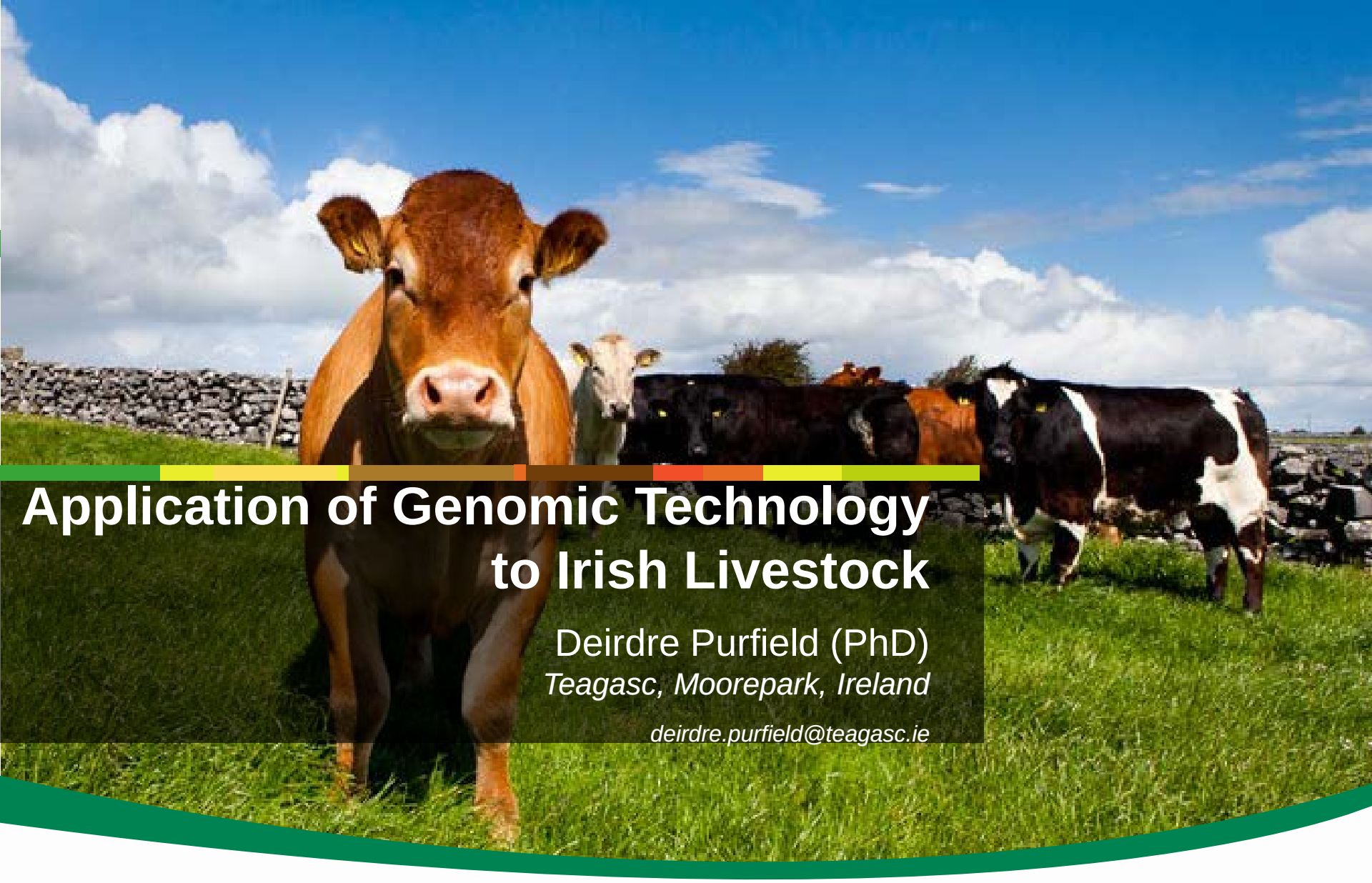

Application of Genomic Technology to Irish Livestock

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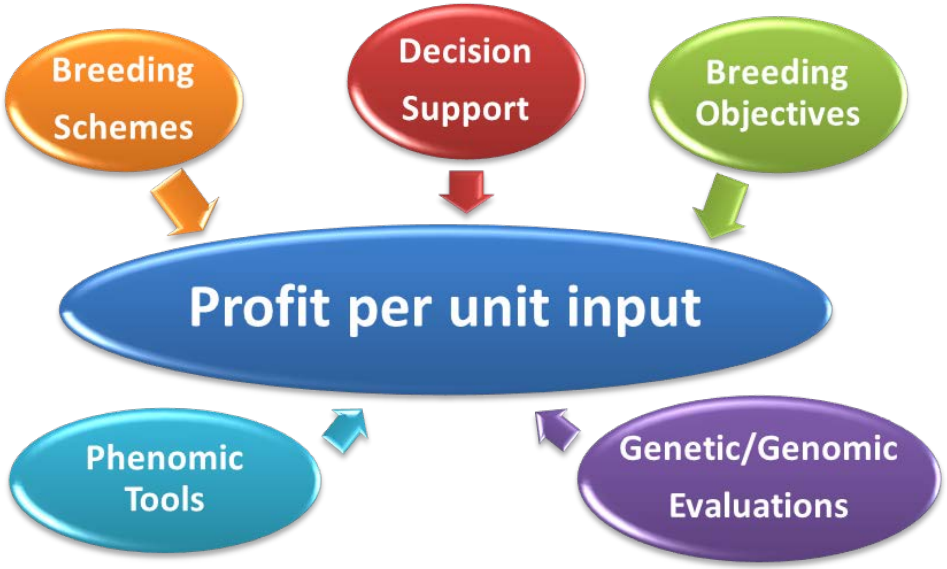
- Genetics Research Team
  - **Researchers:** Donagh Berry, Noirin McHugh, Sinead McParland, Deirdre Purfield, Tara Carthy, Michelle Judge, Jessica Coyne
  - **Post-graduate students:** Siobhan Ring, Alan Twomey, Aine O'Brien, Tom Byrne, Jennifer Doyle, Pierce Rafter, Fiona Dunne, Shauna Fitzmaurice, Stephen Connolly
  - Research focus



- Close relationship with ICBF

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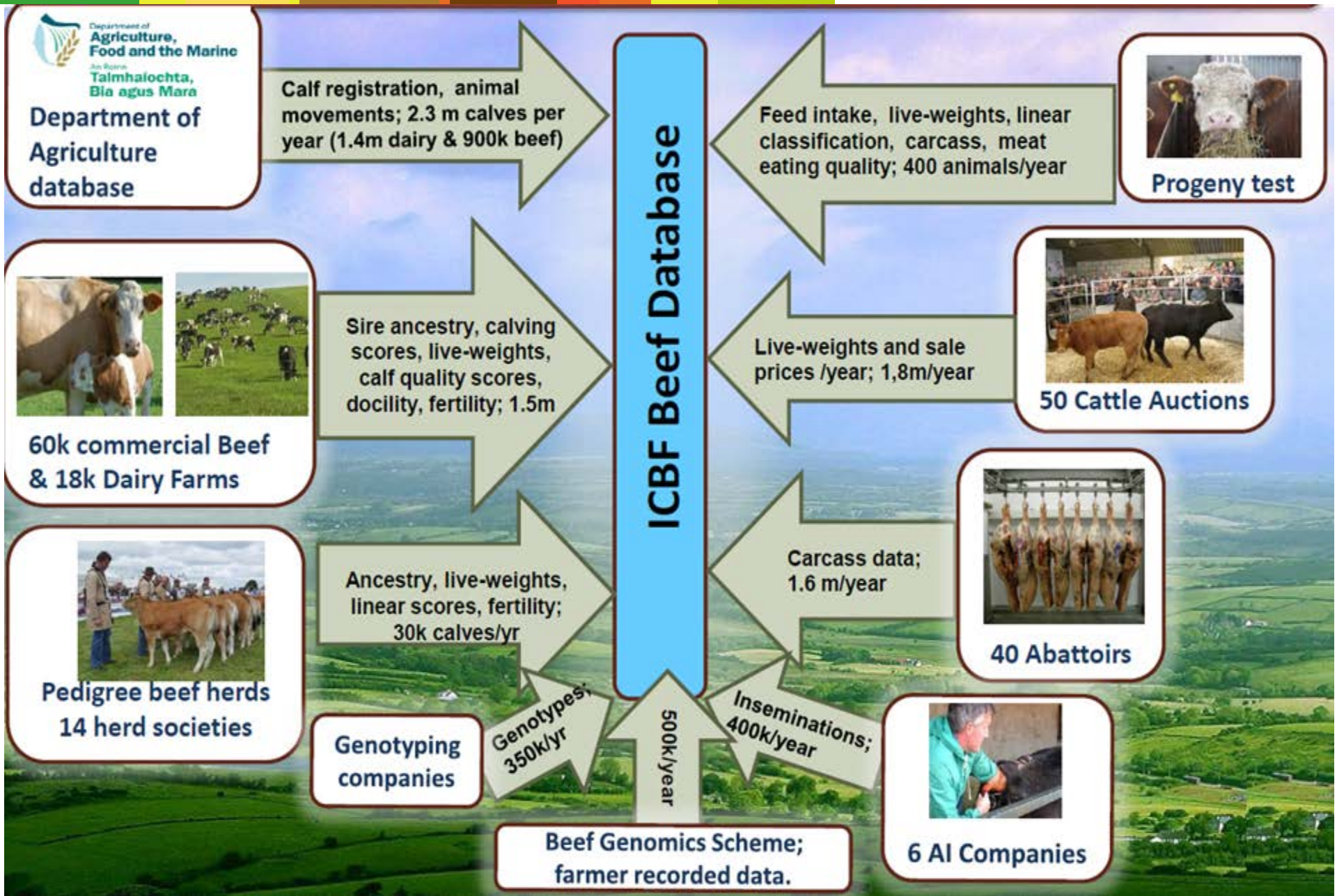
Access to ICBF Database



Industry

Dairy Industry

- 1.4 million dairy cows
- 18,000 Herds
- Avg herd size: 80 cows
- ~93% Holstein-Friesian
- Seasonal grass based
- Export 90% milk produced
- Economic Breeding Index

Beef Industry

- 1.1million beef cows
- 19,000 Herds
- Avg herd size: 40 cattle
- Continental Crossbreds
- Seasonal grass based
- Export 90% beef
- Replacement Index
- Terminal Index

Sheep Industry

- 2.6 million ewes
- 13,000 Herds
- Avg herd size: 133 ewes
- Crossbred
- Seasonal grass based
- Export 70% sheep meat
- Replacement Index
- Terminal Index

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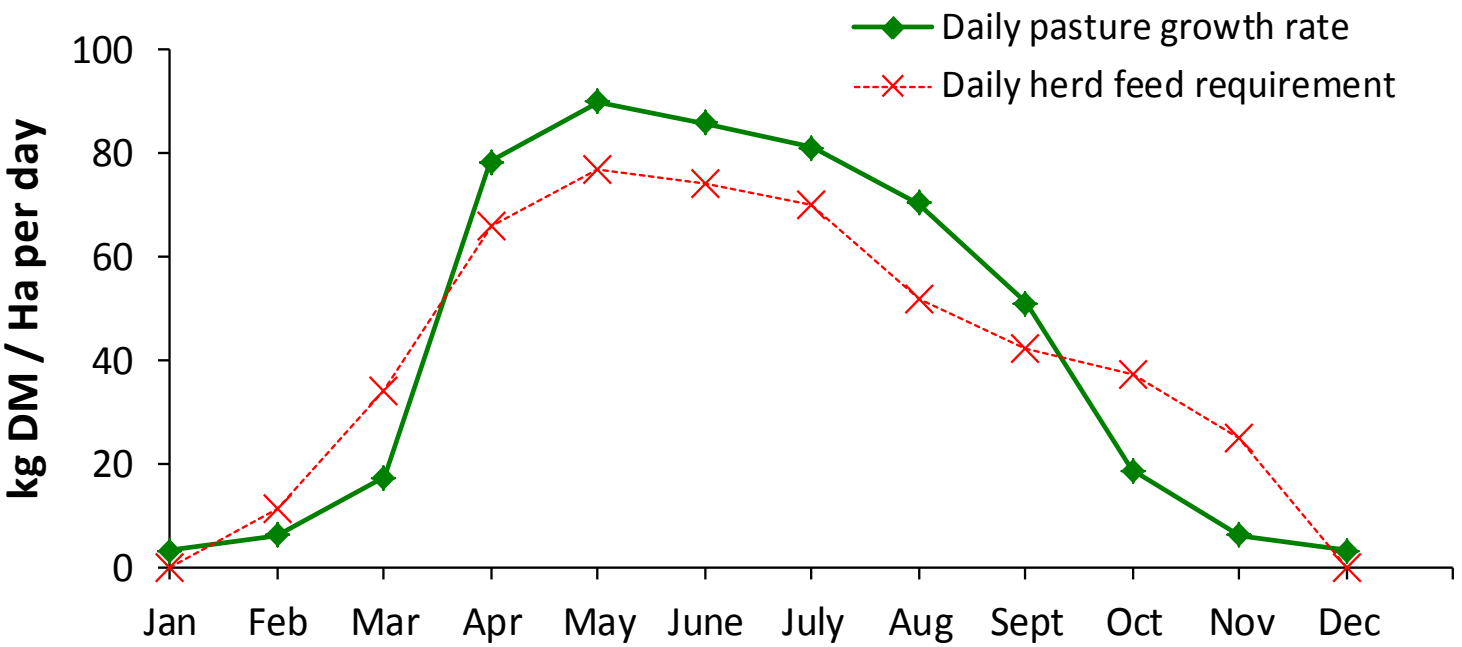
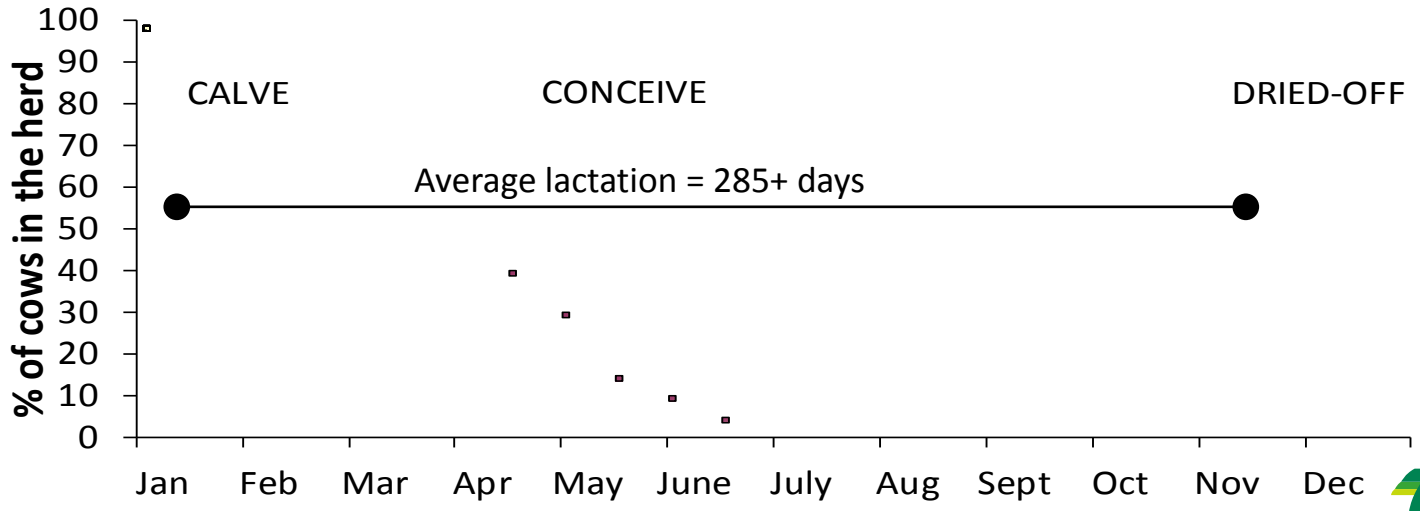
Importance of seasonality





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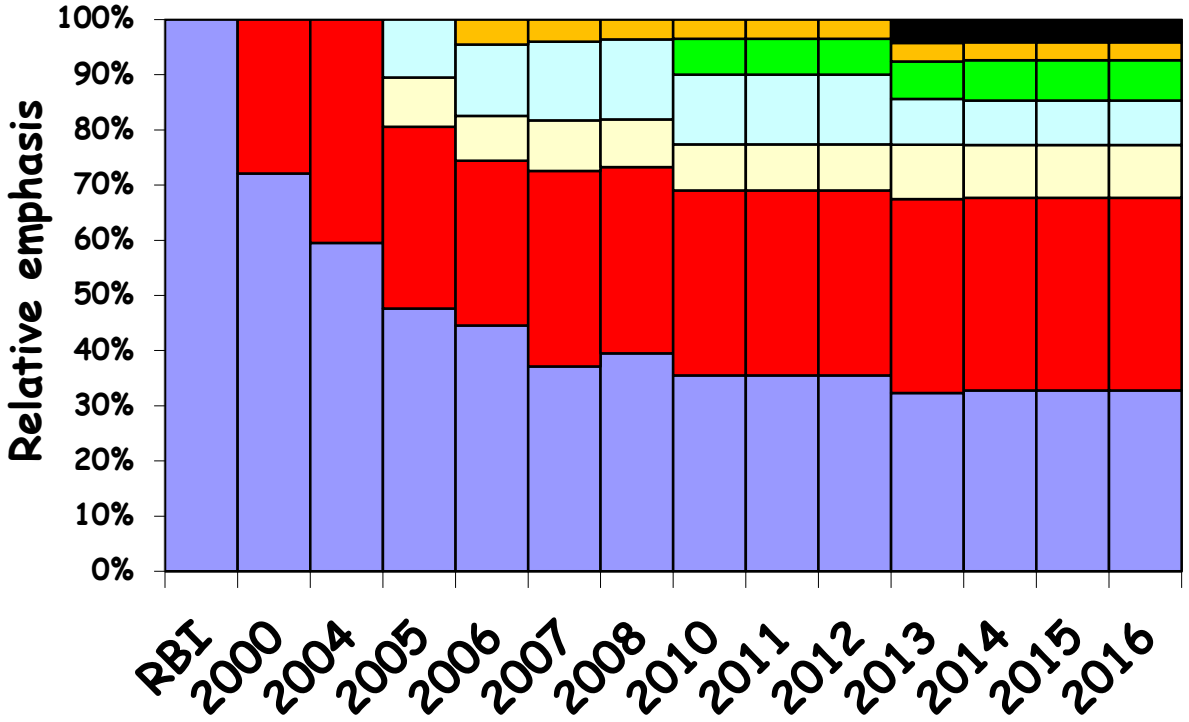
Dairy Breeding



Fertility
35%

Production
33%

Calving
10%

Economic Breeding Index (EBI)

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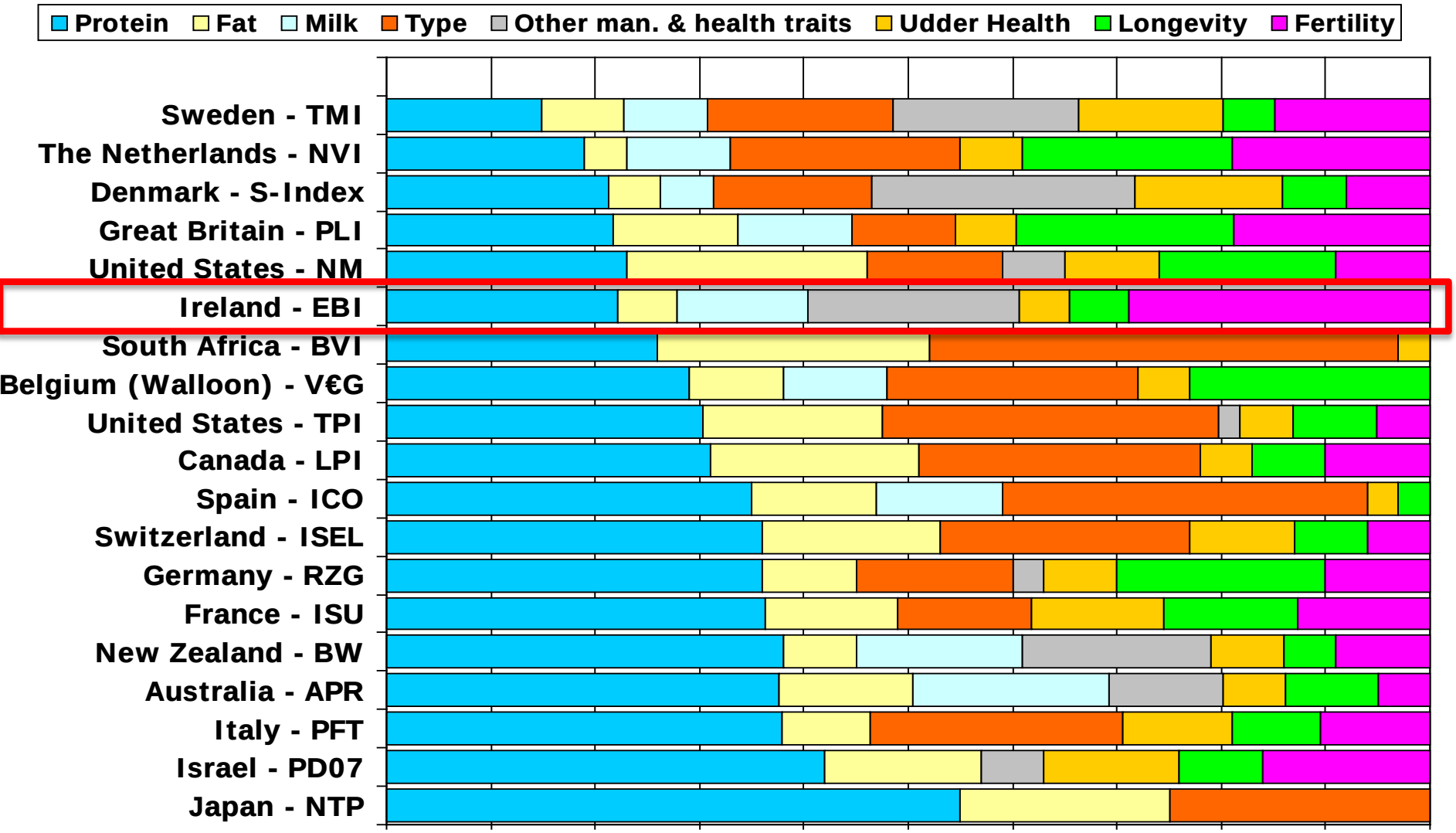
International Dairy Objectives



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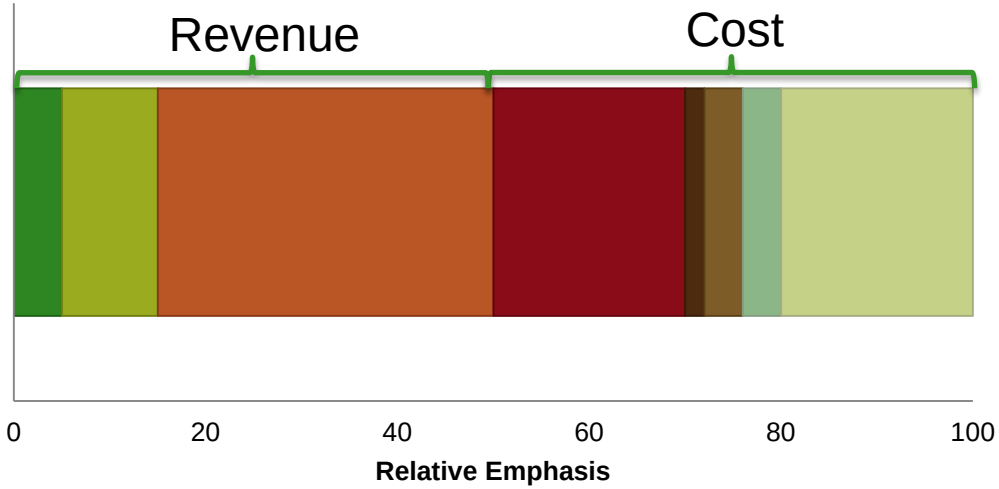
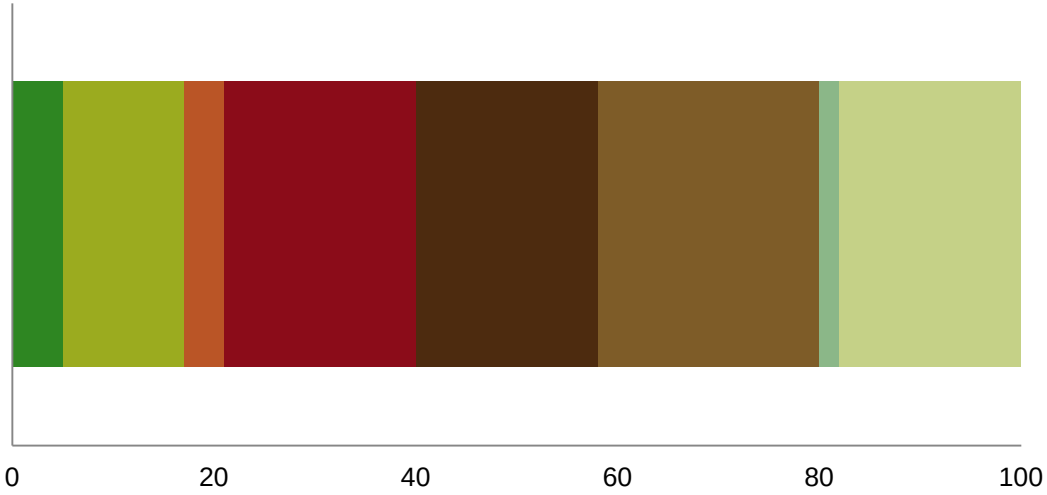
Beef Breeding

- Terminal Index



- Carcass fat
- Carcass conformation
- Carcass weight
- Feed Intake
- Docility
- Direct perinatal mortality
- Direct gestation length
- Direct calving difficulty

- Replacement Index



- Cull cow weight
- Maternal weaning weight
- Maternal calving difficulty
- Fertility and survival
- Progeny Carcass
- Feed Intake
- Docility
- Direct Calving Difficulty

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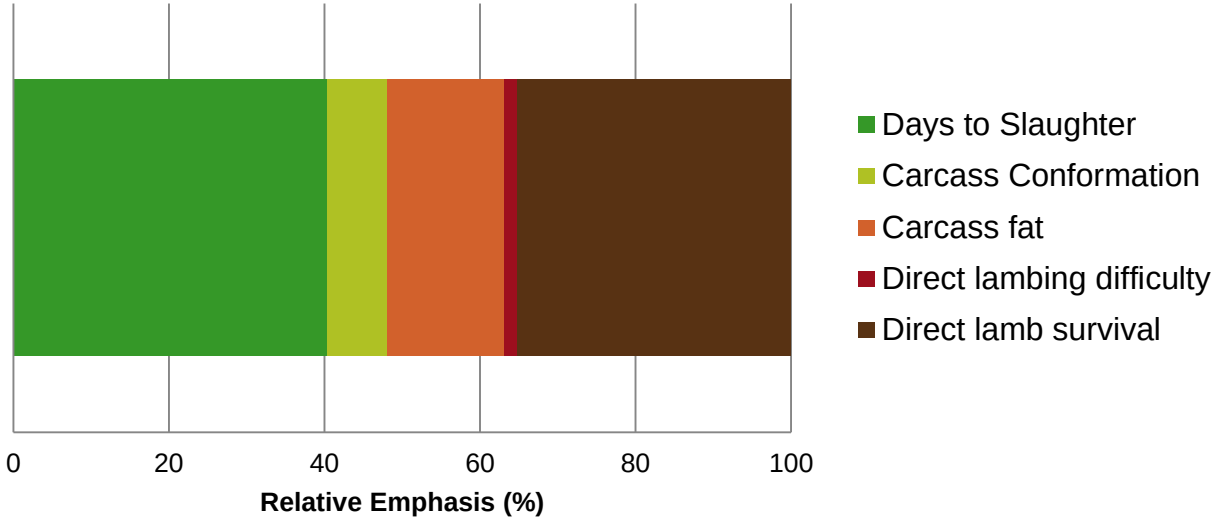
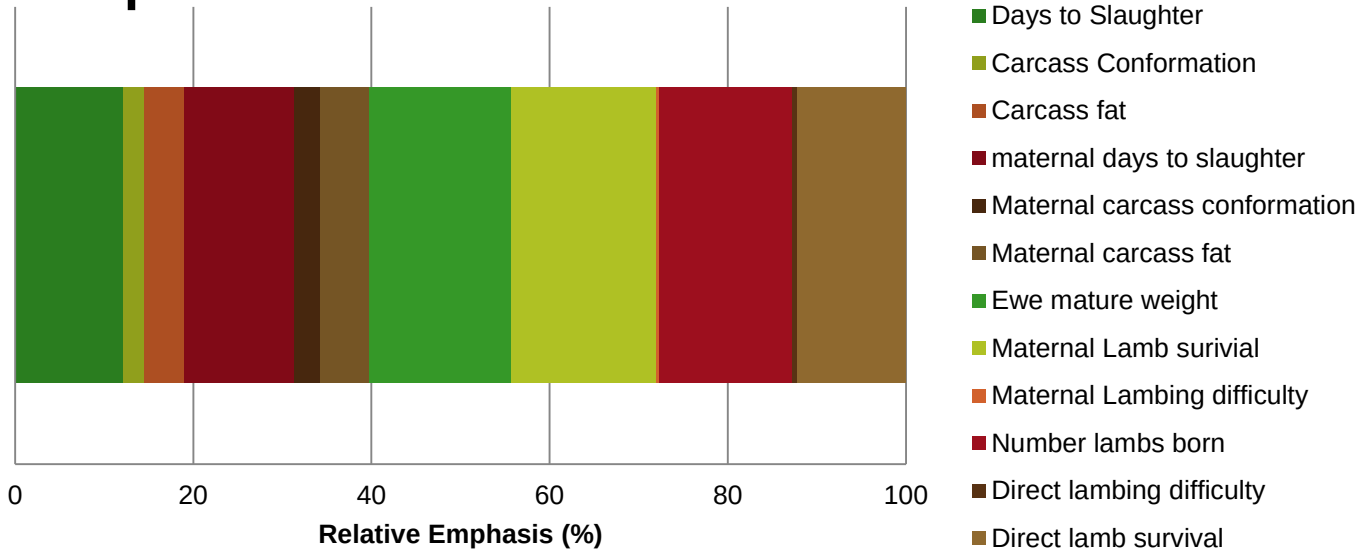
Sheep Breeding

- Terminal Index



- Replacement Index



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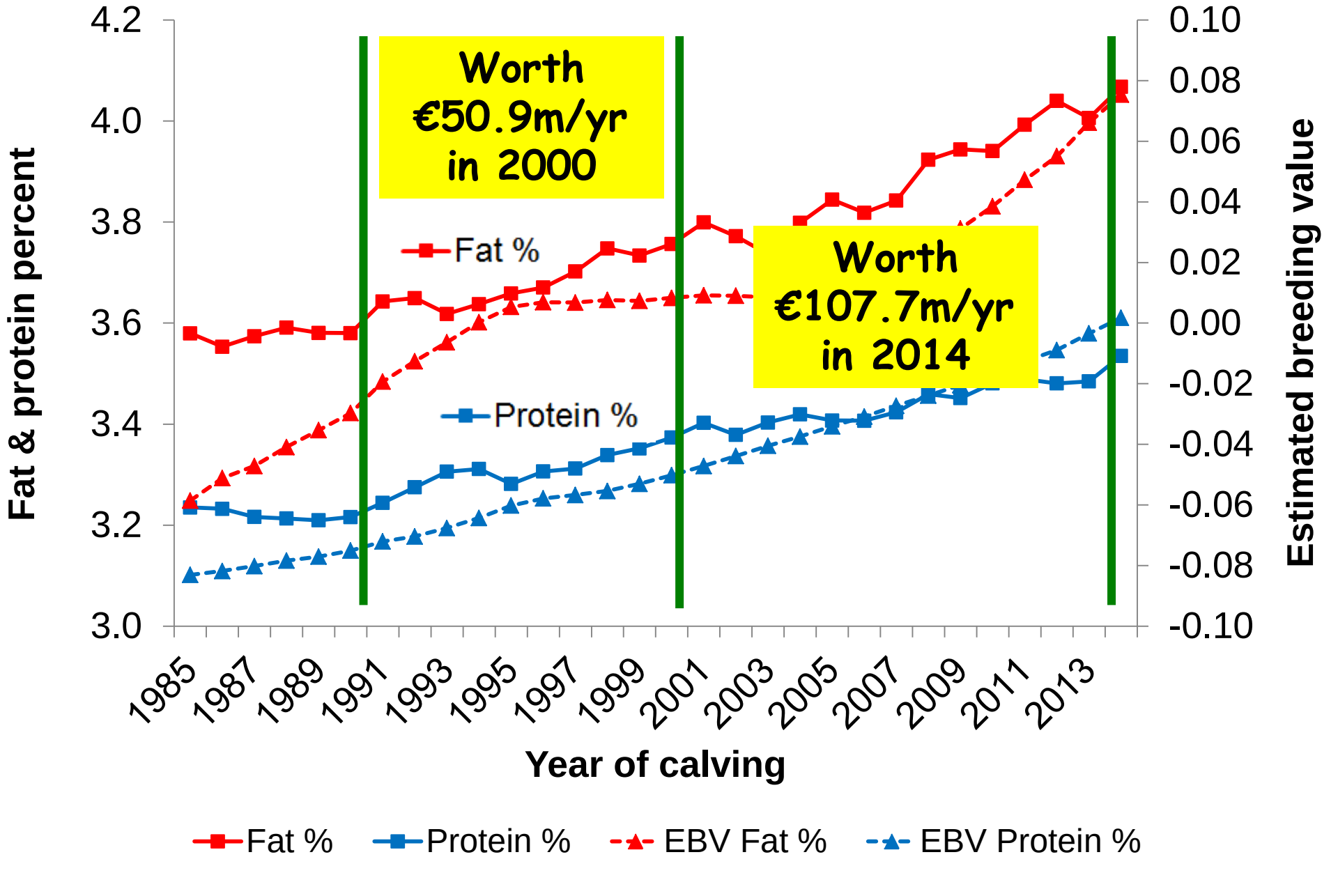
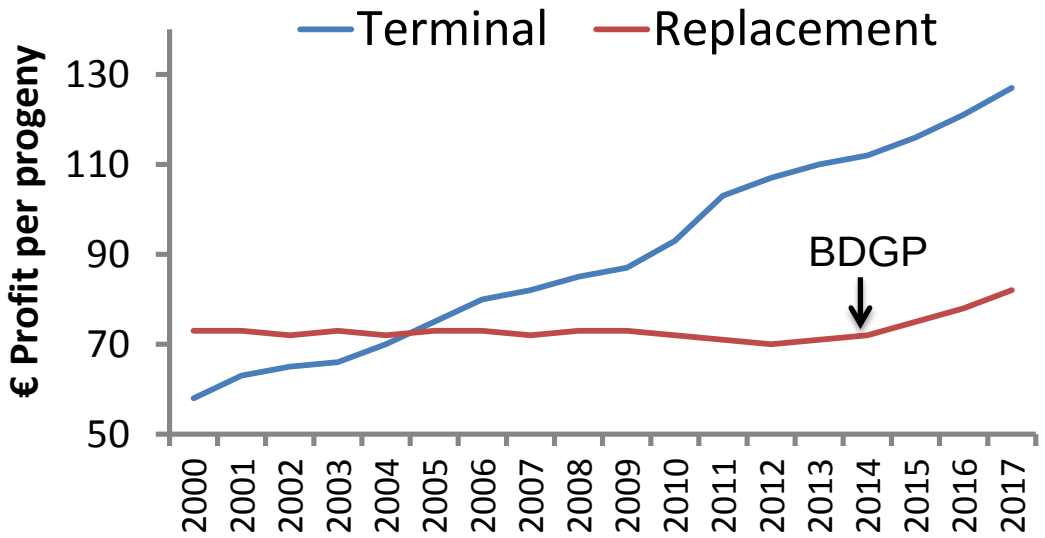
The power of breeding…..

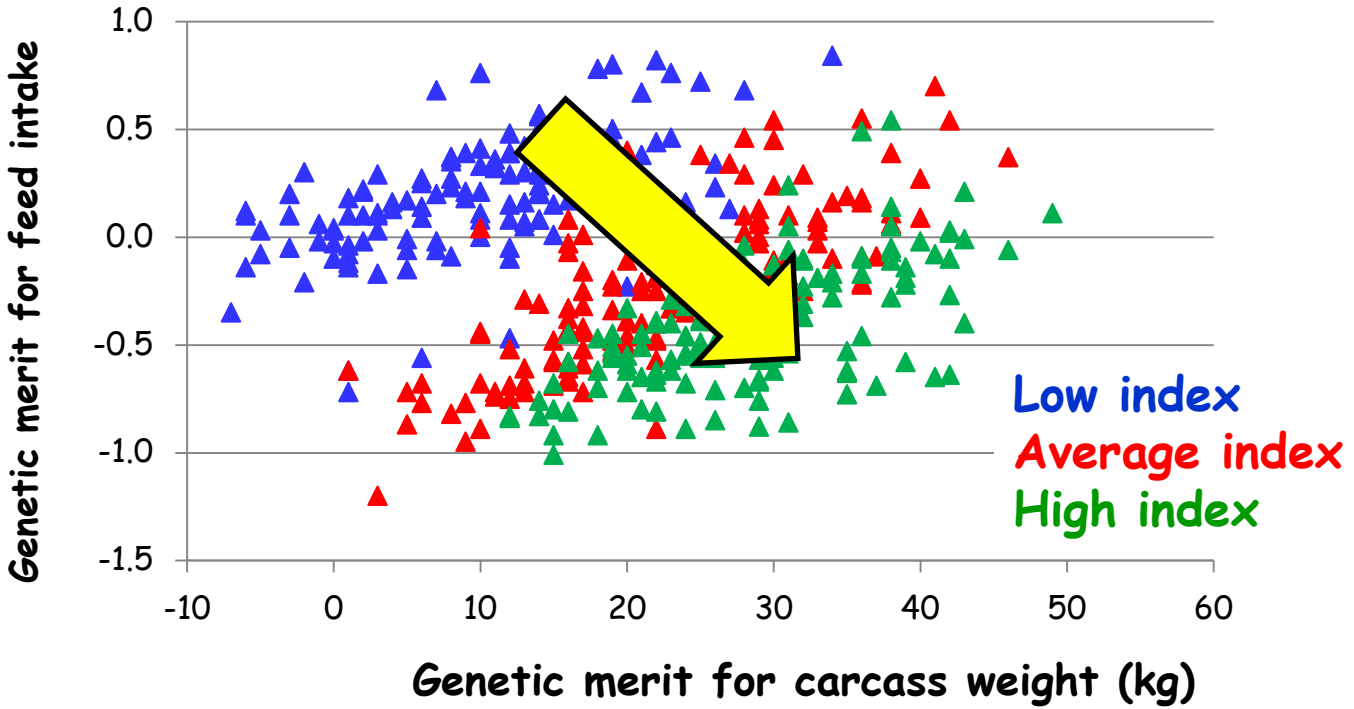


The power of breeding…..

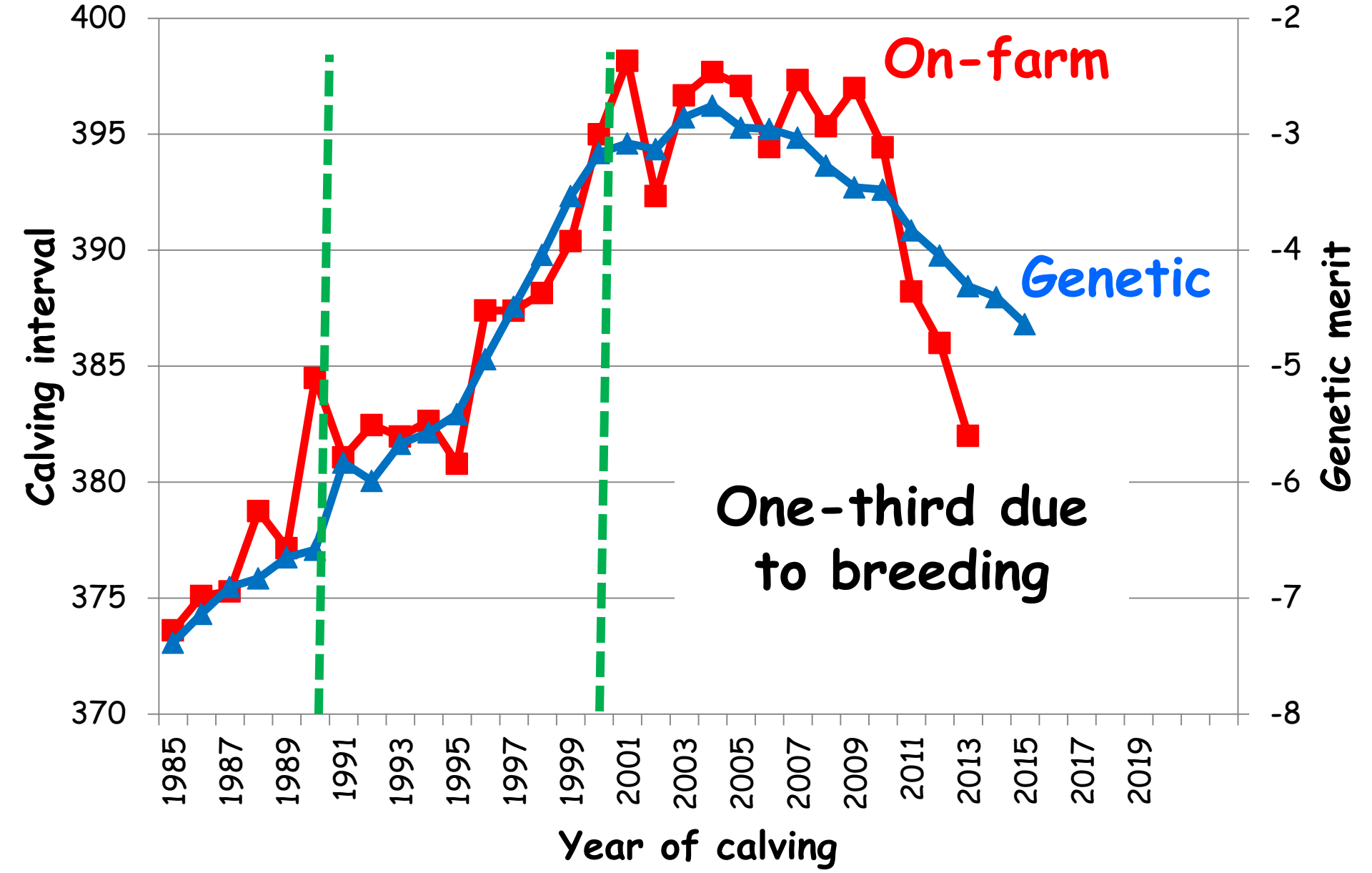


Accelerating Genetic Gain

Less days on feed and less feed per day!



The power of knowledge

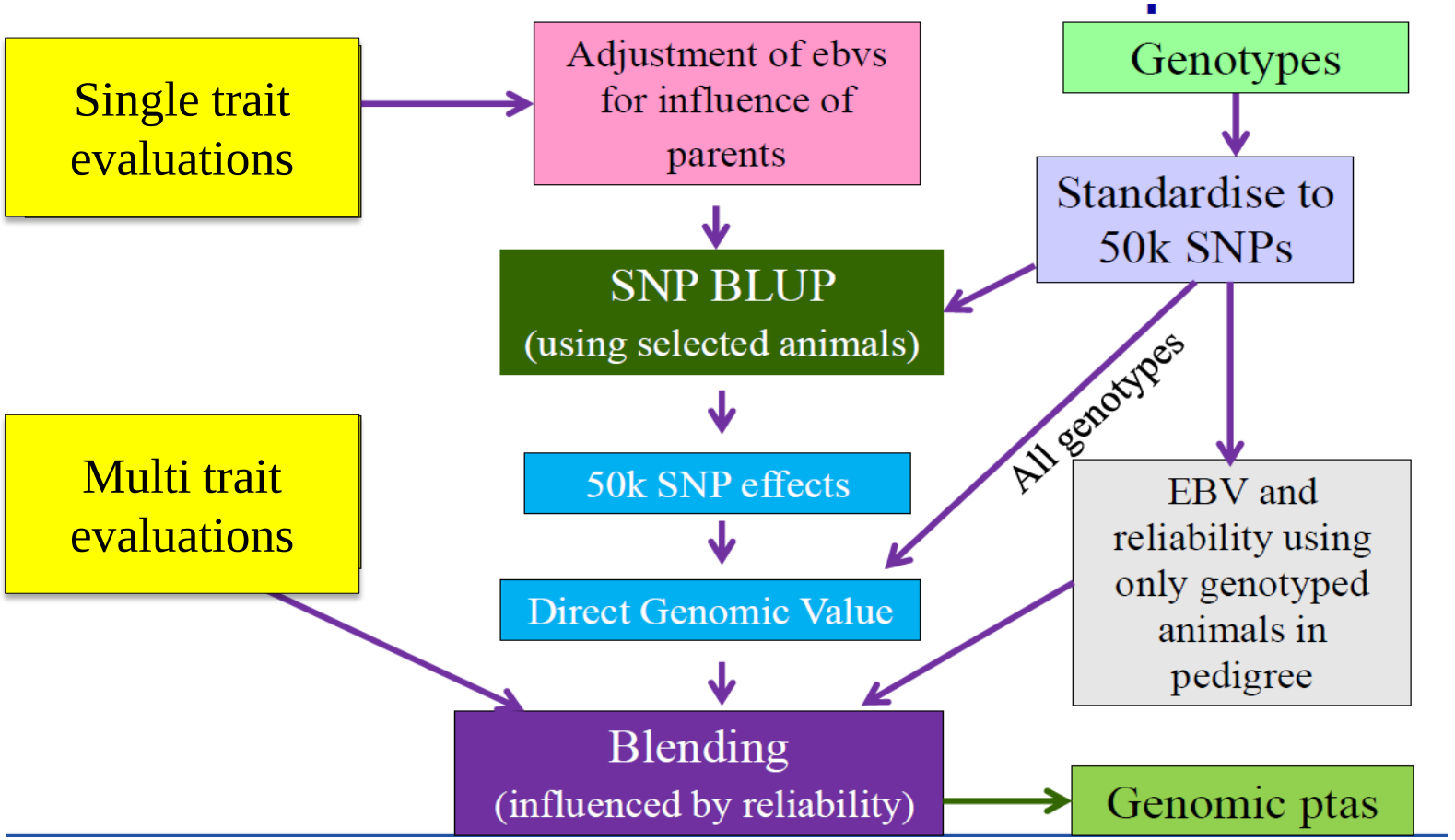


Genomic Selection in Ireland

- Second country in the world to release in 2009
- Young dairy bull reliability increased from 32% to 63% (and increasing)
  - Less fluctuations in bull proofs
  - Recommend bull team use
  - 50% increase in genetic gain
- Large scale genotyping
  - Custom genotyping panel IDB
  - Better heifer selection

Generation of genomic BVs

- Currently two-step approach



Ross Evans, ICBF,2017

- Working on one-step research

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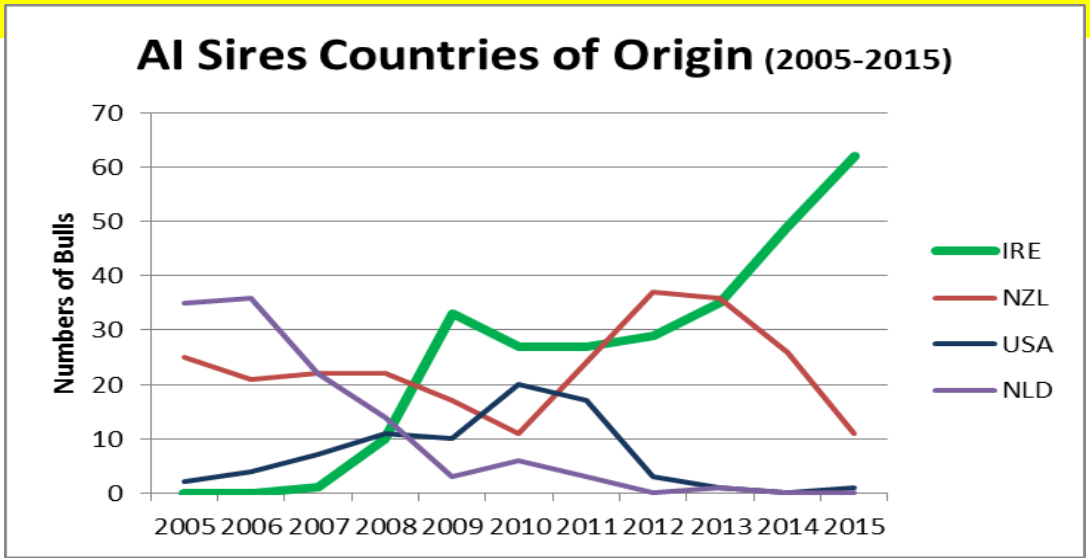
Uptake of genomic selection

	% Use	No. bulls	Ave no. bulls used	Average EBI	EBI Rel
DP-INT	5	165	2.6	€137	59%
DP-IRL	14	314	1.9	€152	88%
GS	80	319	4.8	€237	63%

Number of straws of GS bulls increasing year-on-year



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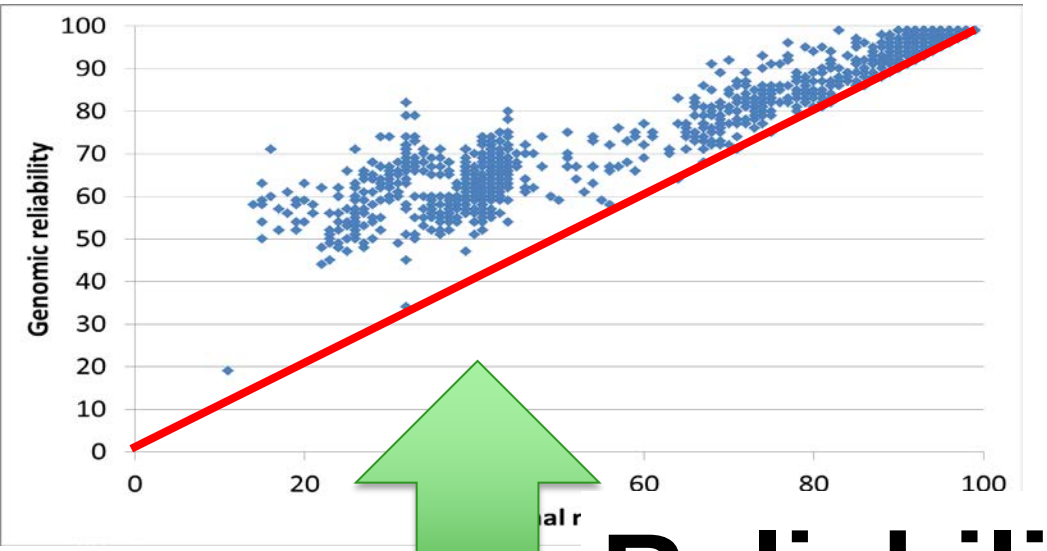
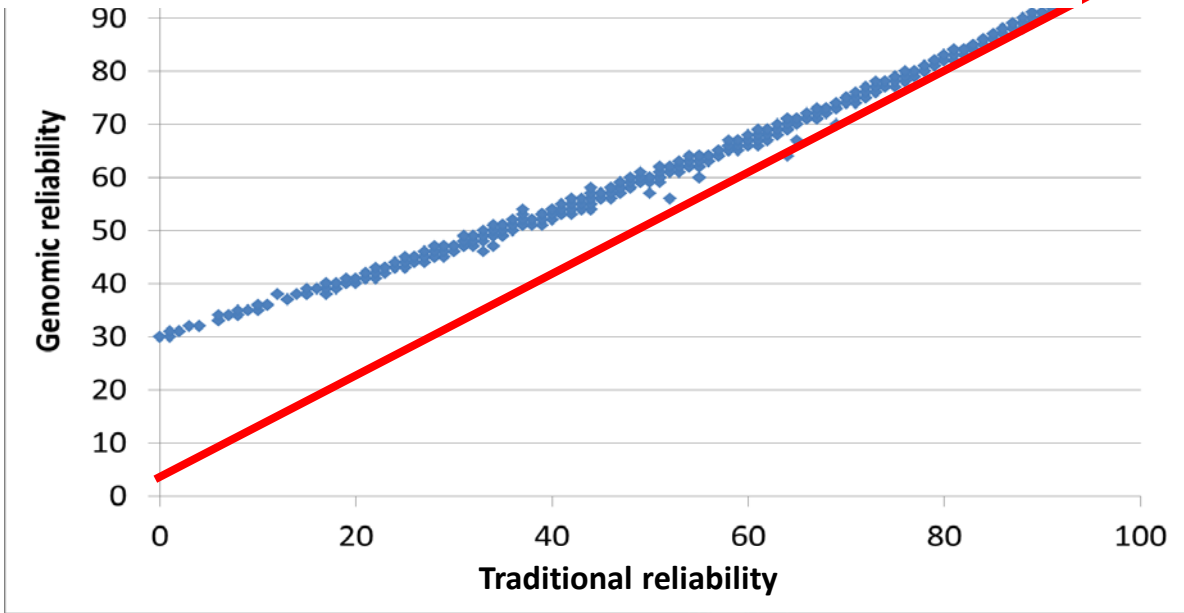
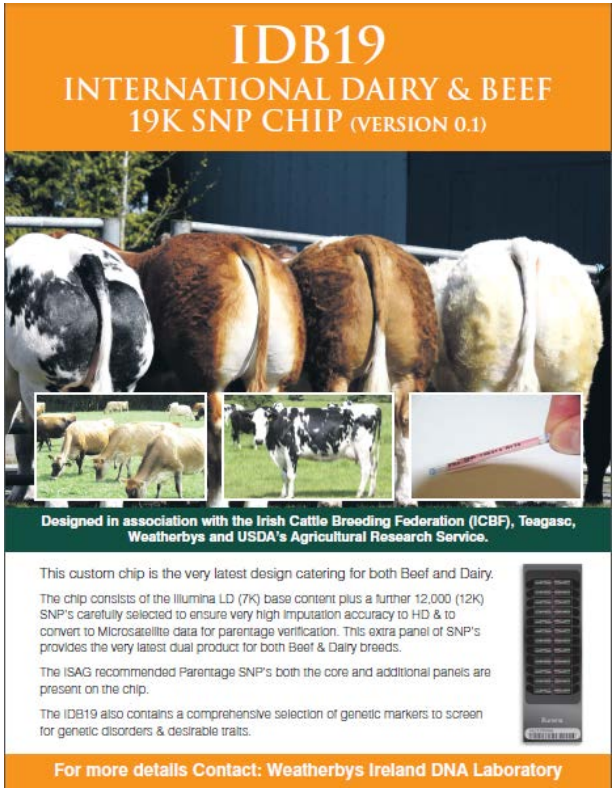
Genomic reliability



Reliability Increases



Custom genotyping panel



IDBV3

53,988 SNPs

Base Illumina Low density
40,446 - dairy genomics
5,765 impute to HD beef
1,927 impute to microsats
800 AA & HE prediction

4 lethal mutations
291 “known major genes”
5,345 research SNPs

IDBV4 in preparation

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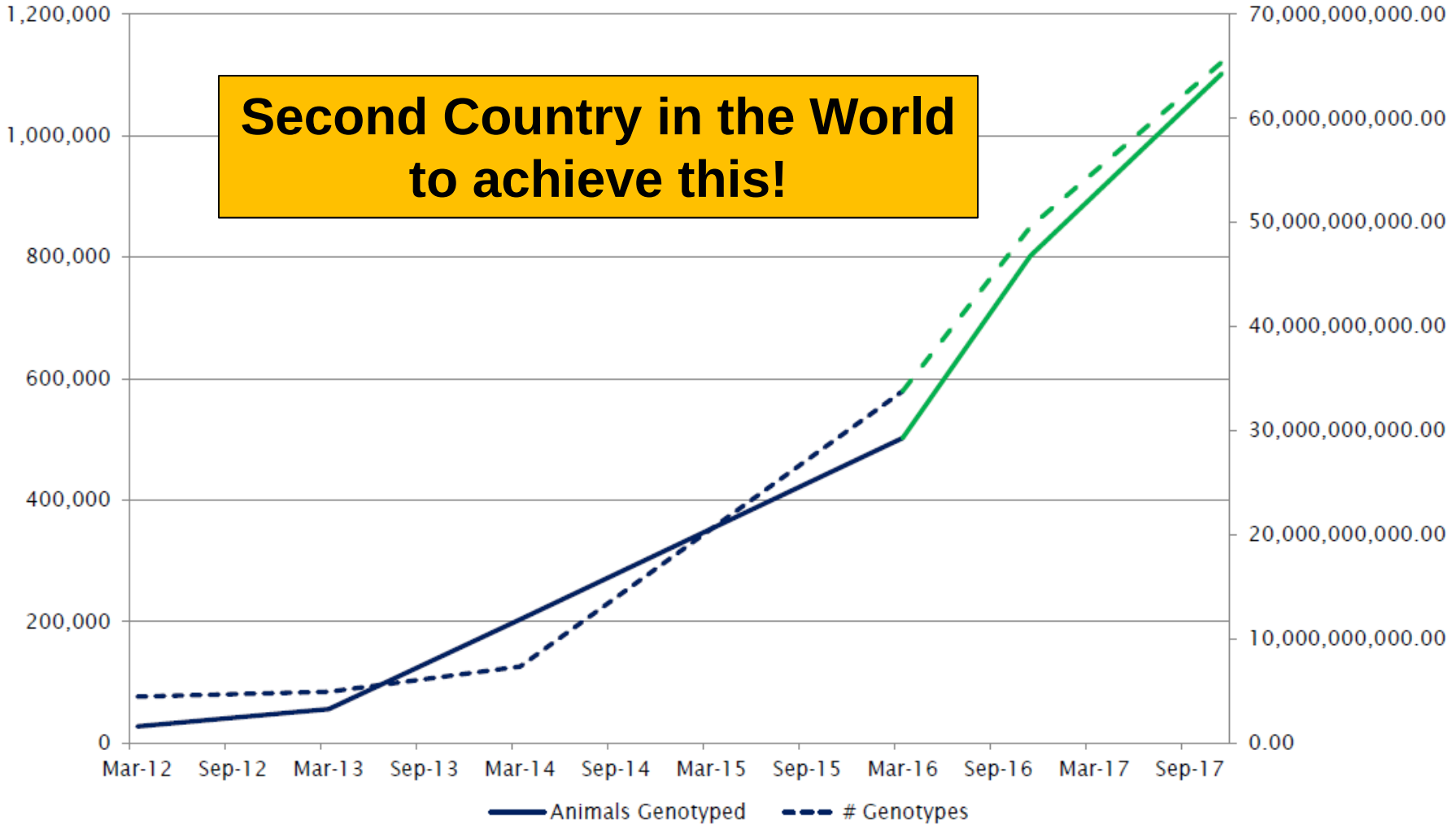
Number of genotyped cattle



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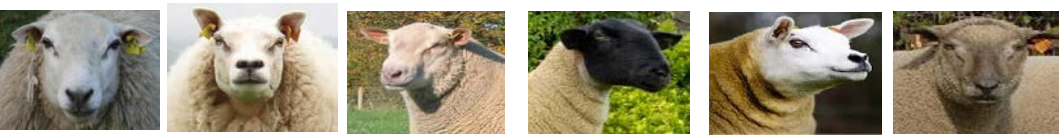
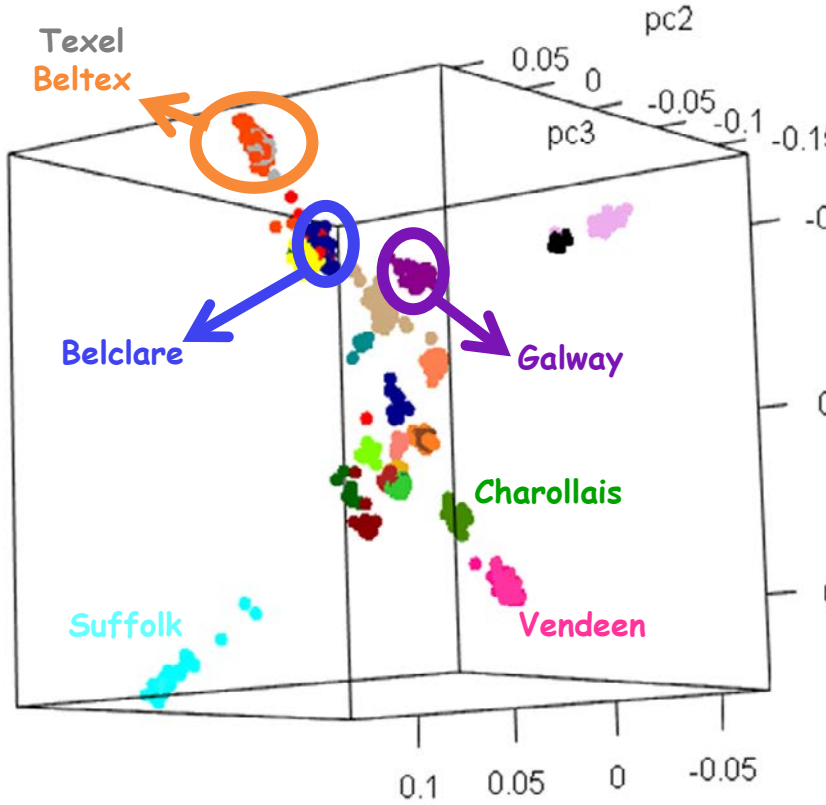
Number of genotyped sheep

Panel	Density	No. of animals
Ovine SNP50	51,135	3,512
Custom Infinium	15,000	9,378
AgR Ovine HD	606,000	303
Custom Axiom	51,135	84
Custom Axiom 11K	11,000	1902
Custom Axiom 50K	50,000	1080

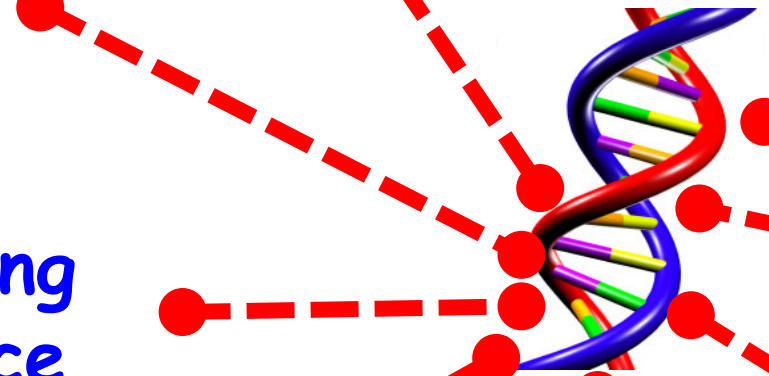
Genomic Selection focusing on 6 main breeds

Belclare Beltex Charollais Suffolk Texel Vendeen





Other applications



Parentage assignment

Increase accuracy of genetic evaluations

Traceability

Breed composition

Mating advice

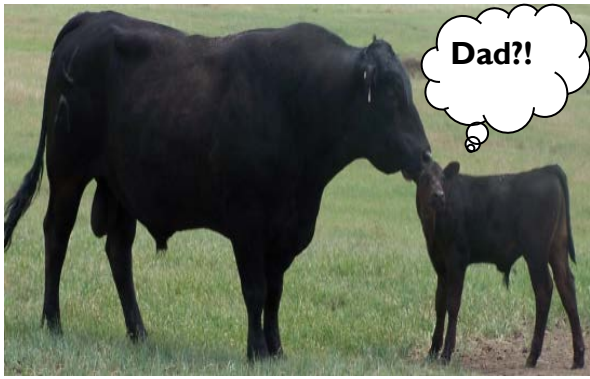
Management

Monitoring lethal genes

Inbreeding

Monitoring major genes

Determining Parentage



Sire

…..TCACCGCTGAG…..

…..CAGATAGGATT…..

…..CAGATAGGATT…..

…..GTTAGCCTGTCA …..

Offspring

Determining Parentage

Sire

…..GTCGCCGCTGAG…..

…..CTAGATAGGATT…..

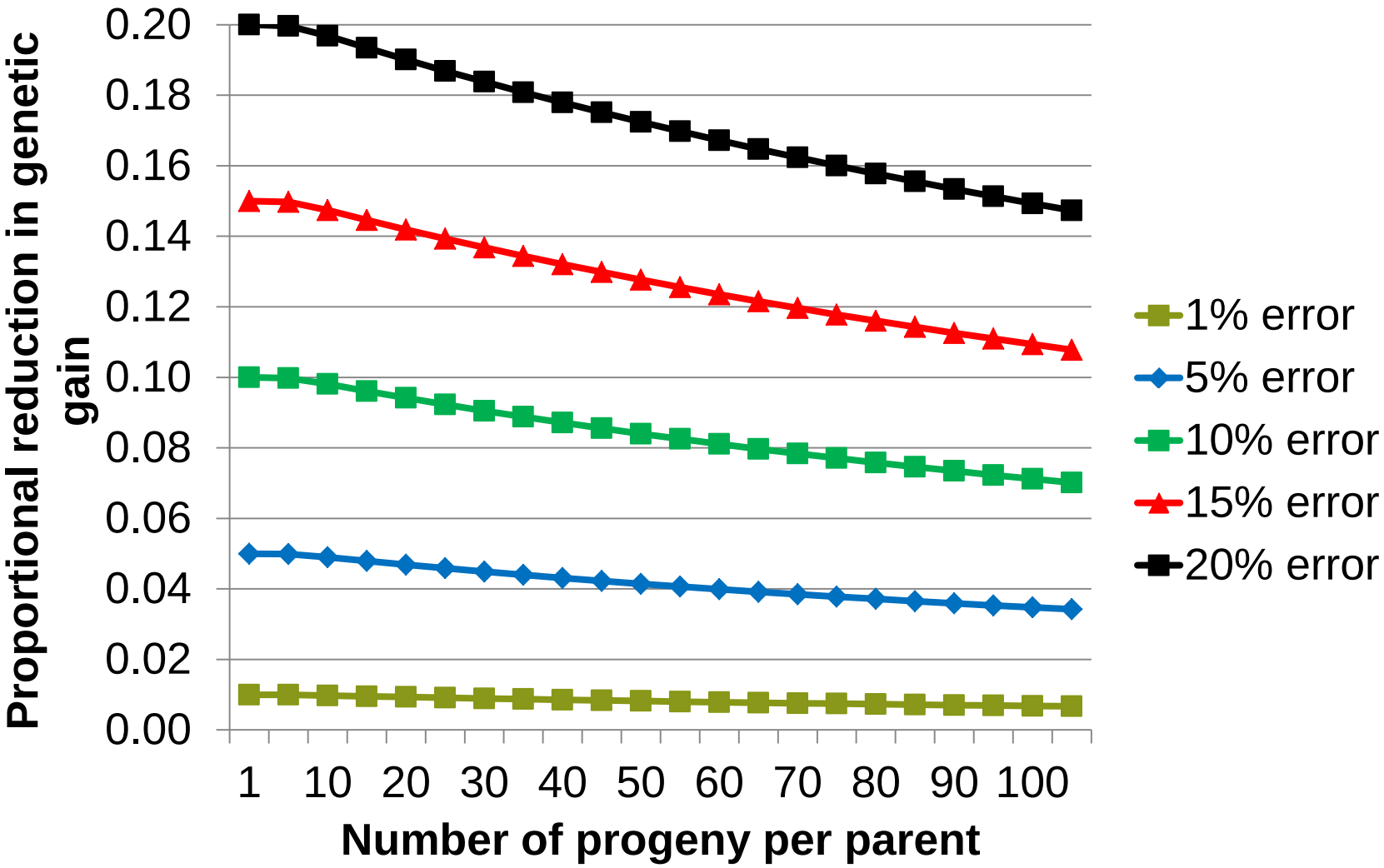
Sire-offspring errors
Dairy ~7.5%
Beef ~14%
Sheep ~13%

…..GCATTCAGTCAT….

…..GCTAGTTACTGG….

Offspring

Impact of parentage error



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Parentage resolution

Database

"Sire 1" …..ATTCGGGCTGTG…..
"Sire 2" …..CAGATAGGATTC…..
"Sire 3" …..GTCACCGCTGAG…
"Sire 4" …..GCATTCAGTCAT…..

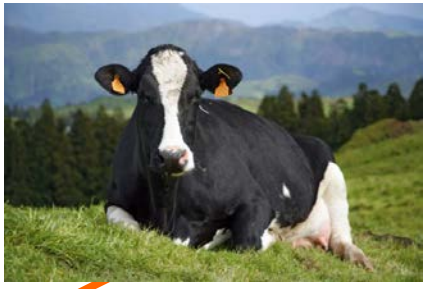
…..GCATTCAGTCAT….

…..GCTAGTTACTGG…..

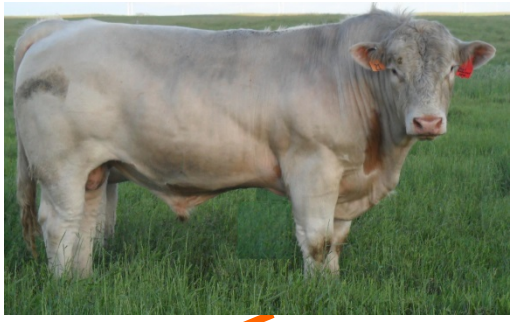
Offspring

By checking against the genotypes of all sires we can correct 80% of parentage errors

Breed Composition



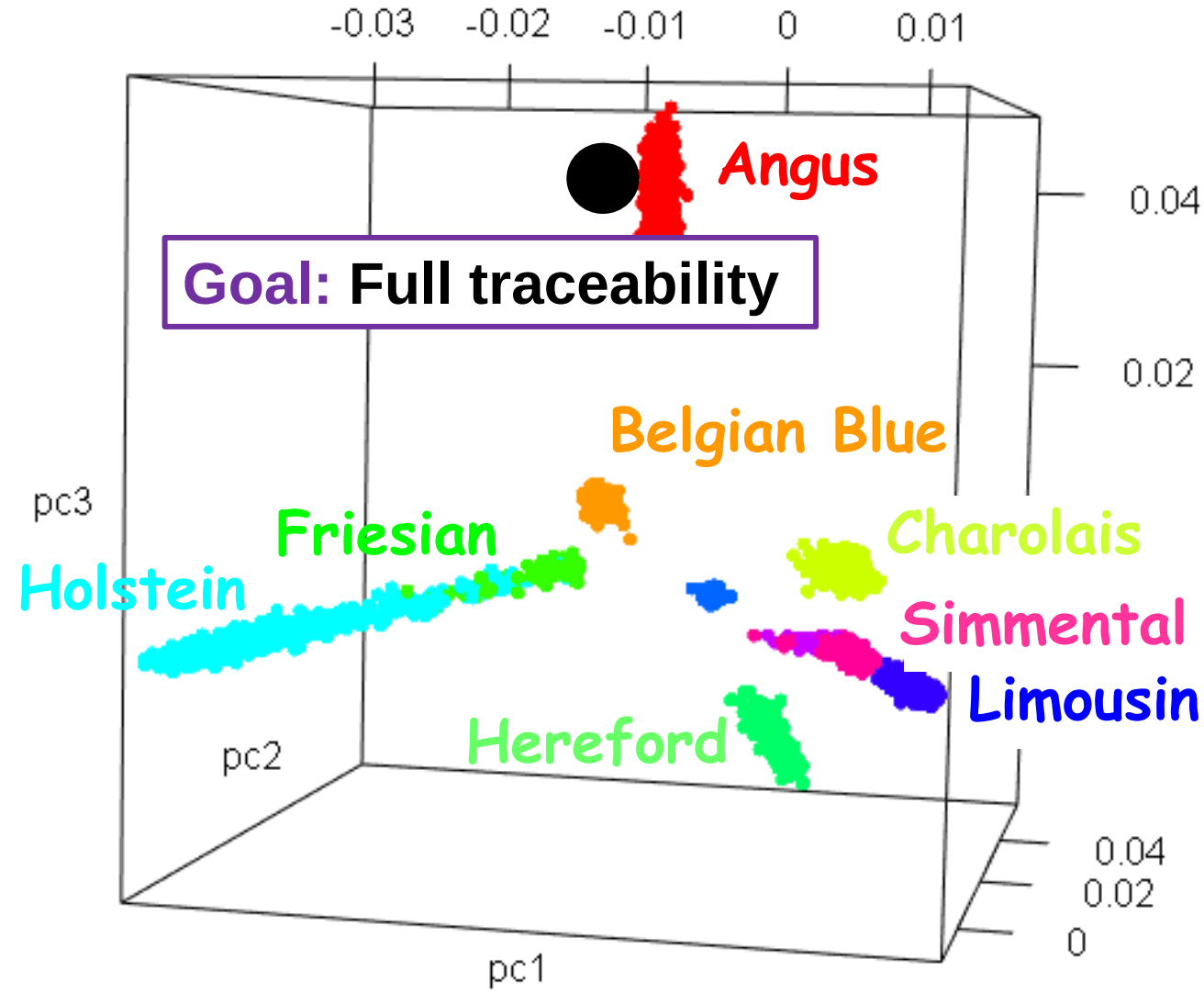
50% LM : 50% HF
(assuming parents are pure)

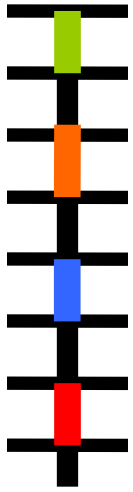


50% CH : 25% HF : 25% LM
50% CH : 50% HF : 0% LM
50% CH : 0% HF : 50% LM

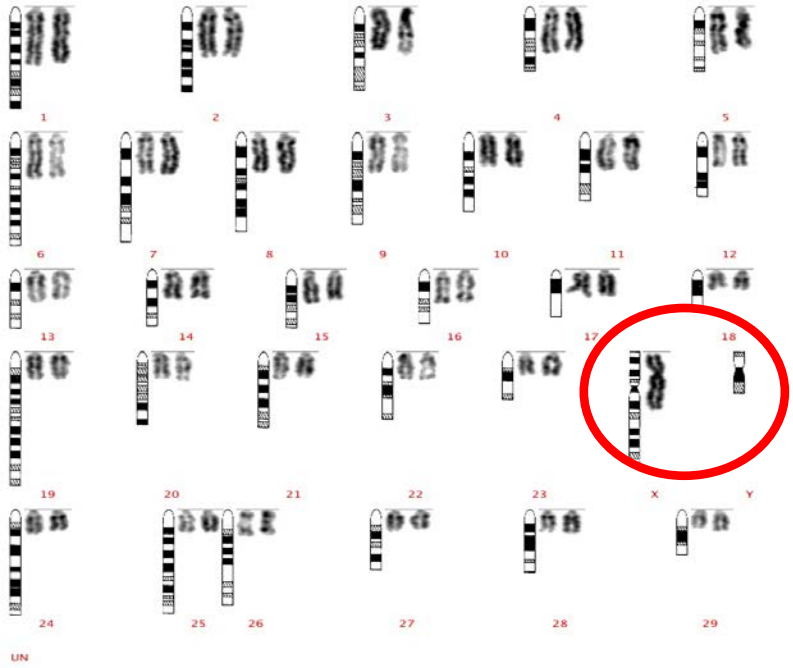
Breed Composition

- What if the animal was not genotyped as a calf?



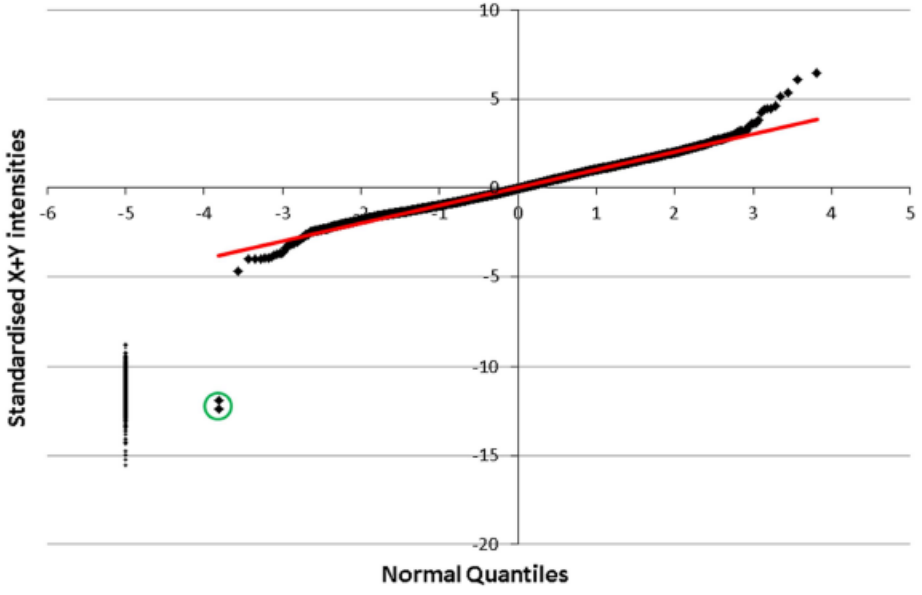


Chromosome abnormalities



- Turner syndrome
- Single X chromosome
- **Will NEVER be fertile!**

Detectable using readily available information from genotype file



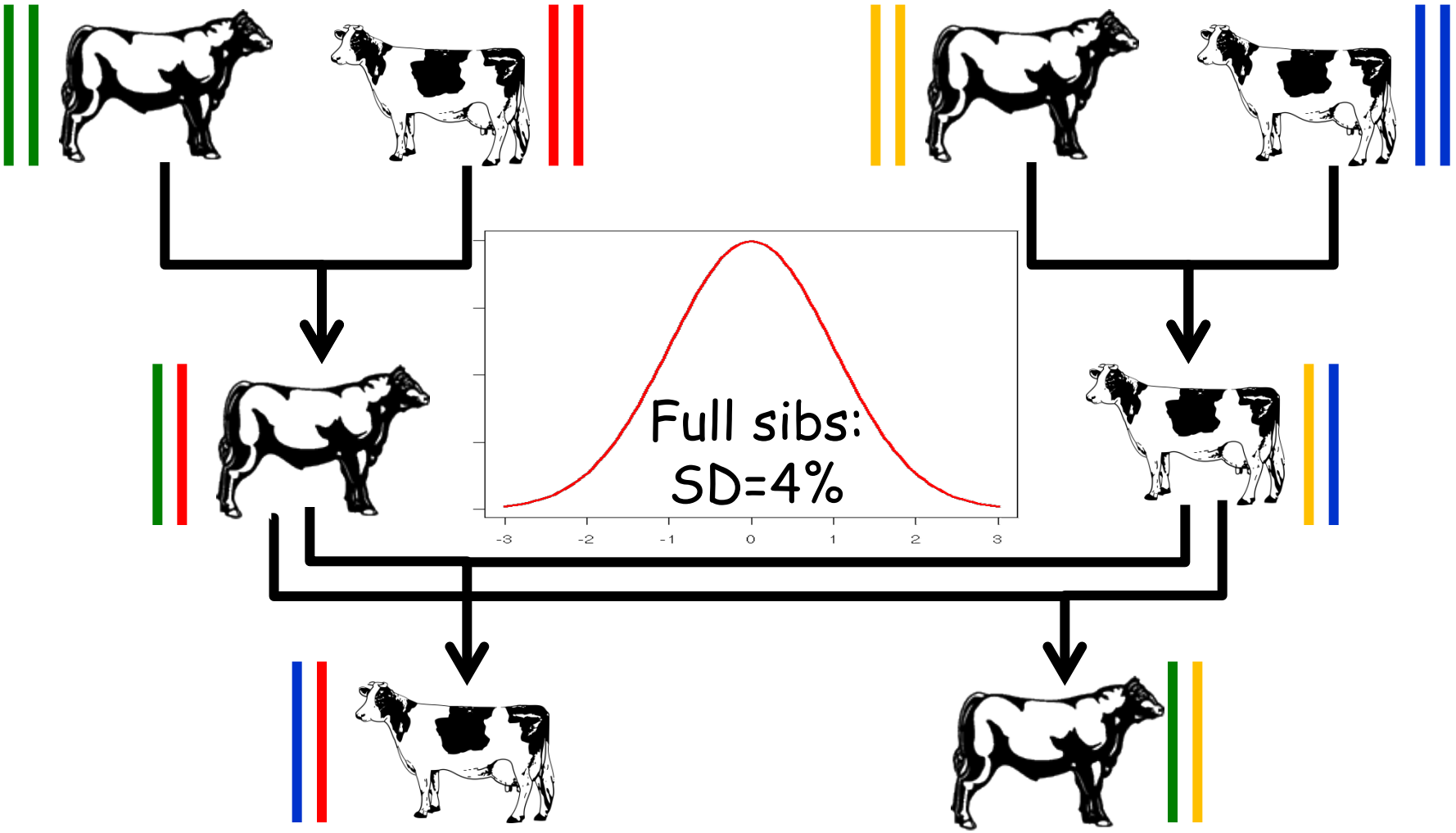
Characterization of an X-chromosomal non-mosaic monosomy (59, X0) dairy heifer detected using routinely available single nucleotide polymorphism genotype data[1]

D. P. Berry,[*2] A. Wolfe,† J. O'Donovan,‡ N. Byrne,* R. G. Sayers,* K. G. Dodds,§ J. C. McEwan,§ R. E. O'Connor,# M. McClure,‖ D. C. Purfield*

Aneuploidy in dizygotic twin sheep detected using genome-wide single nucleotide polymorphism data from two commonly used commercial vendors

D. P. Berry[1†], A. O'Brien[1], J. O'Donovan[2], N. McHugh[1], E. Wall[3], S. Randles[3], K. McDermott[3], R. E. O'Connor[4], M. A. Patil[5], J. Ho[5], A. Kennedy[1], N. Byrne[1] and D. C. Purfield[1]

Genomic Precision Matings



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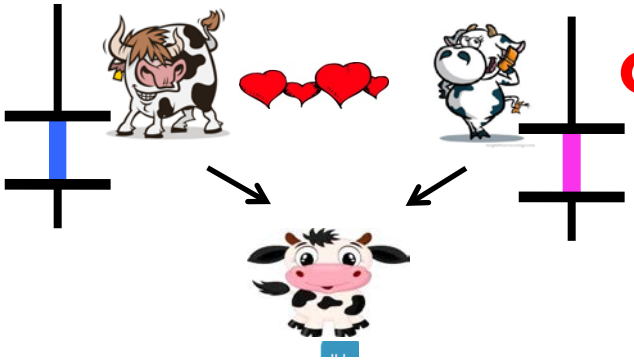
Real Examples

Same sire +same dam

3 Progeny

All Full Sibs



Genomic Inbreeding Coeffiecient

26.26%

Difference

Sire Advice Results The predicted outcome of selected matings

Standard Report | Detailed with Sub Indexes | Detailed with Traits

Showing 1 to 86 of 86 entries

Freeze Band	Tag Number	Bull 1	EBI €	Milk SI €	Fertility SI €	Calving SI €	Beef SI €	Maintenance SI €	Management SI €
165A	IE241649480165	FR2239	184	34	110	32	-2	7	4
260	IE241649440260	FR2385	195	64	95	30	-13	17	4
270	IE241182380270	FR2239	210	41	109	43	-8	14	6
294	IE241649450294	FR2239	203	48	110	42	-6	2	1
313	IE241649470313	FR2239	205	49	91	46	-4	7	6
314	IE241649480314	FR2239	199	62	82	42	-11	17	4

ICBF.com ICBF Web Application

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Click Column Heading to sort by that attribute. Number of Animals Displayed :86 Reset

umbo	Animal Number	Date of Birth	Breed	FR2239 (HO)	FR2385 (HO)	FR4021
165A	IE241849480165	07/02/07	HO (56%), FR (44%)	0.00	0.00	0.0
260	IE241849440260	02/03/09	HO (100%)	0.00	0.00	0.0
270	IE241182380270	23/04/09	HO (47%), FR (47%), UN (6%)	0.00	0.00	0.0
294	IE241849450294	16/01/10	HO (56%), FR (44%)	1.95	0.00	0.7
313	IE241849470313	16/03/10	HO (97%), FR (3%)	0.00	0.00	0.0
314	IE241849480314	20/03/10	HO (94%), FR (6%)	0.00	0.20	0.0
335	IE241849440335	18/01/11	HO (91%), FR (9%)	1.56	0.00	0.7
346	IE241849470346	13/02/11	HO (94%), FR (6%)	1.95	0.39	0.7
353	IE241849460353	18/02/11	HO (100%)	3.13	0.00	1.5
365	IE241849410365	08/03/11	HO (25%), FR (25%), JE (50%)	0.00	0.00	0.0
366	IE241849420366	10/03/11	HO (38%), FR (13%), JE (50%)	0.00	3.13	0.7
371	IE241849480371	21/03/11	HO (88%), FR (13%)	0.00	3.32	0.7
373	IE241849410373	26/03/11	HO (38%), FR (63%)	0.00	6.25	1.5
374	IE241849420374	26/03/11	HO (38%), FR (63%)	0.00	6.25	1.5

Sire Advice

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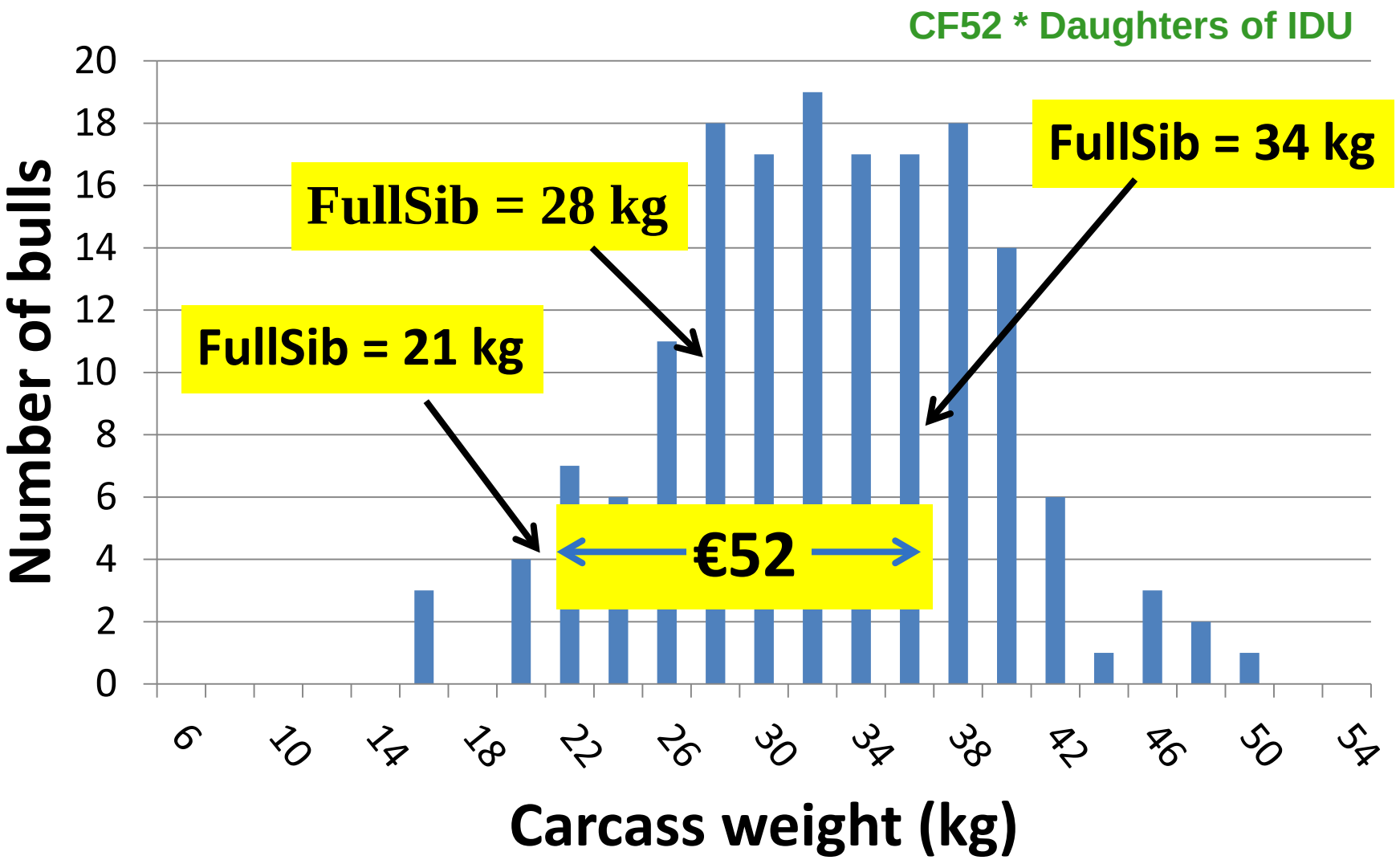
Precision genomic matings



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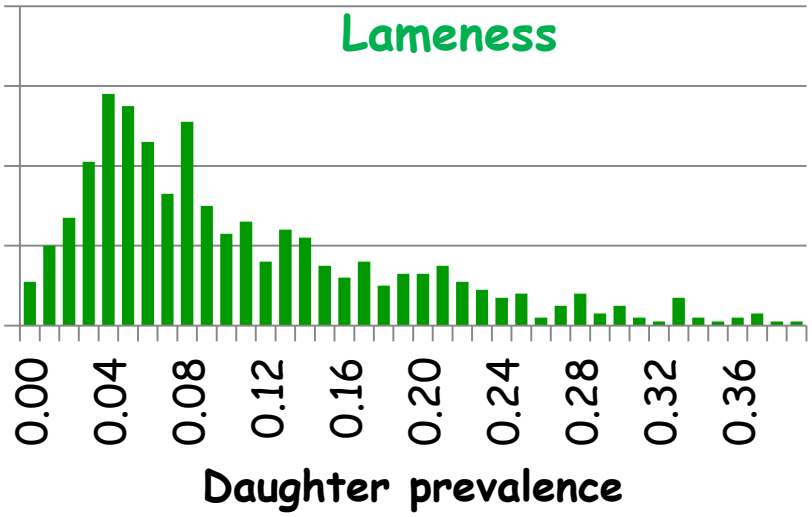
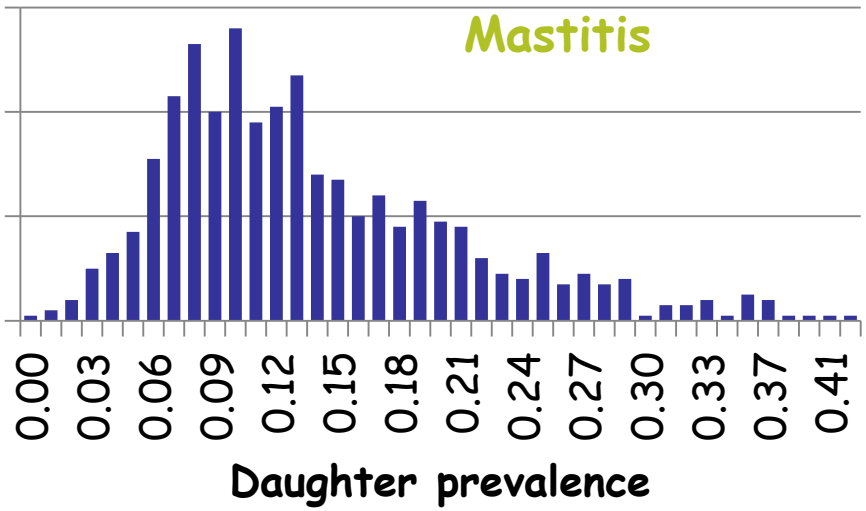
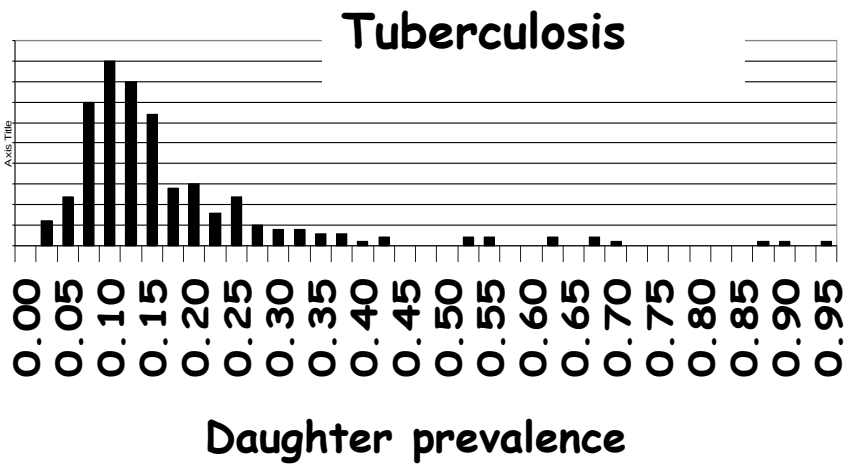
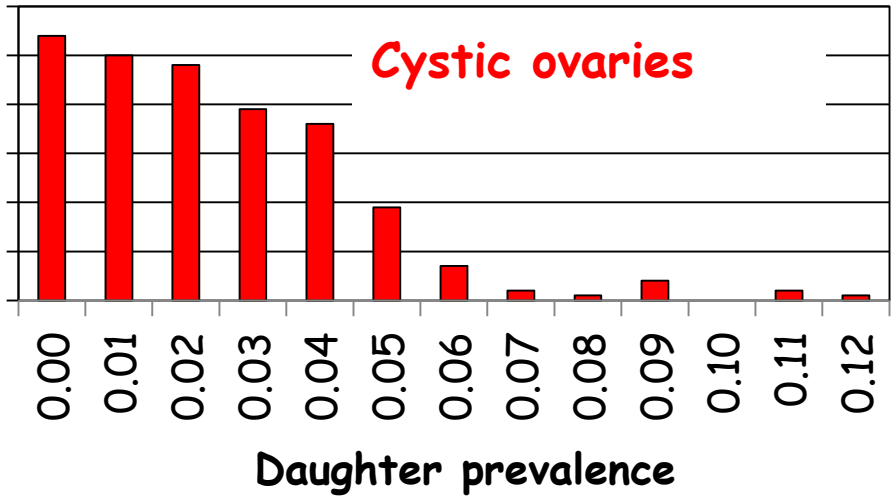
Genomic Management



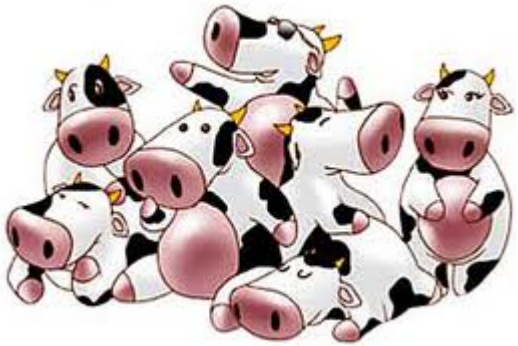




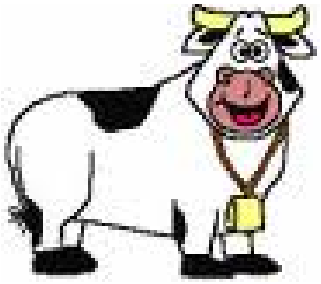


Tracking Lethal Recessives

AB



AB



AA

AB

BB

No CVM

Has CVM

Carries CVM

- Non-CVM allele (B) expressed whenever present
- CVM Allele is recessive “hidden” when with non-CVM
- Identify carriers using IDB chip
- Choose NOT to mate 2 carriers of CVM

Identifying DNA Variants

- Members of the **1000 Bull Genomes Project** + **1000 Ram Genomes Project**
- Imputed 635,000 cattle to sequence

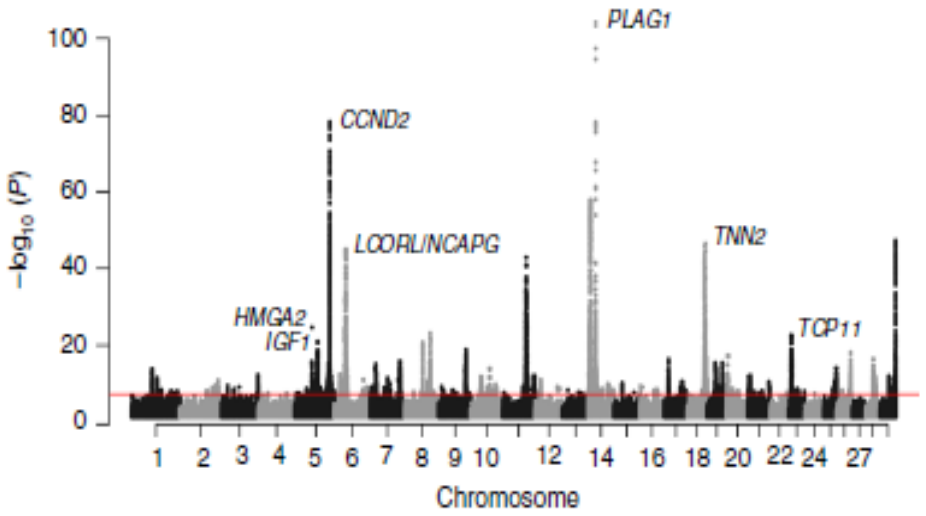
25,400,000,000,000 genotypes

Purpose: To identify DNA variants affecting performance and improve genomic predictions

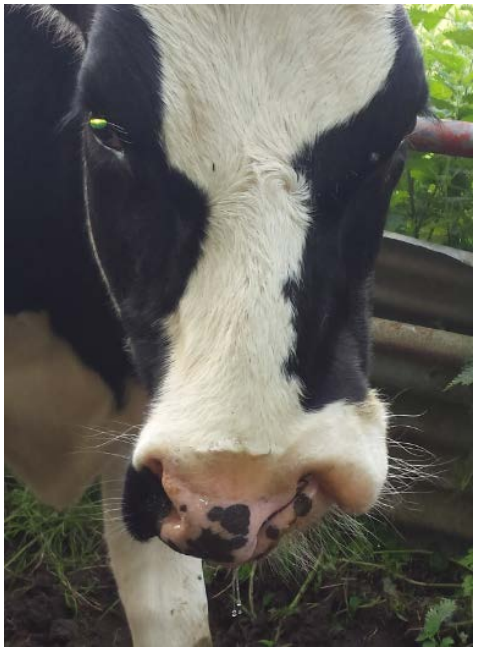
nature genetics

Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals

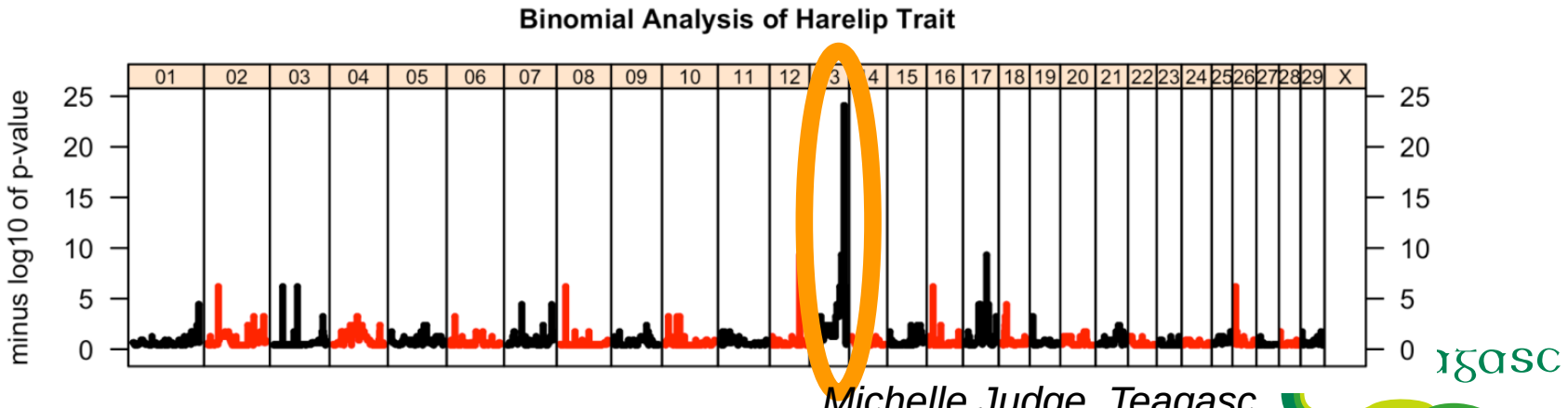
Aniek C. Bouwman, Hans D. Daetwyler, [...] Ben J. Hayes



Example hairlip mutation



- 25 cases & 25 controls
- Analysis being undertaken with sequence
- **Dominant**
  - **Sire did not express phenotype**
  - **De novo, incomplete penetrance, epistasis**
  - **Very small proportion of progeny**
    - **De novo mosaic**



Michelle Judge, Teagasc

Agriculture and Food Development Authority

Conclusions

- Inclusion of genomic information into evaluations clearly **beneficial**
  - Ongoing research for better, more efficient methods
  - Constantly evolving -> new traits
  - **Profit orientated**

•Uptake of Genomic Selection in Ireland has been high

•**Custom genotyping panel** very beneficial

•Multiple uses of DNA
  - •Parentage, traceability, breed prediction, tracking lethal recessives, genomic inbreeding, genomic management.
  - •Access to **high value markets**