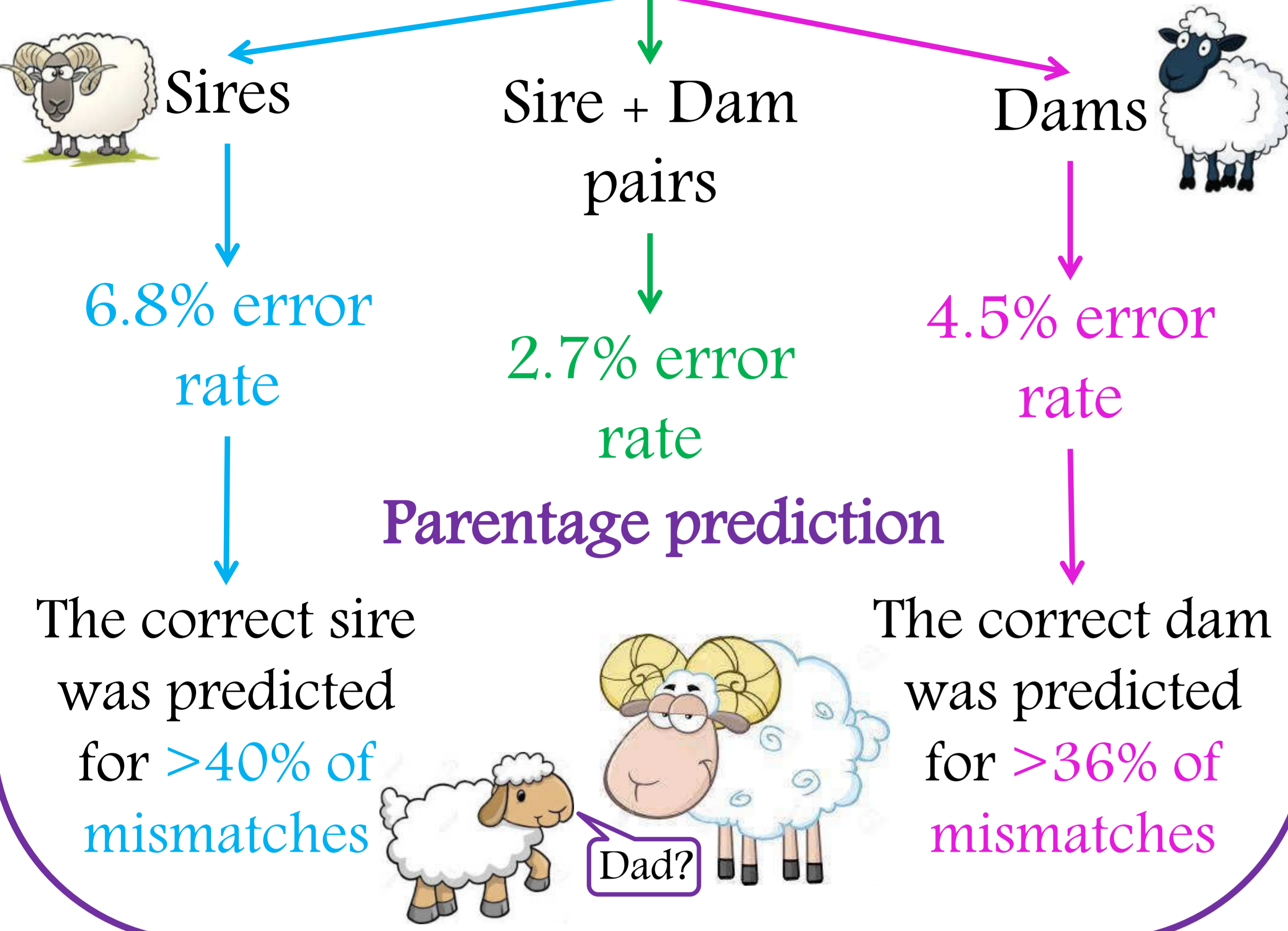


Parentage

21,955 Irish animals genotyped

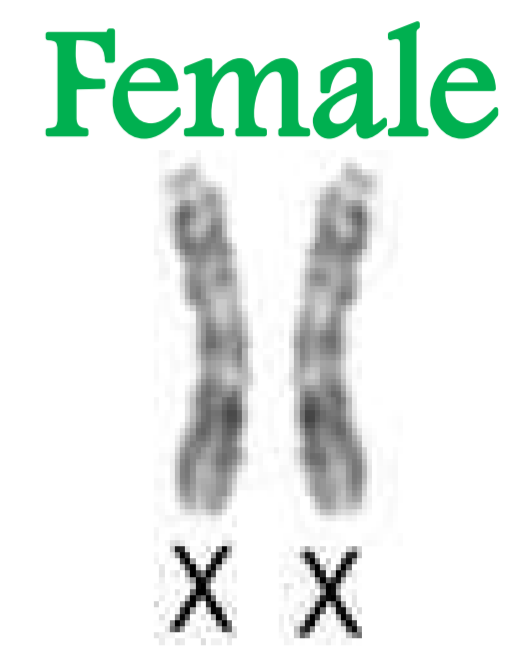
11,963 had a parent genotyped



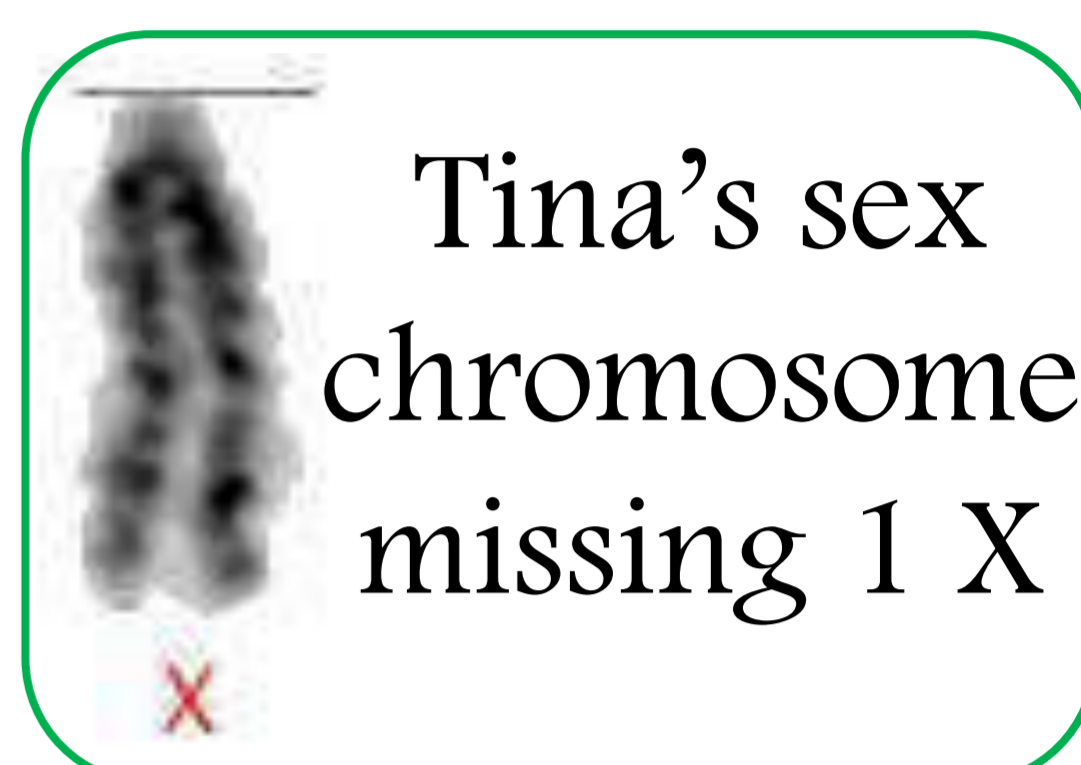
Karyotyping

Karyotype = a "picture" of the chromosomes in the cell of an animal

Sex chromosomes
Always in pairs



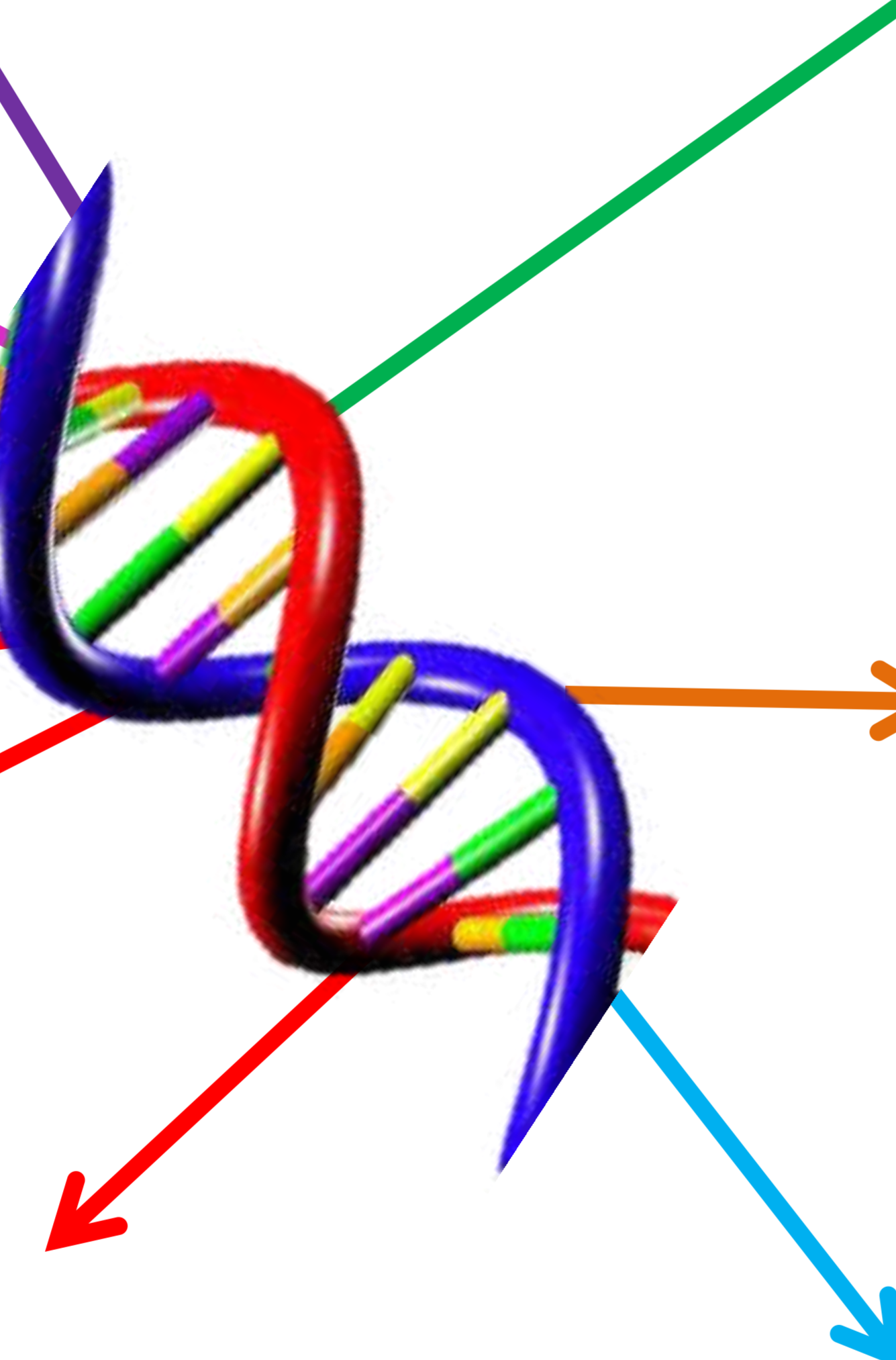
Tina (the sheep) has **Turner Syndrome**



- Missing one X chromosome
- Looks normal
- Loss of ovarian function
- Will **NEVER** become pregnant
- Can be detected at birth

Genomic predictions

- Mating advice
- Inbreeding
- Monitoring lethal genes
- Precision management



Monitoring major genes

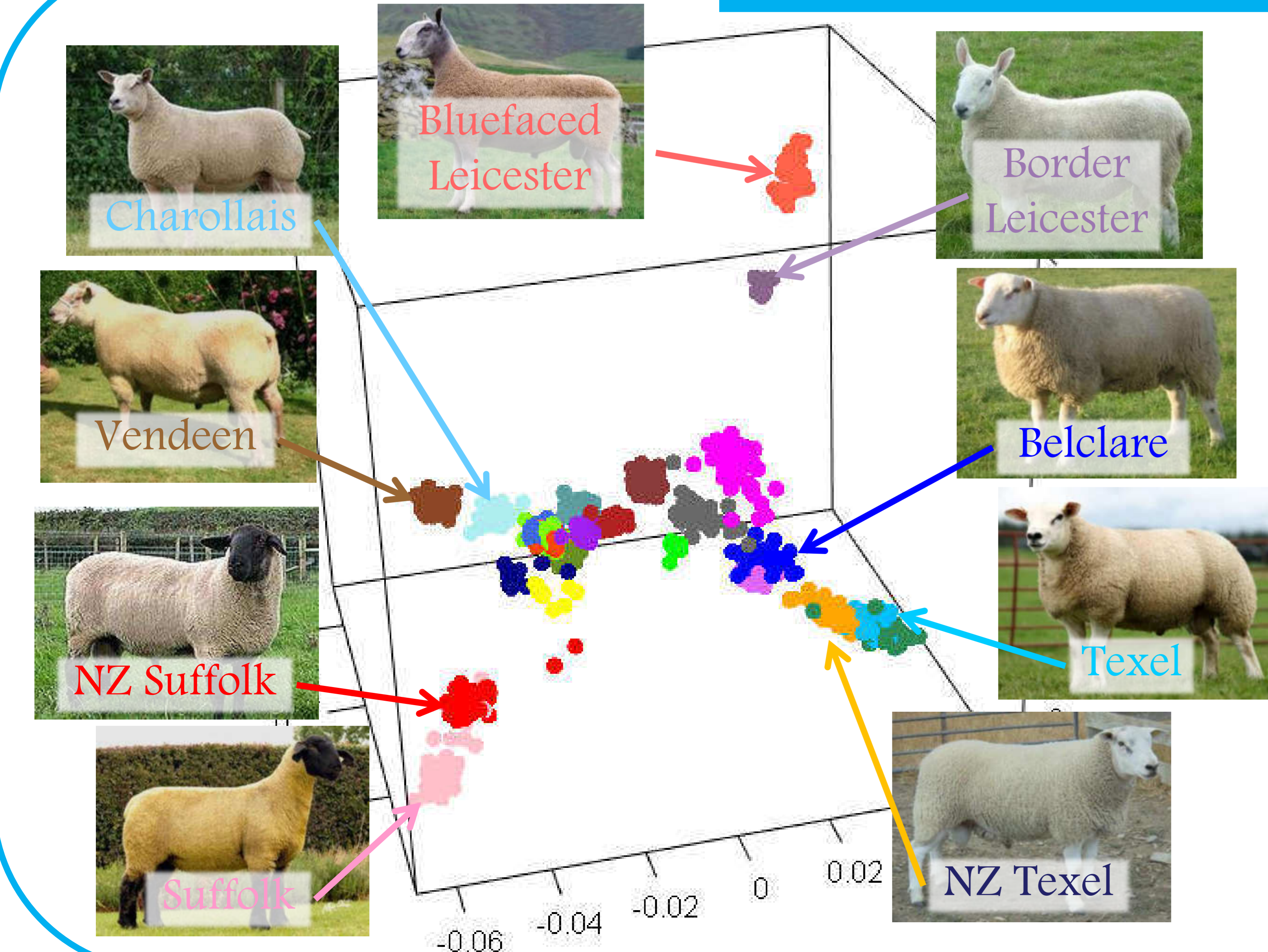
BMP15

- associated with more lambs born
- 1 copy = increased ovulation rate
- 2 copies = sterile animal

Genotyped animals	Frequency
All Irish population	0.07%
Belclares only	9.78%

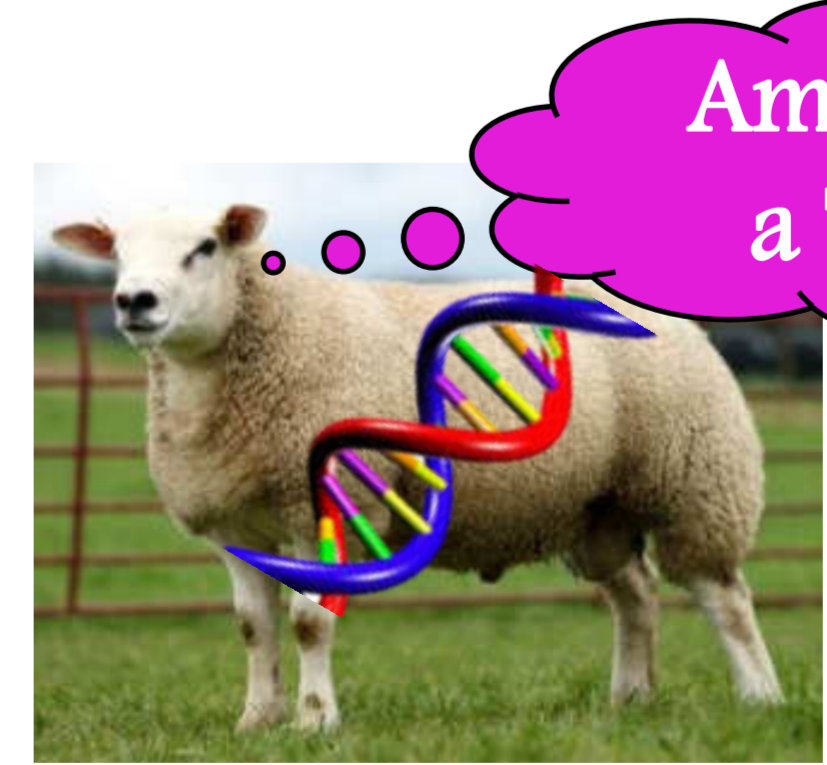
+0.53 lambs born

Breed composition & prediction



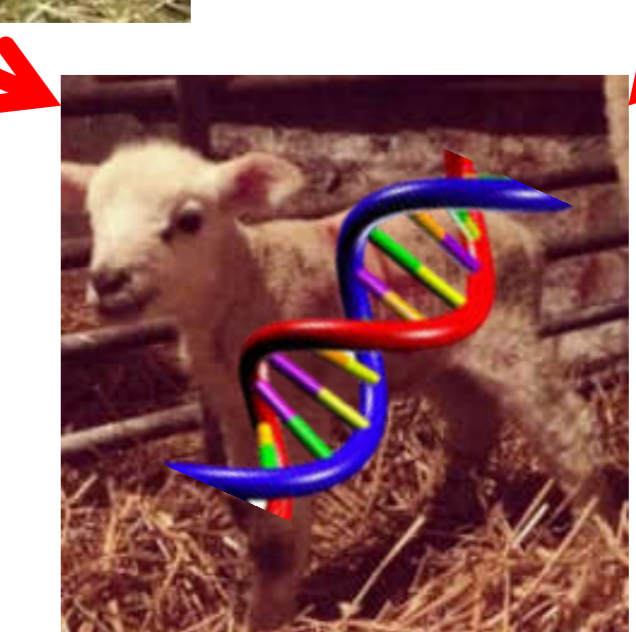
Breed prediction uses

Purebred verification



Yes, 100% Texel

Crossbred breed composition



51% Charollais
12% Texel
37% Suffolk

Carcass Performance Comparison of Suckler Bred Versus Bucket Reared Cattle



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Why do progeny from dairy cows have inferior carcass performance compared to progeny from beef cows?

Genetic merit of the dam



Genetic merit of the sire



Rearing management



Data

- Slaughter information Jan 2017 to Jul 2019 for ~ 2 million animals
- Animals were divided into 4 groups based on genotype and rearing type:

1) Bucket reared dairy sire X dairy dam (DXD)



3) Suckler reared beef sire X F1 dam (BXF1)



2) Bucket reared beef sire X dairy dam (BXD)



4) Suckler reared beef sire X beef dam (BxB)



Analyses

- The 4 rearing groups for carcass traits were analysed:
 - Not adjusted for genetic merit of sire and dam
 - Adjusted for genetic merit of sire (comparison if all animals had same sire)
 - Adjusted for genetic merit of dam (comparison if all animals had same dam)
 - Adjusted for genetic merit of sire and dam (comparison if all animals had same sire and dam)
- Carcass performance for all animals were adjusted to a:
 - parity 3 dam
 - purebred (no hybrid vigour)
 - 24 month (except age at slaughter) steer
 - average finishing herd-year-season
 - carcass weight of 360kg and fat score of 3= (for age at slaughter)

Results

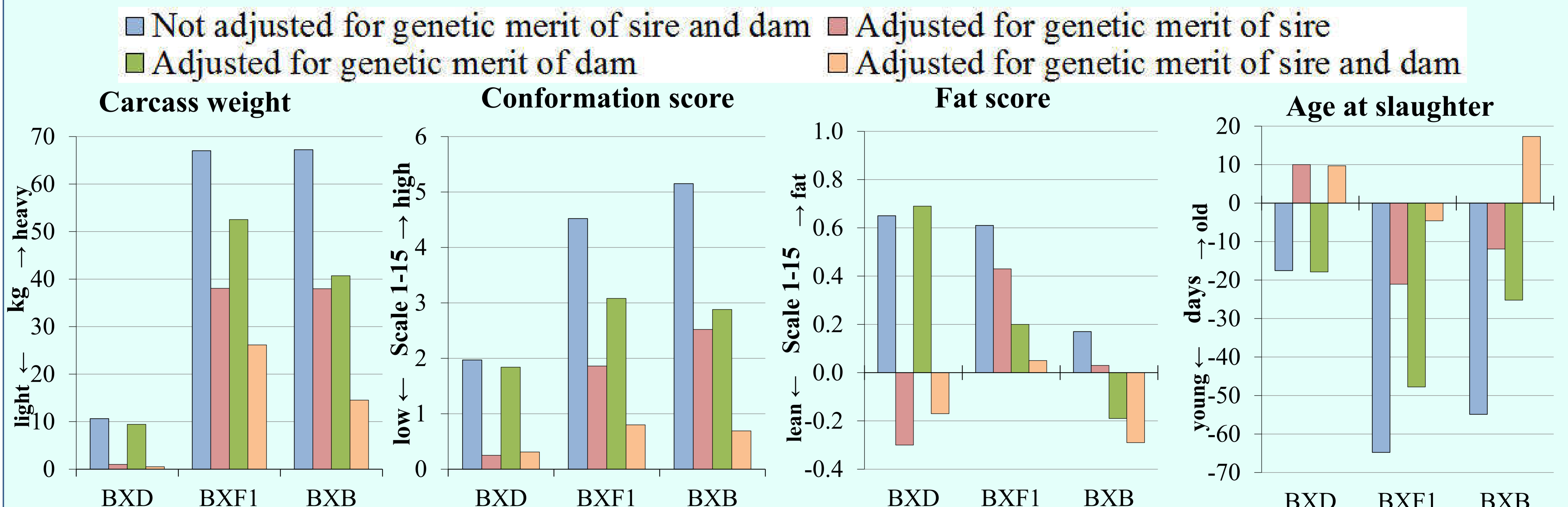


Figure 1. Difference in carcass weight, conformation, fat and age at slaughter for rearing systems compared to a bucket reared dairy sire X dairy dam (DXD)

Conclusion

- Bucket rearing together with the lower genetic merit for carcass traits in dairy dams and the bulls they are mated with, results in inferior carcass performance in their progeny compared to progeny born to beef dams
- If the same sire that was used on suckler cows was also used on dairy cows, the dairy-born calves would still be lighter (38 kg), older at slaughter (25 days) and more poorly conformed (3 units)

Comparison of Holstein Friesian dairy cows of divergent economic breeding index for nitrogen use efficiency and greenhouse gas emissions



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²School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4
³Environment, Soils and Land Use Department, Teagasc, Johnstown Castle, Wexford
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Introduction

Increased pressure to reduce the carbon footprint of dairy farming necessitates sustainable pasture based dairy systems. The Economic Breeding Index (EBI) has facilitated the identification of genetics suitable for profitable pasture based dairy systems. The effect of increased EBI on nitrogen use efficiency (NUE) and greenhouse gas emissions (GHG) emissions remains relatively unknown.

Objective

To model NUE and GHG emissions of animals divergent for EBI

Materials and Methods

The 'Next Generation herd' containing two genetically diverse groups of cows; one representing high EBI (elite; EBI = €154; ICBF, 2018) and the second representing the national average EBI (NA; EBI = €47; ICBF, 2018) was used. The Moorepark dairy systems model (MDSM) was used to simulate outputs from a 40 ha dairy farm carrying 110 cows for each of the two genetic groups. All models took account of fertility and milk production. Nitrogen and GHG models were developed using the outputs of the MDSM to simulate the nitrogen balance and GHG emissions from two dairy farming systems containing the distinctive genetic groups.

Results

Nitrogen balance

The elites had a lower N surplus (nitrogen input – nitrogen output; 204.6 kg / ha) compared to the NA's (209.9 kg / ha). The NUE (nitrogen input / nitrogen output) was greater for the elites (0.336%) compared to the NA's (0.322%).

Greenhouse gas emissions

Total greenhouse gas emissions per ha were similar for both elites (16.2 CO₂-eq, t / ha) and NA's (16.3 CO₂-eq, t / ha). When emissions were expressed relative to fat and protein corrected milk (FPCM), the elite group had the lowest GHG emissions (0.96 CO₂-eq, kg / kg FPCM) compared to the NA's (1.06 CO₂-eq, kg / kg FPCM). Furthermore, the elites had a greater profit per kg of GHG emissions (0.15 €-profit / CO₂-eq) compared to the NA's (0.10 €-profit / kg CO₂-eq).

Conclusion

The results demonstrate that selection using high EBI genetics improves NUE and reduces CO₂-eq / FPCM whilst also improving profitability. Therefore breeding for increased EBI will lead to cumulative and permanent improvements to both environmental and economic sustainability.



The repeatability of feed intake and efficiency in beef cattle offered high-concentrate, grass silage and pasture based diets

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Introduction

- Beef cattle in Ireland are evaluated for feed intake and efficiency indoors on high concentrate diets.
- The majority of a beef animal's lifetime dietary intake comes from grazed grass (~51%) and grass silage (~26%).
- The repeatability of feed intake and efficiency related traits across high concentrate, grass silage and grazed grass diets remains relatively unknown.

Objective

To assess the repeatability of feed intake and efficiency across high concentrate, grass silage and pasture based diets

Materials and Methods

- Ninety seven beef cattle had feed intake and efficiency related traits assessed over three test periods comprising; grass silage with concentrate supplementation (S+C); grazed grass (GRZ) and; high concentrates (HC).
- Animals were on average 319, 486 and 717 days old during the S+C, GRZ and HC test periods, respectively.
- Traits assessed were; dry matter intake (DMI); DMI / kg body weight (DMI / BW); Residual feed intake (RFI); and gain to feed ratio (G:F).
- The relationship between the feed intake and efficiency related traits were assessed using spearman's rank correlations.
- The relationship between predicted transmitting ability (PTA) for feed intake across the three test periods was also assessed using a general linear model.

Results

Table 1. Spearman's rank correlations for feed intake and efficiency traits across the three test periods¹

Trait ²	S+C v GRZ	GRZ v HC	S+C v HC
DMI	0.32**	0.16	0.40***
DMI / BW	0.33**	0.17	0.40***
RFI	0.25*	0.15	0.25*
G:F	0.01	0.09	-0.03

¹S+C = grass silage plus concentrate; GRZ = grazed grass; HC = high concentrate.

²DMI = dry matter intake; DMI / BW = DMI kg / kg of body weight; G:F = gain to feed ratio; RFI = residual feed intake.

Correlation coefficients are different from zero; *P < 0.05; **P < 0.01; ***P < 0.001.

The regression of phenotypic DMI on PTA for feed intake showed a significant increase in DMI per increment increase in PTA for the S+C (0.51 kg; P = 0.01) and HC (3.26 kg; P = <0.001) periods. The relationship during the GRZ period, however, was non-significant (0.42 kg; P = 0.39).

Conclusion

Evaluating animals for both feed intake and efficiency indoors on high-concentrate diets may not reflect their performance when consuming conserved forage-based diets indoors or when grazing pasture.

Acknowledgements

Funding from the DAFM Research Stimulus Fund 13/S/496 RAPIDFEED is gratefully acknowledged.



Large variability exists in feeding behaviour of growing cattle

David N. Kelly^{1,2}, C. Murphy², R.D. Sleator², M.M. Judge¹, S.B. Conroy³, D.P. Berry¹

¹Teagasc, Moorepark, Fermoy, Co. Cork; ²Cork Institute of Technology, Bishopstown, Co. Cork; ³Irish Cattle Breeding Federation, Bandon, Co. Cork.

Background

Feed intake:

- Represents a large variable cost in animal production systems
- Expensive and labour intensive to measure
- Currently measured in cattle at the ICBF, Tully, Co. Kildare as part of national breeding programmes

→ Data collected enables the derivation of feeding behaviour traits

- What is the extent of variability in these feeding behaviour traits?
- Could feeding behaviour help predict feed intake?



Aim

- To derive several feeding behaviour traits in growing cattle and gain a better understanding of their relationship with each other and with other performance and efficiency traits

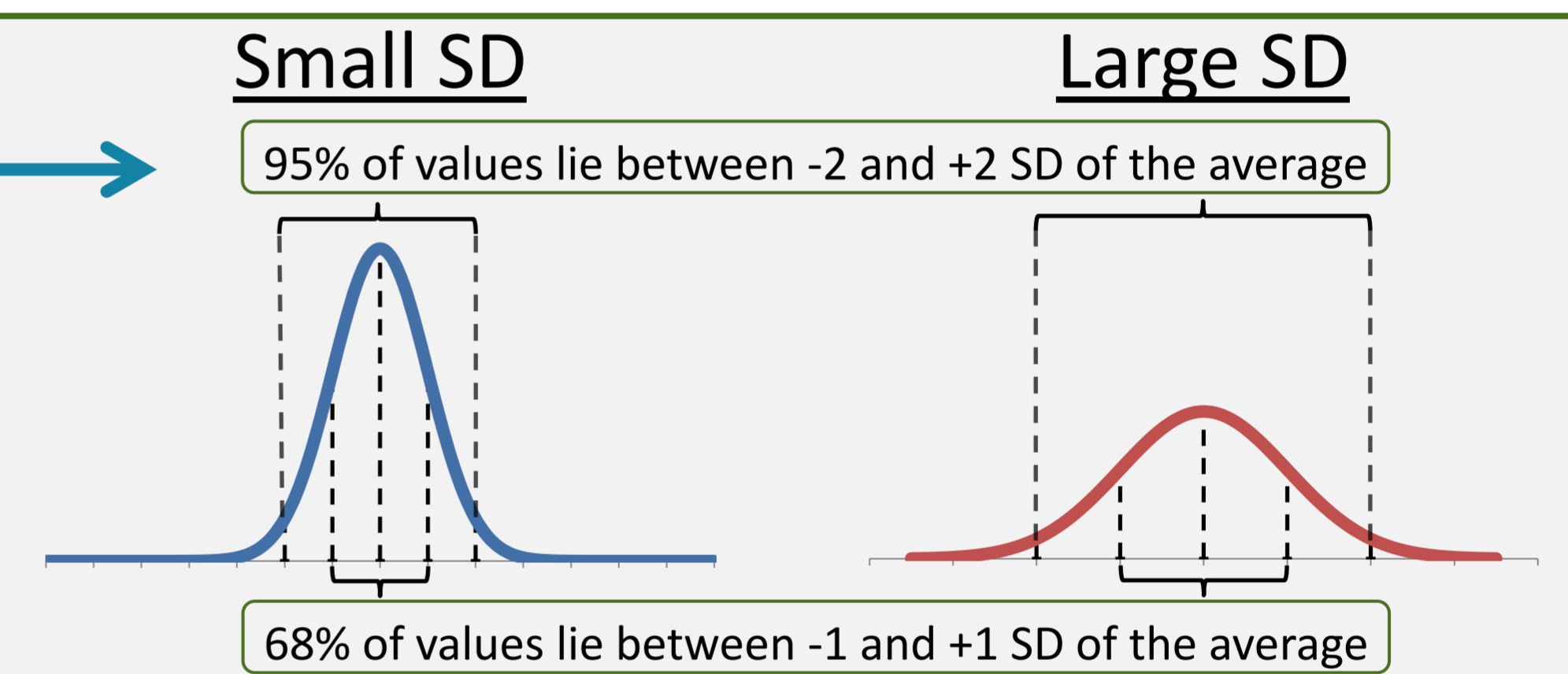
Materials and Methods

- Feeding behaviour, feed intake, and liveweight data were on 624 steers and heifers
- Correlations were estimated among the feeding behaviour, performance, and efficiency traits

Results

Table 1. Raw descriptive statistics for feeding behaviour traits

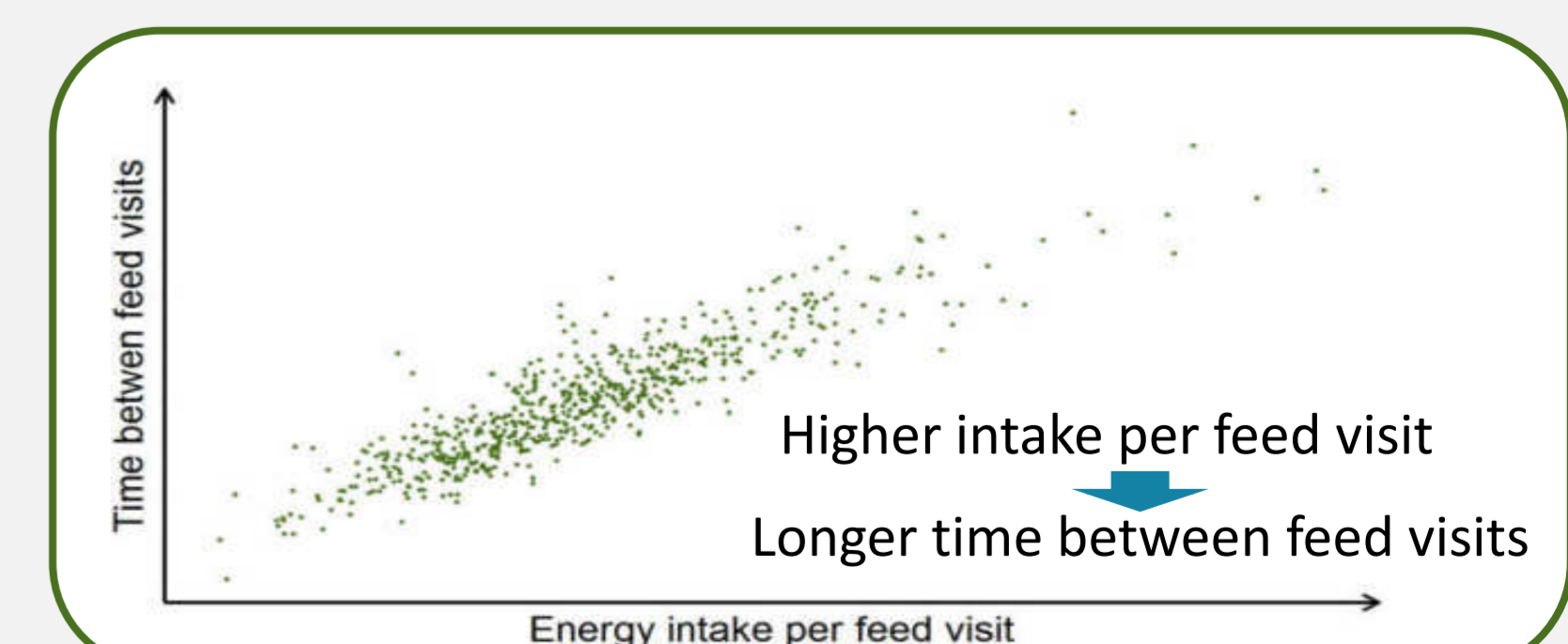
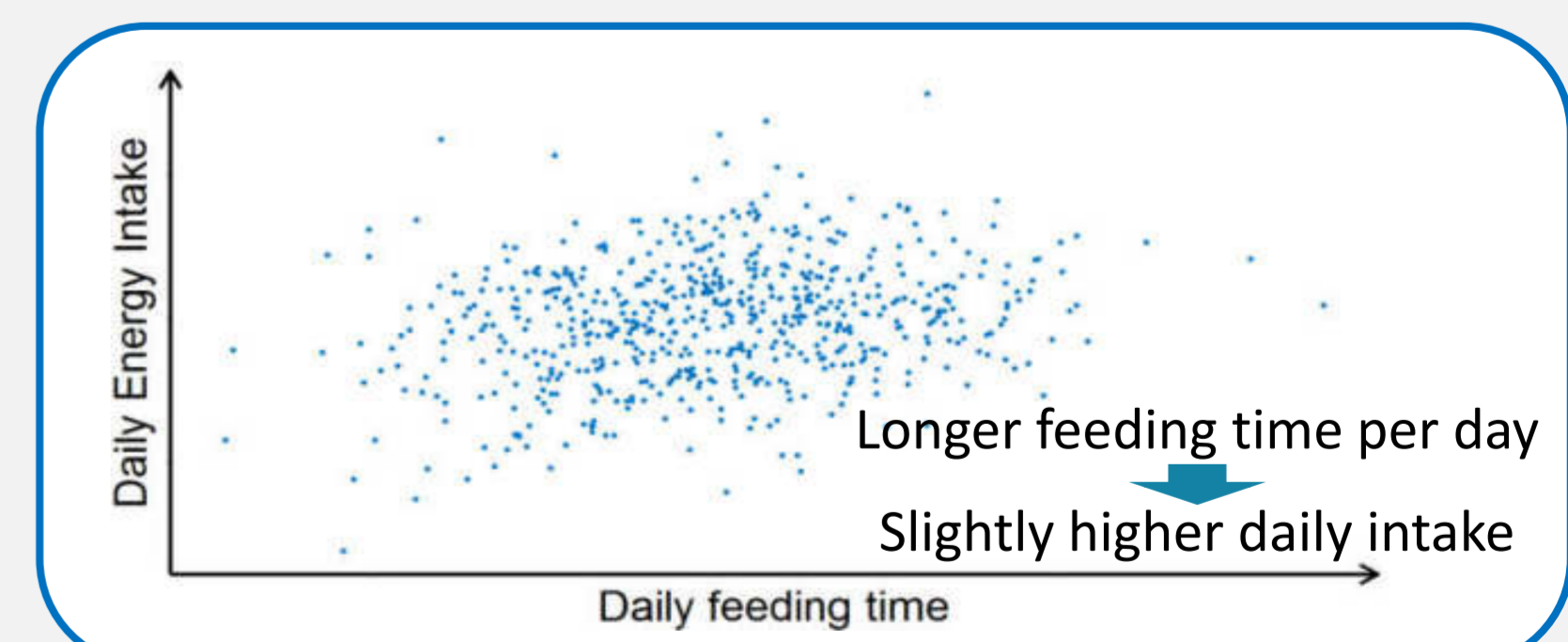
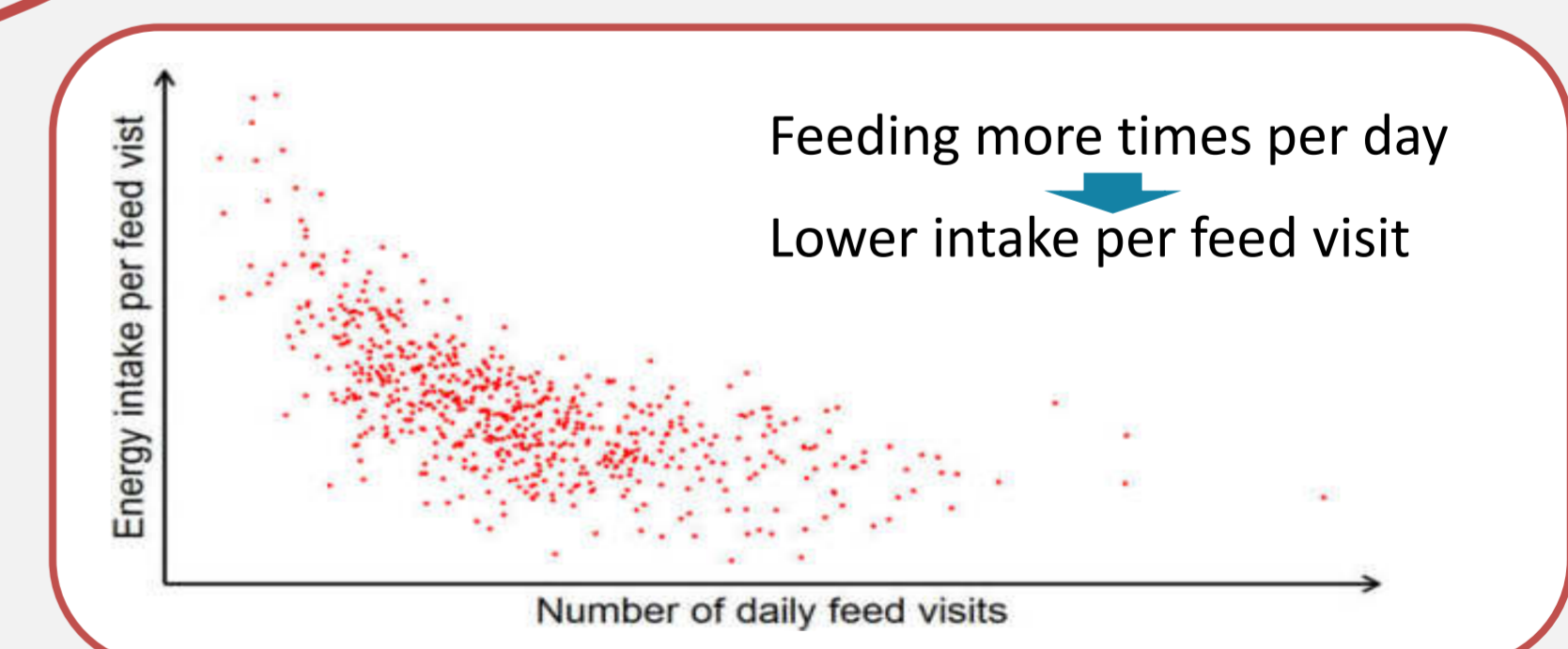
Trait	Average	Standard Deviation (SD)
Daily energy intake (MJ/day)	147.29	22.23
Number of daily feed visits (number/day)	34.39	12.27
Daily feeding time (minutes/day)	142.30	25.06
Feeding rate (MJ/minute)	1.09	0.23
Feeding time per feed visit (minutes/feed visit)	4.88	1.78
Energy intake per feed visit (MJ/feed visit)	5.08	1.94
Time between feed visits (minutes)	42.34	15.15



Cattle, on average, ate **34 times per day** and ate, on average, for almost **5 minutes per visit**

Table 2. Correlations among feeding behaviour traits and between feeding behaviour, performance, and efficiency traits

Trait	Number of daily feed visits	Daily feeding time	Feeding rate	Energy intake per feed visit	Feeding time per feed visit	Time between feed visits
Daily feeding time	0.14					
Feeding rate	0.17	-0.56				
Energy intake per feed visit	-0.70	0.10	-0.01			
Feeding time per feed visit	-0.71	0.34	-0.44	0.87		
Time between feed visits	-0.79	-0.06	-0.14	0.89	0.85	
Daily energy intake	0.23	0.21	0.47	0.12	-0.11	-0.27
Energy conversion ratio	0.14	0.01	0.18	-0.05	-0.13	-0.16



Conclusions

- Large variability exists in feeding behaviour between individual animals
- Complex relationships among the feeding behaviour traits
- Correlations suggest some prediction of intake and efficiency traits is possible from feeding behaviour traits in growing cattle

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Potential exists to breed cattle that better achieve the carcass specs

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¹Teagasc Moorepark, Fermoy, Co. Cork; ²Cork Institute of Technology, Bishopstown, Co. Cork;

³Irish Cattle Breeding Federation, Bandon, Co. Cork

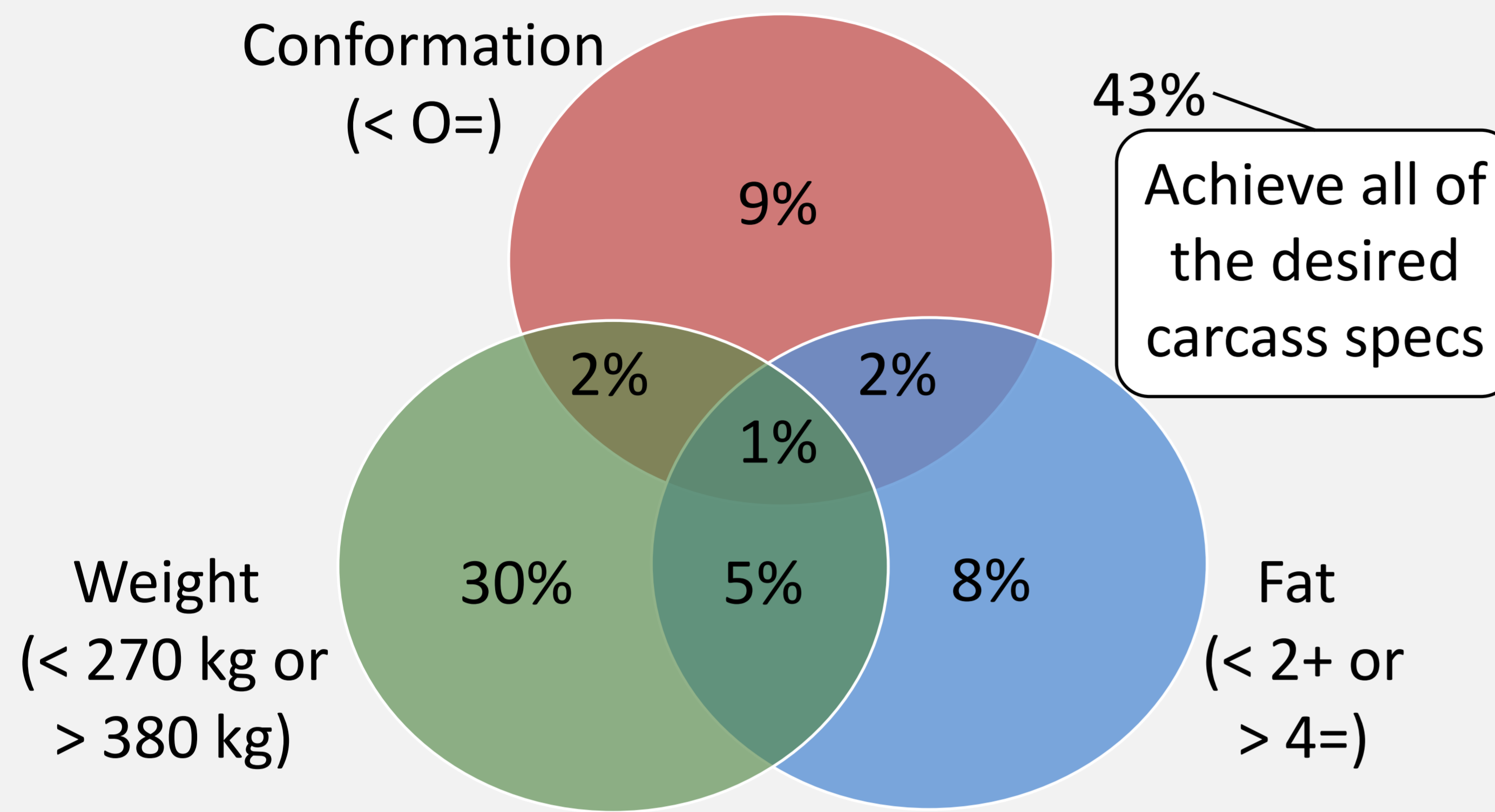
Contact: DavidA.Kenny@teagasc.ie



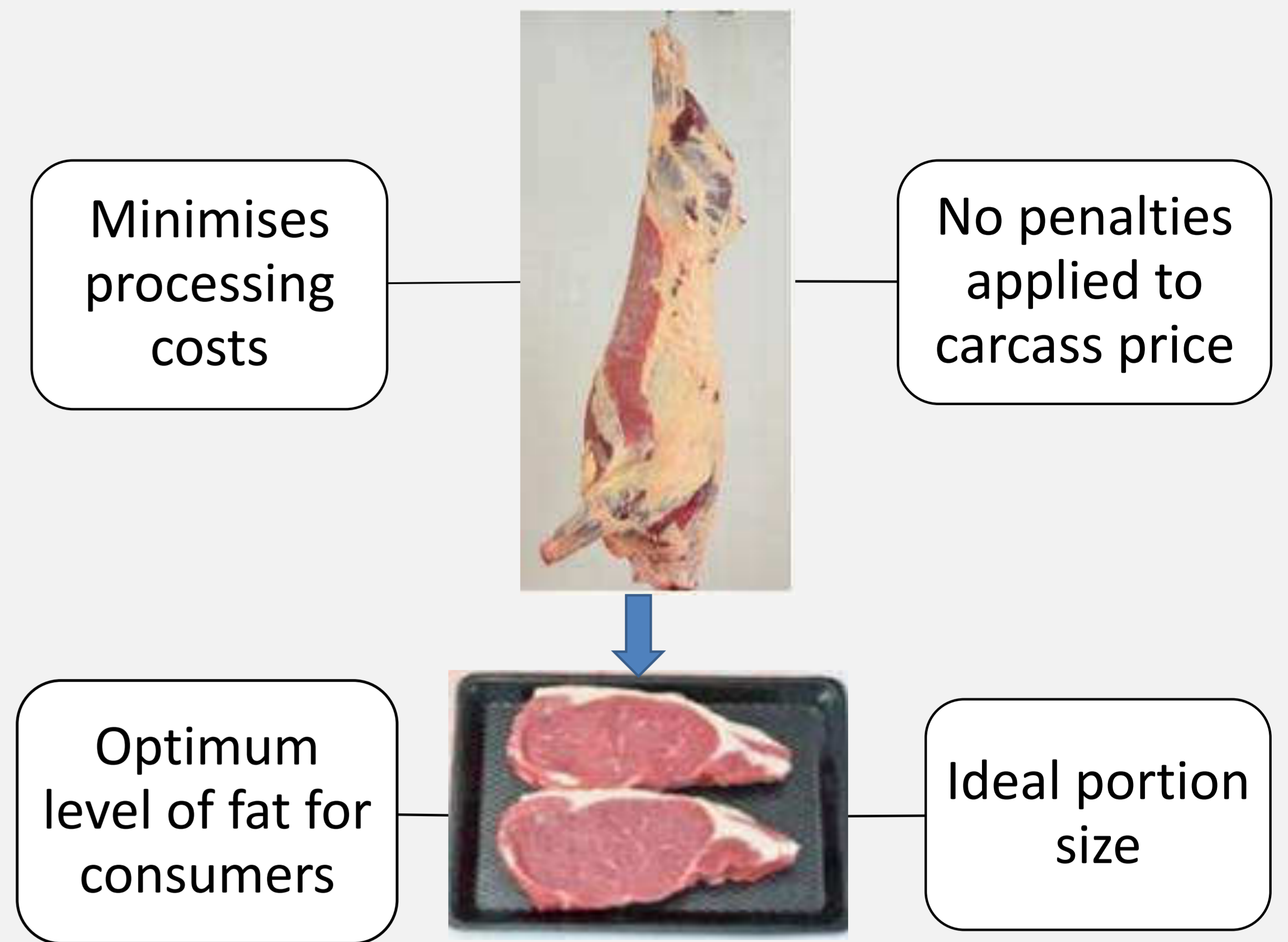
Objective

Quantify potential to breed cattle that better achieve the carcass specs

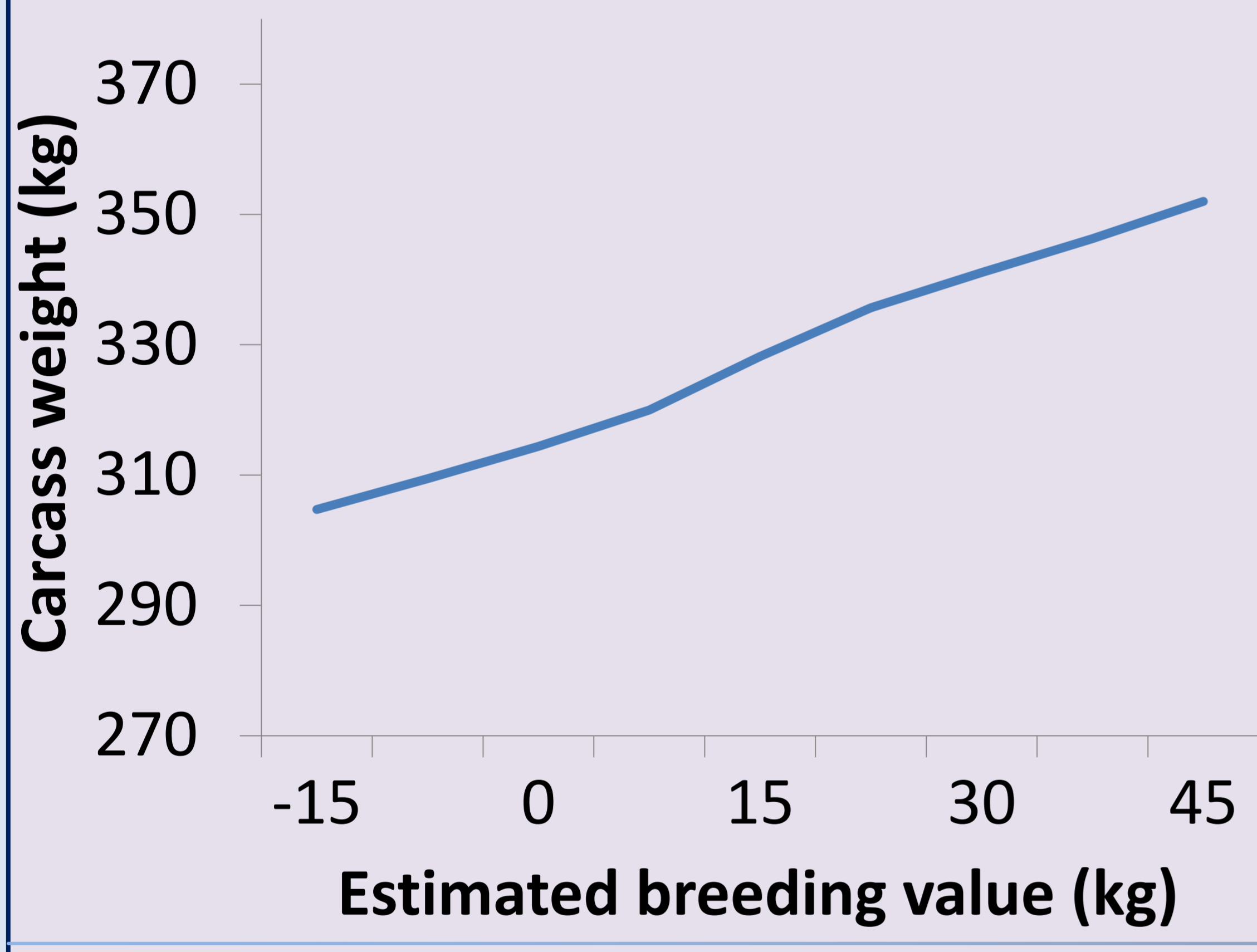
Failure of the desired specs



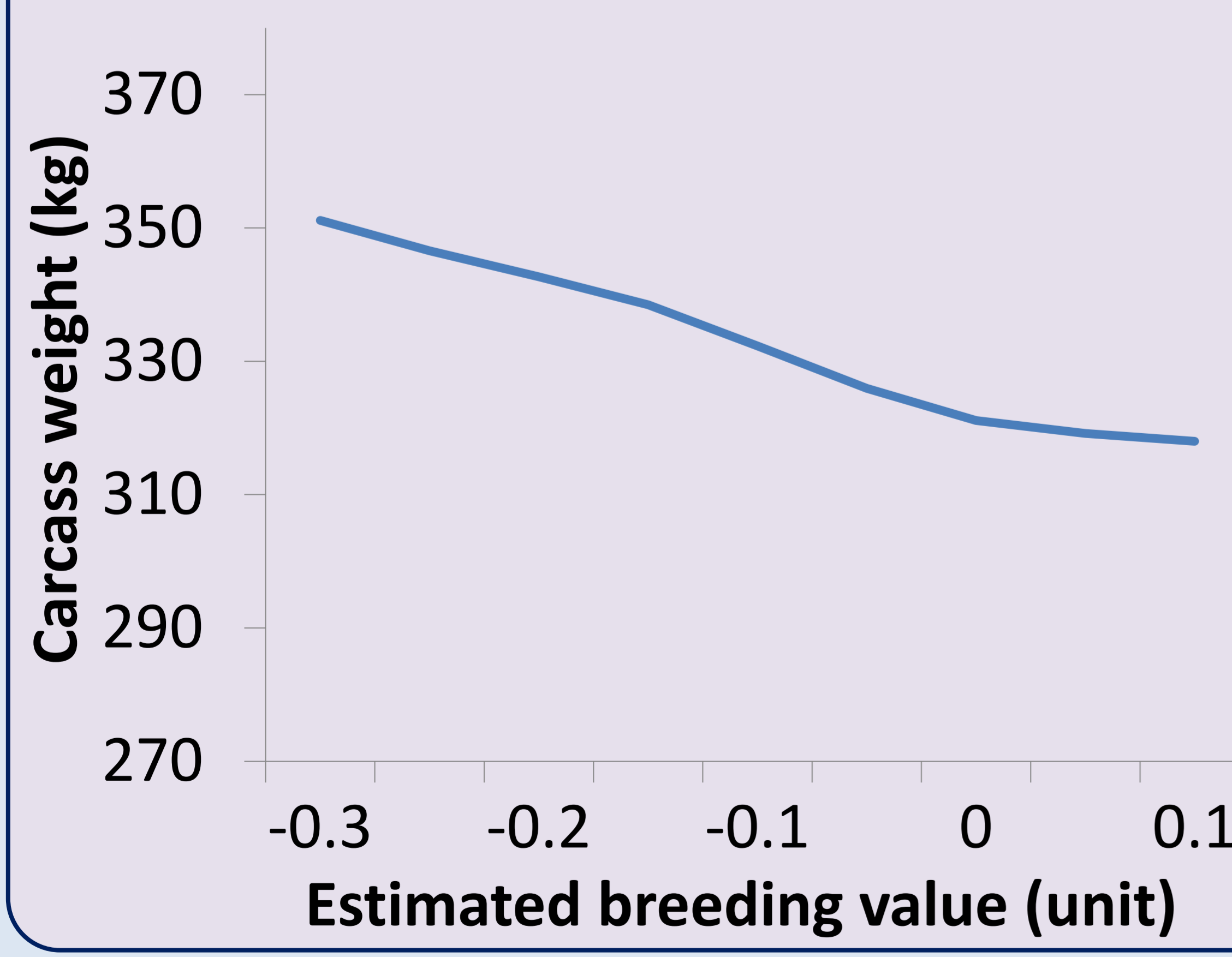
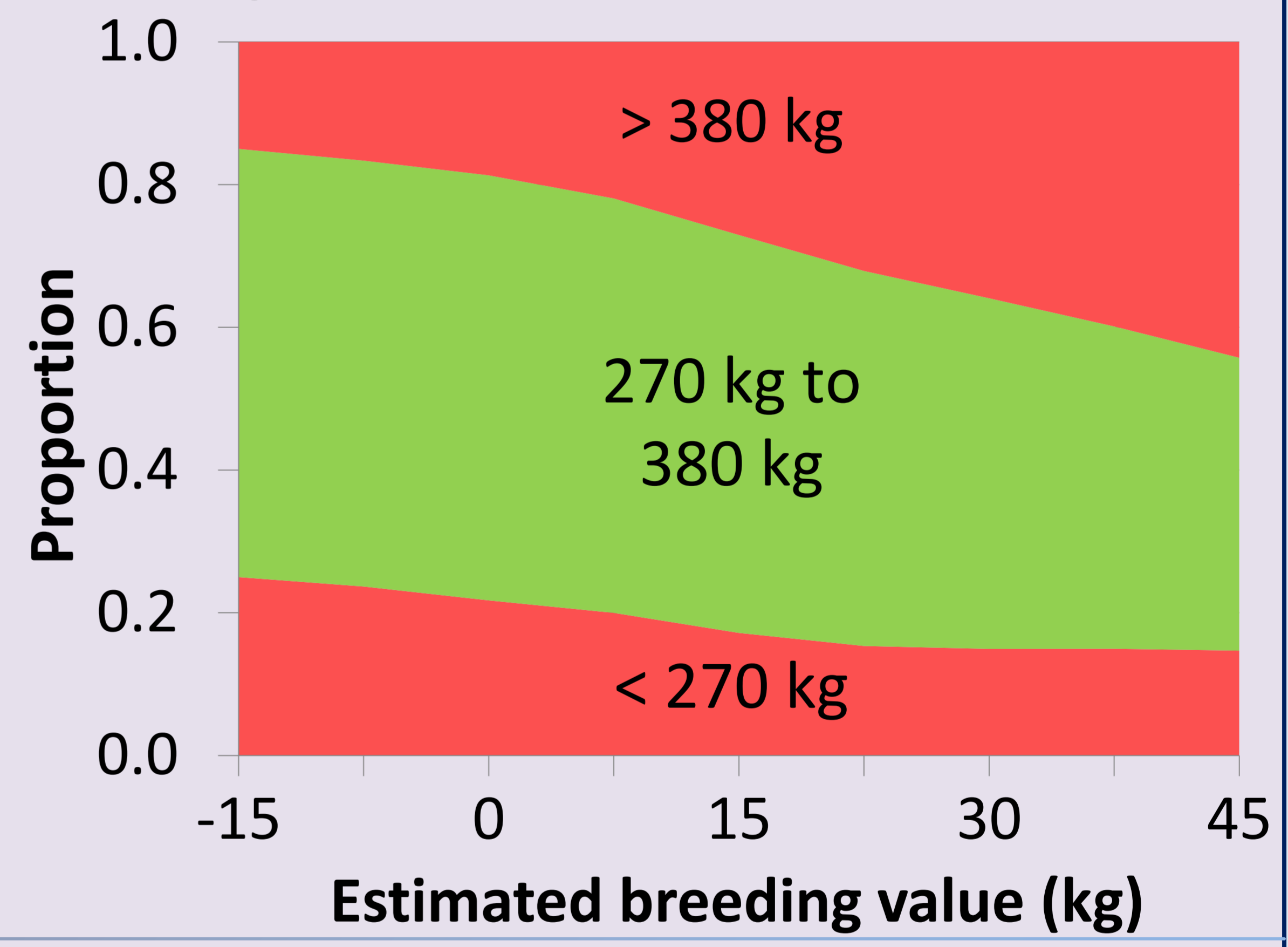
Why breed for the carcass specs?



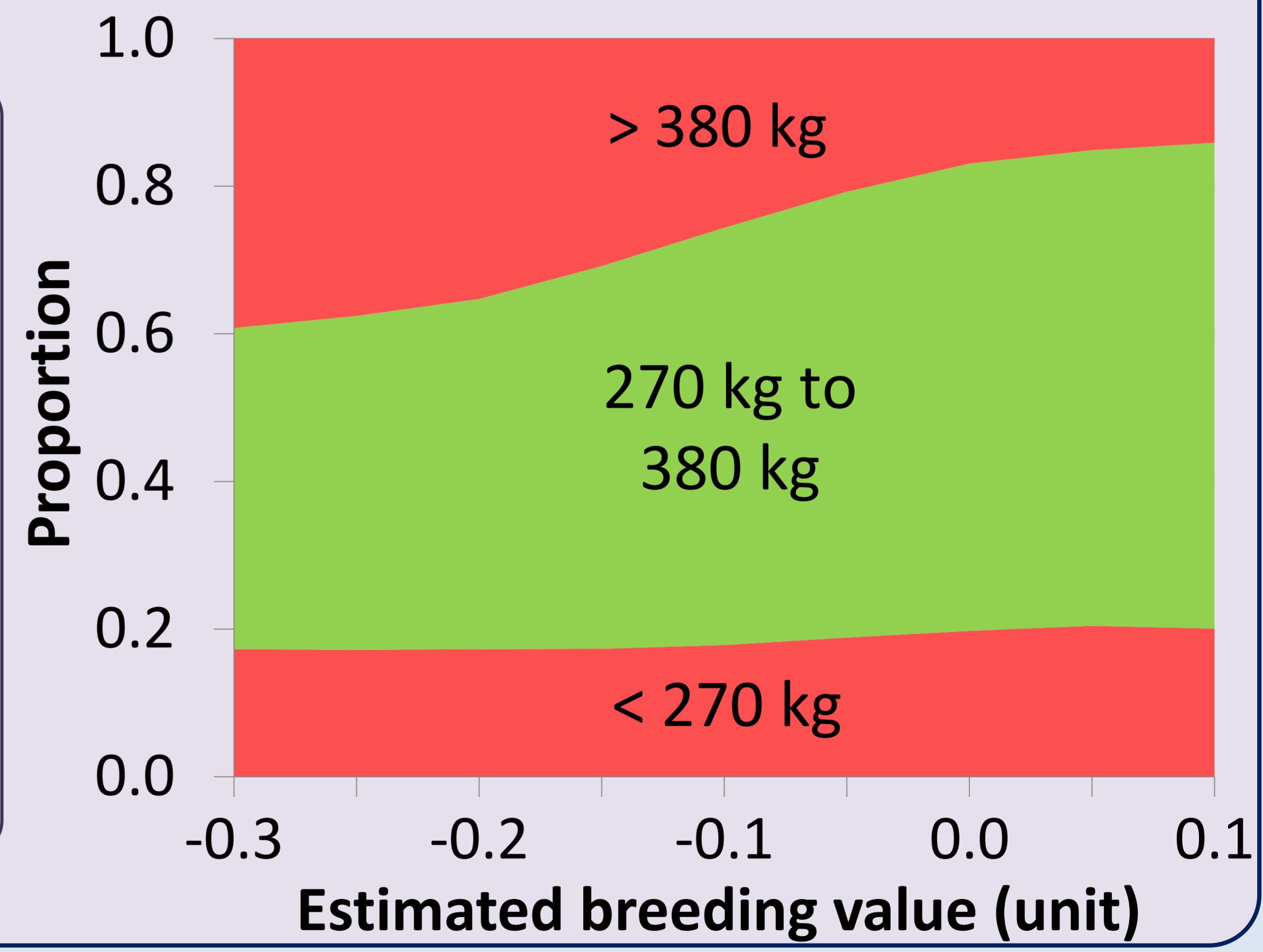
Selection for a desired carcass weight



- Current carcass weight trait**
- 68% of variability is due to genetics
 - Heavier carcasses
 - Less cattle achieve the desired carcass weight spec of 270 kg to 380 kg



- Weight spec trait**
- Binary trait reflecting whether the spec was achieved or not
 - 18% of variability is due to genetics
 - Lighter carcasses
 - More cattle achieve the carcass weight spec



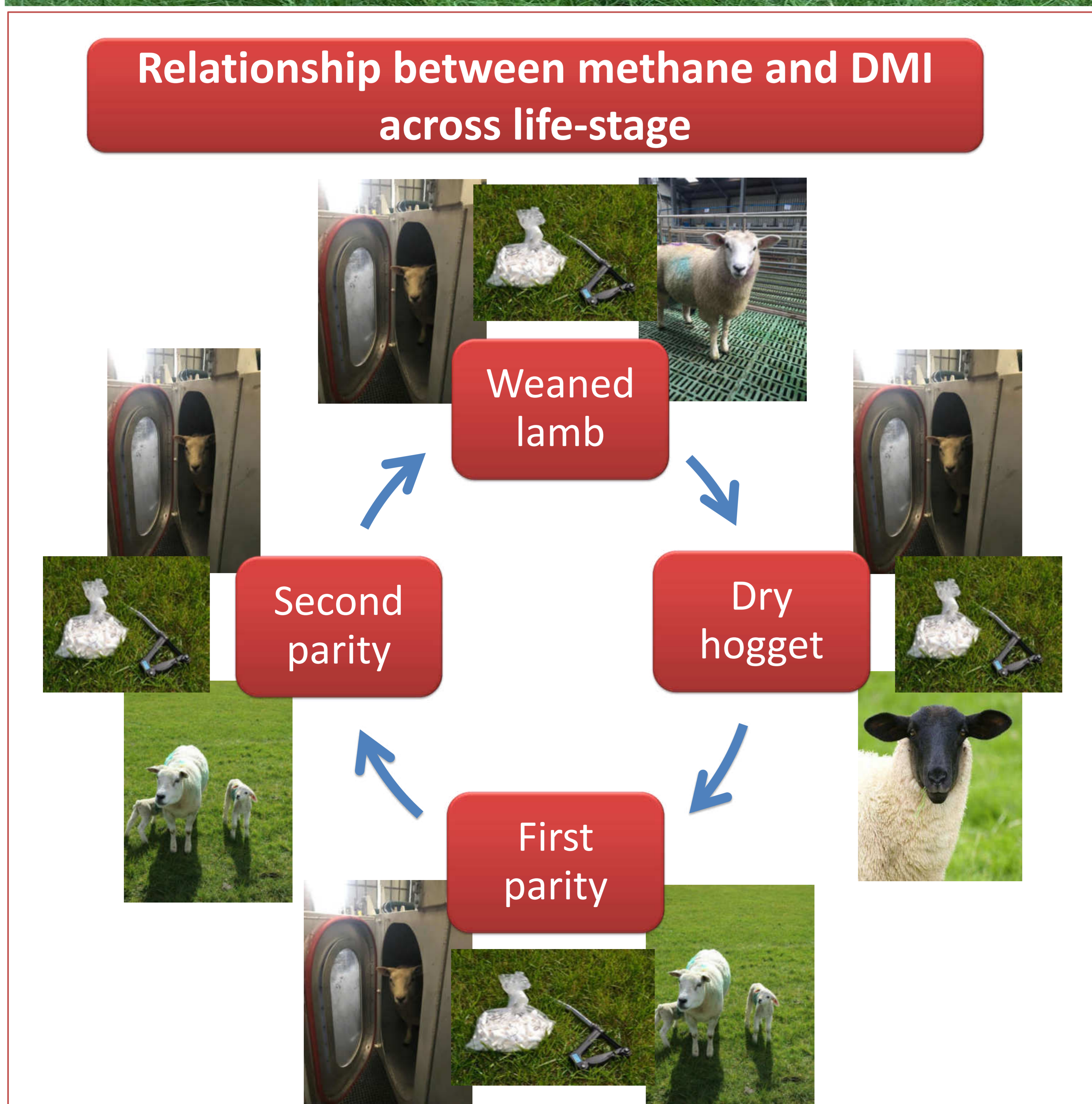
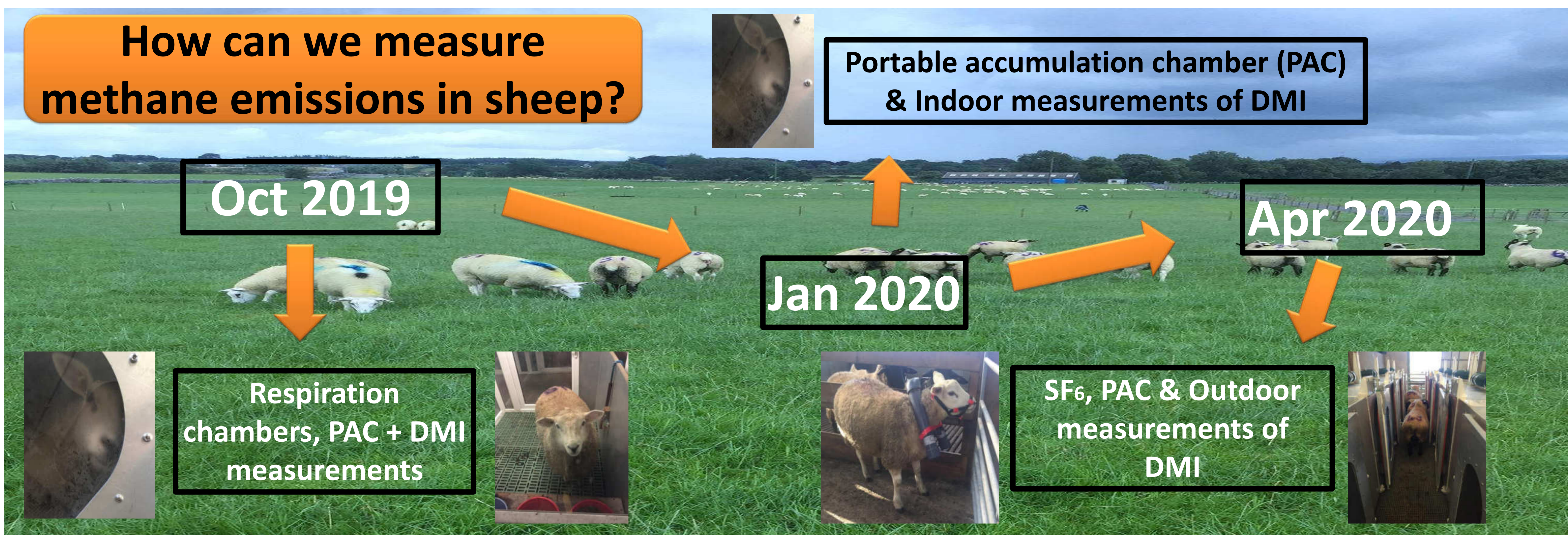
Conclusions

- Massive potential exists to increase the proportion of cattle achieving the desired carcass specs
- Selection for the current carcass traits decrease the number of carcasses achieving the desired carcass specs
- Selection for the spec traits increases the number of carcasses achieving the desired carcass specs



Objective:

- 1) To validate methods of determining methane (CH₄) and dry matter intake (DMI) &
- 2) Using genetics to reduce the environmental 'hoofprint' of sheep



Can we select animals to produce less methane?

Investigate the impact of

- Sire type
- Strain
- Genetic merit

On CH₄ emissions and DMI

International Collaboration

- New GrassToGas Project
- Develop predictors of feed intake and methane emissions



Providing transparency in times of uncertainty

How can you manage it, when you don't measure it?

By measuring how relatives perform in different herd environments,



How do you know what kind of calf you are really buying?

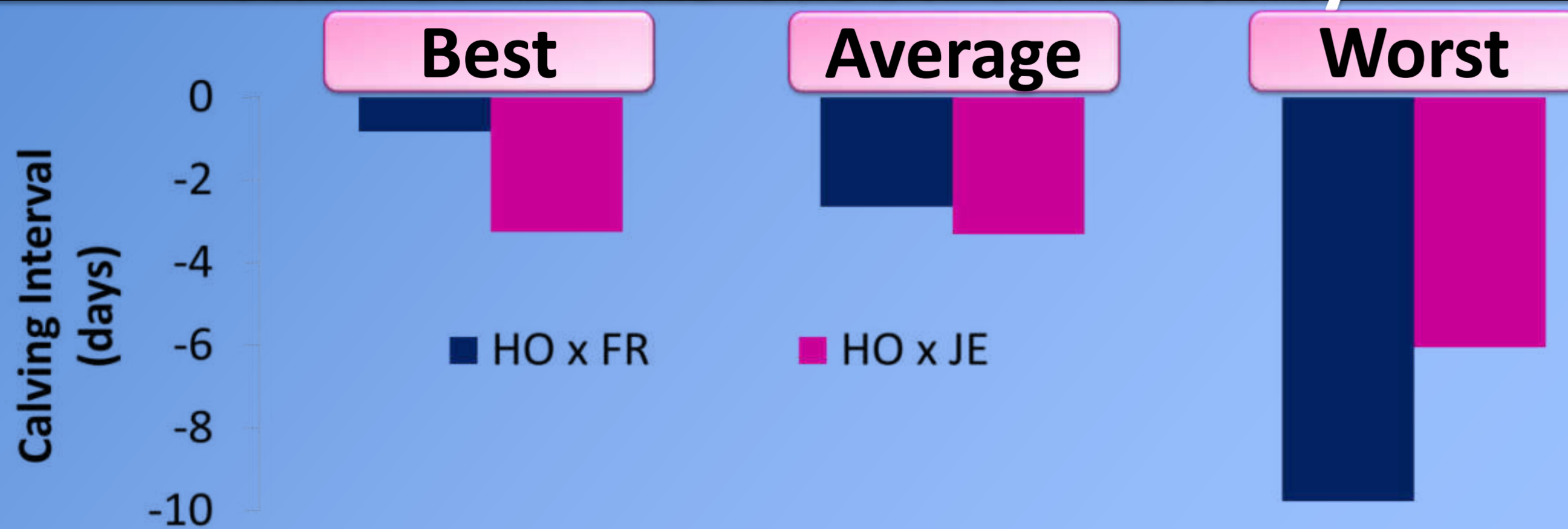
By only using traits that are relevant for animals destined for slaughter,

EUROP Classification													
Fat	Et	E	U	U	U	U	U	U	U	U	U	U	U
1	442	436	430	424	418	412	406	400	400	382	376	370	364
2	442	436	430	424	418	412	406	400	400	382	376	370	364
3	442	436	430	424	418	412	406	400	400	382	376	370	364
4	442	436	430	424	418	412	406	400	400	382	376	370	364
5	442	436	430	424	418	412	406	400	400	382	376	370	364
6	442	436	430	424	418	412	406	400	400	382	376	370	364
7	442	436	430	424	418	412	406	400	400	382	376	370	364
8	442	436	430	424	418	412	406	400	400	382	376	370	364
9	442	436	430	424	418	412	406	400	400	382	376	370	364
10	442	436	430	424	418	412	406	400	400	382	376	370	364
11	442	436	430	424	418	412	406	400	400	382	376	370	364
12	442	436	430	424	418	412	406	400	400	382	376	370	364
13	442	436	430	424	418	412	406	400	400	382	376	370	364
14	442	436	430	424	418	412	406	400	400	382	376	370	364
15	442	436	430	424	418	412	406	400	400	382	376	370	364
16	442	436	430	424	418	412	406	400	400	382	376	370	364
17	442	436	430	424	418	412	406	400	400	382	376	370	364
18	442	436	430	424	418	412	406	400	400	382	376	370	364
19	442	436	430	424	418	412	406	400	400	382	376	370	364
20	442	436	430	424	418	412	406	400	400	382	376	370	364

We can estimate the response in performance due to changes in breeding value when in different environments



And estimate the response in performance due to cross-breeding when in different environments based on fertility



Providing transparency as to what animals can achieve under your management style

And including more pieces of the puzzle when estimating an animals merit for each trait



We can predict the relative carcass revenue of calves



Providing transparency for both the buyer and seller

Host Institution



Partner Institutions



Funded by:



Researched by:

Fiona Dunne*, Margret Kelleher ‡, Ross Evans ‡, Sinead McParland*, Siobhán Walsh †, Donagh Berry*

*Teagasc Moorepark, Co. Cork;

‡ Irish Cattle Breeding Federation, Co. Cork;

† Waterford Institute of Technology, Co. Waterford.





Persistency of the lactation curve

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¹Teagasc, Animal and Grassland Research and Innovation Centre, Moorepark, Co. Cork

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Waterford Institute of Technology
INSTITIÚID TEICNEOLAÍOCHTA PHORT LÁIRGE

Objective

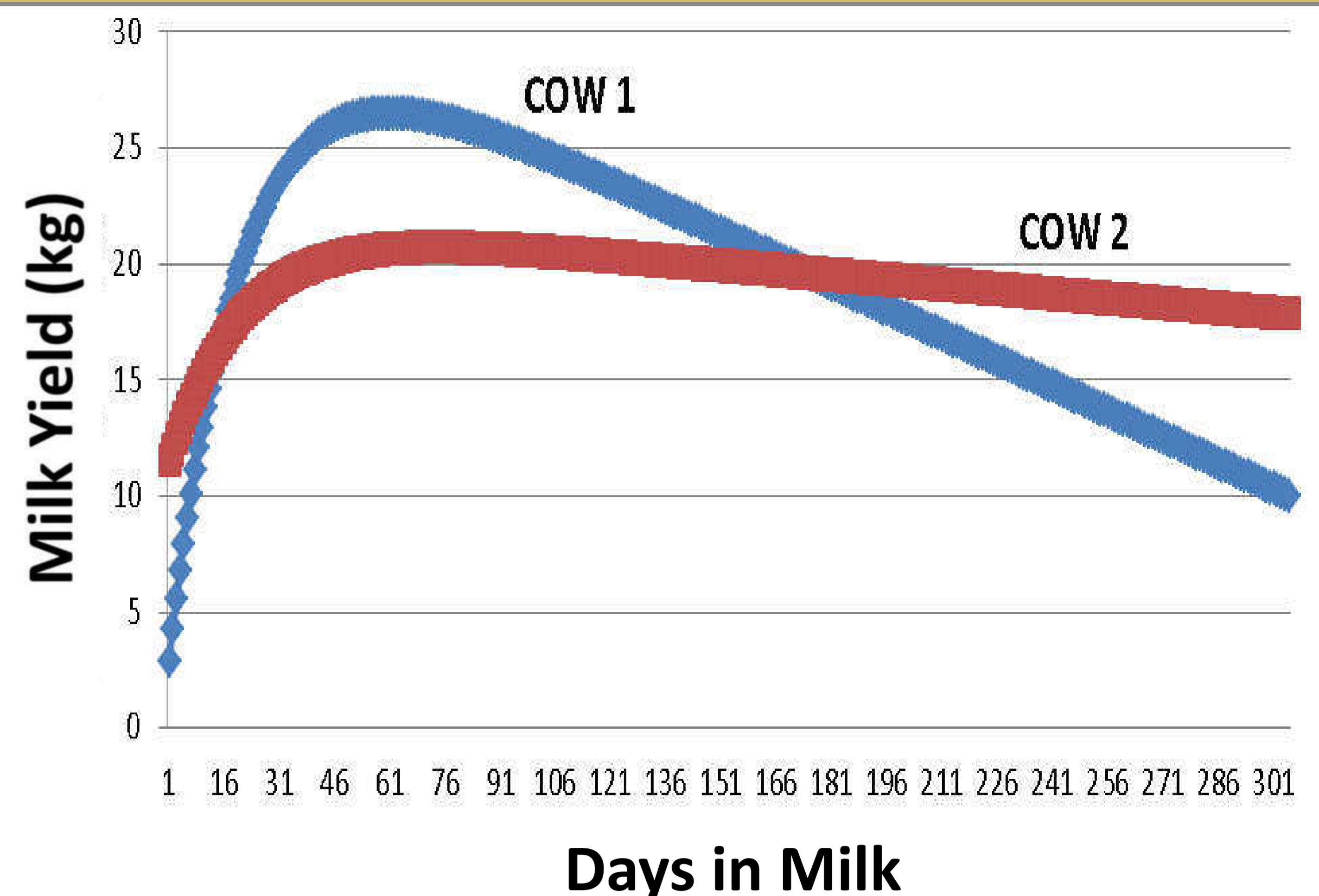
To identify the optimal equation to model lactation curves of Irish dairy cows

To apply the optimal equation to national data to identify persistent cows

Importance of increasing lactation persistency and lowering peak yield

- High peak yields are associated with greater negative energy balance and increased metabolic stress
- Processors will have a more even supply of milk over the year
- Can we breed for a flatter lactation curve?

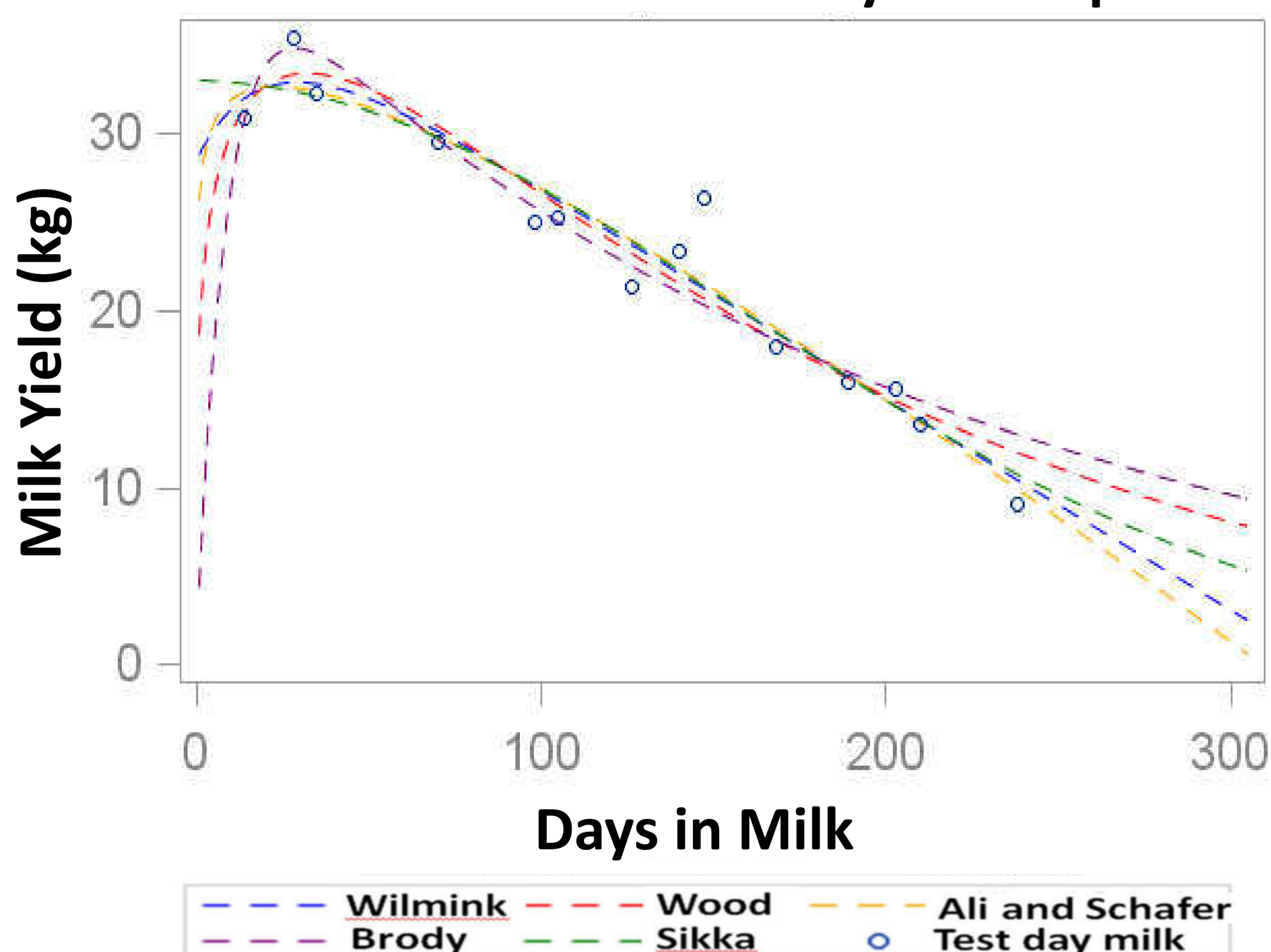
High peak cow vs. High Persistent cow



- Both cows produced 5862 L of milk over 305 day lactation
- Cow 1 has a higher peak and is less persistent than cow 2
- Cow 2 made €57.20 more than cow 1 across the lactation

Alternative equations model lactation curves differently using the same data

Lactation Curve Estimate by each equation



Lactation Curve Equation Results

	Wood	Ali and Schafer	Wilmink	Brody	Sikka
Initial yield (kg)	18.56	26.16	28.76	4.44	32.93
Peak yield (kg)	33.35	32.59	32.84	34.76	32.93
End yield (kg)	7.78	0.57	2.47	9.34	5.28
Average yield (kg)	20.51	19.59	19.86	20.47	20.33
Total yield (kg)	6254	5973	6058	6243	6202

- 5 equations are under investigation: Wilmink, Wood, Ali and Schafer, Brody and Sikka
- Equations were applied to the data of 55,000 lactations. Cows had between 3 and 10 test records
- Initial results indicate woods to have the best fit to the data

DIFFERENTIAL EXPRESSION MRNA AND MIRNA IN THE SPERM OF BULLS OF CONTRASTING FERTILITY

PERRIER J.P., KEOGH K., BERNECIC N.C., SELLEM E., LONERGAN P., KENNY D.A., FAIR S.

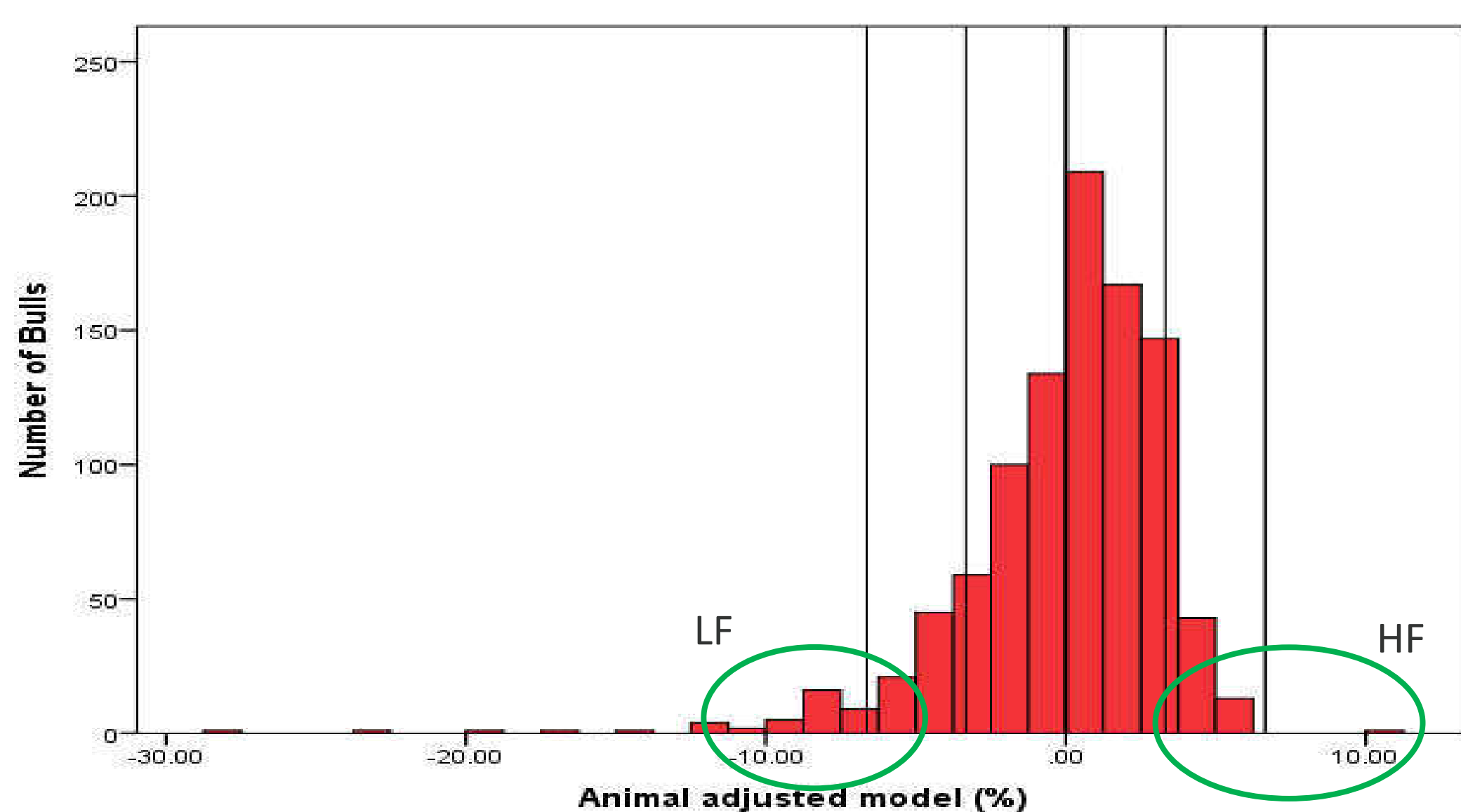
INTRODUCTION

Bulls used in artificial insemination (AI), with apparently normal semen as assessed under the microscope, can vary significantly in their field fertility. A range of more advanced flow cytometric assessments of *in vitro* sperm function have failed to reliably predict the field fertility of bulls. At a molecular level, it is known that the sperm transcriptome contains a rich population of messenger RNAs (mRNAs), long non-coding RNAs (lncRNAs) and small noncoding RNAs (sncRNAs), such as microRNAs (miRNAs). Together, these various transcripts are fundamental for sperm function and for successful fertilisation and embryo development. The objective of this study was to characterize the transcriptomic profile of sperm from High Fertility (HF) and Low Fertility (LF) bulls at the mRNA and miRNA level, in order to identify differentially expressed transcripts that have the potential to be novel markers of fertility.

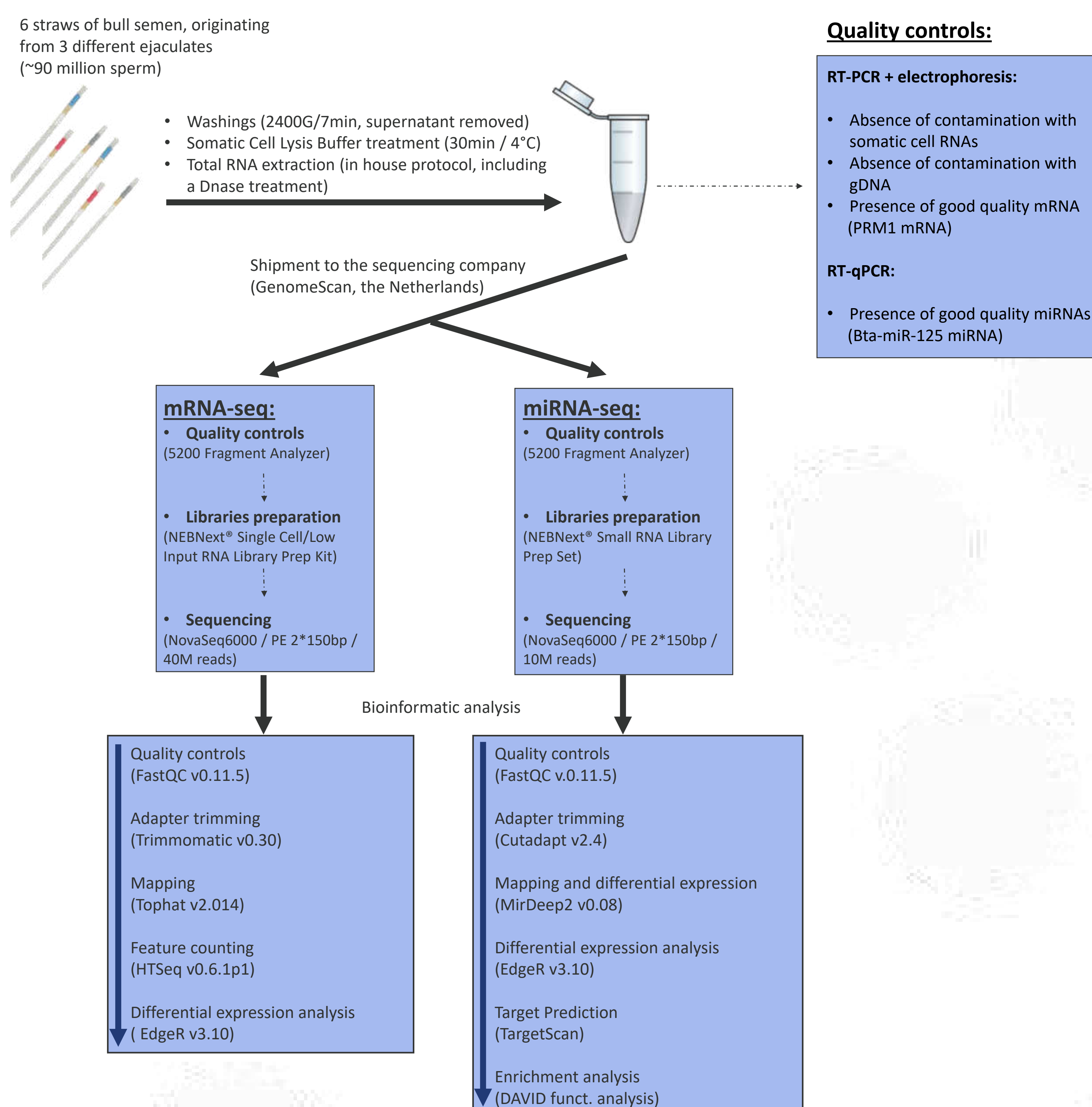
MATERIALS AND METHODS

BULL POPULATION

The HF (n=10) and LF (n=10) Holstein Friesian bulls analysed in this study have been selected from a population of 1665 Irish bulls. They have been ranked based on adjusted fertility scores (Non-Return Rate, or NRR), calculated from a record of at least 500 AI (average = 13,292, min = 519, max = 100,288). The difference, on average, of adjusted NRR between HF and LF bulls is 13.8%.



PROTOCOL FOR TRANSCRIPTOMIC ANALYSIS

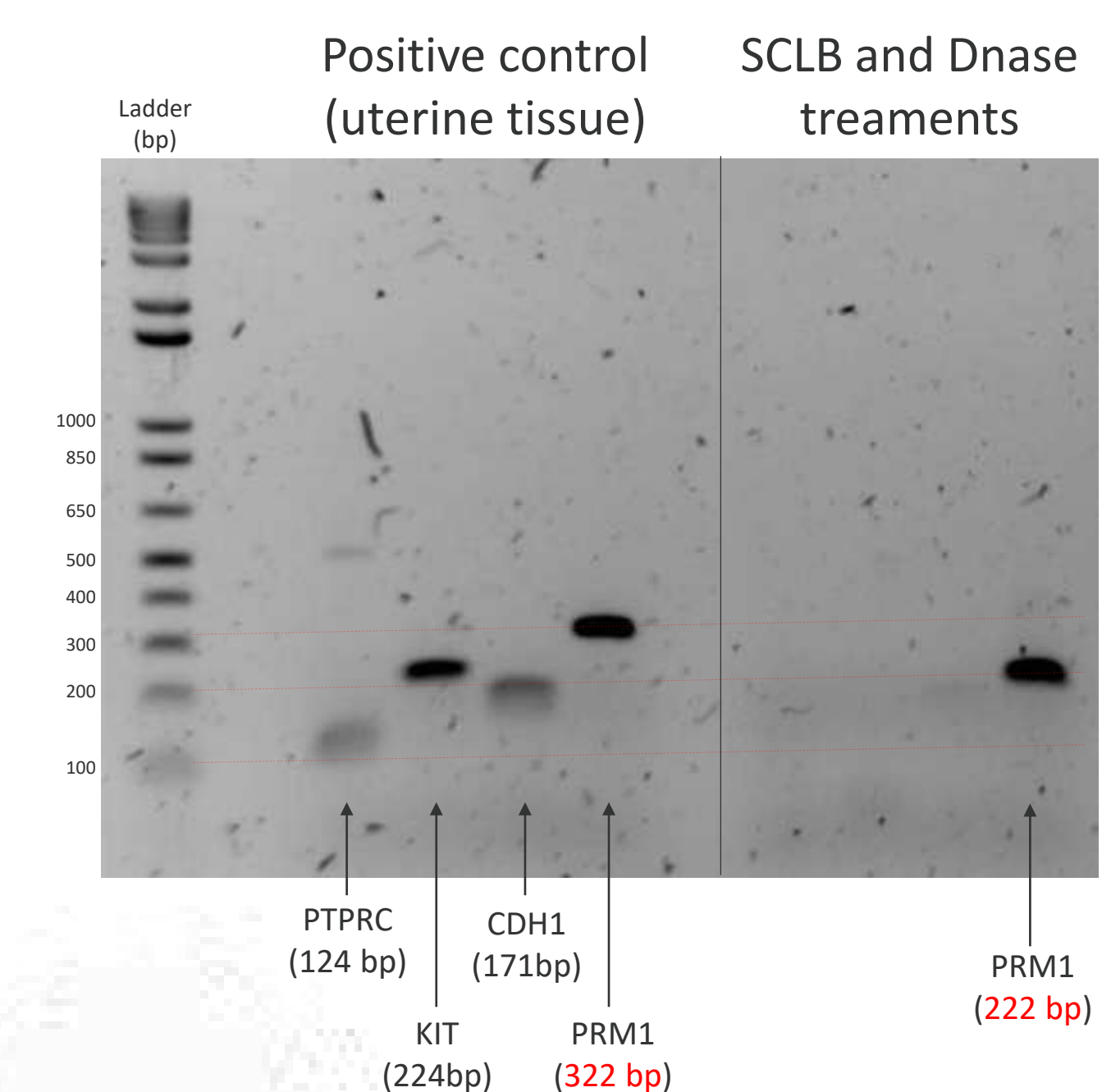
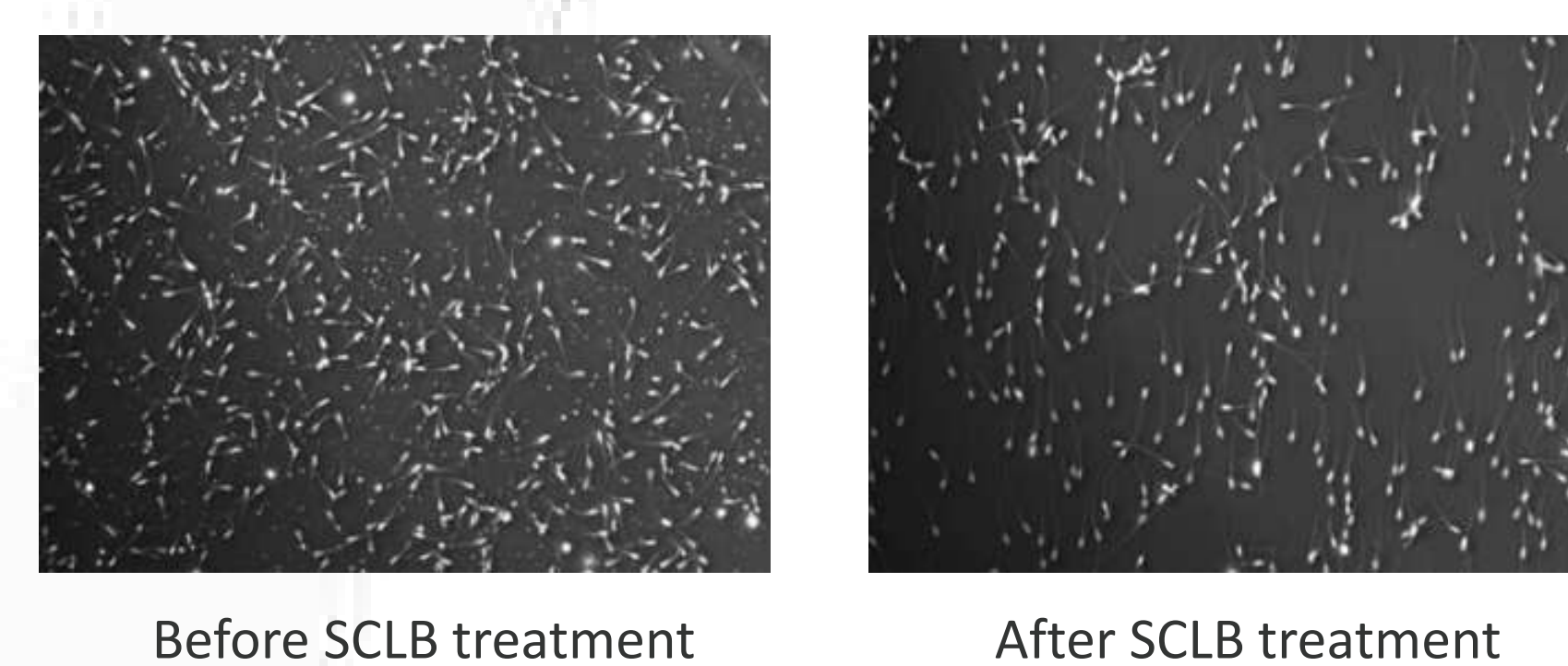


RESULTS

QUALITY CONTROLS

Washings and SCLB treatment efficiently removed debris and somatic cells from the samples (see below), which could bias the results (considering that somatic cells have ~200 times more RNAs than sperm). On the right side is the result of an RT-PCR followed by electrophoresis. Absence of leucocytes, epithelial and germ cell contaminant was tested using primers targeting the genes PTPRC, CDH1 and KIT, which expression is specific to these cell types.

No contamination was detected, for any of the genes. Genomic DNA contamination was tested using intron-spanning primers specific to bovine protamine 1 (PRM1) gene. The signal at 222bp on the sperm sample shows that it is the mRNA, and not contaminating gDNA (322bp, as it includes an intron), which is amplified.



LIST OF DIFFERENTIALLY EXPRESSED MRNAS AND MIRNAS BETWEEN HF AND LF BULLS

Six mRNAs and 13 miRNAs, respectively, were found to be differentially expressed between HF and LF bulls. Notably, the highly abundant protamine 1 (PRM1) mRNA had a higher expression in LF than HF bulls ($P < 0.05$). As PRM1 is involved in sperm chromatin condensation during spermatogenesis, this could suggest that LF bulls exhibit an abnormal sperm chromatin structure.

Gene symbol (Ensembl ID)	Gene name	Fold change	pvalue	miRNA name	Fold change	pvalue
PRM1 (ENSBTAG00000021493)	Sperm protamine P1	2.22	0.018	bta-miR-1298	5.52	0.001
SCP2D1 (ENSBTAG00000005202)	SCP2 sterol binding domain containing 1	2.32	0.020	bta-miR-155	2.03	0.002
Novel gene (ENSBTAG00000048468)	-	2.19	0.024	bta-miR-374b	1.77	0.003
SLC24A1 (ENSBTAG00000025826)	solute carrier family 24 member 1	2.04	0.040	bta-miR-146a	1.57	0.012
RBBP6 (ENSBTAG00000009441)	retinoblastoma binding protein 6	1.65	0.041	bta-miR-885	2.41	0.013
Novel gene (ENSBTAG00000054826)	-	5.41	0.049	bta-miR-98	1.52	0.014
				bta-miR-2285p	2.18	0.015
				bta-miR-338	3.11	0.016
				bta-miR-486	1.64	0.022
				bta-miR-2342	2.17	0.036
				bta-miR-655	2.15	0.037
				bta-miR-502a	1.53	0.047
				bta-miR-2285t	2.44	0.050

TARGET ANALYSIS OF THE MIRNAS

The miRNAs contained in sperm cells are delivered in the zygote after fertilization, where they play key roles during early development by targeting and silencing specific mRNAs. In our study, we identified that the targets of the 13 differentially expressed miRNAs were significantly involved in signalling pathways, such as signalling pathways involved in regulating the pluripotency of stem cells, the mTOR pathway, a central regulator of cell metabolism, growth, proliferation and survival, or even the FoxO signalling pathway, which regulates the expression of genes in cellular physiological events including apoptosis, cell-cycle control, glucose metabolism, oxidative stress resistance, and longevity.

KEGG pathway	miRNA name	Targets involved in the pathway	Corrected pvalue (Benjamini)
Signalling pathways regulating pluripotency of stem cells	bta-miR-2285p	62	1.3E-07
	bta-miR-98	26	9.0E-07
	bta-miR-155	15	1.9E-04
	bta-miR-374b	14	5.0E-02
mTOR signaling pathway	bta-miR-155	9	8.7E-04
	bta-miR-486	6	2.2E-03
	bta-miR-98	11	6.2E-03
	bta-miR-2285p	25	6.6E-03
FoxO signaling pathway	bta-miR-2285p	62	1.9E-08
	bta-miR-98	21	1.5E-04
	bta-miR-486	7	2.2E-03
	bta-miR-155	10	1.9E-02

CONCLUSION

We identified differentially expressed mRNA and miRNAs in the sperm of high and low fertility bulls, which are known to be involved in spermatogenesis or having an effect on embryo development. In the future, these potential biomarkers could be used for improving semen quality assessment and predicting bull fertility. Further experiments could be carried out on embryos in order to determine more precisely how each of these biomarkers positively or negatively influence early embryo development.

Laura Abril-Parreño^{1,2}, Paul Cormican², Anette Krogenæs³, Xavier Druart⁴, Kieran G Meade² and Sean Fair¹

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³ Department of Production Animal Clinical Sciences, Faculty of Veterinary Medicine, Norwegian University of Life Sciences, P.O. Box 369, Sentrum, Oslo, 0102, Norway.

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Introduction

Differences between ewe breeds in the cervix and its secretions are the principal factors why cervical artificial insemination (AI) with frozen-thawed semen works in Norway but not elsewhere. The molecular mechanisms underlying the sperm selection through the cervix remains to be elucidated.

• The **objective** of this study was to use RNAseq to profile the transcriptome of the ovine cervix in four European ewe breeds with known differences in pregnancy rates following cervical AI with frozen-thawed semen.

Materials and Methods

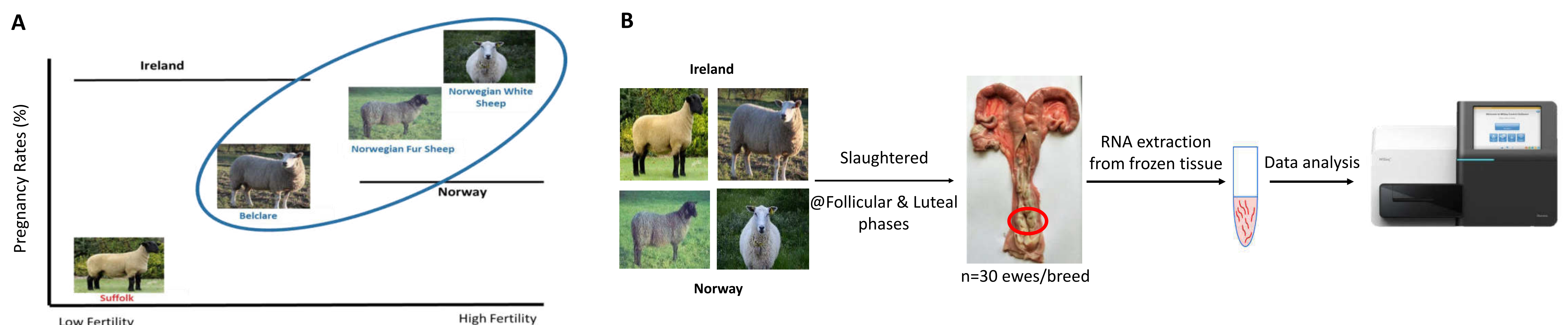


Figure 1. Experimental model. **A)** This study was carried out using two Irish ewe breeds (Belclare and Suffolk; high and low fertility, respectively) and two Norwegian ewe breeds (Norwegian White Sheep (NWS) and Fur; both with high fertility). **B)** Outline of cervical tissue collection. Cervical tissue samples were collected from four ewe breeds (n=30 ewes/breed) at both the follicular and luteal phase of the oestrus cycle.

Results

1. Differential gene expression analysis

• Compared to the Suffolk:

At the **follicular phase** a total of 7232, 7716 and 510 genes were significantly differentially expressed in NWS, Fur and Belclare ewes, respectively.

At the **luteal phase**, 1661, 4984 and 2087 genes were differentially expressed in NWS, Fur and Belclare, respectively.

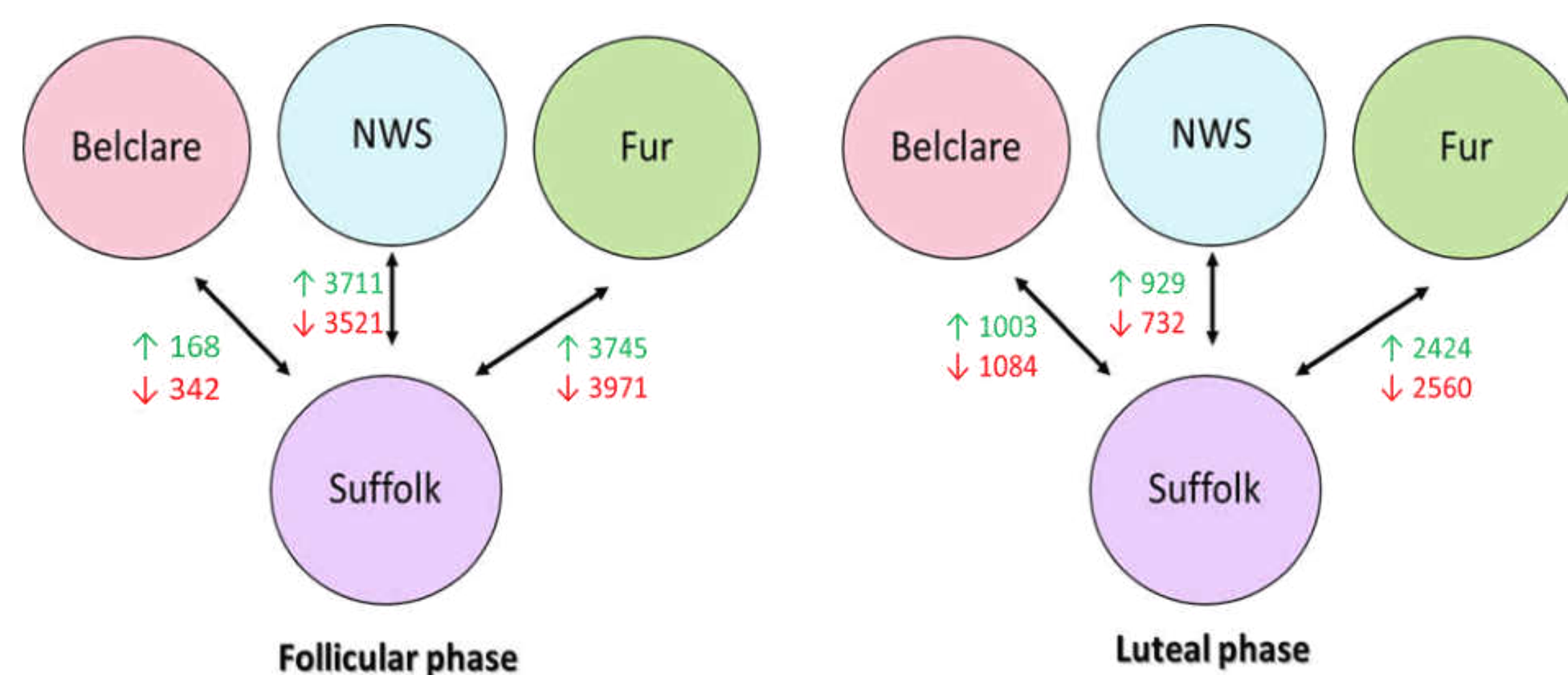


Figure 2. Genes that were up and down differentially regulated (FDR<0.01) in Belclare, NWS and Fur ewes compared to Suffolk ewes (reference level) at the follicular and luteal phases.

2. Conserved transcriptome

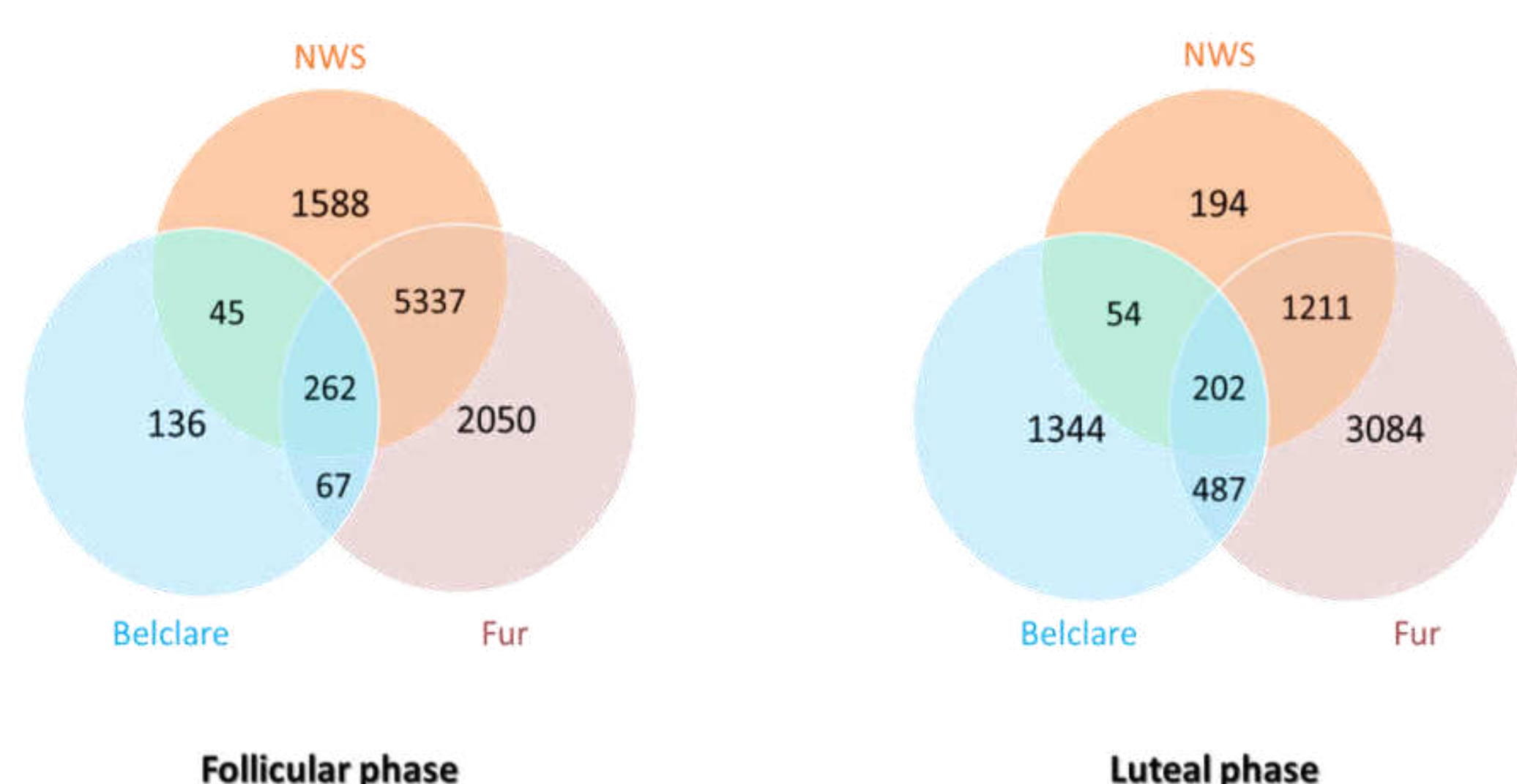


Figure 3. Venn diagrams with genes in common for the 3 comparisons at the follicular and luteal phases.

3. Phase specific differences in gene expression

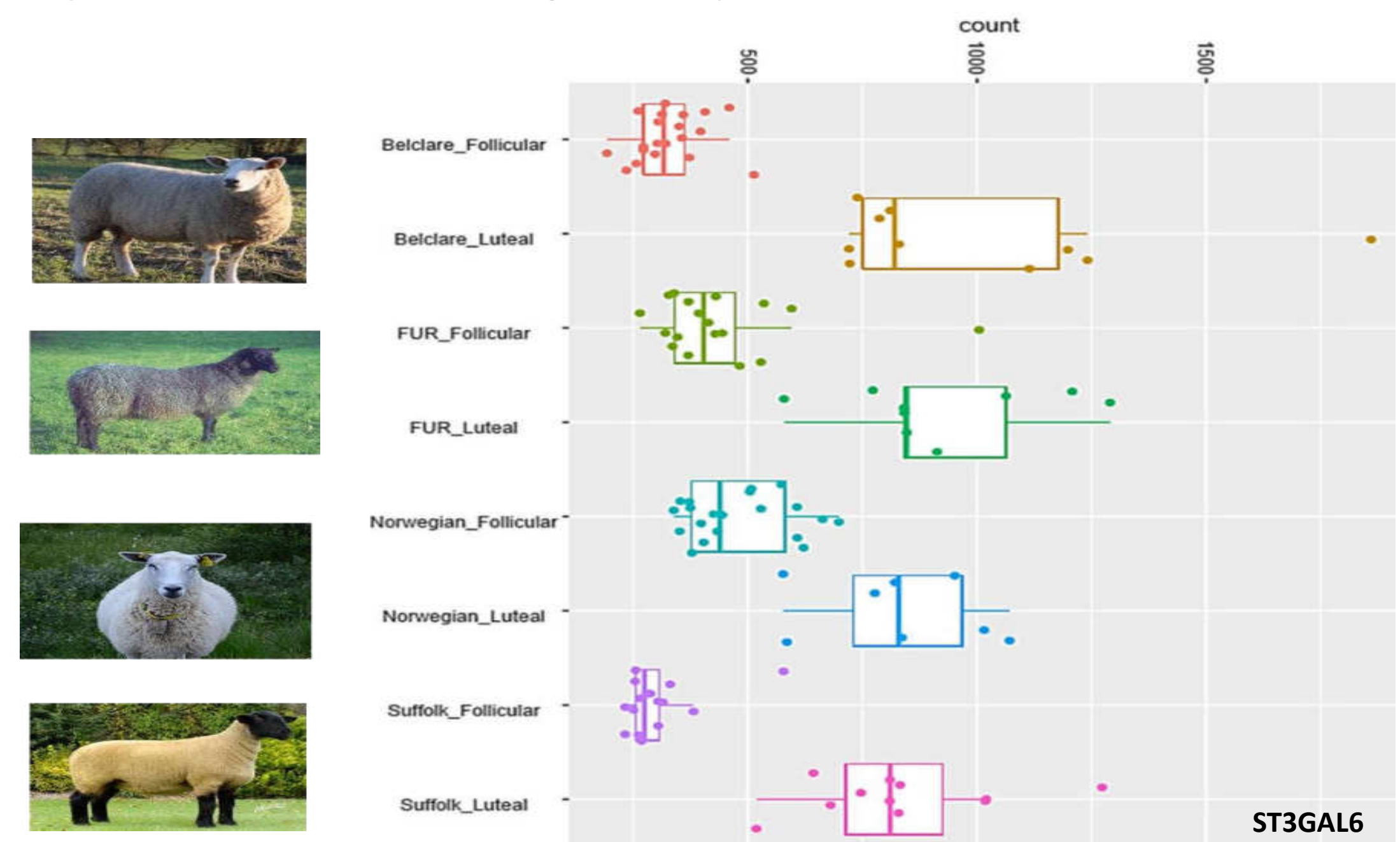


Figure 4. Glycosyl-transferase expression (sorted by normalised read counts) in each ewe breed at the follicular and luteal phases.

4. Breed-specific differences in gene expression

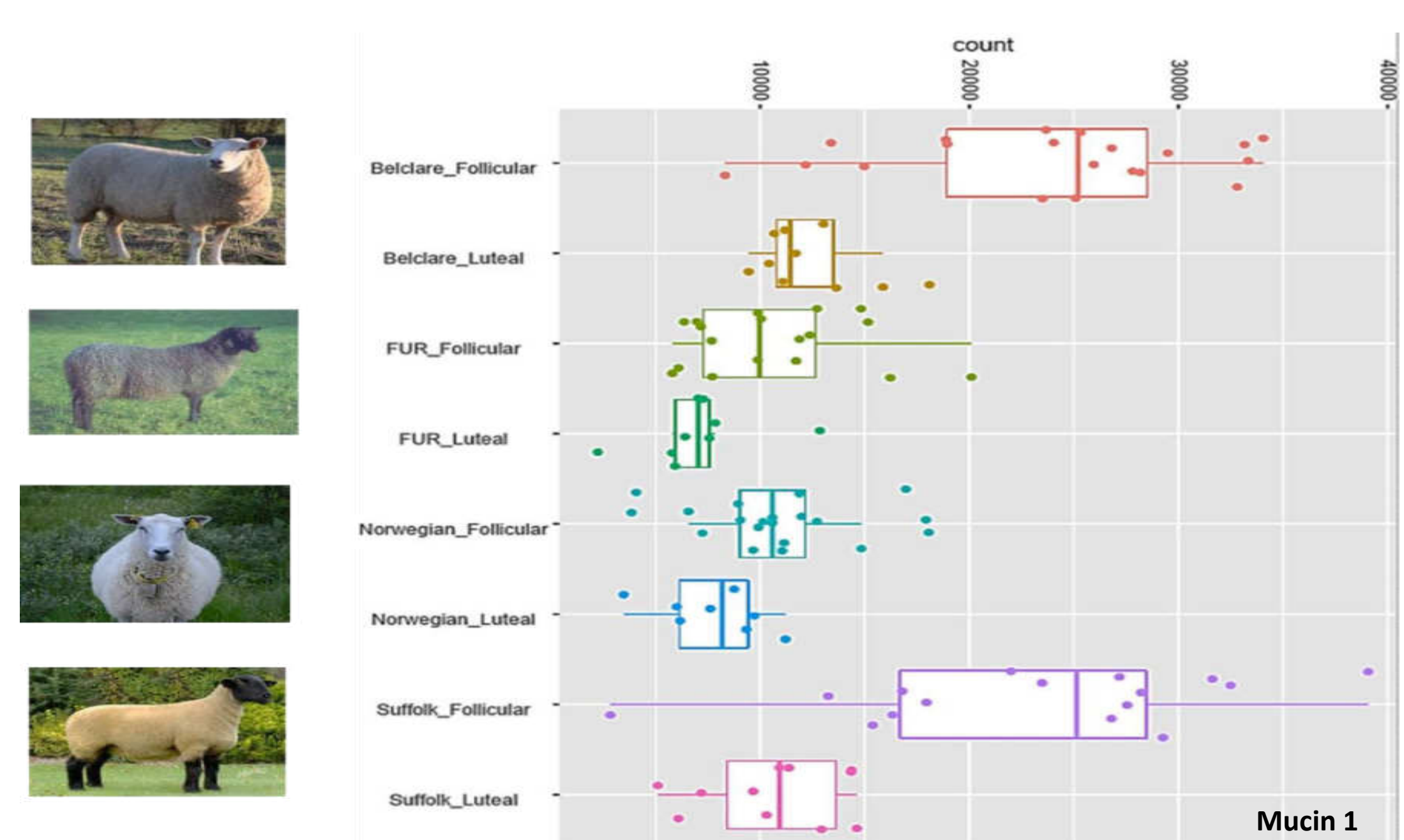


Figure 5. Mucin 1 expression (sorted by normalised read counts) in each ewe breed at the follicular and luteal phases. Mucin 1 is involved in mucus production and protection from infection.

Conclusion

- Significant **differences in gene expression** between **high and low fertility ewe breeds**.
- Pathways involved in **mucin biosynthesis, metabolite transport** and the **inflammatory response**.



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Linear type traits can help predict genetic merit for feed



intake in grazing Holstein-Friesian dairy cows



M. Williams^{1,2}, C. Murphy², R.D. Sleator², M.M. Judge¹, S.C. Ring³, D.P. Berry¹

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Funding from Department of Agriculture, Food and the Marine Research Stimulus 17/S/235 (GREENBREED)

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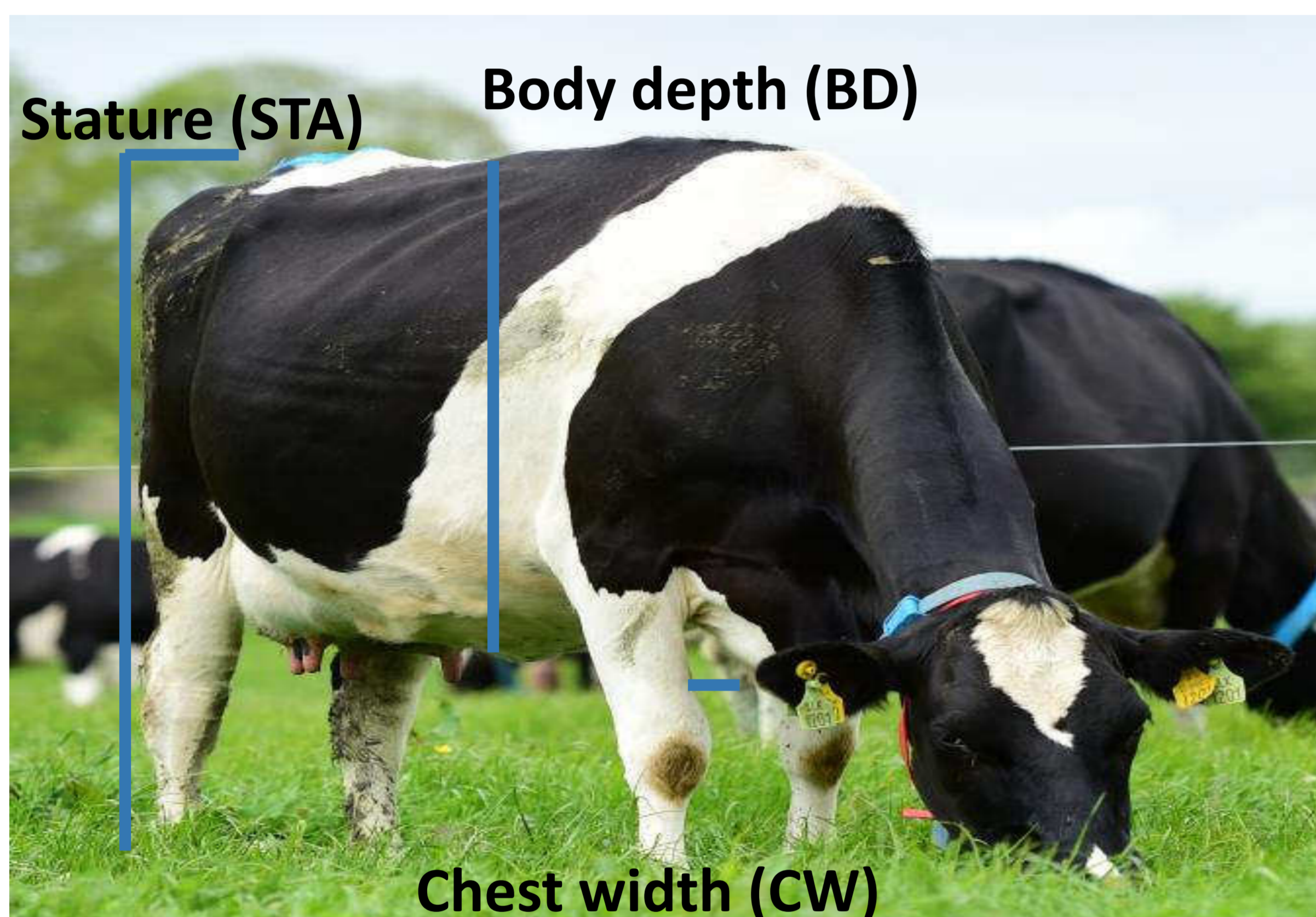
Feed intake

- Difficult and expensive to measure in pasture-based systems
- Readily available body measures may provide a cheaper proxy to direct measurement

Objective

- To estimate the genetic correlations between linear type traits and feed intake
- To quantify the marginal predictive ability of linear type traits in estimating genetic merit for feed intake over and above that predicted by body weight (BW)

Materials and methods



- 7,891 feed intake records for 1,192 Teagasc cows
- 120,739 BW records
- 39,988 linear type trait records for first parity cows

Estimating rumen volume

The four novel traits below were calculated from linear type traits to estimate rumen volume

BD*STA CW*STA CW*BD CW*BD*STA

Results and conclusion

Table 1. Genetic correlations (standard errors) between feed intake (raw and adjusted for genetic differences in BW [Adj_{BW}]), BW, and linear type traits

Linear	Feed intake		Body weight
	Raw	Adj_{BW}	
CW	0.47 (0.12)	0.11	0.50 (0.07)
BD	0.41 (0.12)	0.11	0.42 (0.08)
STA	0.43 (0.09)	0.18	0.40 (0.06)
CW*BD	0.55 (0.11)	0.19	0.55 (0.07)
CW*STA	0.64 (0.10)	0.25	0.63 (0.06)
BD*STA	0.51 (0.10)	0.17	0.50 (0.07)
CW*BD*STA	0.64 (0.10)	0.28	0.62 (0.07)

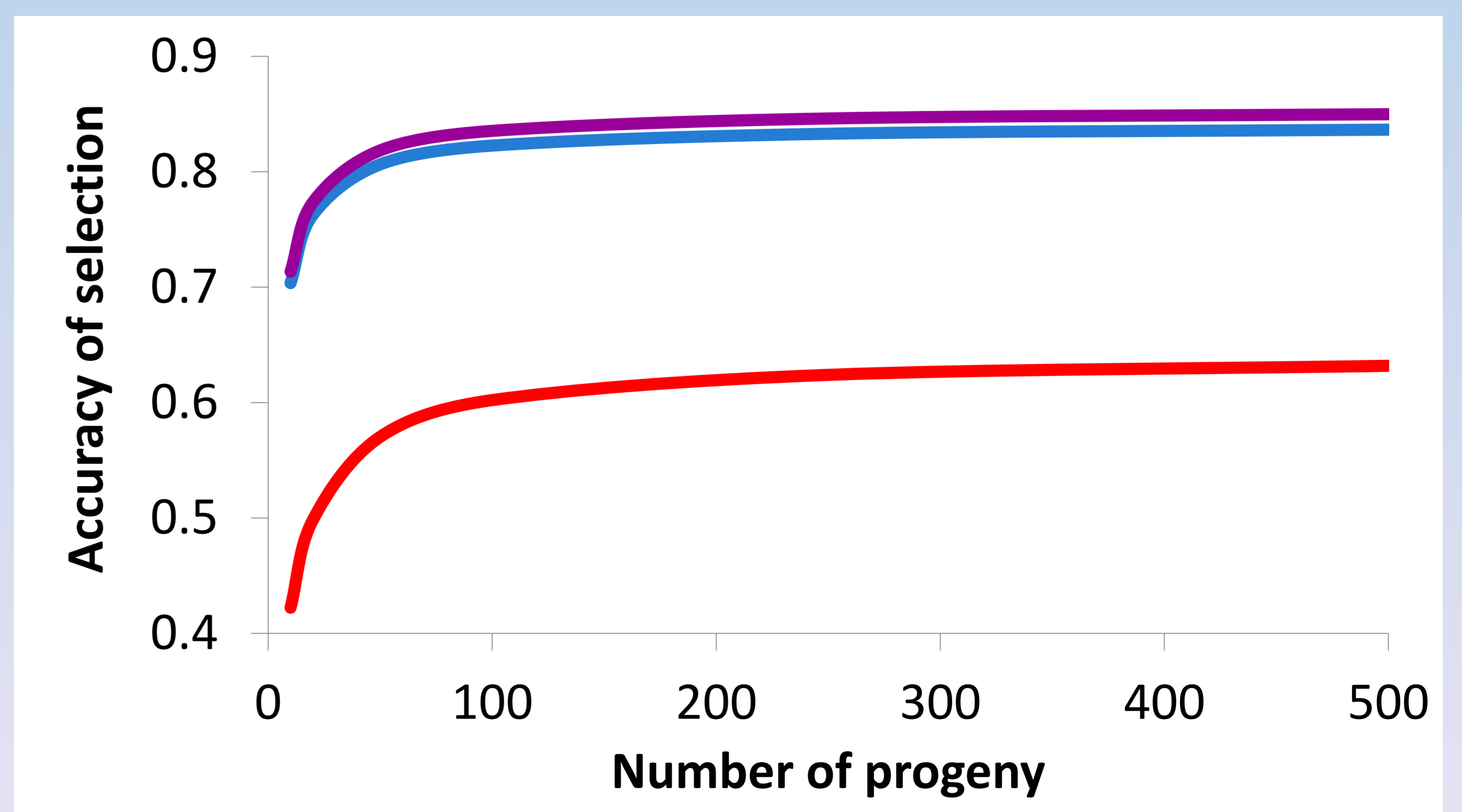


Figure 1. Accuracy of selection for feed intake when based on CW*BD*STA (red), BW (blue), or CW*BD*STA and BW (purple)

Traits estimating rumen volume may be useful to predict feed intake even after correcting for genetic differences in BW





Novel analytical methods to predict milk quality from routinely available spectral data of milk samples



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Objective

Use novel statistical approaches to predict granular milk composition traits in dairy cows from milk mid-infrared spectra (MIRS)

Why MIRS

- MIRS is low cost and non-disruptive approach
- MIRS analyses are available on all milk recorded cows nationally
- Potential to use a single milk sample to predict multiple traits

Why novel approaches

- Partial least square regression (PLS) is the main statistical method used for prediction
- Novel statistical approaches may improve the accuracy of the prediction



MIRS Analyses



- Spectra analyses
- PLS
 - Lasso
 - Machine learning
 - Elastic net
 - Deep learning
 - Ridge

Milk traits

- Fat Content
- Protein Content
- Beta Casein
- Casein Content
- pH
- Rennet coagulation time
- Curd-firming time
- Curd firmness
- Casein micelle size
- Heat Stability

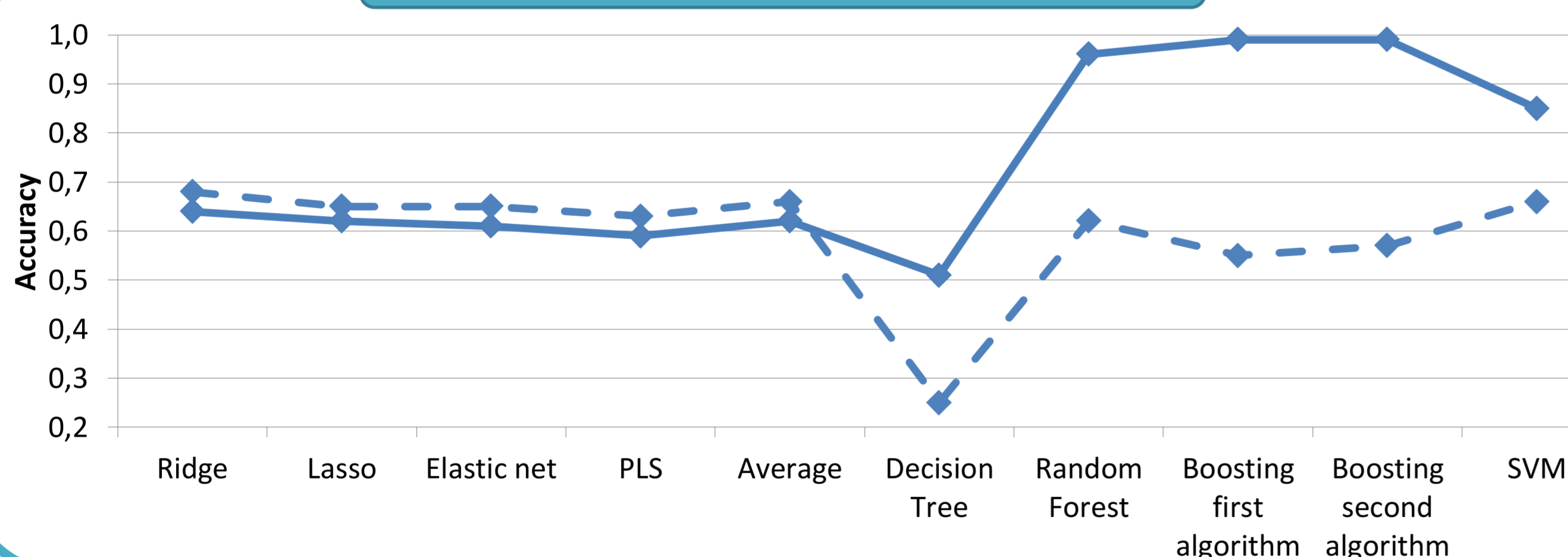
Materials and methods

- 699 milk spectra
- beta casein
 - heat stability
 - pH predicted
- 10 algorithms tested

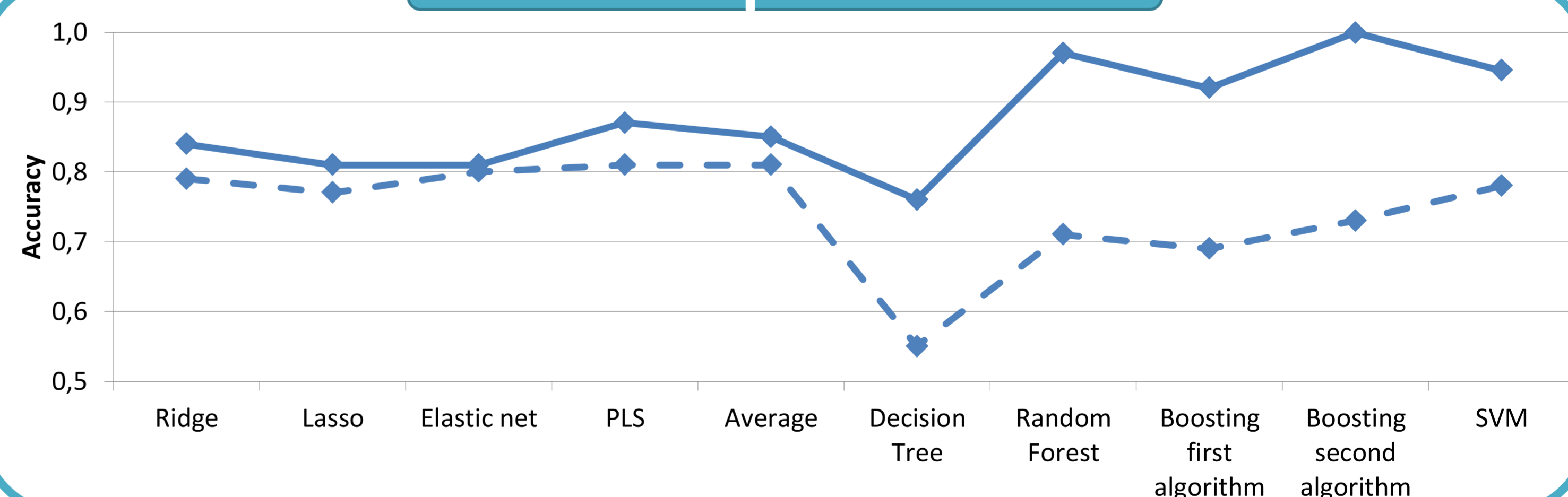
Prediction Results

Prediction accuracy of the cross validation (continuous line) and of the external validation (dotted line) when beta casein, heat stability and pH were estimated

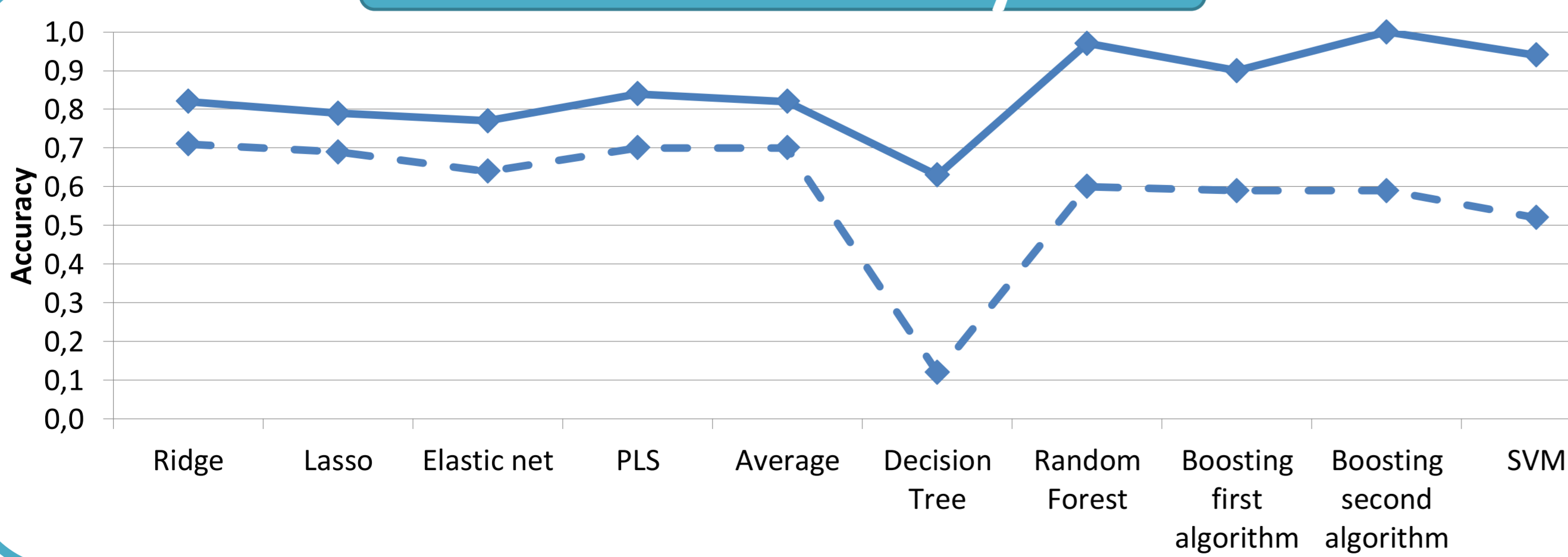
Beta Casein



pH



Heat Stability



Conclusions

- Random Forest, Boosting and Support Vector Machine (SVM) algorithms work well in cross validation
- In an external validation Partial Least Square Regression (PLS) gives the best results



This research is supported by a Starting Investigator Research Grant from Science Foundation Ireland (18/SIRG/5562)

Genetic benefits of the use high genetic merit rams from New Zealand or Ireland in the Irish sheep industry

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¹ Teagasc, Animal and Grassland Research and Innovation Centre, Athenry, Co. Galway

² School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4

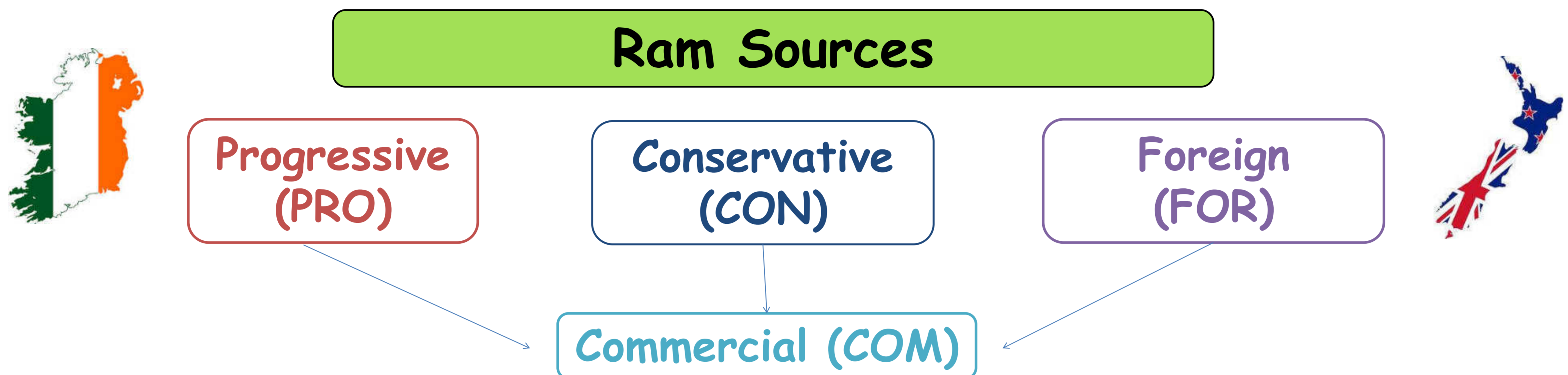
³ AbacusBio, Ground Floor, Public Trust Building, 442 Moray Place, Dunedin 9016, New Zealand.

Background

INZAC highlighted a potential benefit from using superior genetics from Ireland or New Zealand.

Objective

To assess the importance of using high genetic merit animals in the sheep industry.

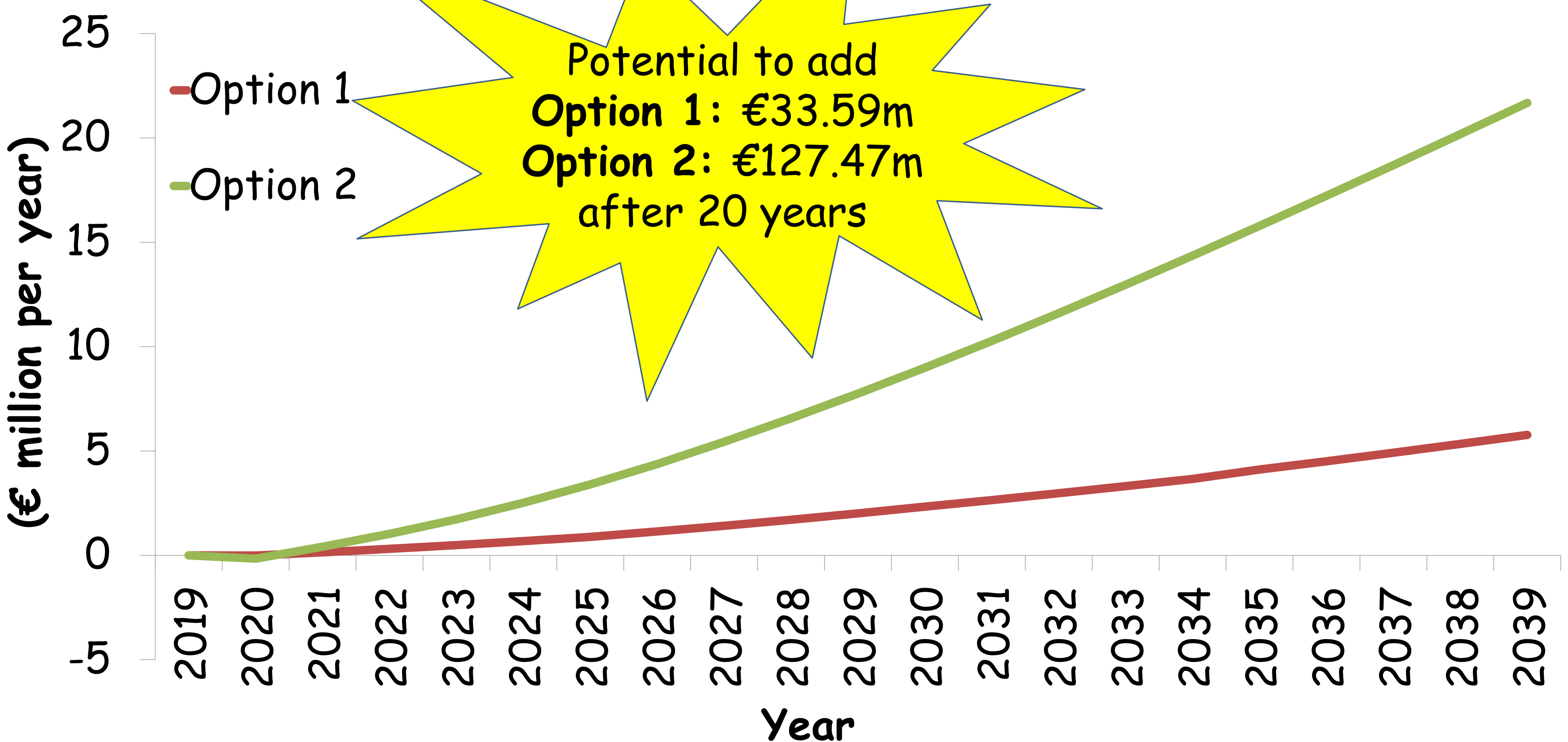


Results

Current Scenario: 93% of sires used in Ireland are not selected on their genetic merit potential

Option 1: Increase the use of high genetic merit rams from NZ or Ireland (no shift in market share)

Option 2: Increase the use of high genetic merit Irish rams by industry (increase market share by 5% per year)



Recommendations

Enormous benefits can be made with widespread use of high genetic merit sires

The Relationship of Methane Output with the €uro-Star Breeding Index

Paul E Smith^{1,2}, Stephen Conroy³, Alan K Kelly², David A Kenny^{1,2} and Sinéad M Waters¹

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²UCD, School of Agriculture and Food Science, University College Dublin Belfield, Dublin 4, Ireland

³ICBF, Tully Progeny Test Centre, Tully, Co. Kildare, Ireland.



Introduction

- **Methane production** (methanogenesis) arising from enteric fermentation, is responsible for ~40% of global agriculture's green house gas emissions.
- The production of **methane** diverts an estimated 2-12% of **gross energy intake** away from animal performance.
- **Over 70%** of variation in ruminant **methane production** is related to individual animal **dry matter intake (DMI)**.
- **Ranking animals** based on **methane yield (grams of CH₄/ kg of DMI)** benefits a more accurate estimation of methane output by accounting for differences in feed intake.
- **Cattle can be selected for reduced methane yield** (heritability of 0.22), however there is a lack of information on the potential effects to animal profitability.

Objective

Thus, the objective of this project was to investigate the relationship of methane yield (MY) with the €uro Star breeding index from the ongoing trial work, as part of *RumenPredict*, at the ICBF Tully Progeny Test Centre.

Materials and Methods

Animal Model

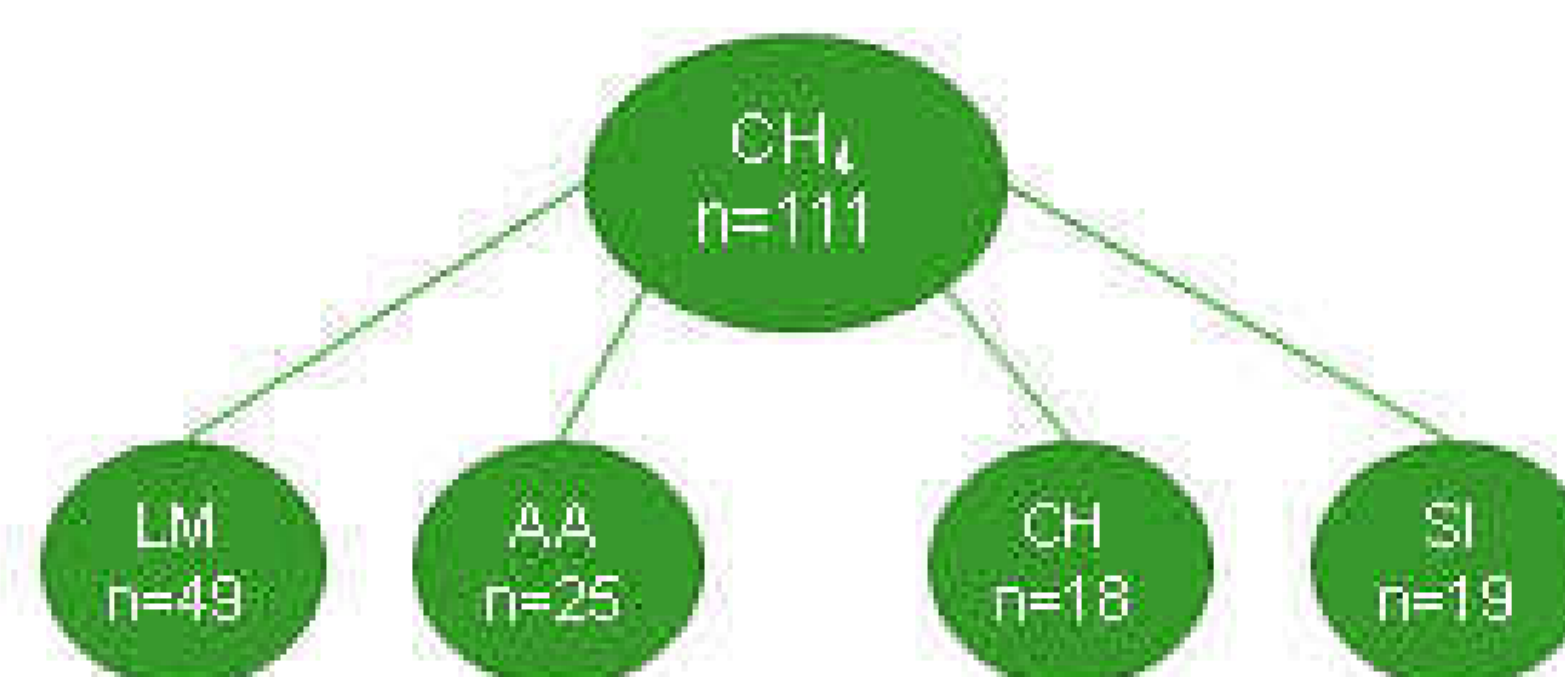
Methane emissions and DMI estimated over a 3 week period at beginning of feed efficiency test (n=111)



GreenFeed System estimating individual animal methane emissions

Roughage Intake Control (RIC) system calculating feed intake

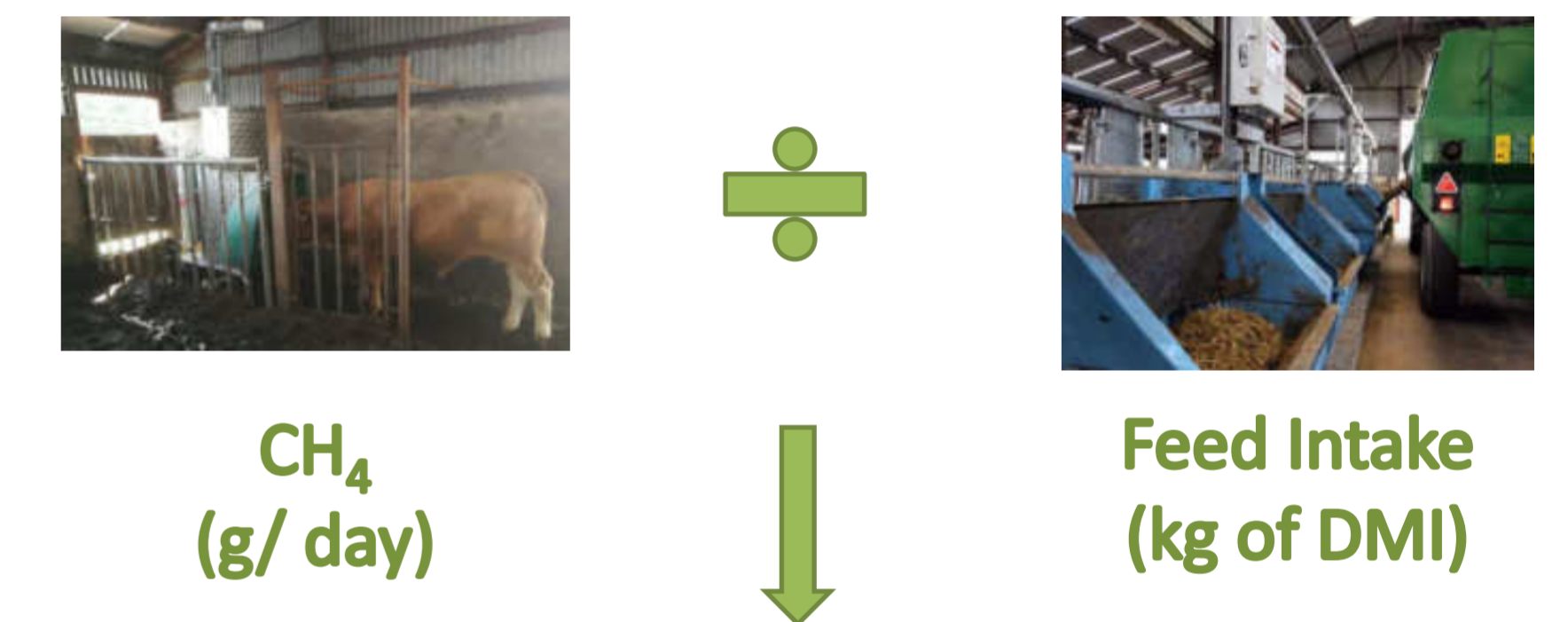
Breed Composition



Main breed composition of cross bred steers included in the study. LM=Limousin; AA=Aberdeen Angus; CH=Charolais; SI=Simmental

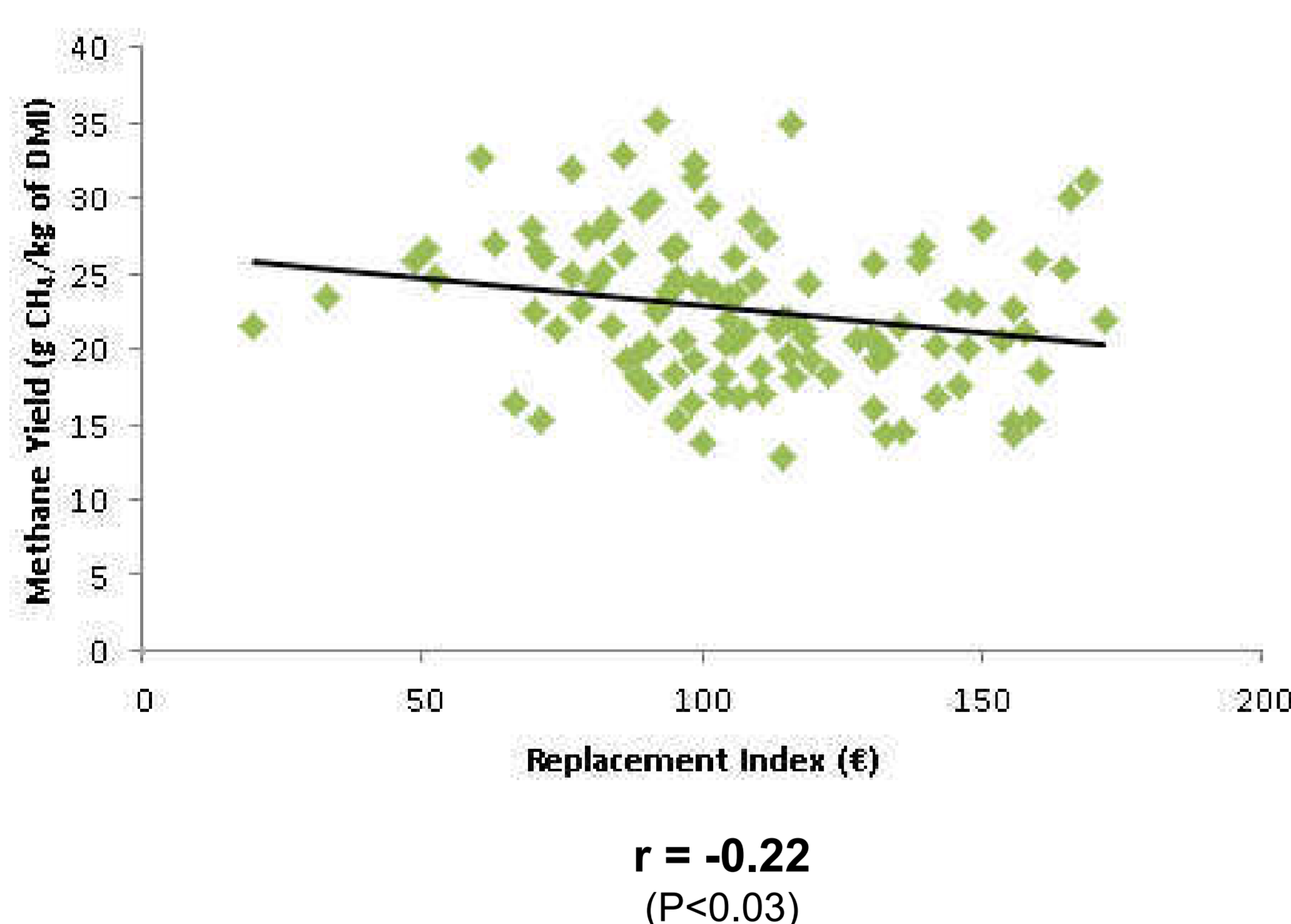
Methane Yield

Methane yield (g CH₄/kg of DMI) calculated and correlated with replacement and terminal index value of individual animals

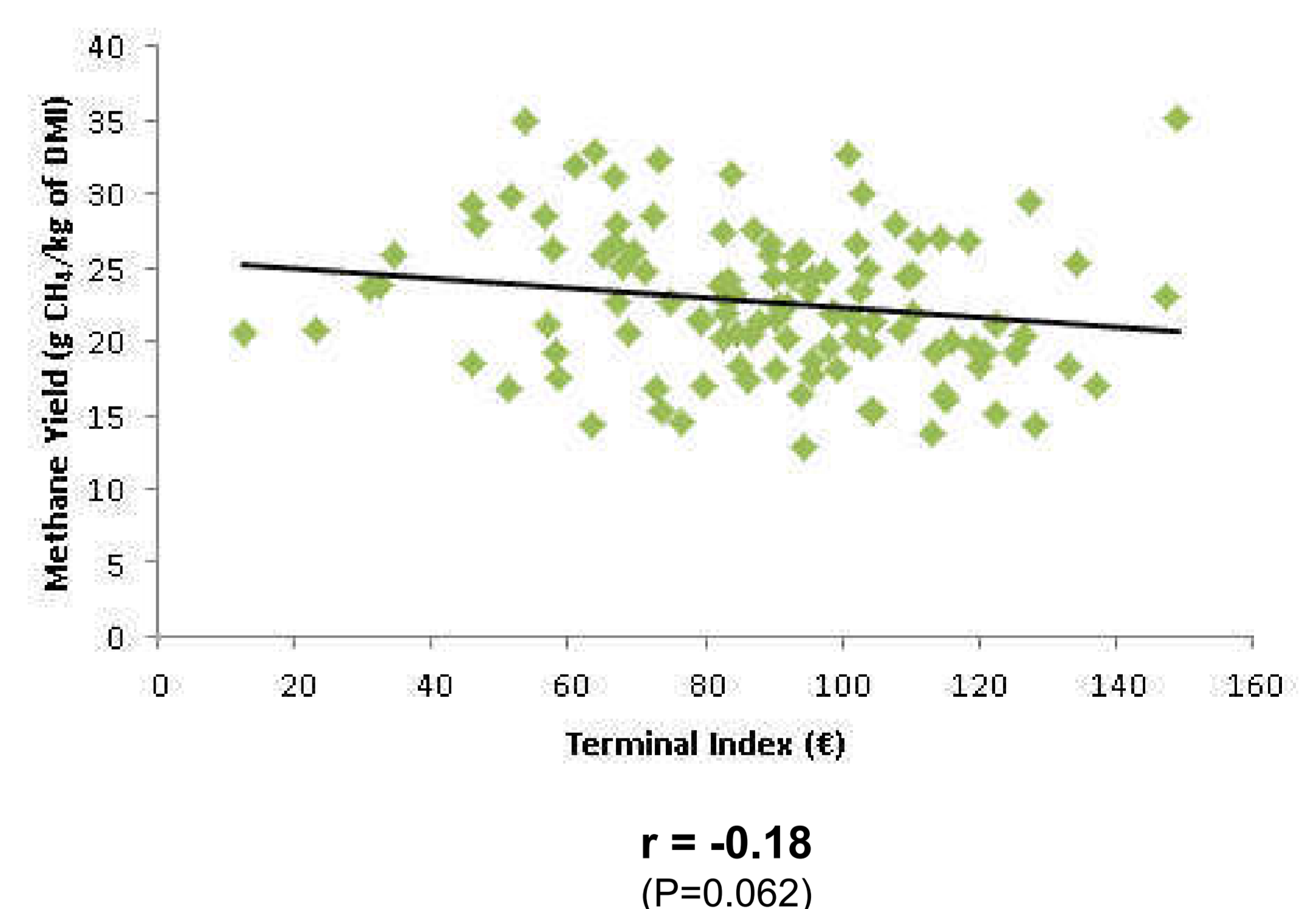


Cattle separated into high (n=55) and low (n=56) MY animals

Results



	Low	High	P-Value
Methane Yield (g/kg DMI)	20.4	26.9	<.0001
Carbon Dioxide Yield (g/kg DMI)	816.6	920.2	<.0001
Daily Methane (g/day)	228.4	264.7	<.0001
Daily Carbon Dioxide (g/day)	9142.7	9044.0	0.65
Age (months)	17.4	16.6	-
Weight (kg)	553.5	501.9	0.49
Feed Intake (kg of DMI)	11.3	9.9	<.001
Replacement Index (€)	111.0	96.5	0.02
Terminal Index (€)	86.6	85.6	0.84



Conclusion

Cattle in the low MY group had an increased level of feed intake but reduced daily methane production. Although feed intake has an 18% economic weighting as part of the Replacement Index, a negative correlation of MY and the index was observed. Based on the current data reducing methane output, by ranking cattle in terms of MY, suggests the potential to select cattle with a greater economic breeding value. In addition, it is probable that cattle with a reduced MY have an enhanced ability to retain energy harnessed from feed. A better understanding of the relationship of MY with the breeding index is likely to become evident as more data is collected.

Acknowledgments

Funding is provided through the FACCE ERA GAS *RumenPredict* grant (16/RD/ERAGAS/1RUMENPREDICT-ROI2017), administered by the Dept. of Agriculture, Food and the Marine, and the MASTER project, having received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 818368.



*Corresponding author: Paul.Smith@teagasc.ie

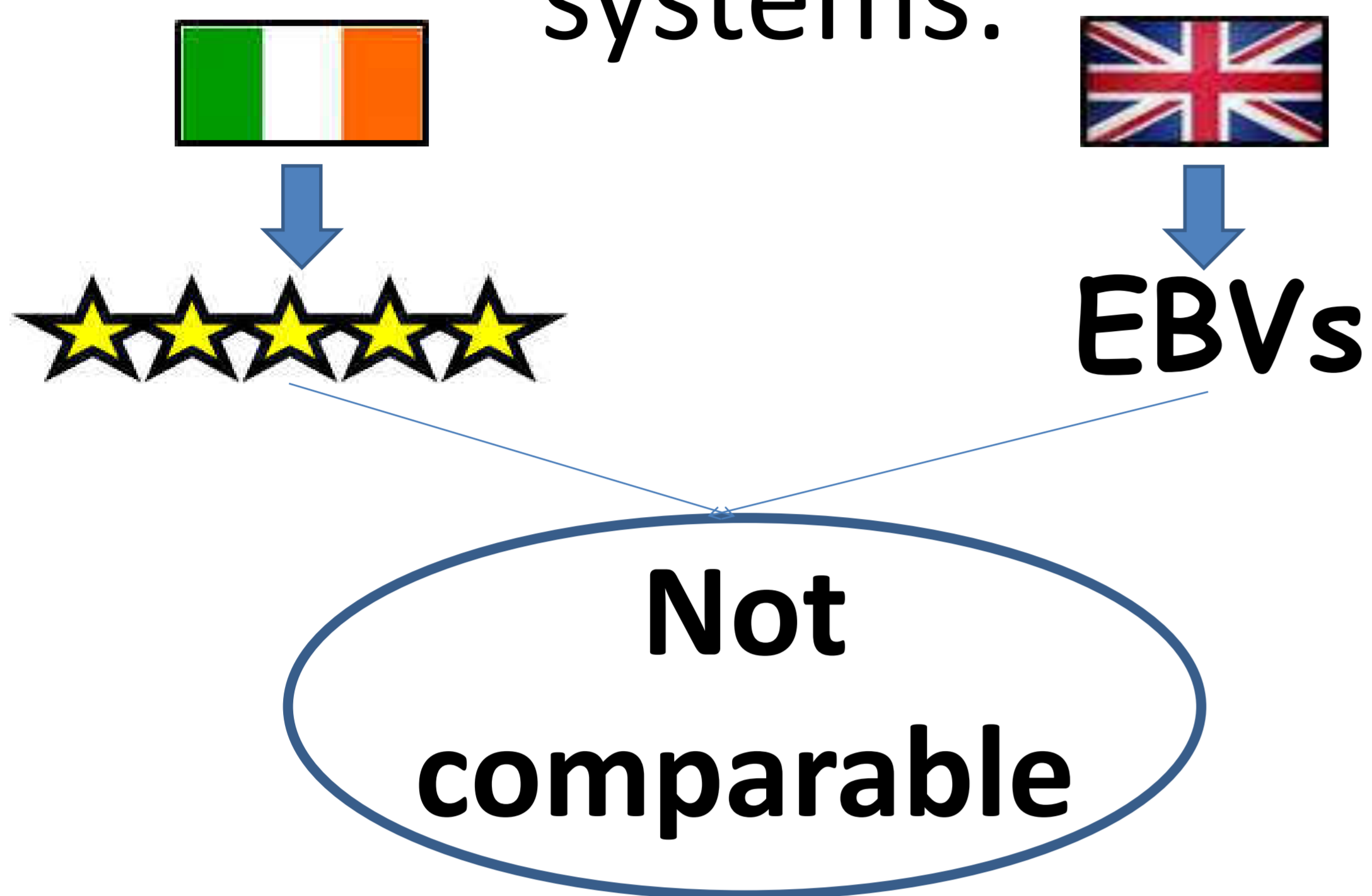


Objective

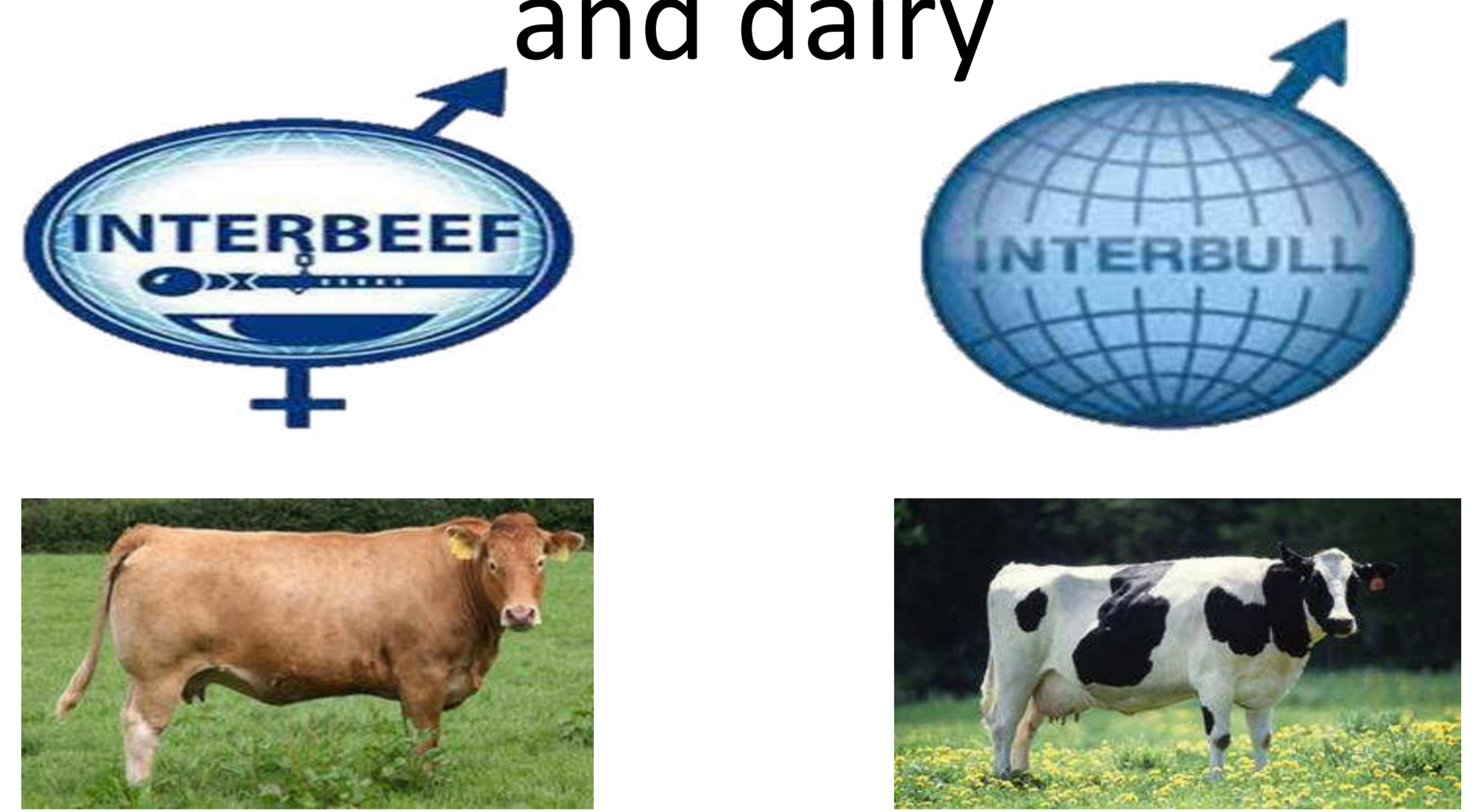
Accurately compare animals based on genetic merit between countries

Why?

❖ Current genetic evaluation systems:

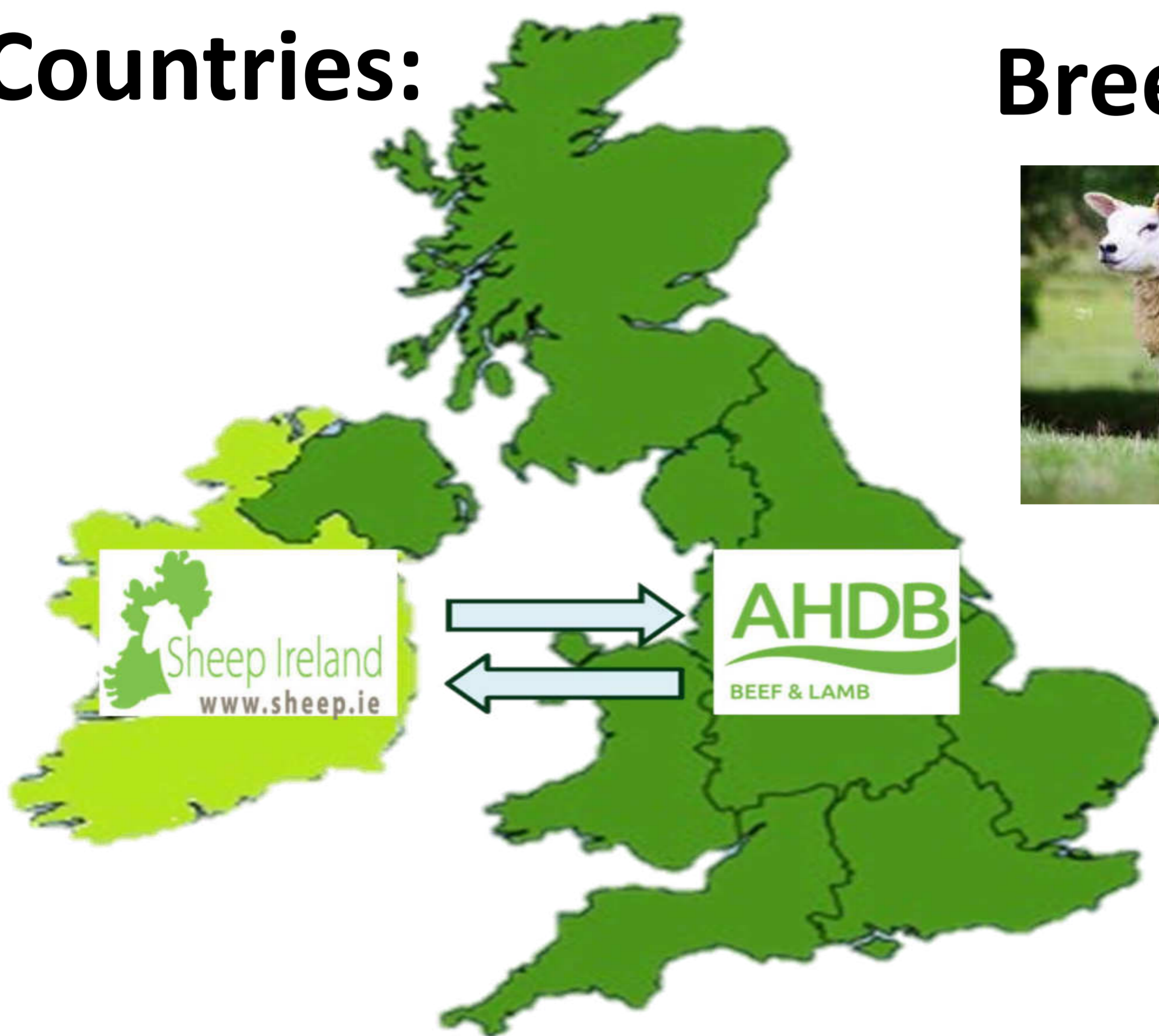


❖ Previous success in beef and dairy

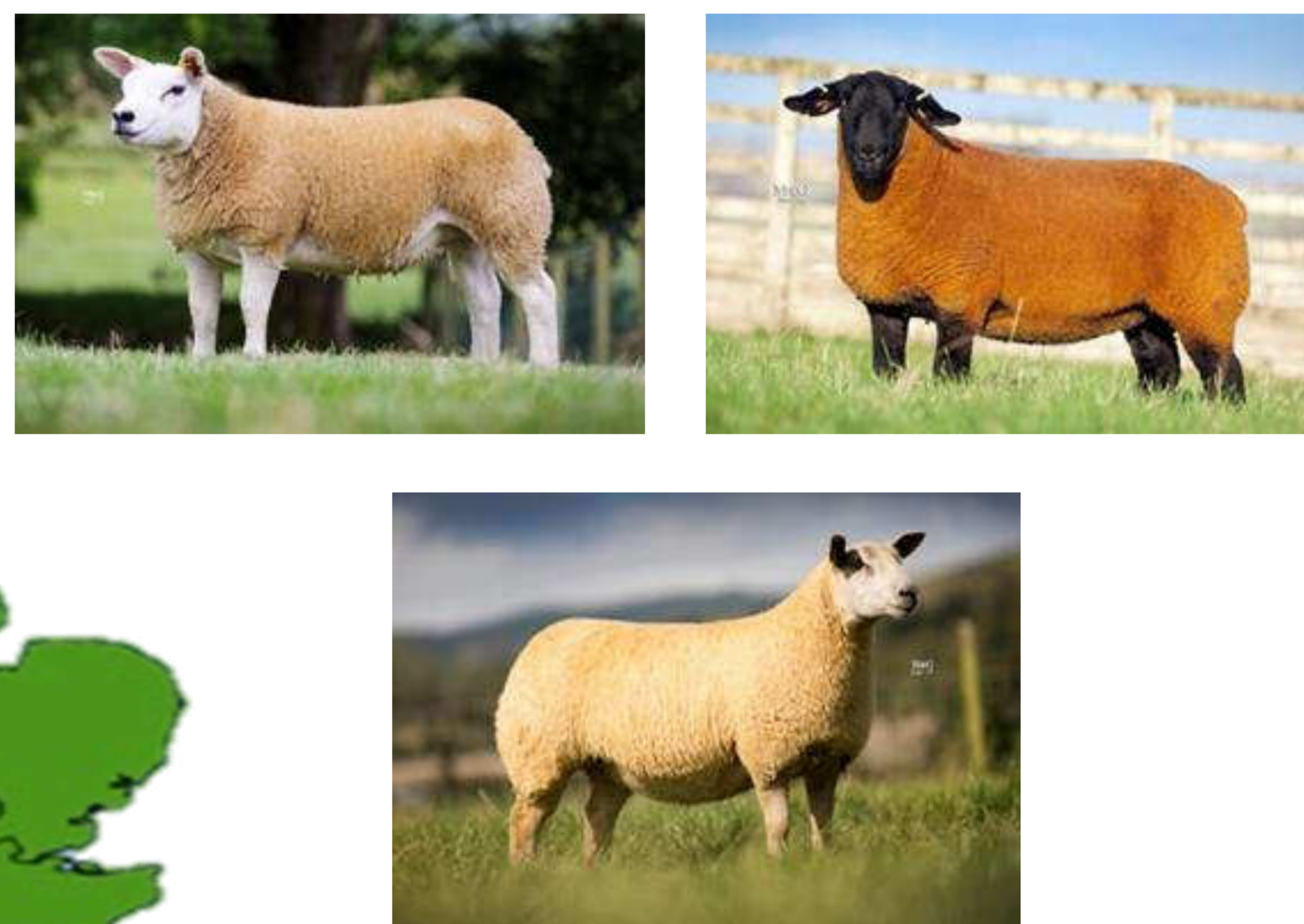


Data

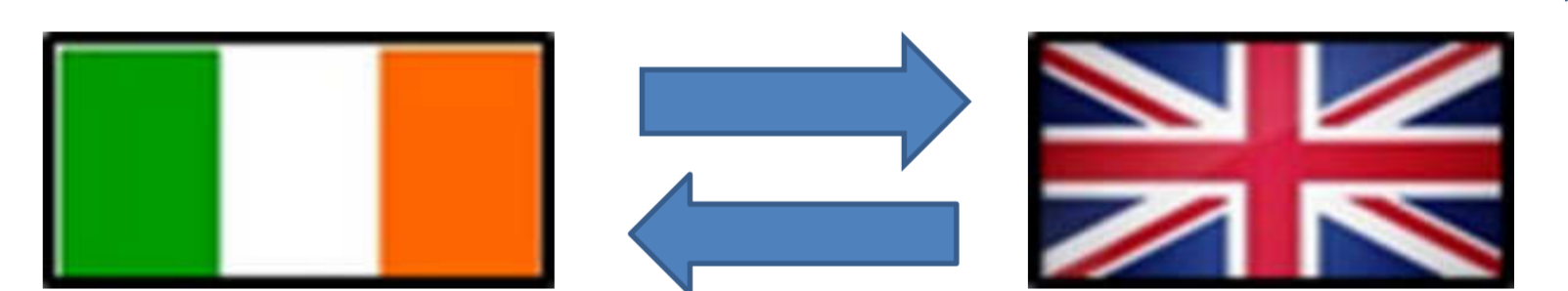
Countries:



Breeds:



Common Traits:

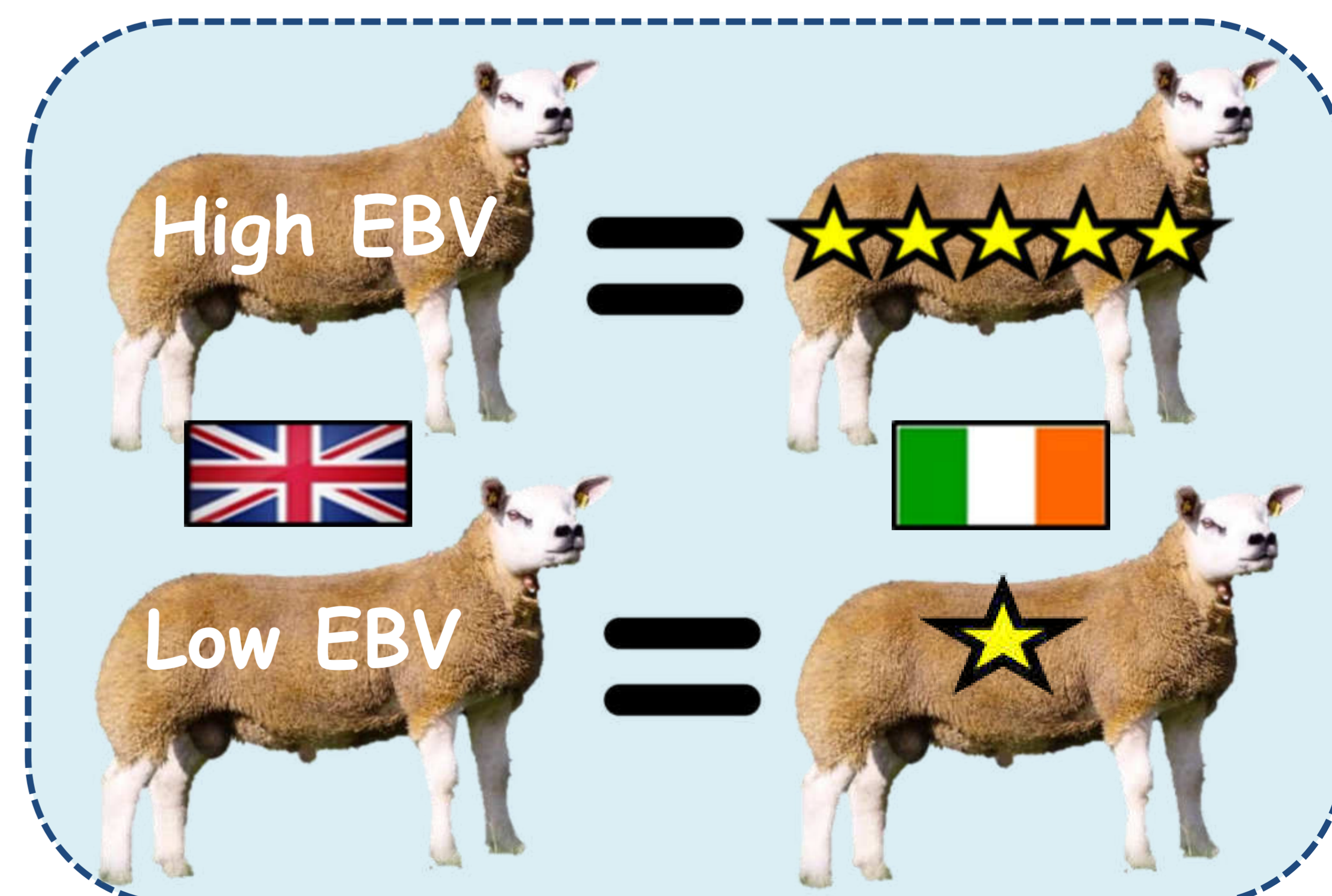


- ❖ Scan weight
- ❖ Muscle depth
- ❖ Fat depth

Results

Sire EBV Correlations		
Trait	n	gCORR
Scan weight	420	0.87
Muscle depth	342	0.85
Fat depth	341	1

What does this mean ?



Conclusion

- ❖ Large overlap of common animals between Ireland and the UK
 - ❖ Strong correlations between common traits
- ❖ Across country evaluations are possible within the sheep industry

Effect of early life plane of nutrition on the molecular regulation of testicular development in the Holstein Friesian bull calf

S. Coen^{1,2}, K. Keogh¹, C.J. Byrne³, P. Lonergan², S. Fair³ and D.A. Kenny^{1,2}

¹Animal and Bioscience Research Department, Teagasc Grange, Dunsany, Co.Meath, Ireland; ²School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4, Dublin, Ireland; ³Laboratory of Animal Reproduction, Department of Biological Sciences, University of Limerick, Limerick, Ireland.

Introduction

- In seasonal dairy production systems demand for semen from young genetically elite AI sires often exceeds supply.
- Consequently there is a requirement to identify appropriate rearing management strategies to ensure;
 - I. Early onset of puberty and sexual maturity
 - II. Timely availability of high quality semen
- We have clearly shown that improved early life nutrition advances the development of the hypothalamic-pituitary-testicular (HPT) axis and age at puberty onset in bull calves. However, the precise underlying biological mechanisms are unknown

Objective: To examine the effect of plane of nutrition during early calthood on aspects of the molecular control of testicular development in the dairy bull calf.

Materials & Methods

- 30 Holstein Friesian bull calves with a mean (SEM) age and bodyweight of 17.5 (2.8) days and 48.8 (5.3) kg, respectively, were assigned to either a high (H; n=15) or moderate (M; n=15) plane of nutrition, to achieve an average target growth rate of 1.0 and 0.5 kg/day, respectively. Calves on H and M diets received 1.5 and 0.5 kg of milk replacer (MR) per day, reconstituted at 15 and 12.5% (w/v), respectively. Calves on H diet were offered concentrate *ad libitum*, while M calves received 500g/day. Both milk replacer and concentrate allocation was delivered using an electronic calf feeder. In addition, all animals received 500 g of hay daily.
- Calves were weighed and blood sampled regularly for the evaluation of reproductive (anti-Mullerian hormone, luteinising hormone, follicle stimulating hormone and testosterone) and metabolic hormones (IGF-1, insulin, leptin) as well as metabolite (β -hydroxy butyrate, non-esterified fatty acids (NEFA) cholesterol, and glucose) concentrations.
- At 87 (\pm 2.1) days of age, all calves were euthanized and target tissues recovered including the testes for subsequent molecular analyses.
- Recovered testes samples were then subjected to miRNA and mRNA sequencing as well as global proteomics. miRNA and mRNA sequencing were performed on Illumina HiSeq2500 and Illumina NovaSeq sequencing platforms, respectively. Global proteomics analysis was undertaken utilising a Q-Exactive mass spectrometer.



Results

- Calves offered a higher plane of nutrition were heavier at slaughter (112 v 88 kg, $P < 0.001$), reflective of their higher ADG (0.88 v 0.58 kg, $P < 0.001$). Similarly, H also had heavier testes (29.2 v 20.1 g, $P < 0.05$) compared to M calves.

Results contd.

- Metabolites and metabolic hormones including BHB, glucose, IGF-1 and insulin, in general, reflected the improved metabolic status of the calves on H compared with M.
- There was no effect of diet on serum concentrations of either anti-Mullerian hormone or testosterone, indicative of testicular maturity.
- Of the 14,344 genes expressed in the testes, 37 were identified as differentially expressed (DE) between H and M groups ($P_{adj} < 0.1$; fold change > 1.5). Additionally 7 miRNA were DE along with 191 differentially abundant proteins ($P < 0.05$, fold change > 1.5).
- Biochemical pathway analysis DE mRNA genes identified a biochemical network (Figure 1) involved in lipid metabolism based on the DE genes. Additionally *CLDN11* gene which is involved in Sertoli cell development and ultimately sexual maturation was also up-regulated in the H compared to the M calves.

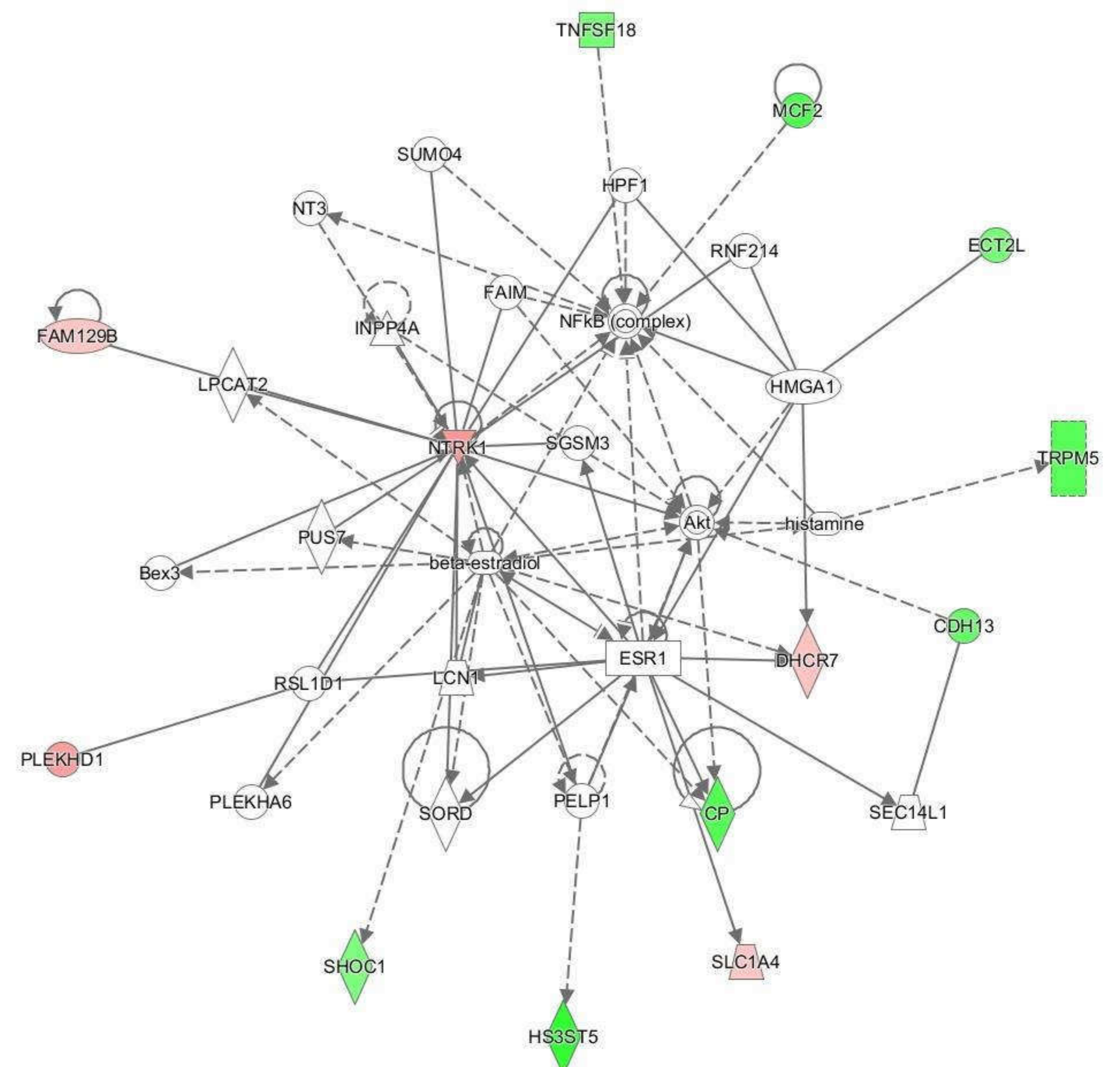


Figure 1. Lipid metabolism network in testicular tissue of calves on high versus moderate plane of nutrition. Node colour intensity indicates expression of genes, red representing up-regulation, green representing down-regulation in high versus moderate planes of nutrition

- The lipid metabolism network in Figure 1 also highlights the DE of *FAM129B* which has previously been identified as DE in testes tissue of bull calves following altered plane of nutrition for the first 18 weeks of life (English et al., 2018).
- bta-miR-2419-5p miRNA was up-regulated in H versus M, with transcription of its target gene, *CDH13*, down-regulated in H calves, suggesting transcriptional repression by this miRNA as a consequence of prevailing dietary intake.

Conclusions

- Data indicate that enhanced early life nutrition advances the molecular development of testicular tissue in the bull calf
- The results of this study, together with complementary analyses of other key HPT tissues, will be utilised in the development of nutritional and genomic based strategies to consistently advance

Acknowledgements

- This work was funded by Science Foundation Ireland. 16/IA/4474



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¹Teagasc, Moorepark, Fermoy, Co. Cork,

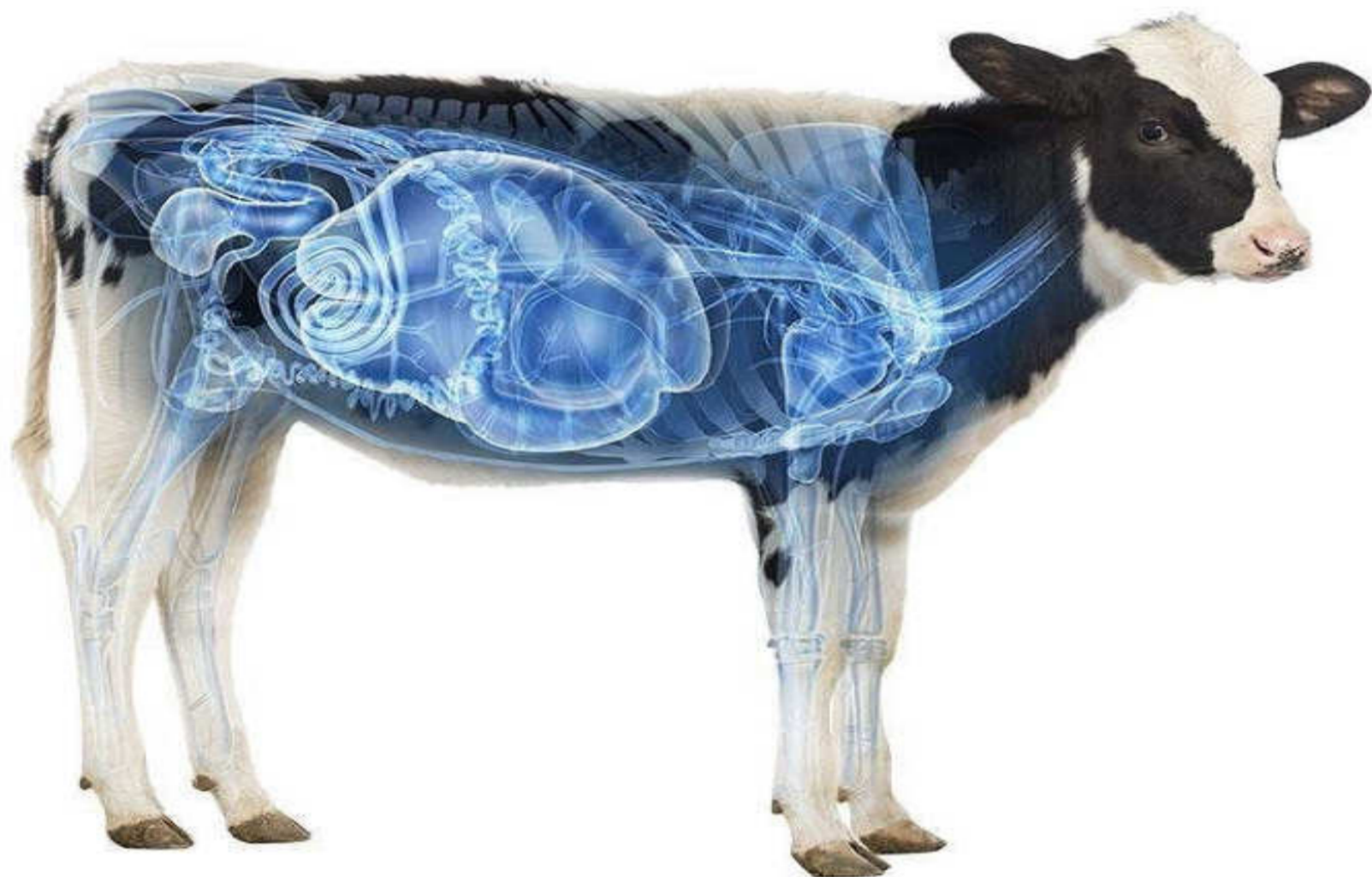
²Cork Institute of Technology, Bishopstown, Co. Cork

³Irish Cattle Breeding Federation, Bandon, Co. Cork

thomas.condon@teagasc.ie

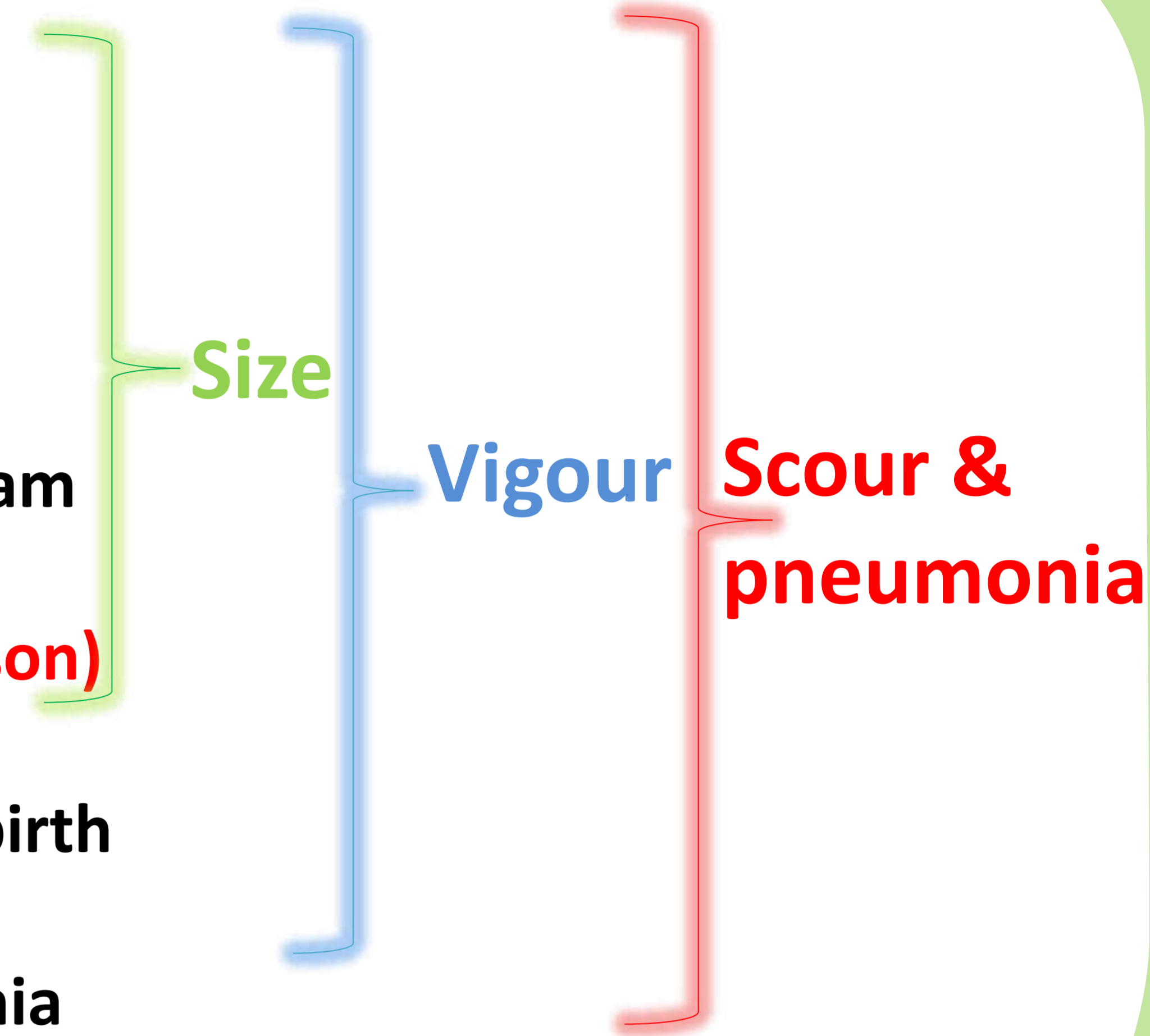
Aim

Quantify the risk factors associated with calf **size**, **vigour**, **scour** and **pneumonia** and determine the genetic parameters



Risk factors

- Sex
- Singleton/twin
- Age at calving
- Dam parity
- Heterosis of calf and dam
- Recombination loss of calf and dam
- Breed
- **Contemporary group (hd/yr/season)**
- Timing of calving period
- % calved within 7 day's of calf's birth
- Herd size
- Age at scoring of scour/pneumonia



Materials & Methods

➤ 2015 to 2018

- 10,927 herds

➤ 236,696 calves

- 173,346 scour
- 172,383 pneumonia
- 44,784 vigour
- 45,957 size

➤ Analysis

- Linear mixed models

Take home message

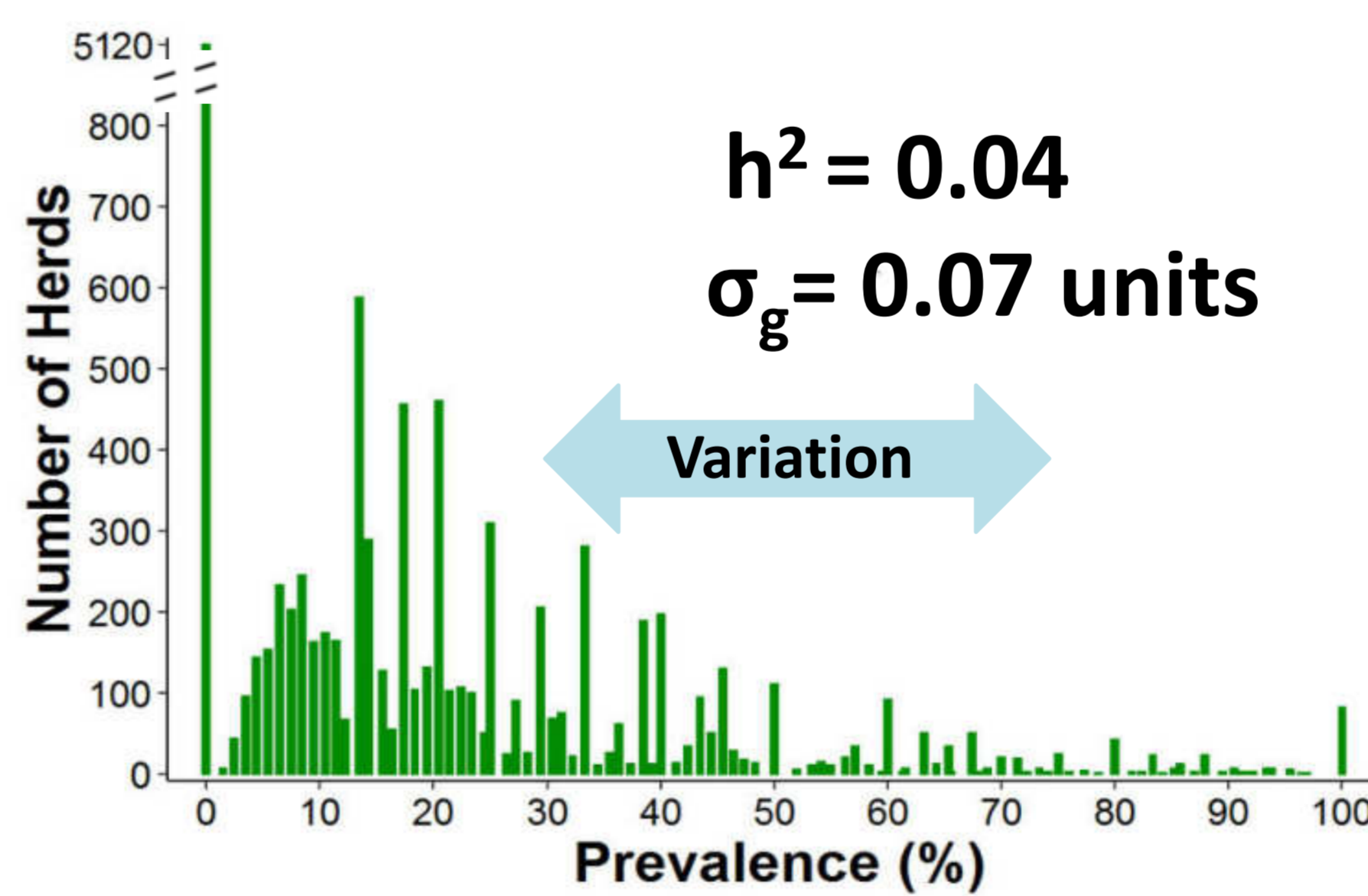
Potential exists to change, through breeding, calf **size**, **vigour**, **scour** and **pneumonia**

Fixed effect – black
Random effect - red

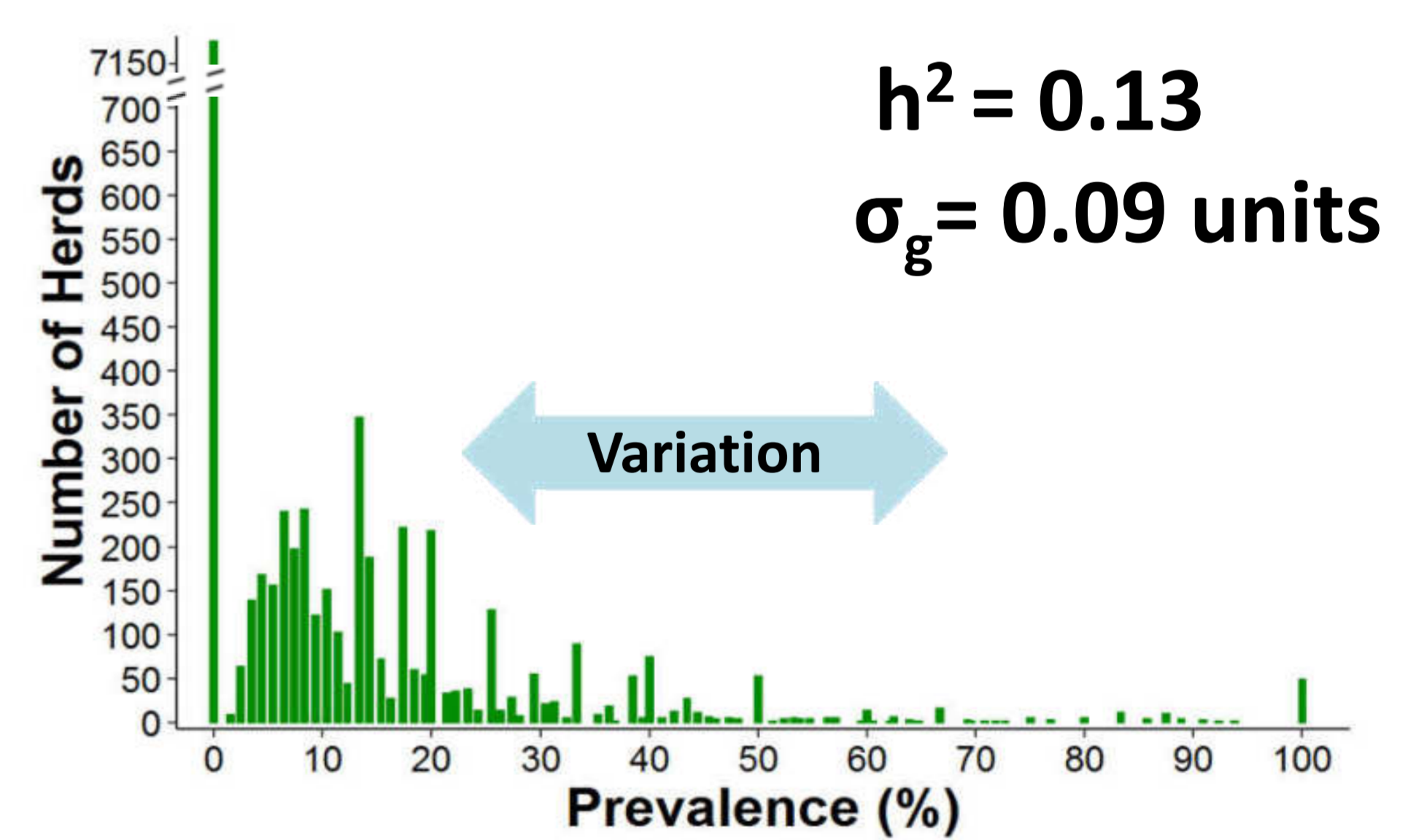
Heritability (h^2) is the amount of phenotypic variation that is attributable to individual genetic differences
Genetic standard deviation (σ_g) is a measure of the extent of variability that exists within a trait

Results

Scour



Pneumonia



Could I have been born bigger and stronger Mam?



Yes, the heritability of **vigour** and **size** is **0.26** and **0.49** with a genetic standard deviation of **0.38** and **0.46** units

