ 0.23]

Striploin - steers



Opportunities to better differentiate carcasses



Genetic Parameters



- 81,785 VIA records, 1 site
- Basic Data Edits
 - Heifers and steers aged 450 to 900 days
 - Kill dates with large amount of missing data
 - outliers
- 30,530 record remained
 - 63% steers, 37% heifers
 - 72% cross bred, 28% purebred
 - Breed types 22% Limousin, 19% Continental beef, 42% dairy, 8% native beef and 9% other
- 5 generation pedigree
 - 98,505
 - 31% of VIA animals had sire recorded

genetic parameters

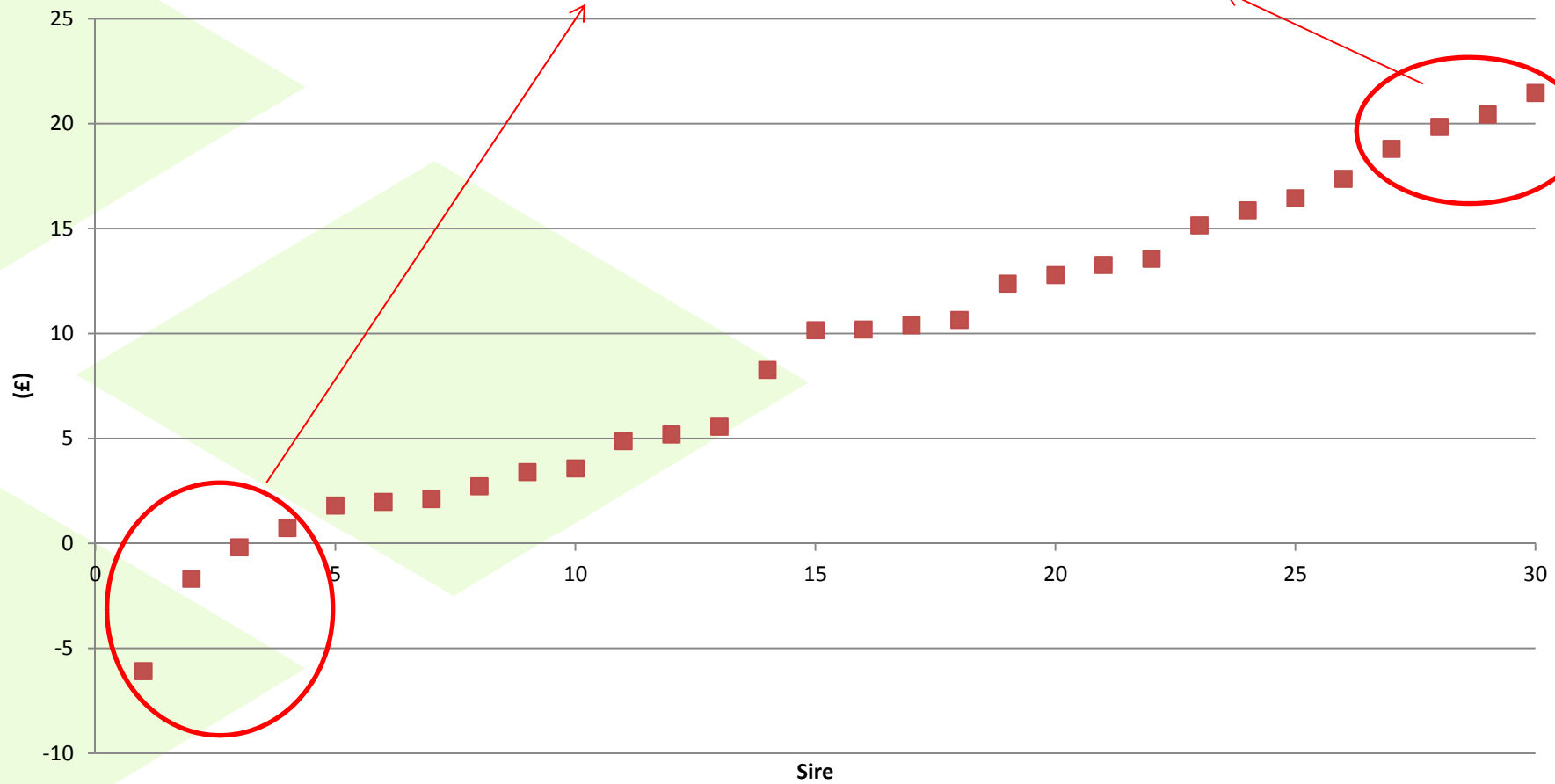


	Phenotypic variance	h²
Carcase weight	43.48 (1.15)	0.25 (0.04)
Conformation	15.63 (0.35)	0.50 (0.04)
Fat	43.48 (1.15)	0.25 (0.04)
Fillet	0.03 (0.001)	0.19 (0.05)
Striploin	0.11 (0.002)	0.37 (0.05)
Topside	0.35 (0.01)	0.29 (0.04)
Rump	0.16 (0.003)	0.29 (0.05)
Silverside	0.48 (0.01)	0.28 (0.05)
Knuckle	0.15 (0.003)	0.33 (0.05)
Flank	2.57 (0.06)	0.28 (0.05)

30 Limousin sires EBVs



£447 vs £910 (£463 difference in raw retail value)



Building the Limousin reference population



- Aiming for 2,000 Limousin's
 - VIA phenotype (accuracy of preliminary VIA EBVs)
 - medium density (50k) chip type
 - Project genotypes
 - Currently 662 genotypes
 - ~300 sampled
 - 716 HD Limousin
- 48 Limousin Sequences

Implications



- Massive benefit to the industry
 - Large numbers of records – thousands not hundreds
 - Traits of importance £
 - Stronger links in the supply chain
 - Increase efficiency ~ greenhouse gas emissions
 - Selection for dairy-beef
 - First EBVs of their kind in the UK
 - Genetic improvement
 - Stimulate the industry

Conclusions



- Developments Industry focused
- Large scale with big data sets
- Carcase traits and genomics
 - projects that are the first of their kind in the UK
- Provides a solid platform to expand and address further areas for improvement
 - Feed efficiency
 - Female fertility traits

Acknowledgements



Food Group

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British Cattle
Movement Service



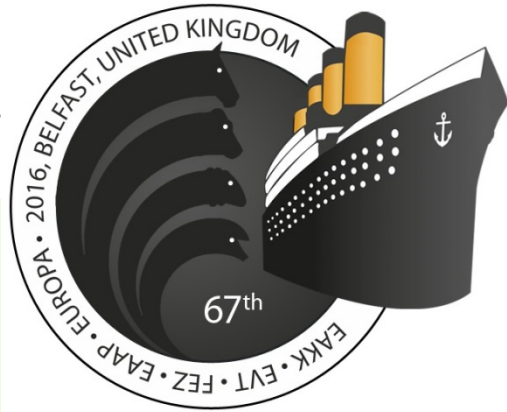
LIMOUSIN

Iain Kerr
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Simon Mead

Funding:

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Driving Innovation





Belfast

EAAP 2016

European Federation of
Animal Science Annual
Meeting – Livestock
Systems and Science

Belfast

28 August–1 Sept 2016

www.eaap2016.org

