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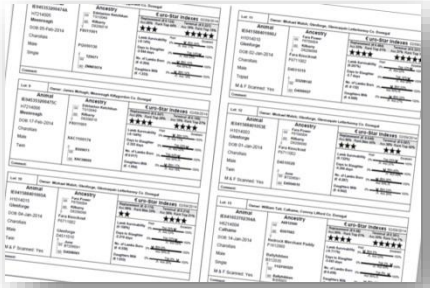
Lots of small changes make a BIG DIFFERENCE

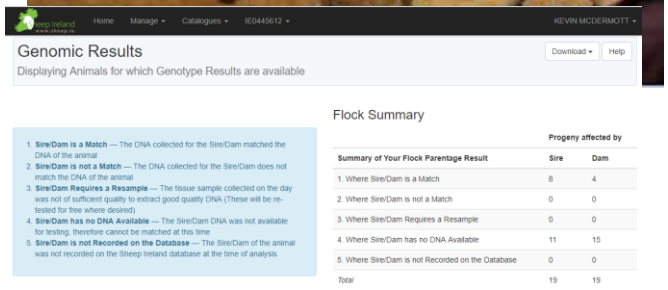


Sheep Ireland Industry Meeting
18/04/2018

Why do we need €uroStars?

To make the most informed breeding decisions possible in order to have a more profitable & sustainable industry and farms

Since the last Meeting



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Genomic Results

Displaying Animals for which Genotype Results are available

Download | Help

1. **Sire/Dam is a Match** — The DNA collected for the Sire/Dam matched the DNA of the animal
2. **Sire/Dam is not a Match** — The DNA collected for the Sire/Dam does not match the DNA of the animal
3. **Sire/Dam Requires a Resample** — The tissue sample collected on the day was not of sufficient quality to extract good quality DNA (These will be re-tested for free where desired)
4. **Sire/Dam has no DNA Available** — The Sire/Dam DNA was not available for testing, therefore cannot be matched at this time
5. **Sire/Dam is not Recorded on the Database** — The Sire/Dam of the animal was not recorded on the Sheep Ireland database at the time of analysis

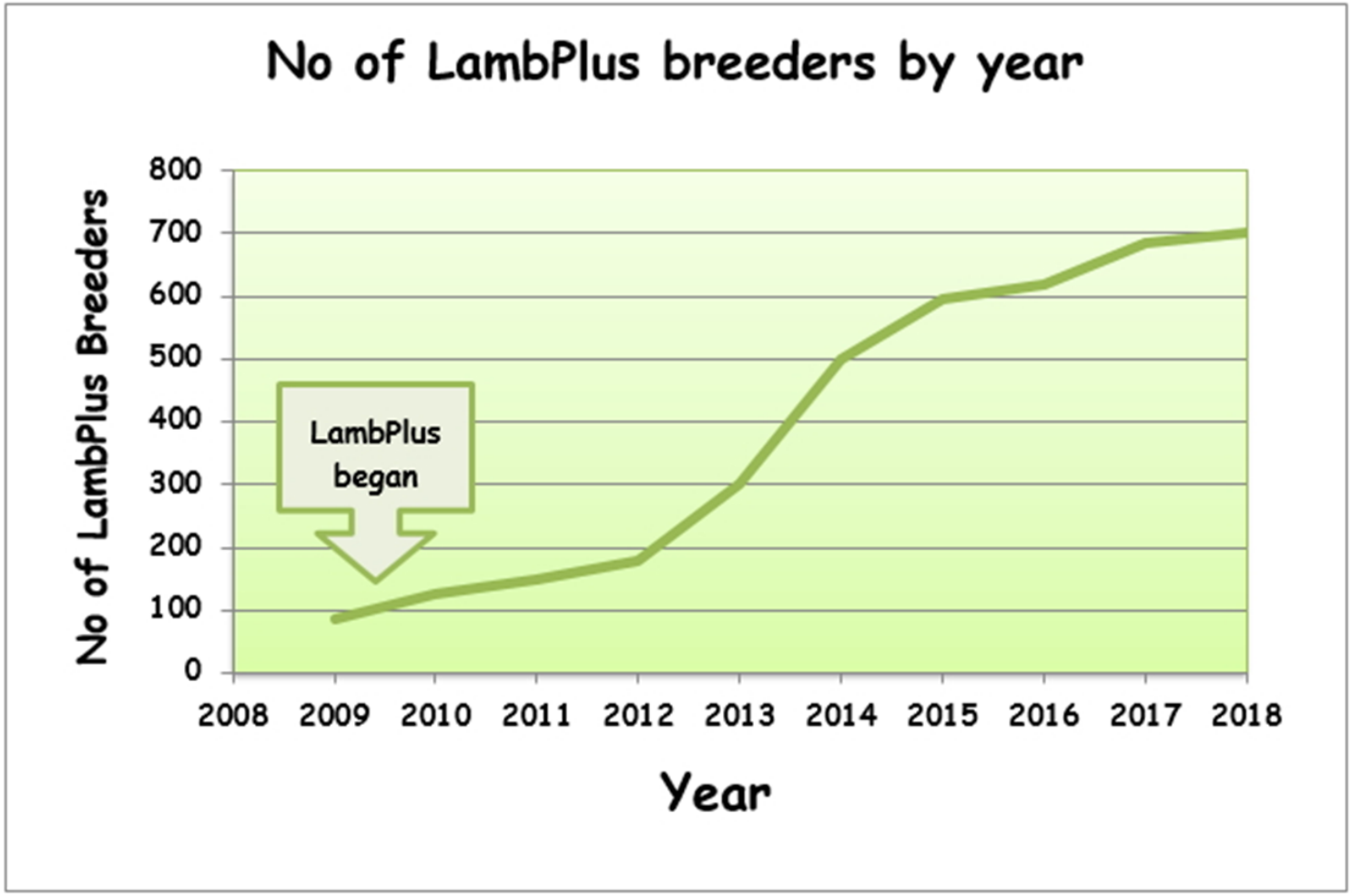
Flock Summary

Summary of Your Flock Parentage Result	Progeny affected by Sire	Progeny affected by Dam
1. Where Sire/Dam is a Match	8	4
2. Where Sire/Dam is not a Match	0	0
3. Where Sire/Dam Requires a Resample	0	0
4. Where Sire/Dam has no DNA Available	11	15
5. Where Sire/Dam is not Recorded on the Database	0	0
Total	19	19

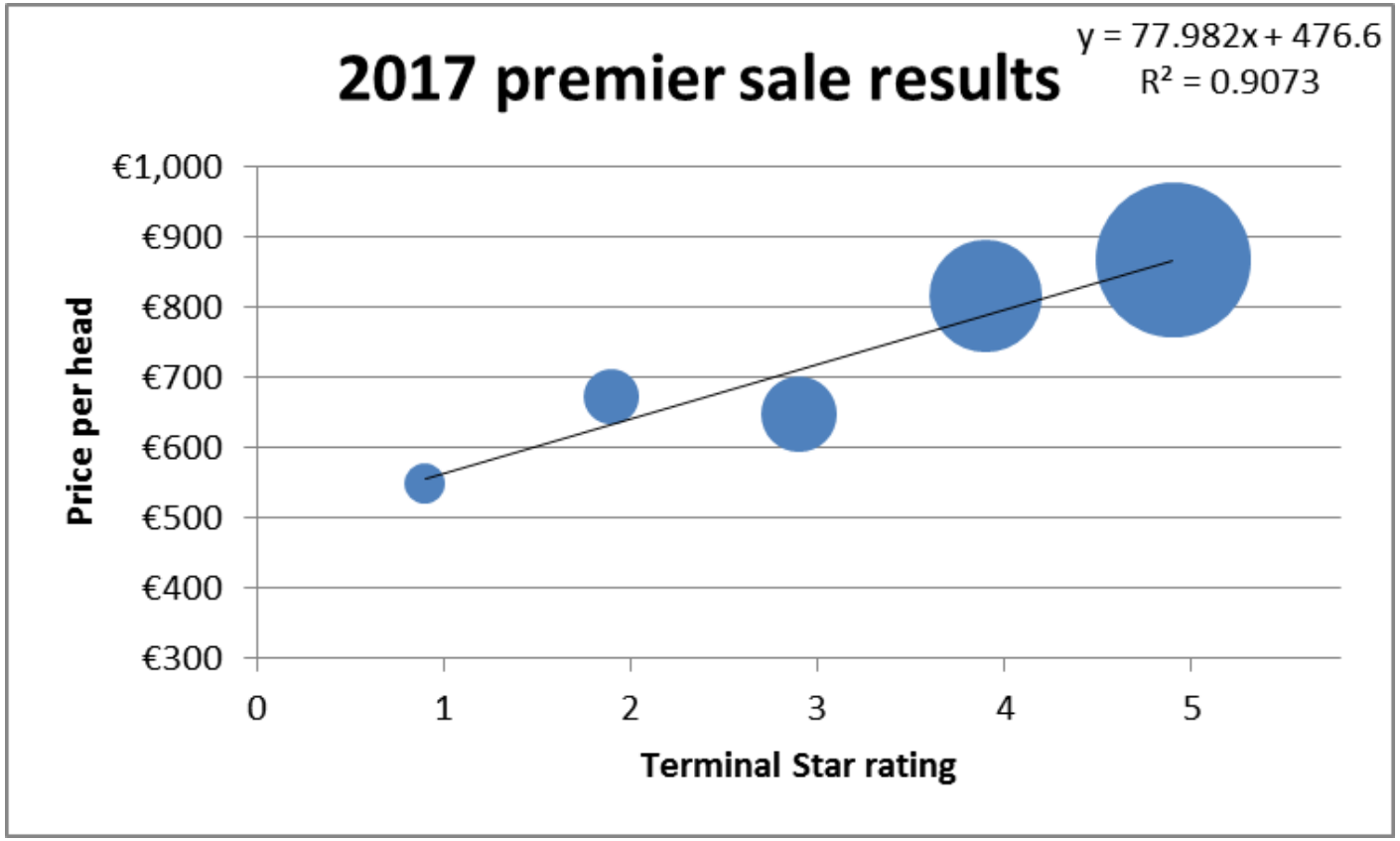
In progress

Across-breed Eval

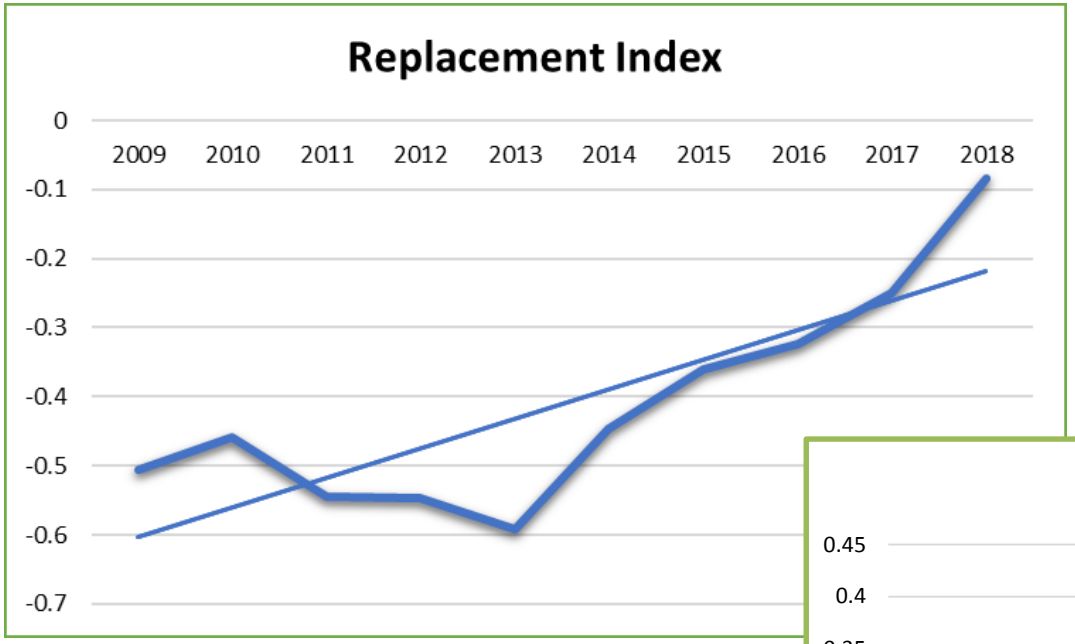
LambPlus membership

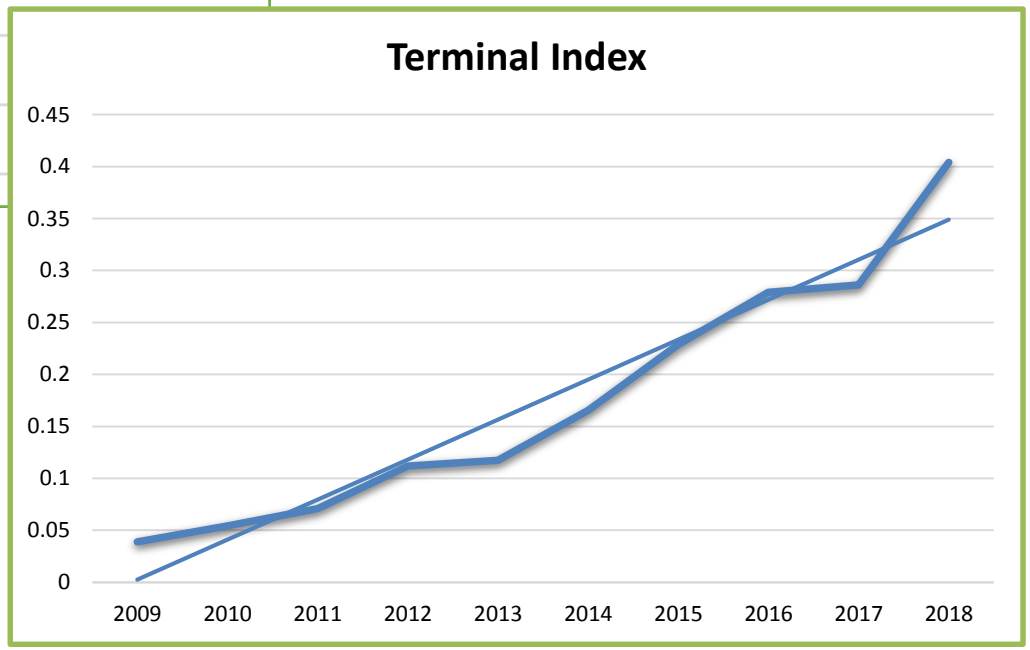


2017 Premier Sale results



Genetic Gain





Research Projects

- **OviGen** - Genomics
- **OviData** – Using DNA to assign parentage
- **SusShep** – Ewe Longevity, Labour & Cervical AI

Calculating economic values using a whole farm bio-economic model

A. Bohan [1, 2], L. Shalloo[1], P. Creighton[3], D.P. Berry[1], T. M. Boland[2], A.C. O'Brien[1], T. Pabiou[4], E. Wall[4], K. McDermott[4] and N. McHugh[1]

[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland.*
[2]*School of Agriculture & Food Science, University College Dublin, Belfield, Dublin 4, Ireland.*
[3]*Animal & Grassland Research and Innovation Centre, Teagasc, Athenry, Co. Galway, Ireland.*
[4]*Sheep Ireland, Highfield House, Shinagh, Bandon P72 X050, Co. Cork, Ireland*

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Agriculture and Food Development Authority

The Irish Agriculture and Food Development Authority

Breeding objectives

Economic Value

€

Genetic Component

Breeding Values

Terminal Index

Replacement Index

Bio-economic model

Flock net energy

Grass, Silage
& Concentrate

Land
Animals
Production
Mortalities
Variable costs
Fixed costs
Labour

1.Financial
2.Economic
3.Physical

EV calculation: Mastitis

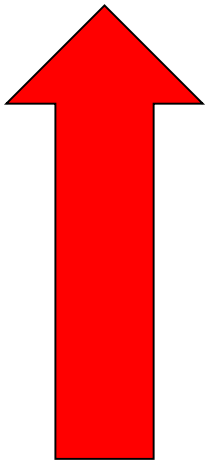
- Clinical mastitis increased from 5% to 20%

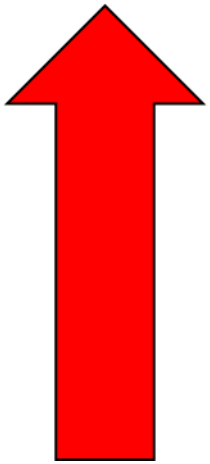
- Increased vet costs
- Increased labour costs
- Reduced lamb sales

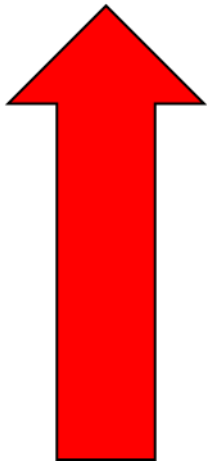
- Does not accounted for:
  - Ewe mortality
  - Ewe culling
  - Lamb performance

EV Calculation: Days to slaughter

- Growth rate reduced by 5% (221 to 210g/day)
- Increased days to slaughter (+29 days)







Maternal traits

Trait Group	Trait	Unit	Economic value
Maternal	Number of lambs born	Lamb	€39.76
	Ewe mature weight	Kg	-€1.40

Lambing traits

Trait Group	Trait	Unit	Economic value
Lambing	Lambing difficulty single	%	-€0.27
	Lambing difficulty single (mat)	%	-€0.30
	Lambing difficulty multiple	%	-€0.25
	Lambing difficulty multiple (mat)	%	-€0.27
	Lamb survival	Lamb	€54.84

Production traits

Trait Group	Trait	Unit	Economic value
Production	Days to slaughter	Day	-€0.25
	Carcase conformation	Grade	€3.70
	Carcase fat	Score	-€0.84

Health traits

Trait Group	Trait	Unit	Economic value
Health	Lameness ewe	%	-€0.24
	Lameness lamb	%	-€0.08
	Mastitis	%	-€0.25
	Dag Score	Score	-€0.34
	Faecal egg count	%	-€0.08

Indexes

Replacement

12 traits

Number of lambs born
Ewe mature weight

Lambing difficulty
Lamb survival

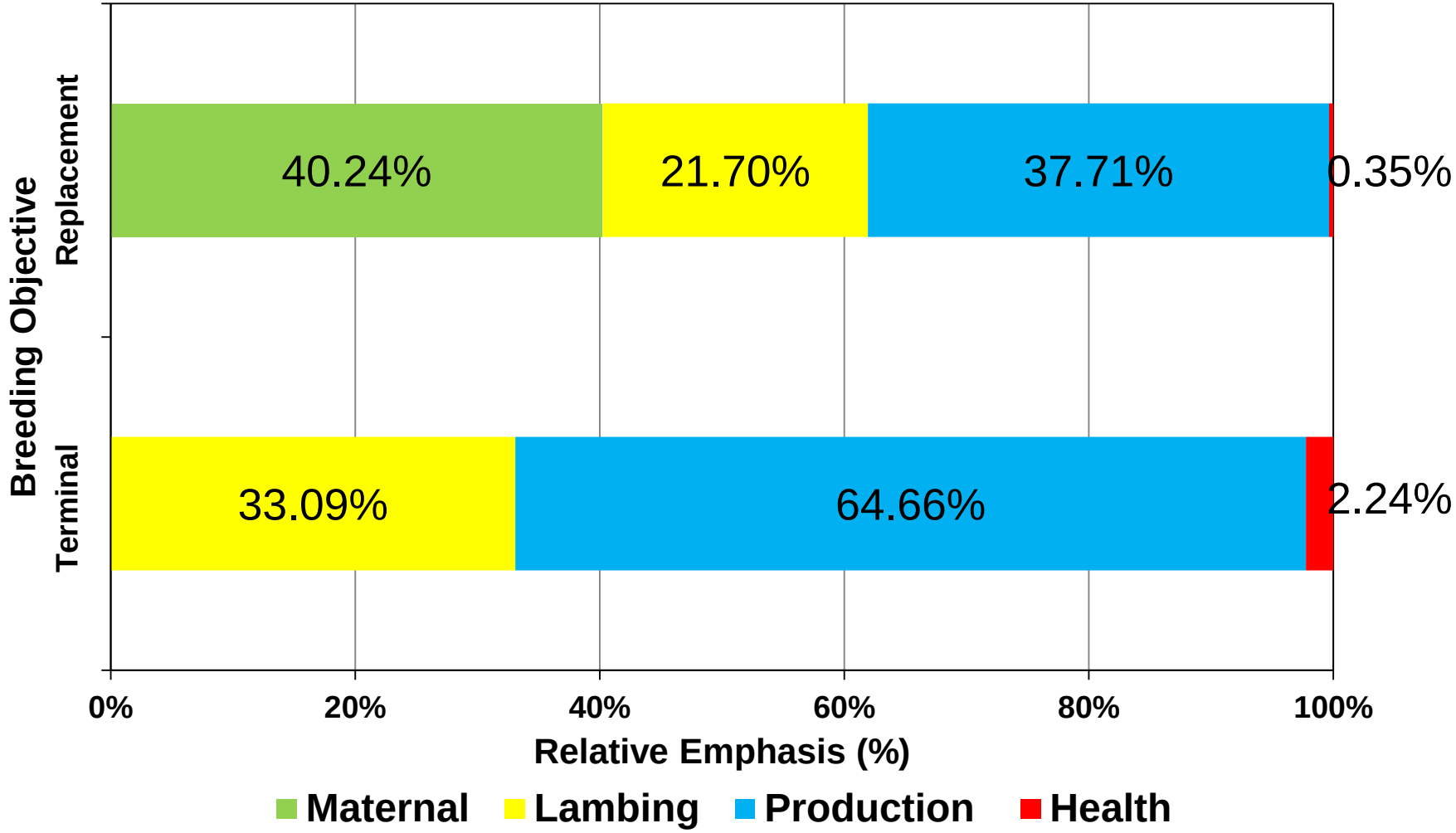
Days to slaughter
Carcass conformation
Carcass fat

Ewe lameness
Lamb lameness
Mastitis
Dag score
Faecal egg count

Terminal

8 traits

Relative emphasis



Conclusions

- Improved calculation using a whole farm model
- Updated and improved economic values
- Rapid response to industry change

Thank you

Questions ???

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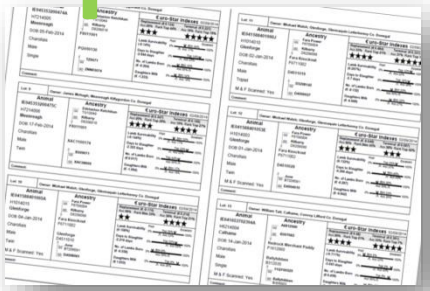
Genetic Evaluation Model Updates



Thierry Pabiou

+ SheepIreland, & Teagasc teams

Agenda

- What's new for 2018
  - New genetic parameters for lambing
  - New economic values
- Impact on breeding values and accuracies
  - Using 1,412 rams with progenies in 2017

What's new for 2018

- New Lambing Module
  - Applying Noirin's research
- New Economic Values
  - Applying Alan's research

Lambing module update

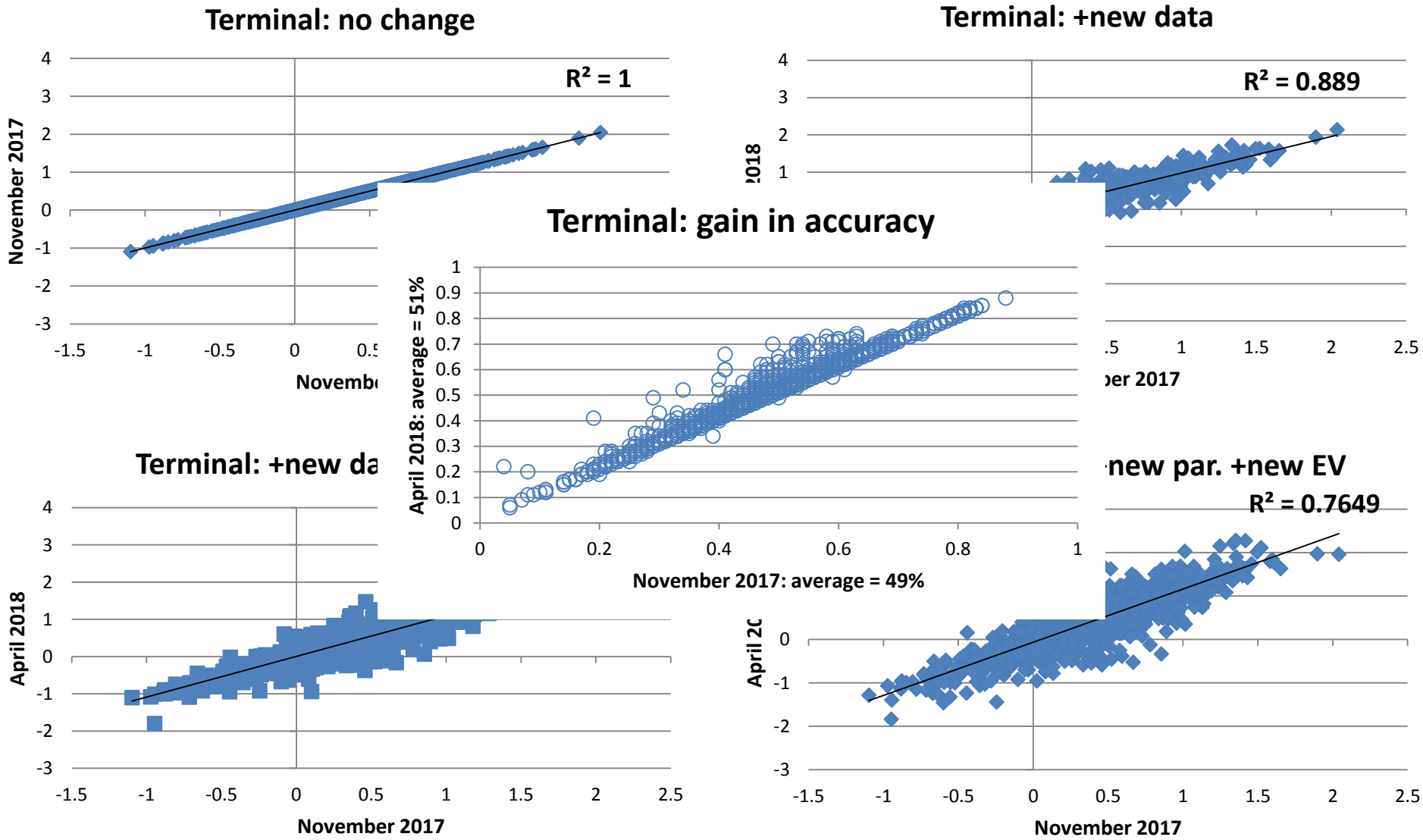
- Because last update was done in 2009
- More accurate data since from pedigree and commercial flocks
  - ➢ New genetic parameters

Heritability for lambing traits								
	Ram traits (direct effect)				Ewe traits (maternal effect)			
	Birth weight	Lamb survival	Lambing ease single	Lambing ease multiple	Birth weight	Lamb survival	Lambing ease single	Lambing ease multiple
'Old'	15.0%	2.0%	5.0%	5.0%	20.0%	2.0%	1.0%	1.0%
New 2018	24.6%	2.7%	6.4%	7.0%	23.4%	2.3%	3.2%	3.1%

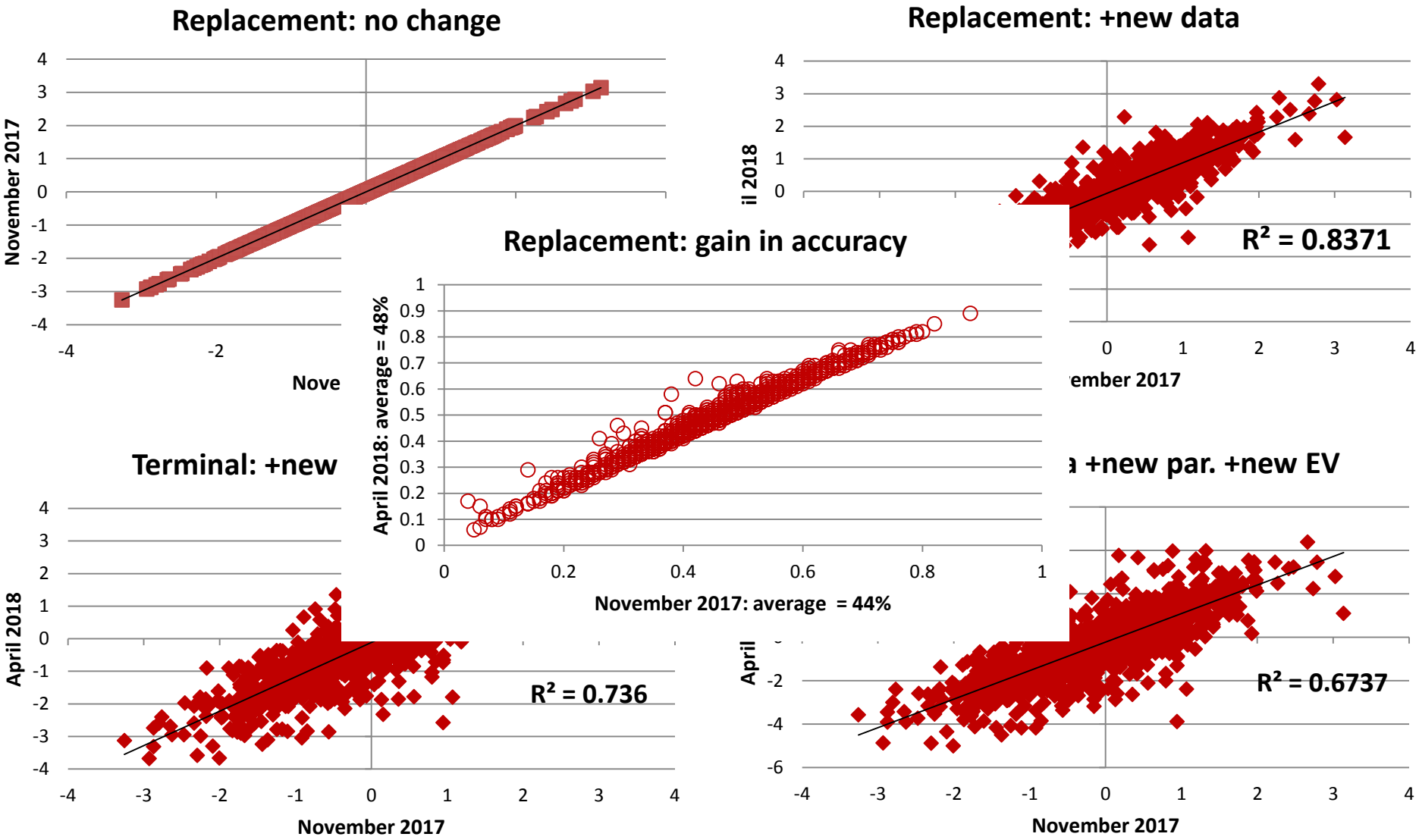
= More accurate breeding values

Economic value update

Terminal index in April 2018



Replacement Index in April 2018



Relation Terminal index with phenotypes

- Rams with progenies in 2017

For increase of 1€ in Terminal index					
	Texel	Suffolk	Charollais	Belclare	Vendeen
Number of rams	404	230	298	97	62
%dead lambs	-2.1%	-4.1%	-2.2%	-3.8%	-4.4%
%lambing diff. single	-5.1%	-5.9%	0.2%	-0.2%	-0.3%
%lambing diff. multiple	-5.9%	-12.0%	-5.4%	-5.0%	-4.1%

- Better accuracy in 2018 compare to previous model: gain average -0.2%

Summary

- 2 major novelties
  - Revamping of lambing module
  - New economic values

- 2 major impacts
  - Better selection
  - Increase in accuracy

International Genetic Evaluations

Shauna Fitzmaurice

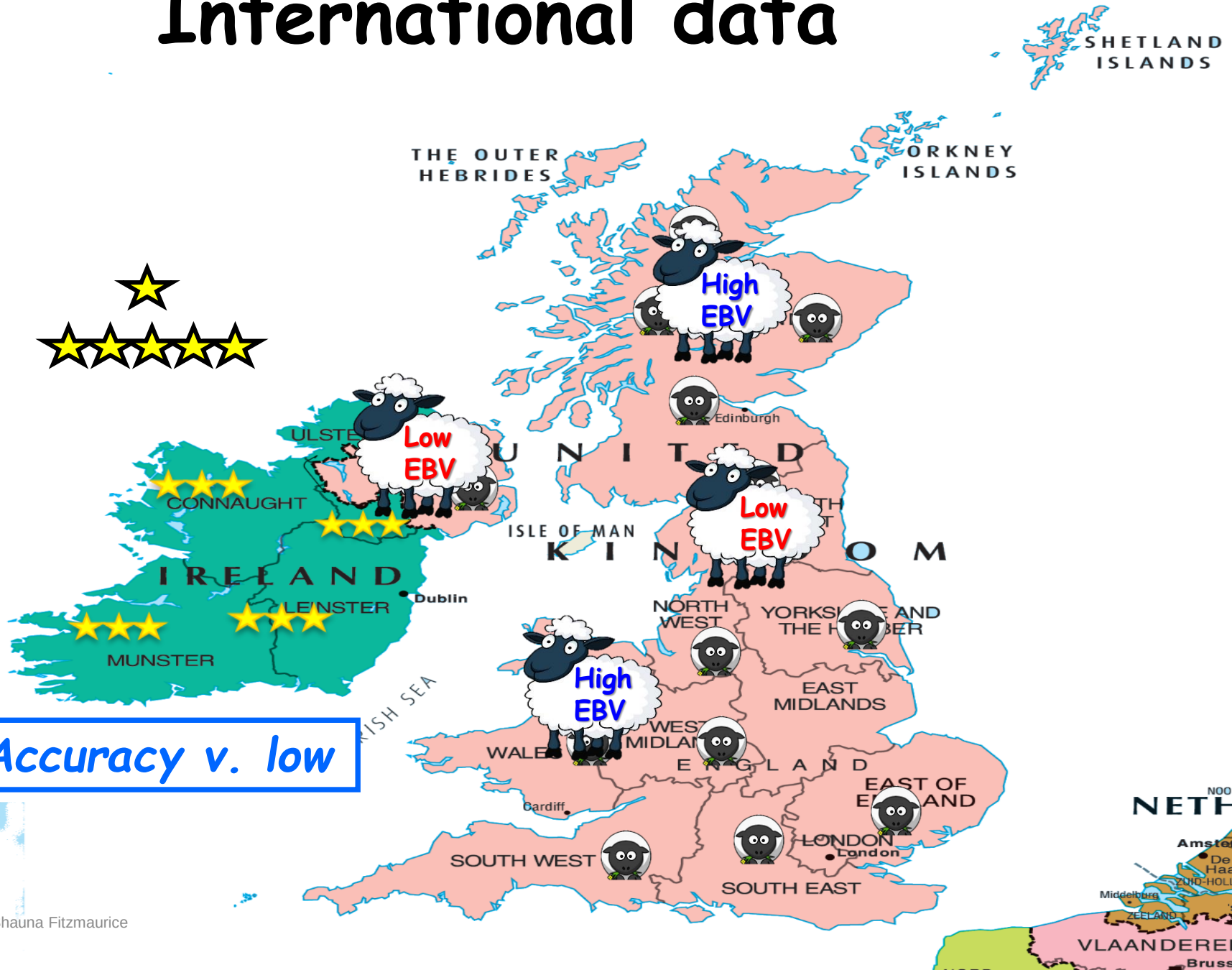
SRUC

Teagasc
Agriculture and Food Development Authority

The University of Edinburgh

Success in Beef & Dairy

International data



Accuracy v. low

International data

Steps:

1. Identify UK animals in national database
2. Research phase
3. Implementation ??

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AHDB
BEEF & LAMB

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Texel Data

8,392 common animals between Ireland and the UK

Males

2,594 with progeny in Ireland

1,188 with progeny in both countries

Animals must have breeding values in both countries

Females

5,798 with progeny in Ireland

2,323 with progeny in both countries

Shauna Fitzmaurice

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Suffolk Data

3,313 common animals between Ireland and the UK

Males

1,040 have progeny in Ireland

Females

2,273 have progeny in Ireland

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Charollais Data

1,727 common animals between Ireland and the UK

Males

604 have progeny in Ireland

Females

1,123 have progeny in Ireland

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Next Steps

- Compare Irish and UK breeding values for common animals
- Compare phenotypic data between the 2 countries

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Measuring ewe efficiency

Nóirín McHugh

Teagasc
Agriculture and Food Development Authority

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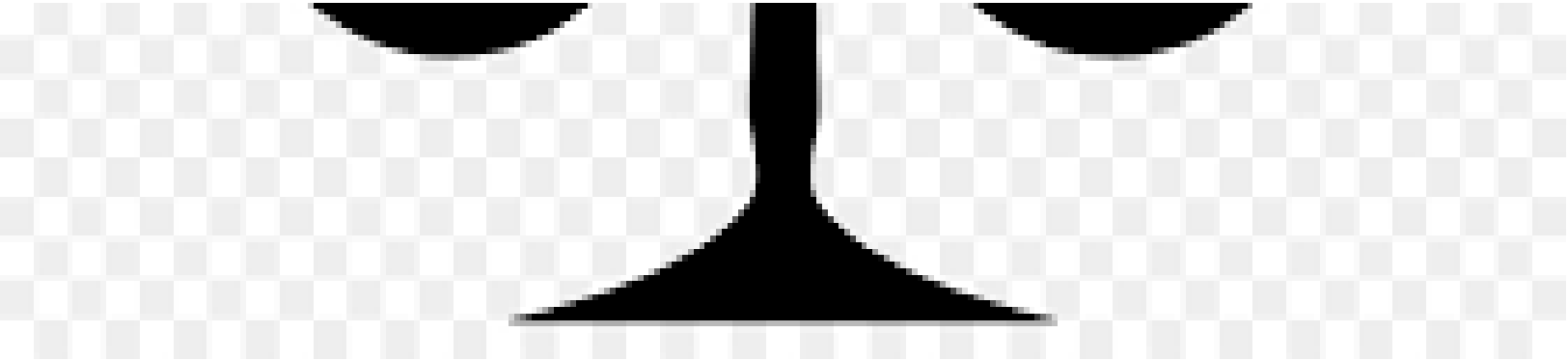
How to measure ewe efficiency

- Whats the variation between ewes of the same weight??
- New concept → deviation in animal performance from a population



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Data

Live weight records

Ewe weights

Lamb weights

Investigate the variation- combined litter weight relative to ewe weight at same time

Set relative to population

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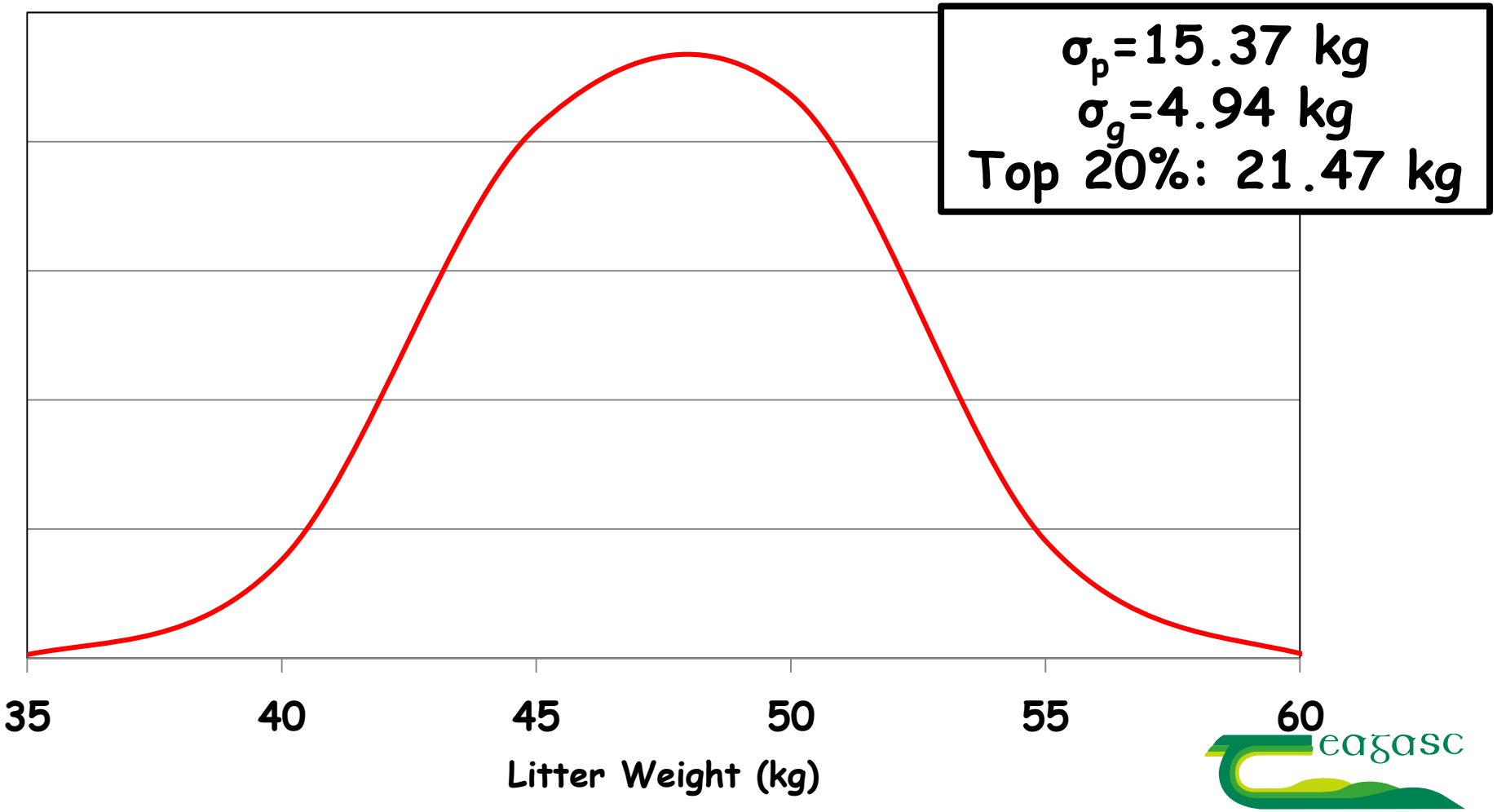
Ewe Efficiency

Combined litter weight relative to ewe weight at same time



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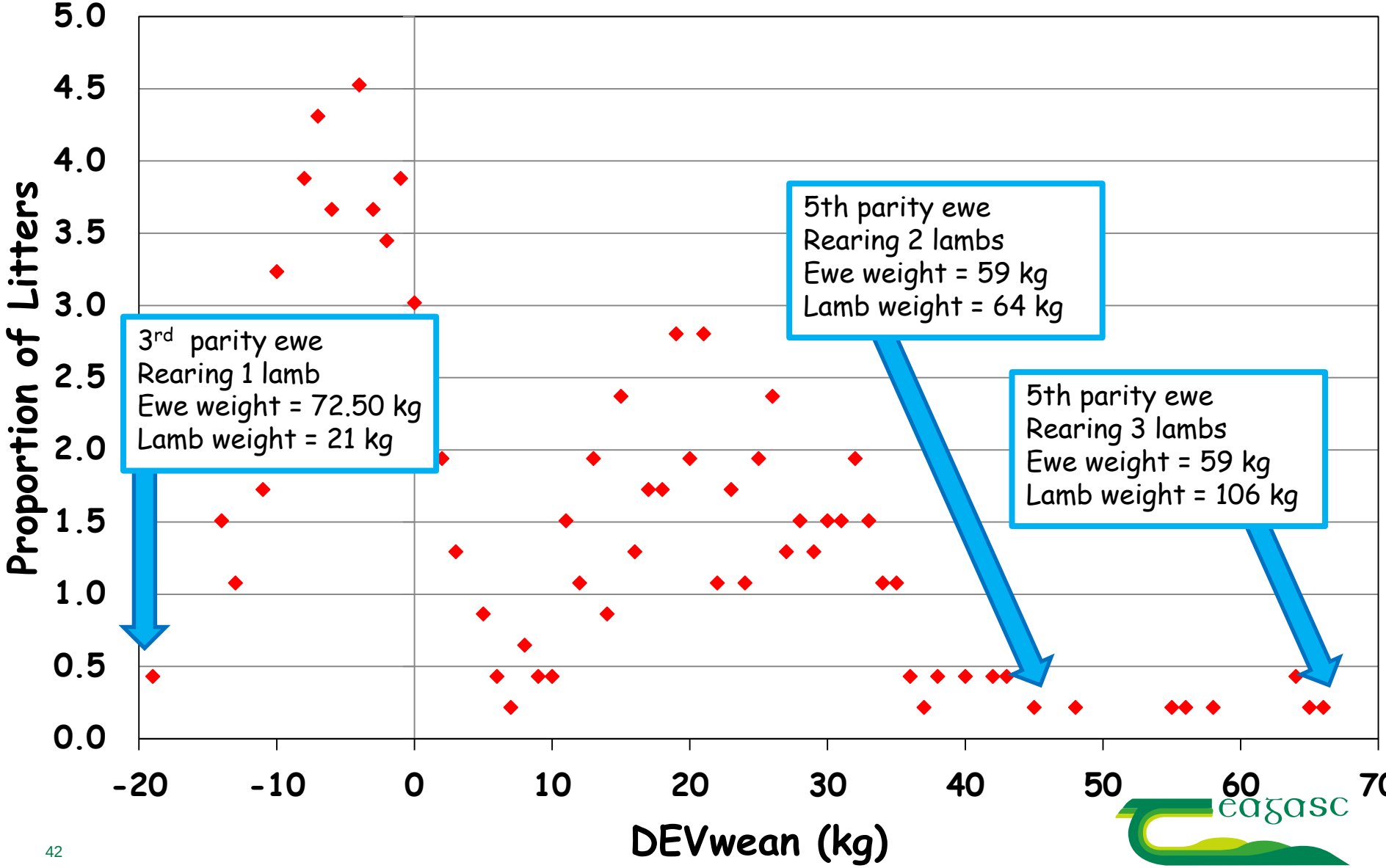
Benchmarking – Flock A



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Conclusion

- New ewe efficiency trait
- Information required to derive these phenotypes is routinely available
  1. Exploitation through breeding programs
  2. Routine benchmarking within and between flocks

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Genomics

Áine O' Brien

Sheep Ireland Industry meeting

Athenry, April 2017

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DNA - From the tip of your nose to the tops of your toes!!

DNA is the same in every cell of your body and doesn't change throughout your life

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What is a SNP?

- 99.9% of our DNA is identical – most of the differences are in the form of SNPs

...ACGTACGTCAATGACTTTTACGTAT...

...ACGTACGACAATGACTTTTACGTAT...

- Single Nucleotide Polymorphism

Change

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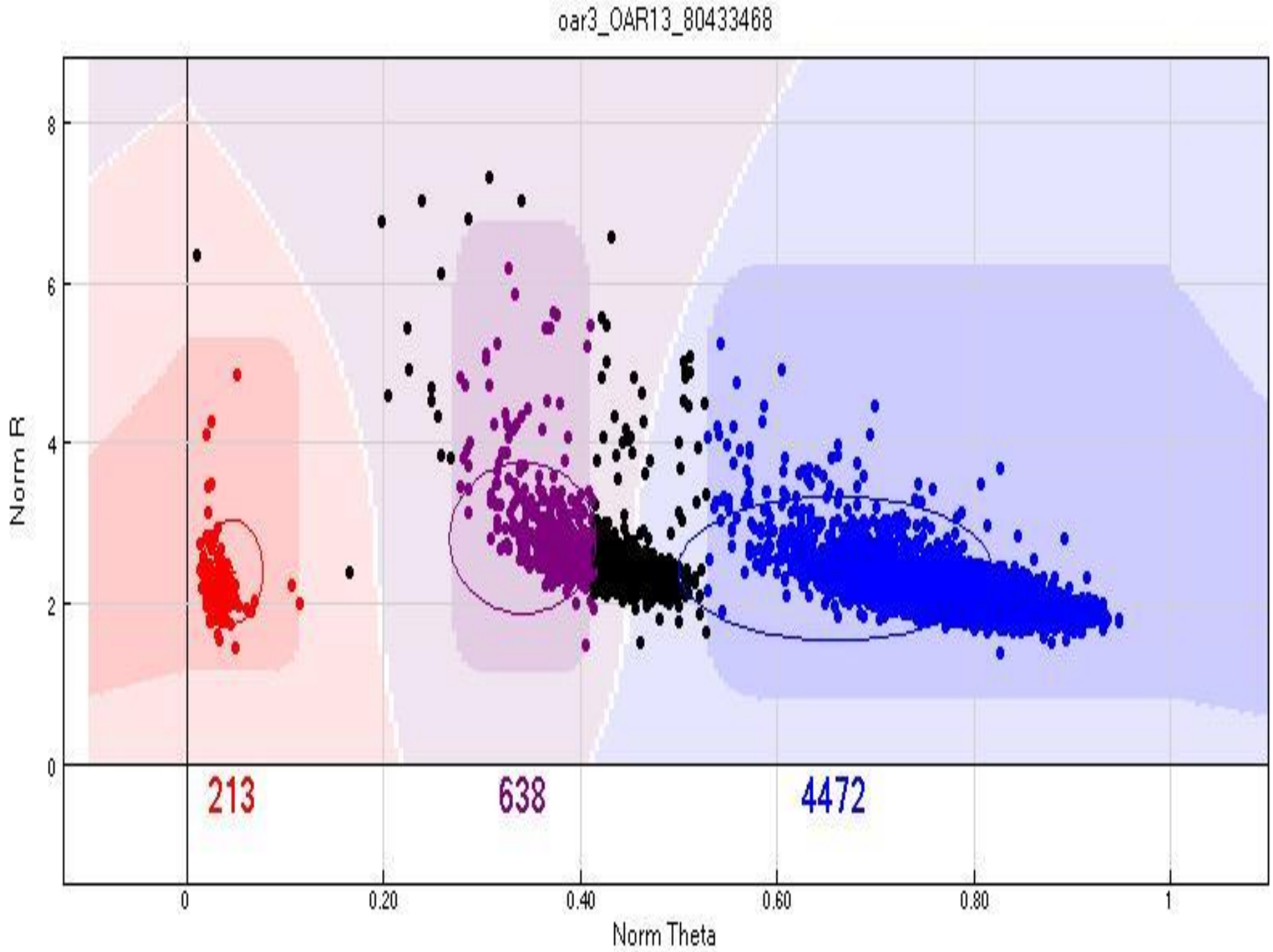
oar3_OAR13_80433468
Norm R
Norm Theta
0
2
4
6
8
0
0.20
0.40
0.60
0.80
1
213
638
4472

Genotyping panels

Year	Panel density (no. of SNPs)	Cost (€)	Cost per SNP (€)
2015	606,000	Research only	Research only
2015	50,000	62.50	0.00125
2016	15,000	28.50	0.00190
2017	11,000	25.00	0.00227
2018	50,000	22.00	0.00044

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Genotyping by breed and panel

	SNP panel			
	50K	LD	HD	Total
Belclare	884	595	20	1499
Charollais	1049	2355	23	3427
Suffolk	1047	1293	14	2354
Texel	1353	3138	27	4518
Vendeen	699	129	9	837
Other - pedigree	379	249	189	817
Other - crossbred	1989	3490	14	5493
Total	7400	11249	296	18945

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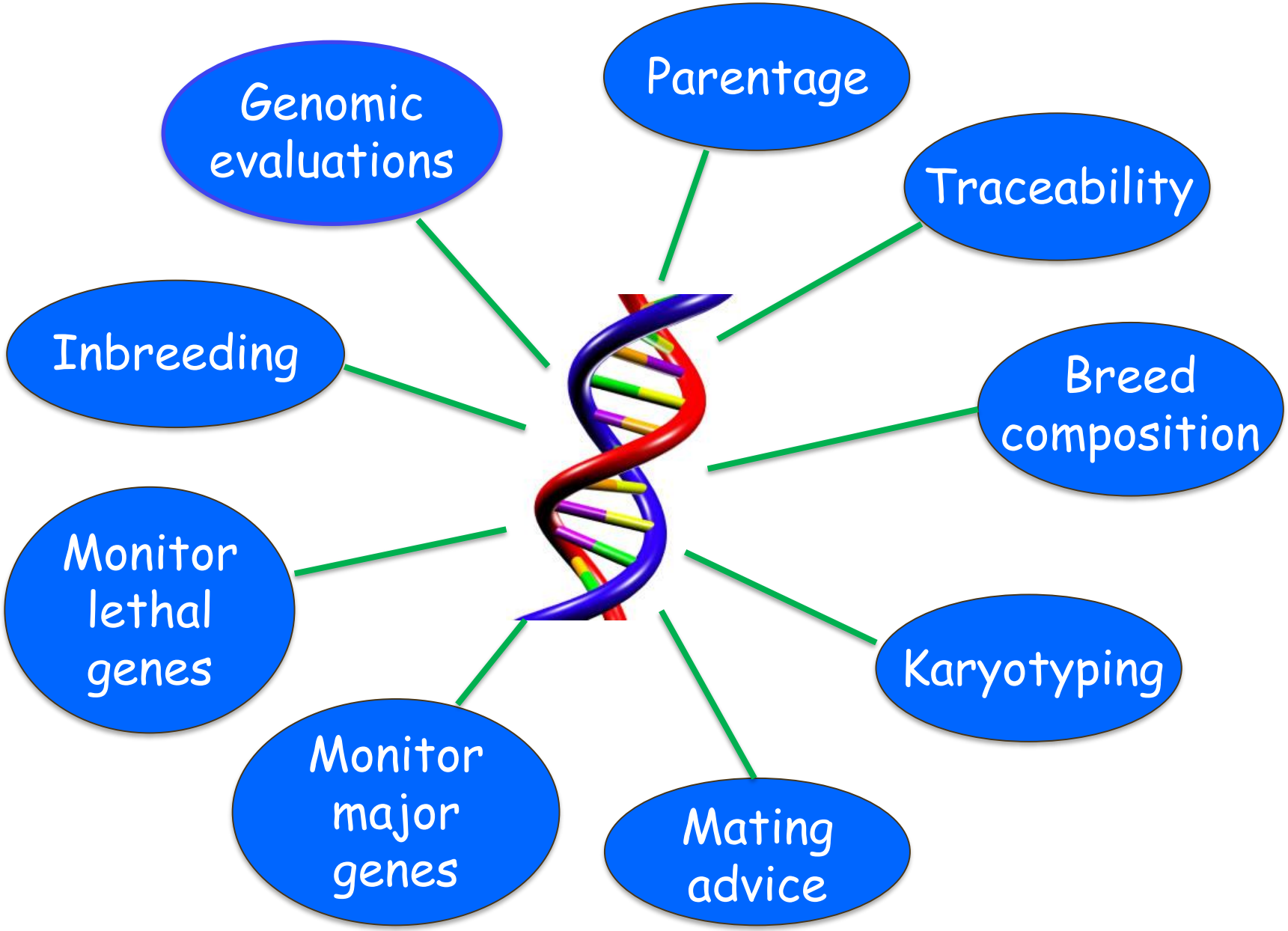

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Parentage & Impact on Genetic Evaluations

Nóirín McHugh

Teagasc
Agriculture and Food Development Authority

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Determining Parentage

Sire

Dam

Parents must also be genotyped

Animal genotyped

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Parentage

2% failed genotyping

17,991 animals genotyped

5,066

mals had a
typed

699 sires we
13.80

103 anim s had n paren wrong
(3.64%)
367 animals had either parent wrong
(12.98%)

re incorrect
8.68%

Total parentage errors (~20%)

What's the impact of these errors??

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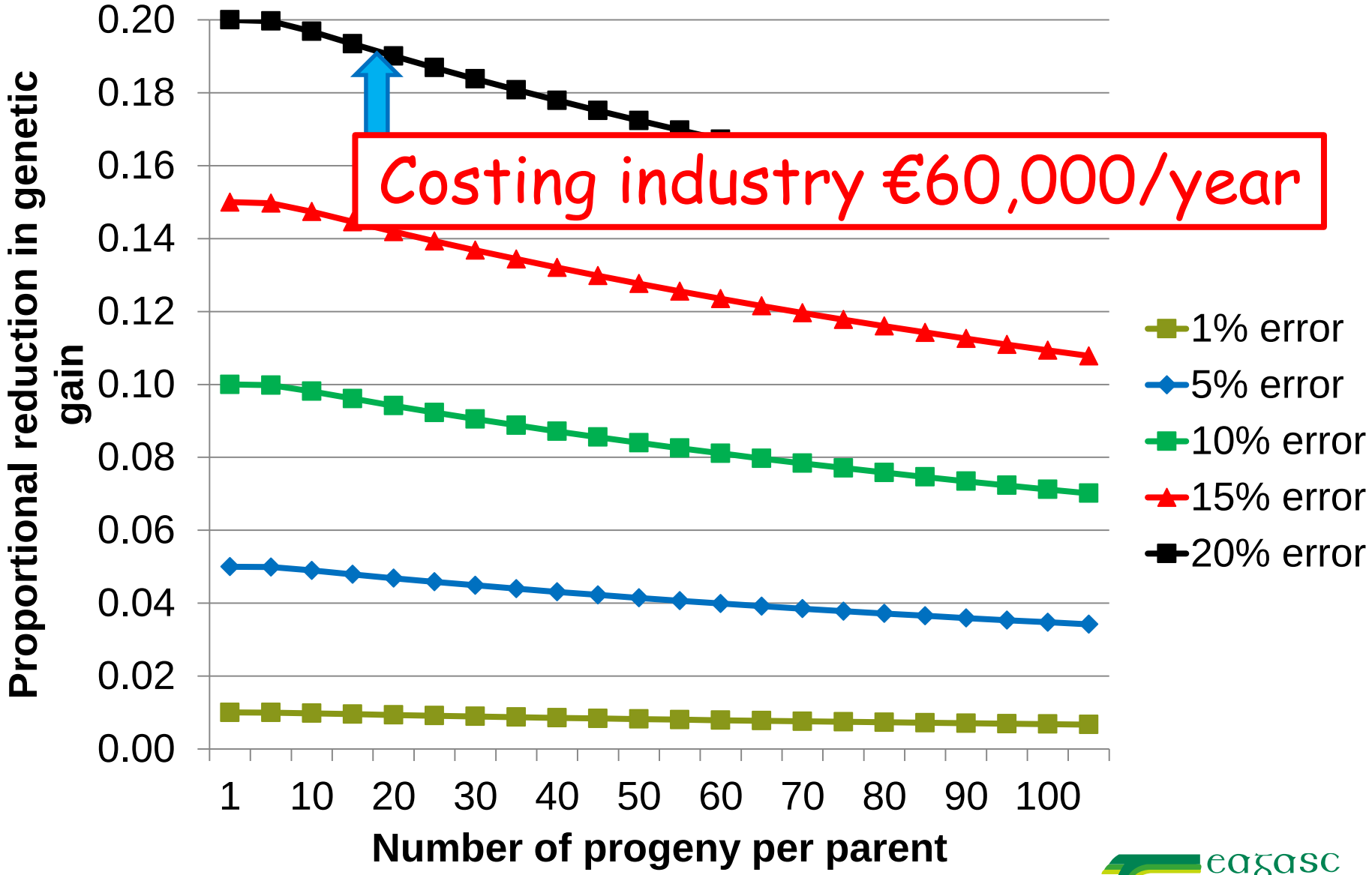
Impact of parentage errors - theoretical



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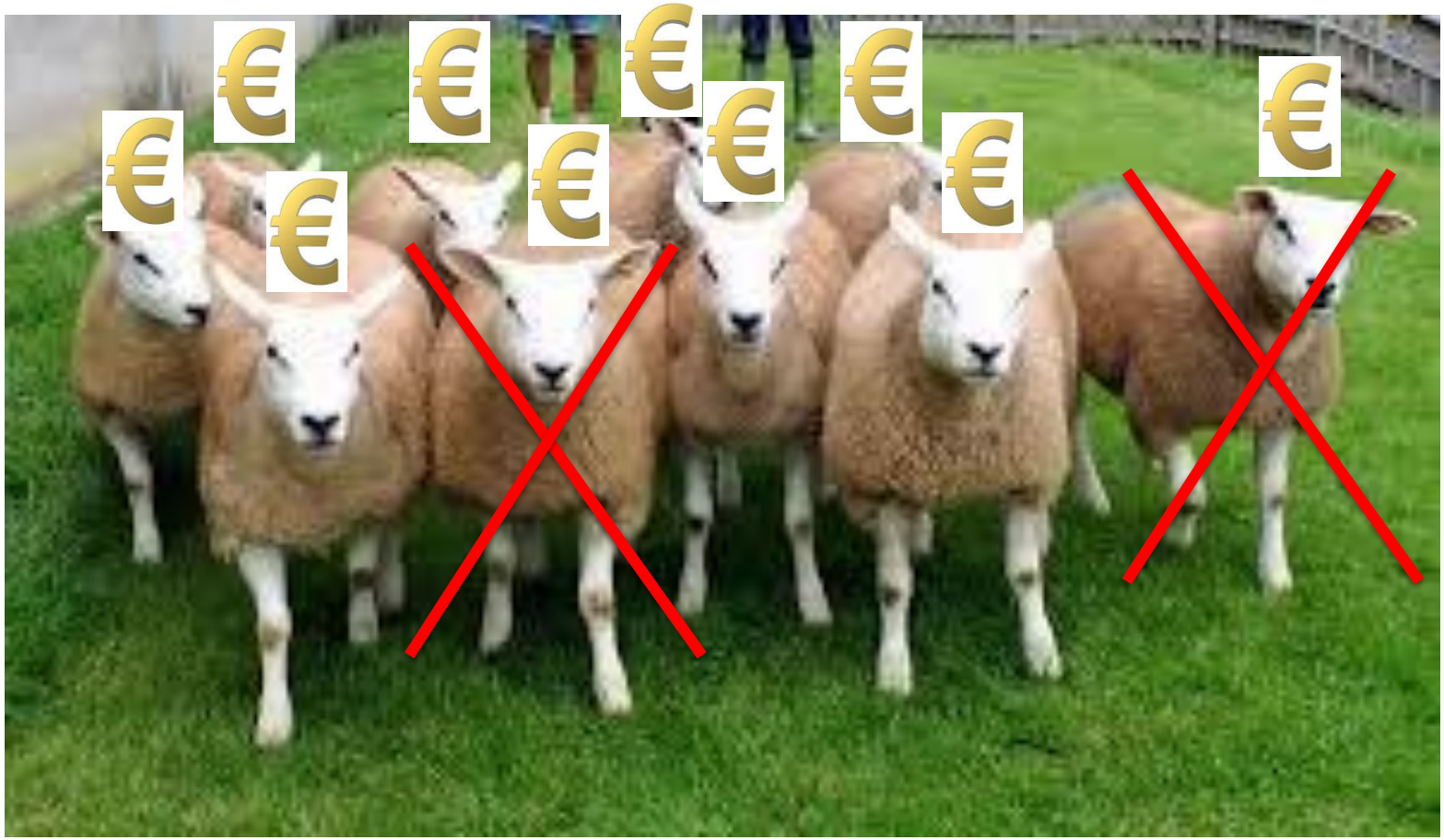
Impact of parentage errors – reality



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Impact of parentage errors – reality

- Individual animal
  - -€0.13 (range -€1.37 to €0.69)
- Sire
  - <5 progeny -€0.08
  - Sire 6 to 30 progeny -€0.04
  - Sire >30 progeny -€0.02
- Dam
  - -€0.05
- Flock mates
  - -€0.17

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Conclusion

- Genomics:
  - new accurate tool for parentage prediction
  - Impact of parentage errors
    - Individual animal, back pedigree and flock
- Future priorities:
  1. Routine parentage reports through LambPlus screens
  2. Parentage assignment from bank of available genotypes

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Scrapie

Donagh Berry

Teagasc, Moorepark

donagh.berry@teagasc.ie

Sheep Ireland Industry Meeting, April 2018

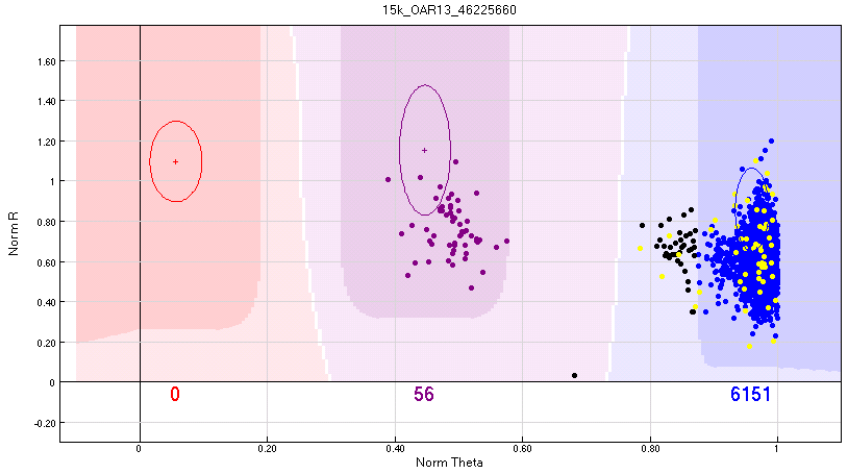
Scrapie

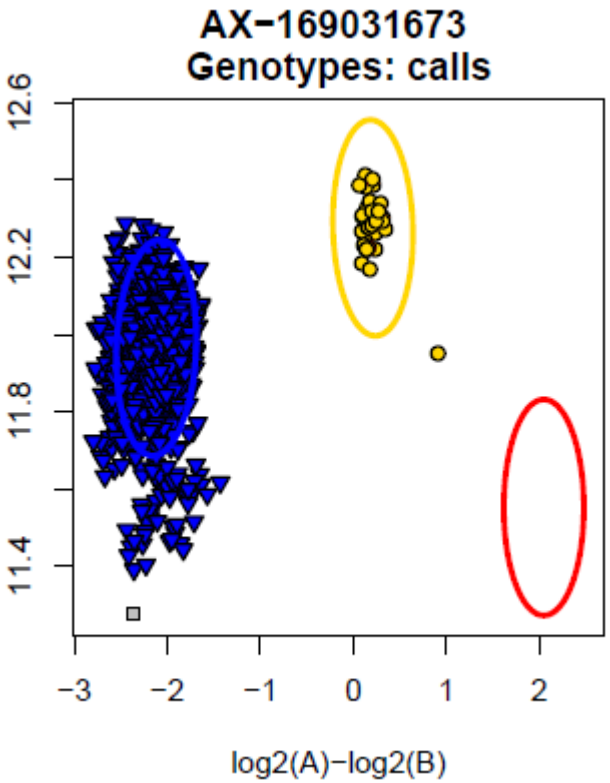
- **5 different DNA variants**
  - **1 + 1 + 3**

Name	Chr	Position
oar3_OAR13_46225660	13	46225660
15k_OAR13_46225714	13	46225714
15k_OAR13_46225764	13	46225764
15k_OAR13_46225765	13	46225765
15k_OAR13_46225766	13	46225766

Codon 136

- 15K_OAR_46225660
- Determine amino acid at codon 136: Alanine (A: GCC) or Valine (V: GTC)
- Very nice

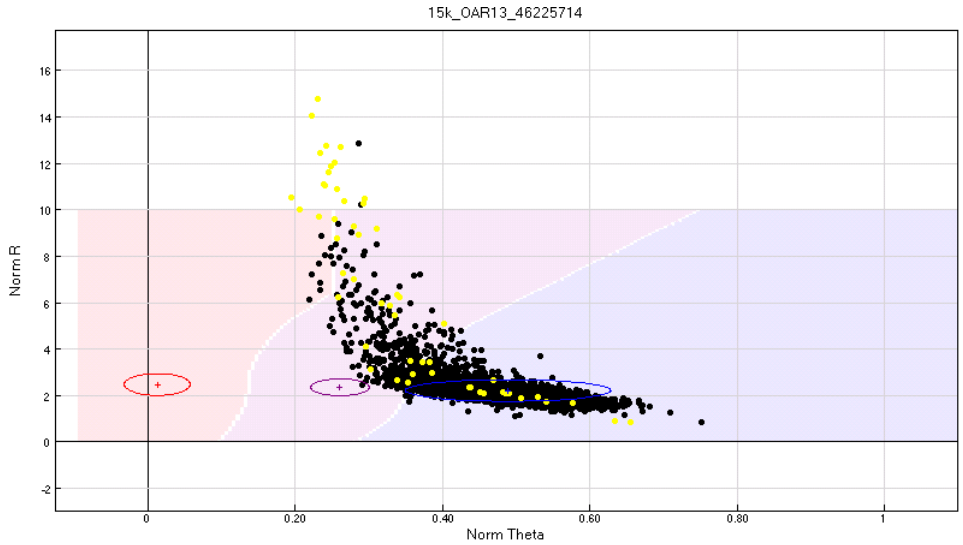


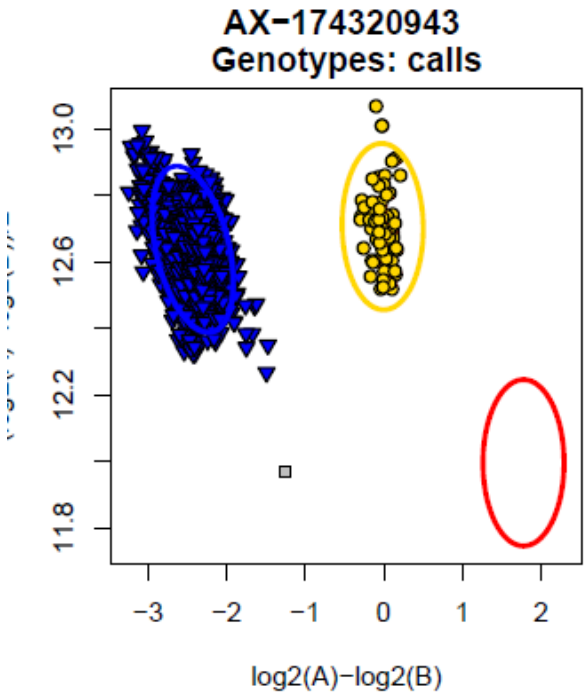


Codon 154

15K_OAR13_46225714

Identify the amino acid at codon 154: Argenine (R: CGT) or Histadine (H: CAT)

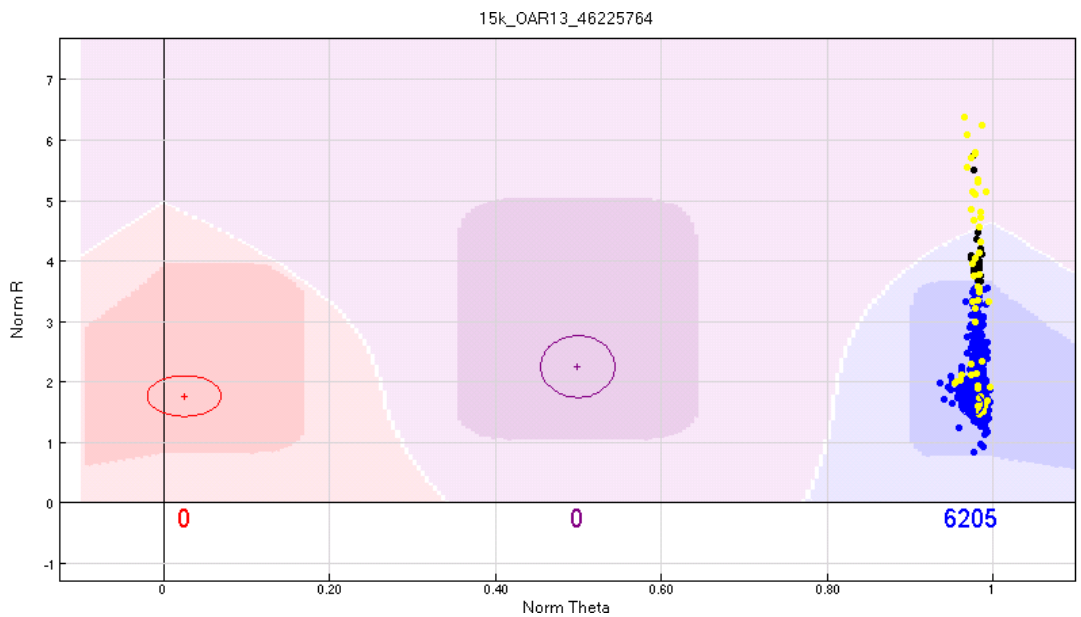


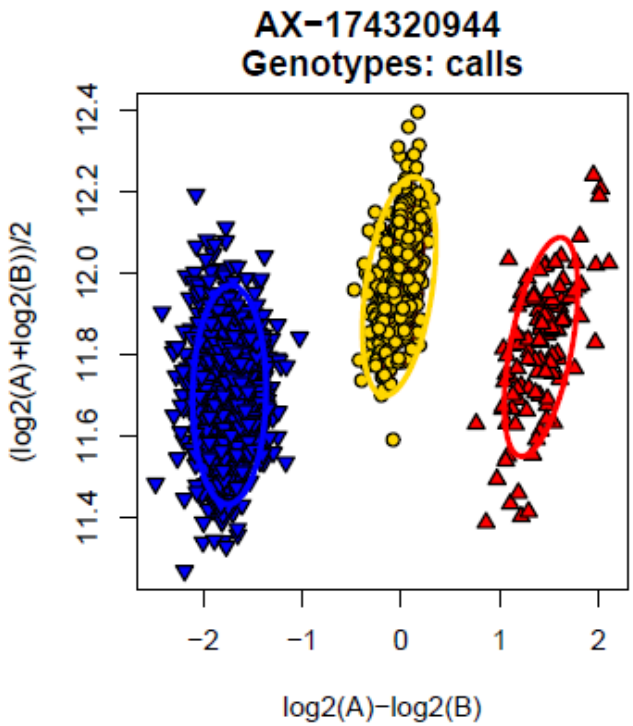


Codon 171 (3 bases)

- **15K_OAR13_46225764 – 1st base**

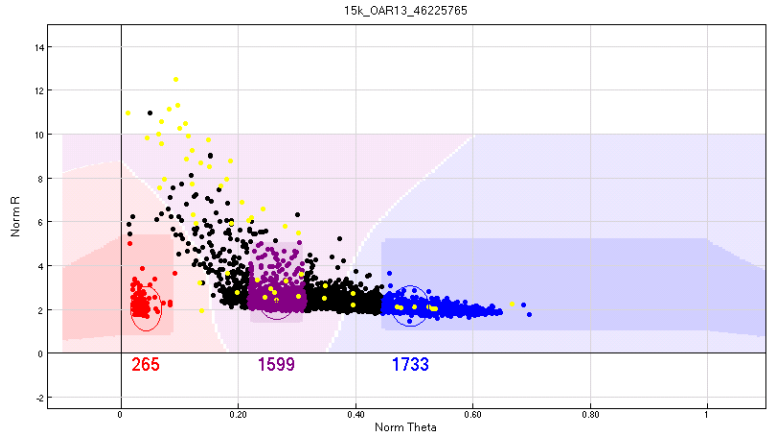
- **Looks good**

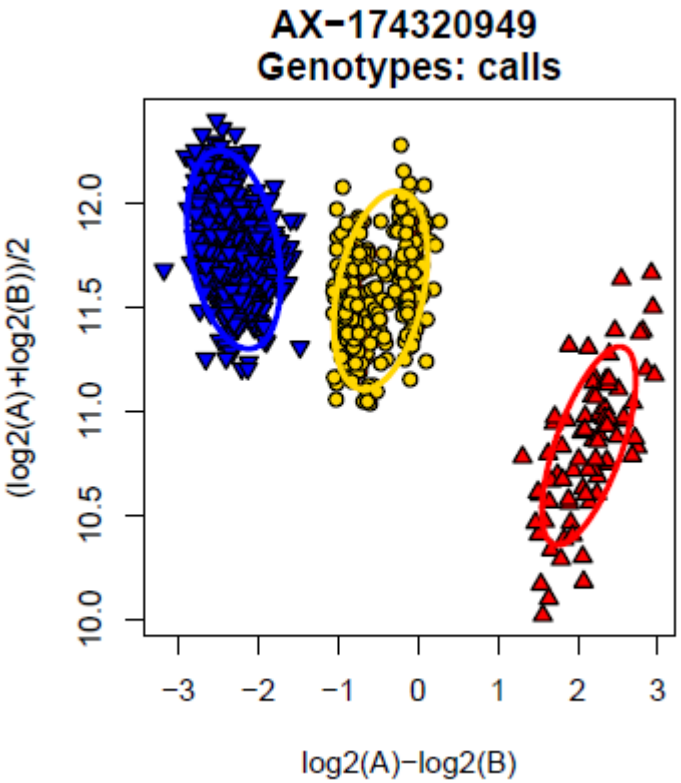




Codon 171

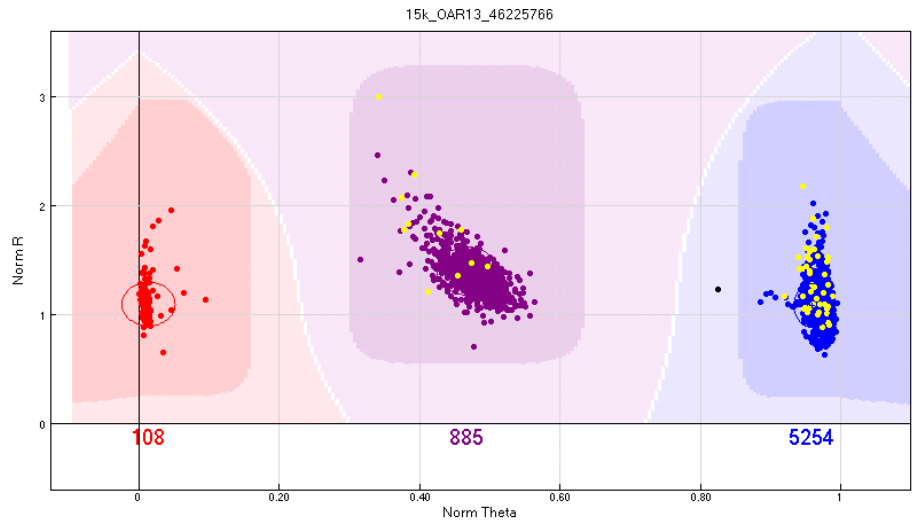
- **15K_OAR13_46225765 – 2nd base**
- **Though one but now good**

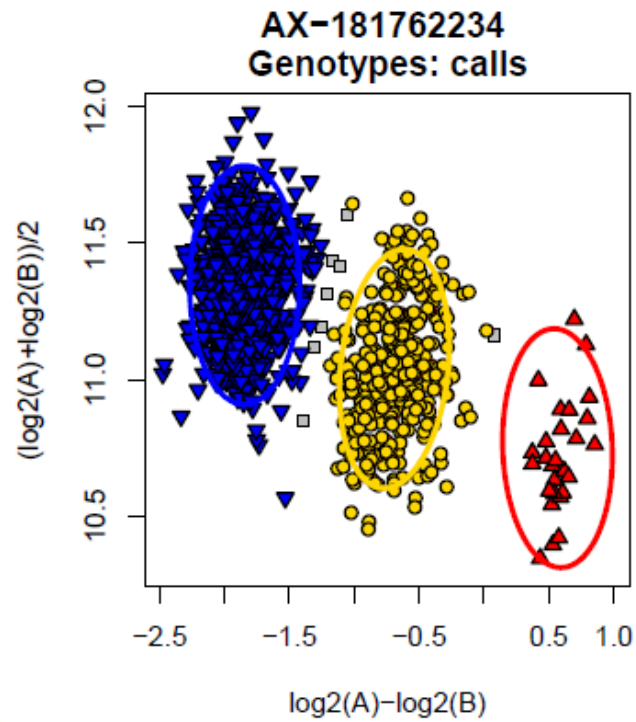




Codon 171

- **15K_OAR13_46225766 – 3rd base**
- **Problem one the last time (my fault)**





Genotype result	Type	Degree of resistance/susceptibility
ARR/ARR	1	Sheep that are genetically most resistant to scrapie.
ARR/AHQ ARR/ARH ARR/ARQ	2	Sheep that are genetically resistant to scrapie, but will need careful selection when used for further breeding.
AHQ/AHQ AHQ/ARH AHQ/ARQ ARH/ARH ARH/ARQ ARQ/ARQ	3	Sheep that genetically have little resistance to scrapie and will need careful selection when used for further breeding.
ARR/VRQ	4	Sheep that are genetically susceptible to scrapie and should not be used for breeding unless in the context of a controlled breeding programme approved by NSPAC.
AHQ/VRQ ARH/VRQ ARQ/VRQ VRQ/VRQ	5	Sheep that are highly susceptible to scrapie and should not be used for breeding.

First SNP differentiates type 4 & 5 from the rest

V v others**

Only need to know ARR & VRQ

Courtesy of Hayley Baird & John McEwan

Testing

- 54 samples of Type 3, 4, & 5 from DAFM
- Type 1 & 2 from OVIGEN

- 100% correct in calling scrapie type

Prevalence (n=2022)

Type	BR	CL	SU	TX	VN
1	69	71	73	49	72
2	25	24	24	41	26
3	3	3	0	5	2
4	2	1	3	3	0
5	1	2	0	2	0

4.5% not called

Conclusion

- Genotypes now give 100% concordance with scrapie type (1, 2, 3, 4, 5)
  - Still a small proportion “didn’t work” – WIP
  - Calling of actual scrapie genotype – WIP
- Future validation with larger number
  - Work in retrospect
  - Locate different types from those already tested
- Continuous spot checks

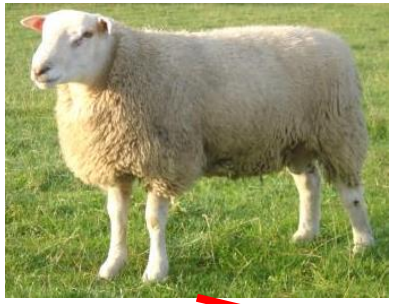
Breed prediction

Áine O' Brien

Sheep Ireland Industry meeting

Athenry, April 2017

Crossbreeding – dilemma 1



50% BR : 50% SU
(assuming both parents are pure)

50% CL : 25% BR : 25% SU

50% CL : 50% BR : 0% SU

50% CL : 0% BR : 50% SU

Crossbreeding – dilemma 2

50% TX : 50% SU

X

50% SU : 50% TX

100% TX

50% TX : 50% SU

50% SU : 50% TX

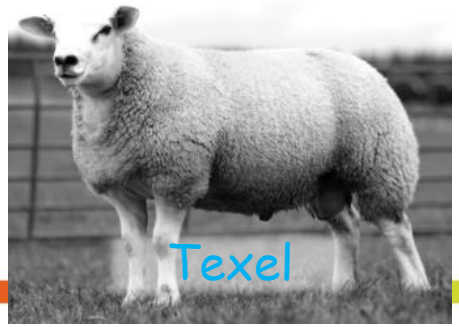
100% SU

The Belclare

The question:

How much Lleyn is in the modern day Belclare?

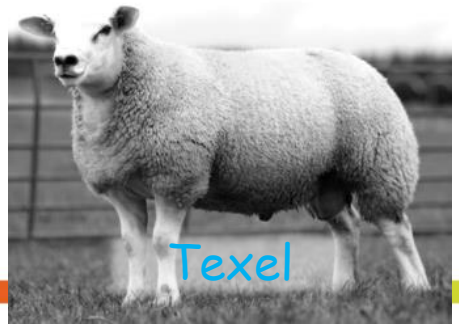
The Belclare



% in Belclare

- Minimum = 0%
- Maximum = 8.64%
- Average = 0.3%

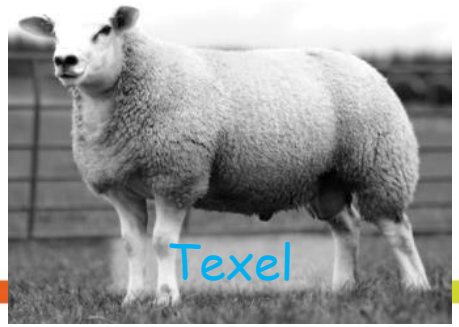
The Belclare



% in Belclare

- Minimum = 0%
- Maximum = 81.9%
- Average = 35.0%

The Belclare



% in Belclare

- Minimum = 0%
- Maximum = 91.7%
- Average = 16.0%

The Belclare

% in Belclare

- Minimum = 0%
- Maximum = 28.6%
- Average = 0.6%

On-going work

Quantifying breed proportion in crossbreds

- CPT flocks, Research Flock

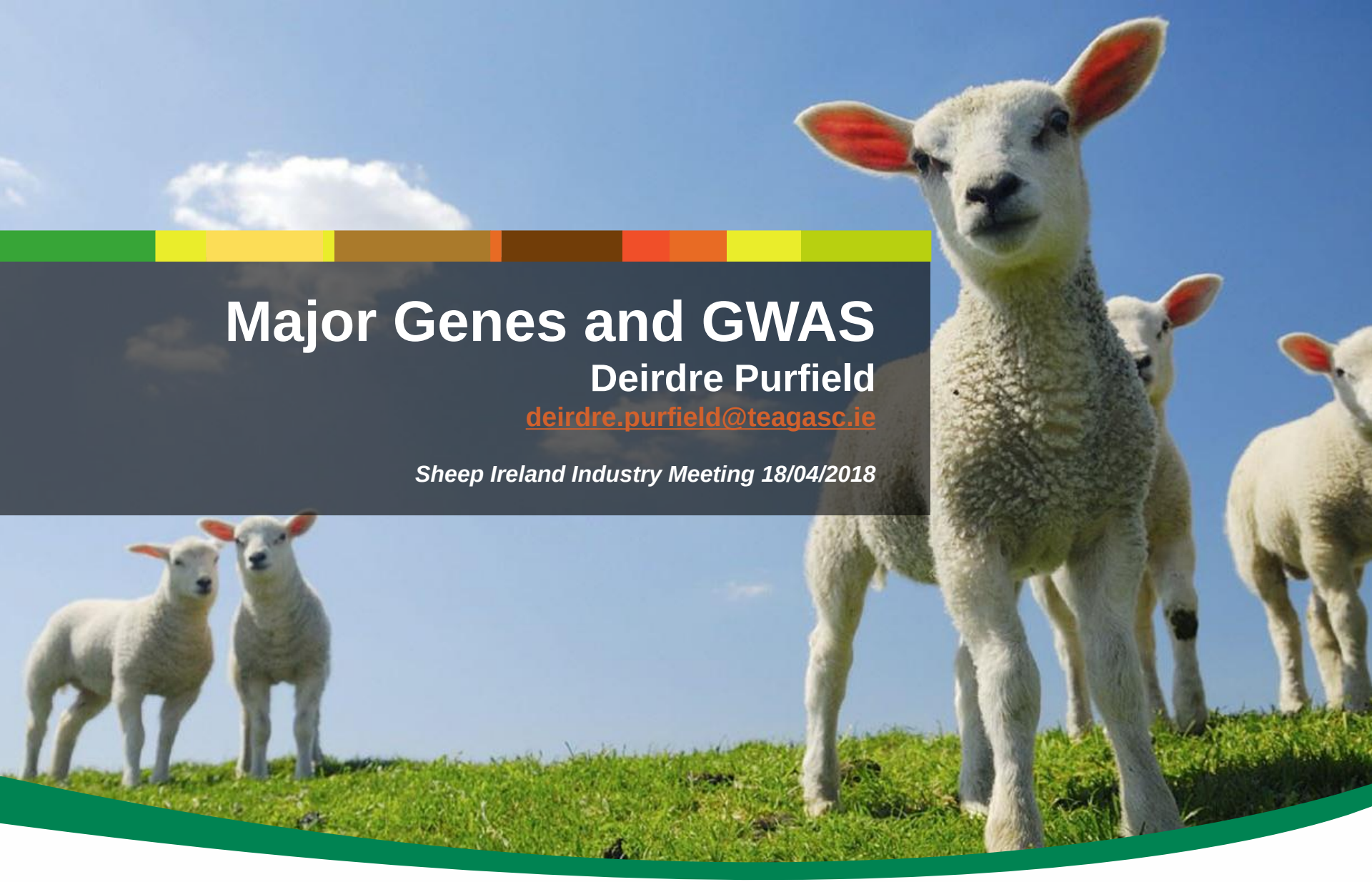
Belclare and other composites

- EasyCare, Highlander, Primera

Major Genes and GWAS

Deirdre Purfield
deirdre.purfield@teagasc.ie

Sheep Ireland Industry Meeting 18/04/2018



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Major Genes

Major gene: A gene that substantially influences a trait

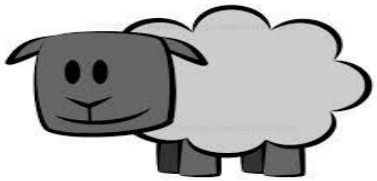
Gene	Symbol	Species	Effect
Myostatin	GDF8	Sheep Cattle	Double muscling
Bone morphogenetic protein 15	BMP15	Sheep	Ovulation rate
Growth differentiation factor 9	GDF9	Sheep	Ovulation rate
Diacylglycerol O-acyltransferase1	DGAT1	Sheep Cattle	Milk yield
Melanocortin 1 receptor	MC1R	Cattle Sheep	Coat colour
Calpains	CAPN	Cattle	Meat quality

Prevalence of major genes

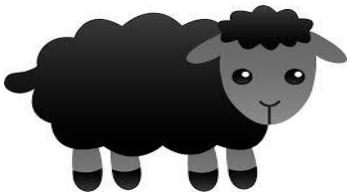
All animals have “major” genes

Different DNA variants in major genes = **Different Phenotypes**

0 copy
AA



1 copy
AB



2 copy
BB

Prolificacy Genes

BMP15 Xb → associated with Belclare breed

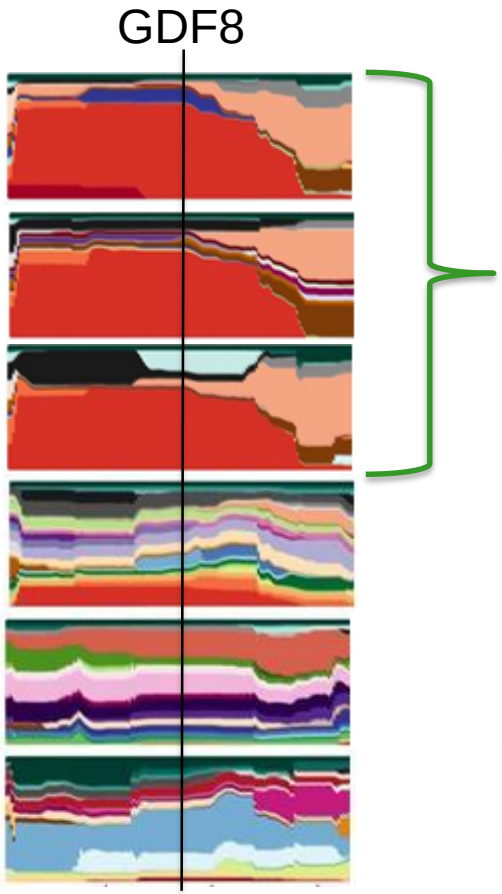
1 copy of DNA variant (T) increased ovulation rate

2 copies sterile (TT)

+0.53 lambs born

Genotyped	1 copy
All population	0.07%
Belclare	9.78%

GDF8-double muscling



	0 Copy (AA)	1 Copy (AG)	2 Copy (GG)
Texel	97.0	2.7	0.3
Beltex	97.8	2.2	0
Belclare	69.7	28.7	1.6
Charollais	2.6	26.6	70.8
Galway	0	21.1	78.9
Suffolk	0.2	0.3	99.5
Vendeen	0	0	100

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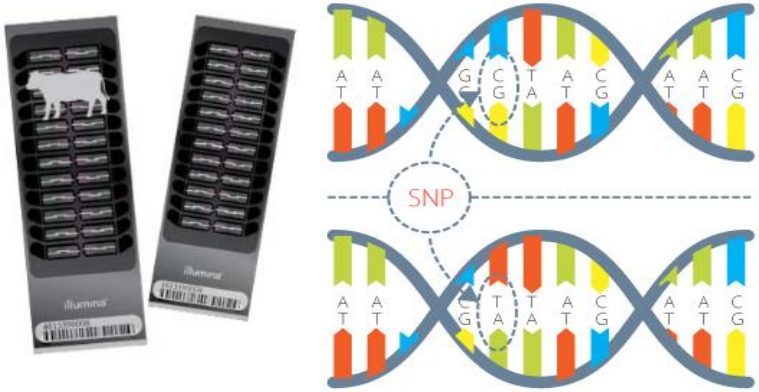
How to identify DNA associations?

Genome Wide Association Study

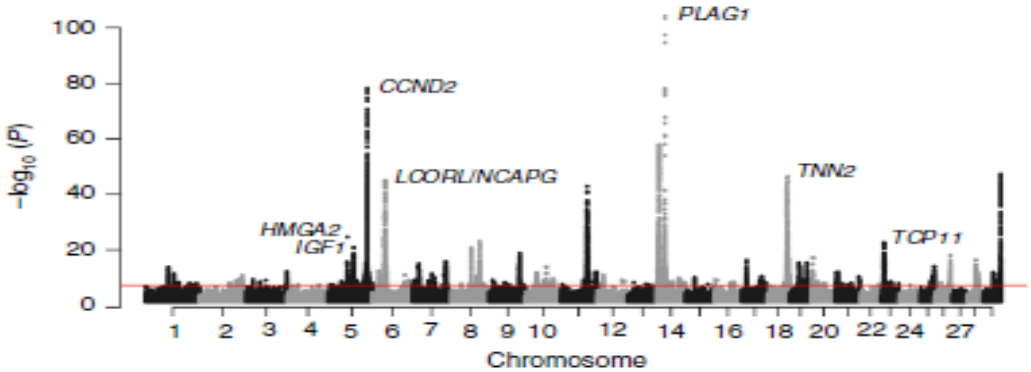


~50,000 SNPs

SNP1G

SNP1A

Associate DNA variations with differences in performance



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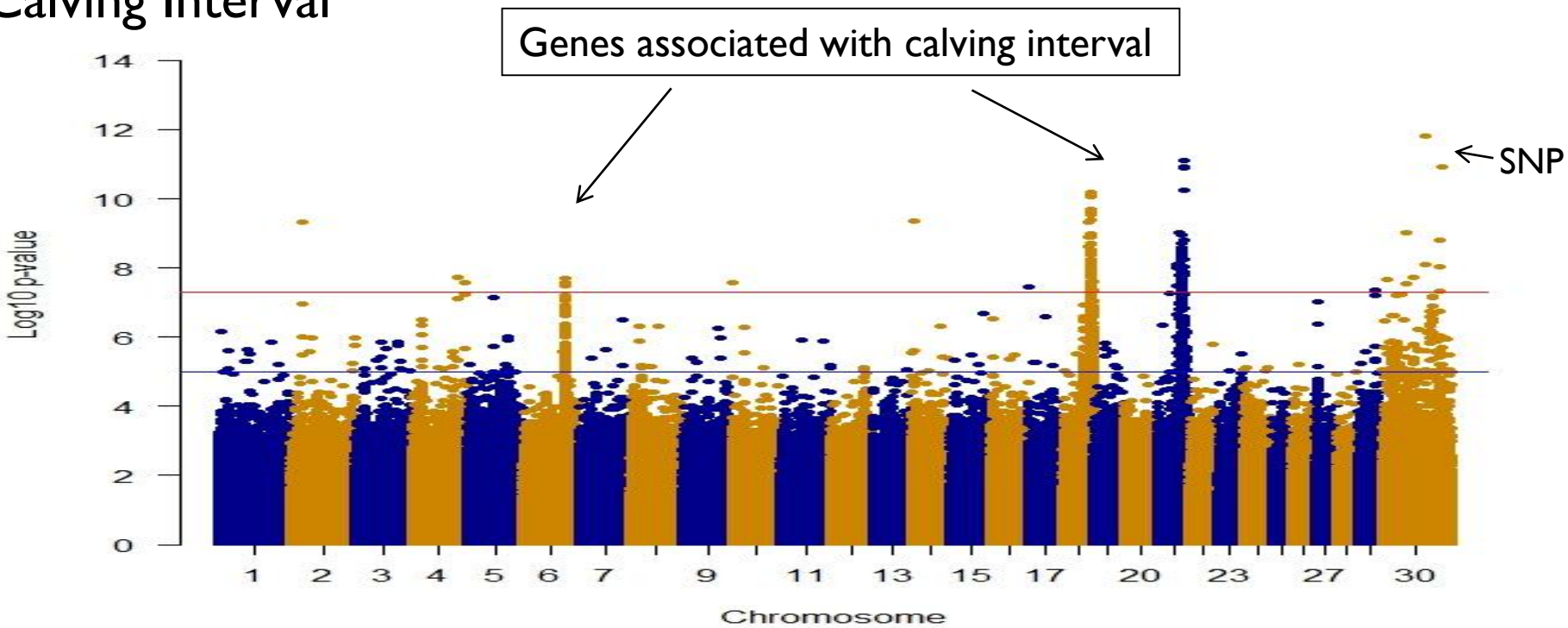
Cattle Example

Most Performance traits are **polygenic**

Influenced by small effects of thousands of SNPs

Calving Interval



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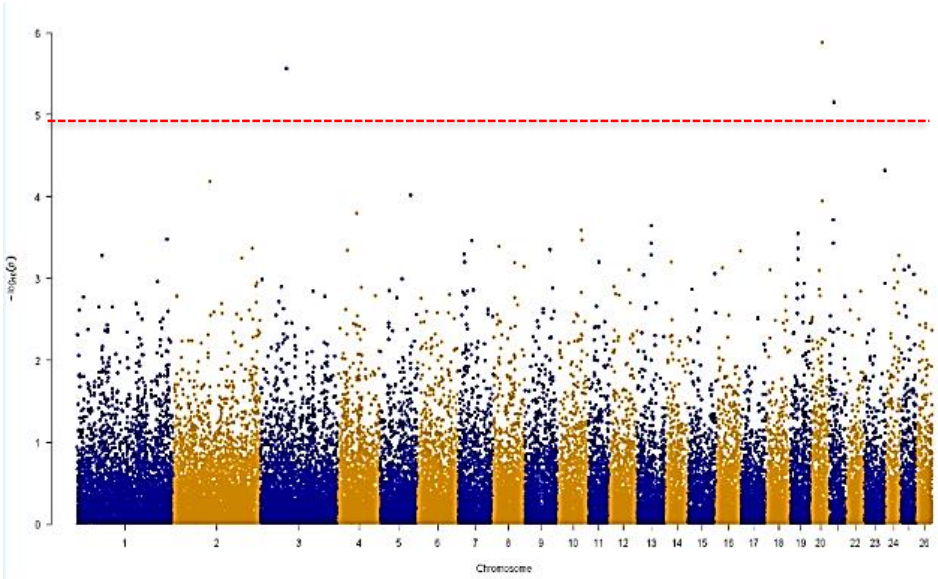
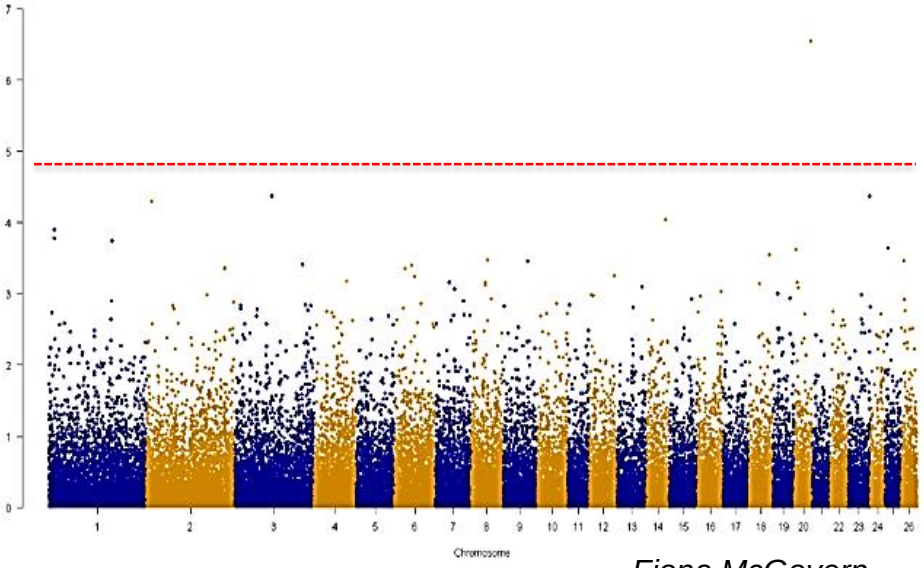
Sheep example

- 9,909 Sheep with EBV for direct birth weight
- Five breeds
- No clear signal of association -> influenced by many SNPs



Charollais
N=2,895



Fiona McGovern

Texel
N=3,148

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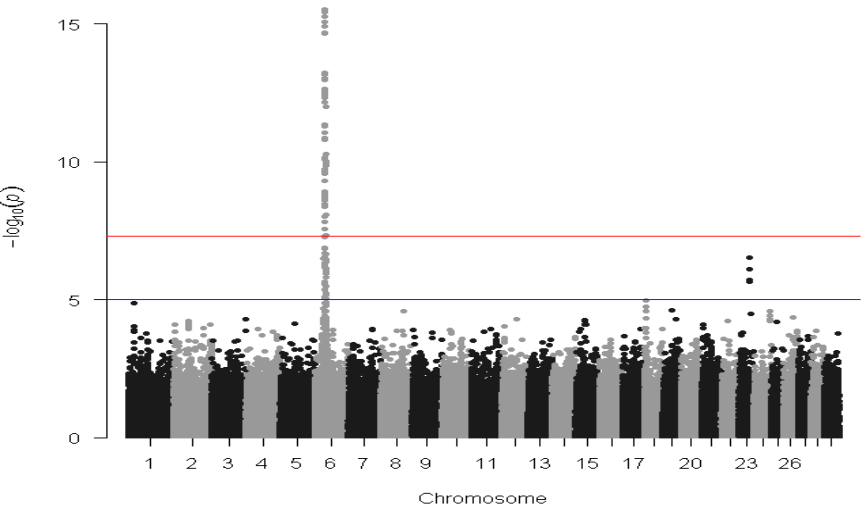
Refine DNA associations

- Although can find DNA region, still difficult to identify which gene
- 1000 Rams project ~ 1000 Bulls genome project
  - Resource tool which each partner can use for imputation
  - Provides whole genome sequence (~50 million SNPs) on key rams

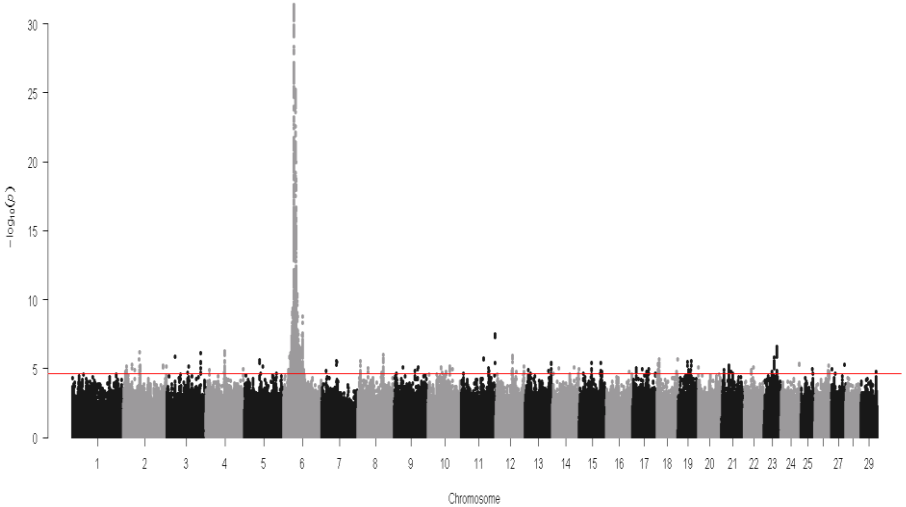
Height of Withers

Limousin cattle (n=39,821)



600,000 SNPs

Pinpoint gene
Increase significance



15 Million SNPs

On-going Work

- Complete association studies for multiple traits
  - Investigate if other major genes exist in sheep
  - Identify SNPs for possible inclusion in a custom panel
  - Validate association results

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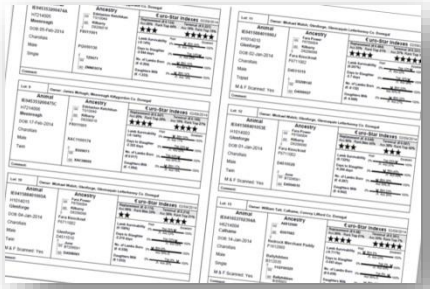
Genomics Next Steps



Eamon Wall

Current Situation

- Ovigen budget
  - Research completion – Dec 2018
  - Budget has now been spent – huge investment in pedigree sheep breeds
  - Long term legacy for Irish sheep breeding

Delivery of Genotype Results

- Current status
  - Results of 2017 genotyped animals are yet to be delivered
  - Why?
    - A change in SNP chip being used
    - Up to now a manual process of assessing the results
    - Work nearing completion on a automated system to process genotypes & results in SI
  - This will deliver results in a timeframe similar to beef (currently 3-4 weeks from sample submission)
  - Unable to commit to this turnaround in 2018

2018 Genotyping

- Genotyping in 2018
  - SI will subsidise genotyping in 2018
  - Females & Stock rams remain priority
  - Fee will be €10 per sheep (male or female)
  - SI will contribute €12 per animal (Total cost €22)
  - This will kick-in on April 30th
  - Policy will need to be reviewed throughout the year
  - Alternative funding streams will be investigated!

Validation of genetic indexes

Fiona McGovern & Noirin McHugh

Sheep Ireland Industry Meeting
18th April 2018

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Overview

- Why we need validation
- Results –
  - INZAC Flock
  - CPT
- Economic Efficiencies

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Why we need validation…

- Accurate genetic evaluations are key to sustainable genetic gain
- Must be reflective of on-farm performance
- Access to accurate genetic evaluations → selection of superior animals for breeding

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Index Validation

A.

B.

€ uro-Star Indexes 11/07/2016	
Replacement (€ 0.813)	Terminal (€ 1.026)
Acc 41% Rank Top 8%	Acc 44% Rank Top 2%
★★★★★	★★★★★

€ uro-Star Indexes 11/07/2016	
Replacement (€ -0.85)	Terminal (€ -0.197)
Acc 33% Rank Btm 18%	Acc 37% Rank Btm 6%
★	★

Index validation

Terminal Index

Replacement Index

Results:

Do genetic indexes work?

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CPT Data

1 Star ★ V's 5 Star ★★★★★

Index	Trait	★	★★★★★	Diff
Replacement	Lamb Mortality (%)	10.65%	9.45%	-1.20%
	Number of lambs born	1.92	1.97	0.05
	Ewe mature weight (kg)	78.7	76.8	-1.9
Terminal	Lambing Difficulty (%)	23.06%	18.17%	-4.89%
	40 day weight (kg)	18.1	20.2	2.10
	Weaning weight (kg)	31.9	34.5	2.60

INZAC Data

Index	Trait	★	★★★★★	Diff
Replacement	Lamb Mortality (%)	11.00%	5.10%	-6.00%
	Number of lambs born	1.76	1.81	0.05
	Lambing Difficulty (%)	22.00%	21.00%	-1.00%
	Ewe weight (kg)	77.9	76.6	-1.3
	40 day weight (kg)	16.9	18.4	1.5
	Weaning weight (kg)	32.9	34	1.1

What does this mean for us??

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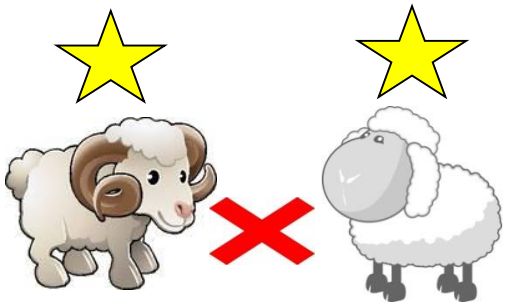
Flock Scenario



A flock with 5 star animals has:

1. Less lambing difficulty - less labour
2. More lambs born & lower lamb mortality
3. Lighter ewes –increase stocking rate?
4. Heavier lambs at weaning - shorter DTS

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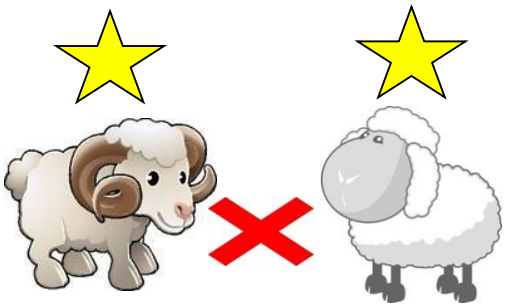
Economic Efficiency – 100 ewe flock



€7
Net profit / ha

€217
Net profit / ha

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Conclusion

- Genetic evaluations key to sustainable genetic gain
- Genetic merit for maternal and performance traits was associated with superior performance
- Importance of indexes for improving profitability across a range of traits

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