IRISH CATTLE BREEDING FEDERATION

ICBF Industry Meeting; Dairy.

14th October 2014.

National Development Plan
Transforming Ireland

Dairy; 10.00 - 10.45.

- Test Day Model – John McCarthy.
- Dairy Genomics – Francis Kearney
- Next Generation Dairy Herd – Sinead McParland.

Dairy & Beef; 10.45 – 1.00

- New calving evaluations – Ross Evans.
- Health & disease data – Jen McClure.
- AI codes – Pat Donnellan.
- Data quality for genetic evaluations – Andrew Cromie.
- Interbeef genomics workshop – Andrew Cromie.

Beef; 2.00 – 4.00

- Suckler Beef Genomics – Donagh Berry.
- Value of €uro-Stars – Stephen Connolly.
- Meat eating quality – Ross Evans.
- Maternal milk score – Ross Evans.
- G€N€ IR€LAND Update – Stephen Conroy.

IRISH CATTLE BREEDING FEDERATION

Test Day Model for Milk Production Traits

14-Oct-2014

National Development Plan
Transforming Ireland

Background

- Currently calculate 305 day values for each lactation
- 305 day model uses one 305 day figure for Milk/Fat/Protein/Scc which summarises whole lactation
- Operated on contract by CRV Holland
- The 305d figures are calculated using “lactation curves” software – assume lactation curves just differ in level

Background

- Change from 305 day model to test day model where all individual recordings are directly included in evaluation.
- Instead of calculating 305 day yield and then evaluating, evaluate actual individual test day yield
- Significantly more computation required
- Use new software
- Collaboration with Finnish research institute (MTT)

Where are we

- Participated in Interbull test run Jan 2013 with initial model and HO/FR bulls for milk/fat/prot
  - Model passed that test
- Further changes made to model over summer 2013
  - Correction for Heterogeneity of Variance
  - Inclusion of later parities (5-15)
  - Other breeds (Red/Jersey/Sim-Mont)
- Participated in Interbull test run Sep 2013 with updated model milk/fat/prot for HOFR/JER/Red/Sim-Mont evaluations
  - Model passed that test

Where are we

- HO/FR Test proofs distributed 4th Oct 2013
- Industry meeting 8th Oct 2013
- Other Breeds Test proofs distributed 18th Oct 2013
- Specific heterosis included (instead of general heterosis)
- i.e. heterosis from HO*JE is NOT same as HO*FR or HO*SR
- Include breed specific heterosis (ho*fr, ho*je, ho*mo, ho*mri, scandavian red * HF)

Where are we

- Decision taken end Oct 2013 not to go with test day proofs in Dec 2013 run as had been planned

What’s happened since

- Complete re-analysis of model, focusing in particular on Fat
  - Genetic parameters
  - Evaluation Model (incl HV)
- Genetic Parameters
  - Strict data edits
    - non-ediy
      Milk recorded each year (between 06 and 13) with >=6 tests each year
    - Had >85% sire recording on replacements each year
    - Had > 50 cows (across the whole time period)
    - Had > 1000 individual tests across the whole time period
    - Remove 40 high phenotype records (Milk >60,Fat>3.5,Prot >2.2)
    - Cows had to be >24 parts ho/fr, with recorded sire
    - Parity n included only if parity n-1 already present

What’s happened since

- Genetic Parameters
  - Variants on Model for VCE tested
    - Calving Season effect
    - Herd curve effect
    - Inclusion of Wilmink (negative exponential) term
    - Reduced lactation length (scarce data at end of lactation)
    - Remove Later lactation (4,5)
    - Separate individual parities

What’s happened since

Genetic Parameters

- Variants on Model for VCE tested *(continued)*
  - Effect of bull used different times in breeding season
  - Contemporary group size (especially parity 3)
  - Age calving effect(non normal distribution)
  - Effect of “milking on” cows over winter and whether they are in calf or not
  - Effect of different profile bulls used across parity
  - Specific behaviour of residual (particularly at end of lactation)
  - Effect of calving interval
  - Effect of calving season (early/mid/late/autumn)

What's happened since

Evaluation Model

- Mostly builds on the Genetic Parameter Model
  - Ensure logical genetic groups
  - Examine changes to herd curve – and solutions
  - Examine solutions to other fixed effects
  - Specific heterosis
  - Genetic trend

What’s happened since

- External Input from MTT
- Martin Lidauer
  - Finish Research Institute
  - >16 years experience working on dairy test day models internationally
  - Has (together with student PhD Timo Pitkanen) been involved in all section of development
  - Has expressed confidence in model, from beginning

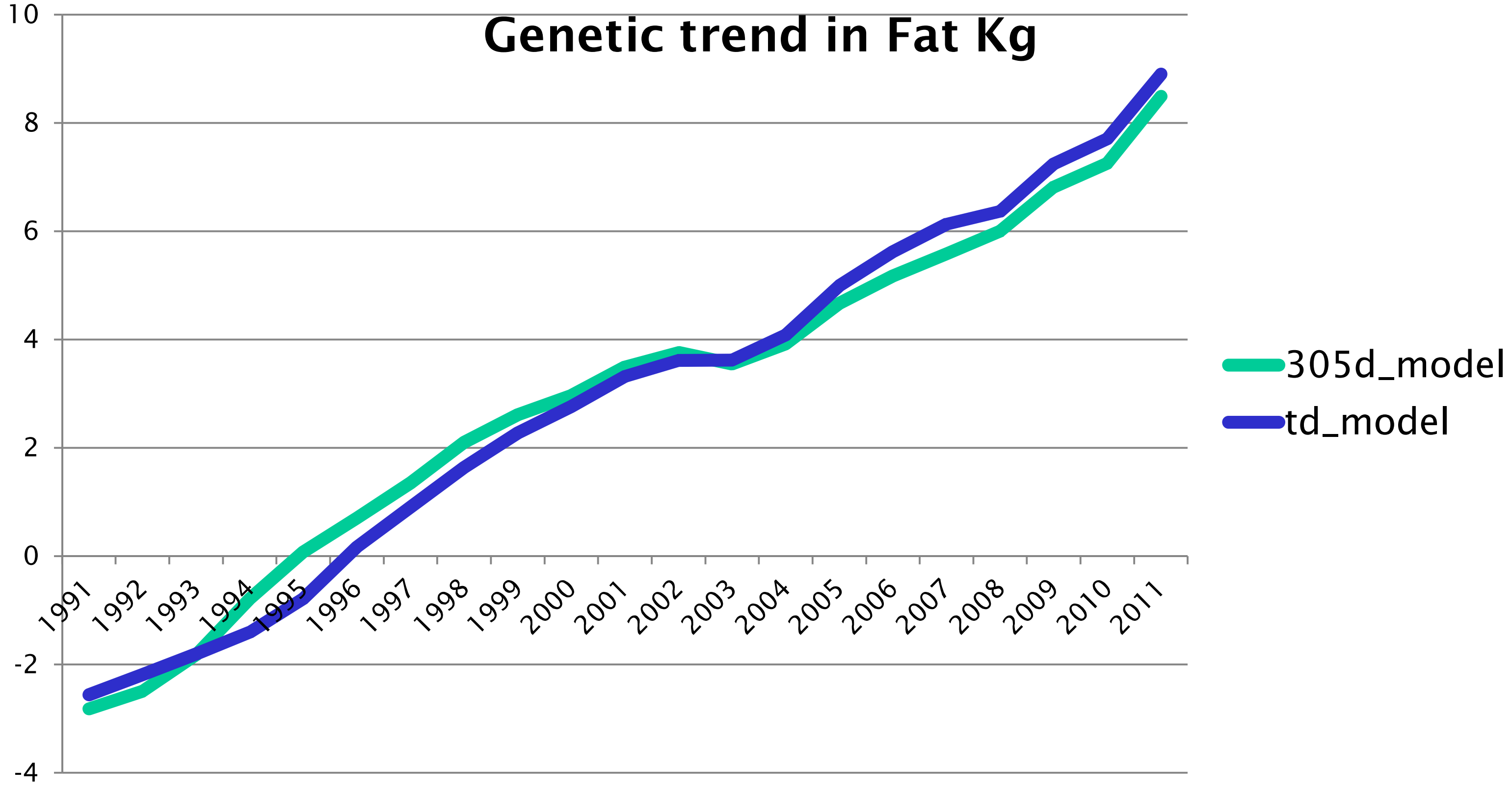
Results

- After extensive analysis (internal and external) no discernable improvement can be found to previously proposed model

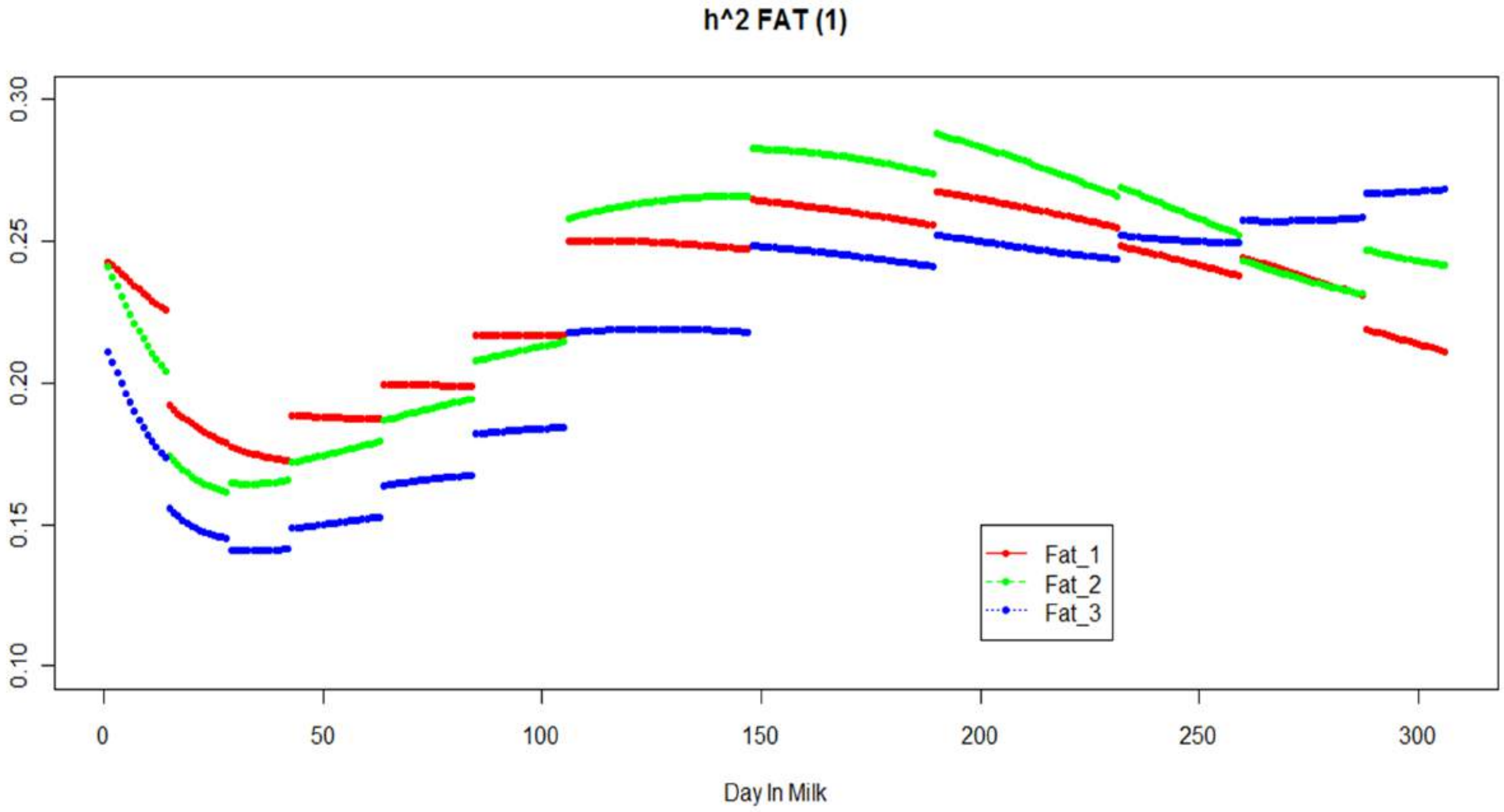
- Correlations (fat)

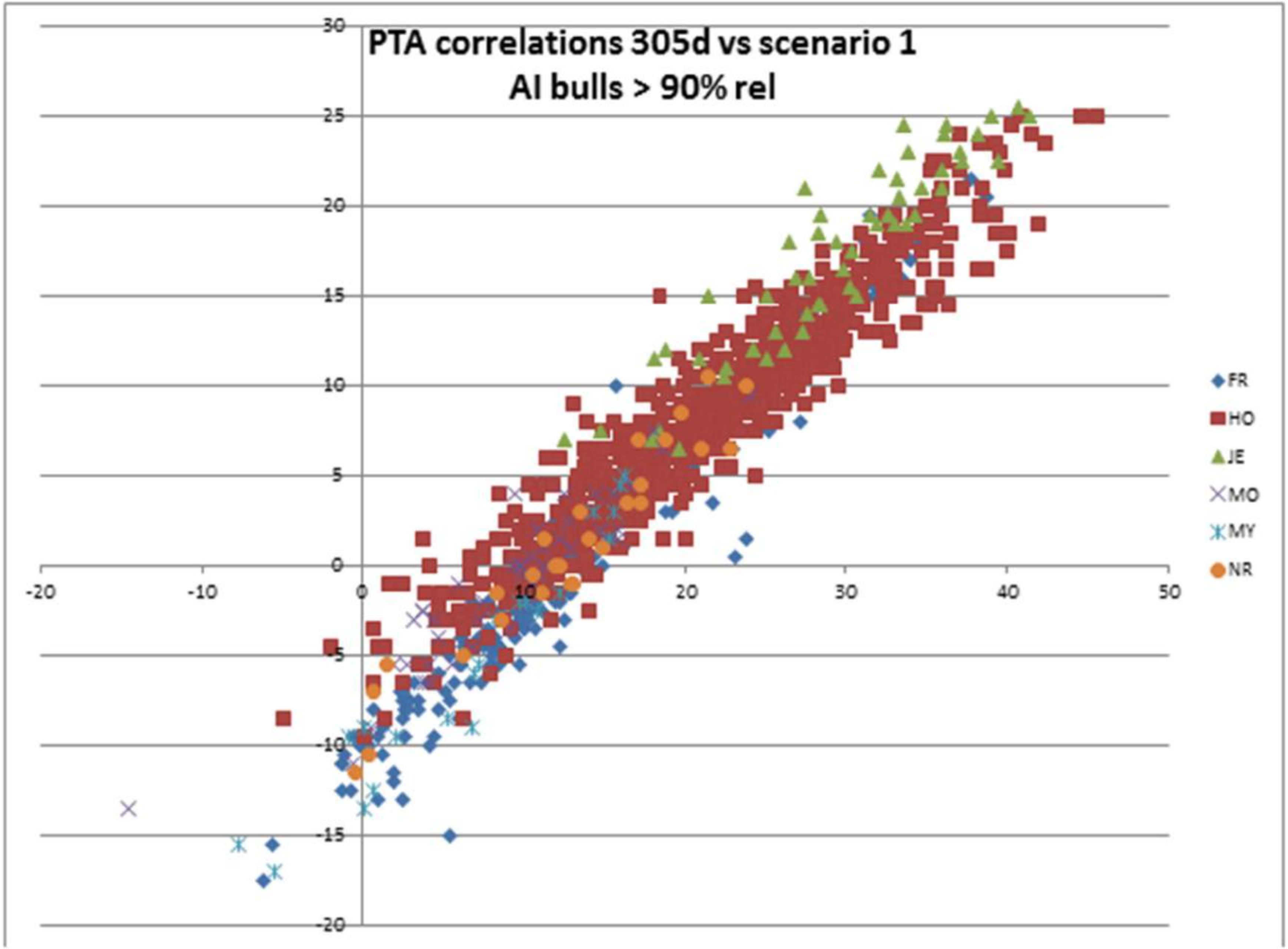
AI bulls >=99% rel	0.9688
AI bulls >=90% rel	0.9598
Cows (no hv)	0.8852

Results


Genetic trend in Fat Kg
10
8
6
4
2
0
-2
-4
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
305d_model
td_model

Results
Fat Heritability




PTA correlations 305d vs scenario 1
AI bulls > 90% rel
30
25
20
15
10
5
0
-5
-10
-15
-20
-20
-10
0
10
20
30
40
50
FR
HO
JE
MO
MY
NR

Results

- JE and NR relatively slipping back (~1Kg Fat)
- Due to Specific Heterosis

Corr	Avg Difference (Fat KG)	Breed	Num Bulls
0.95	0	HO	1048
0.97	-0.04	FR	190
0.93	-0.97	JE	55
0.93	-3.1	MO	44
0.97	-0.95	MY	21
0.96	-1.58	NR	20
0.95	0.41	SR	6

Results
Specific heterosis effects

Effect	Parity	Solution	Parity	Solution	Parity	Solution	Total effect (full Lact)
fr*ho	1	0.010	2	0.010	3	0.012	3.25
ho*je	1	0.040	2	0.045	3	0.051	13.83
ho*mo	1	0.028	2	0.027	3	0.033	8.95
ho*my	1	0.013	2	0.014	3	0.016	4.37
srs*hf	1	0.015	2	0.021	3	0.027	6.41
rec	1	0.001	2	0.002	3	0.001	0.41

Units are KG Fat/day

KG Fat/lact

Couple High Profile Bulls

Bull	Change in Fat Kg
GMI	-0.57
JOS	-1.06
LBO	1.12
MAU	-1.46
MFX	-1.34
NHS	-0.62
RDU	0.95
RUU	1.37
TIH	-3.31
UYC	2.92

Remember value of Fat in EBI is €1.04 per Kg fat

Only differences shown as any base change will effect actual level

Example bulls; Big movers up

TAG	NAME	YOB	BREED	Change Fat KG
MMU	MACOMBER O-MAN BOGART	2004	HO	9.47
RUD	RUTLAND DURBAN	1975	FR	9.18
DZM	DANSIRE OMAN OMAR	2004	HO	9.08
ROY	ROBINVIEW ROYALIST	1987	FR	8.78
TTY	TIMMER TYSON	2004	HO	8.68
GDZ	HALLSTONE GRAND MAN 1	2006	HO	8.38
GJM	GRAN-J OMAN MCCORMICK	2004	HO	8.17
JAY	GENUS JAYSON	1996	HO	8.15
OJI	O-BEE MANFRED JUSTICE ET TV	1998	HO	7.3
ORL	DANSIRE OMAN ORLA	2004	HO	7.3
PGI	PENN-ENGLAND GARRISON-ET	2000	HO	7.27
TPO	TOPSPEED H POTTER	2000	HO	7.16
HBX	HOLBA MORTLANE	2003	HO	7.13
BQN	BRIDEPARK OMAN	2007	HO	6.94
GWY	BRAEDALE GOLDWYN	2000	HO	6.9

Example bulls; Big movers down

TAG	NAME	YOB	BREED	Change Fat KG
HAP	HALLALI	1992	MO	-14.5
FAA	FREEBROOK SEXATION ANDY ET	1982	HO	-11.34
PEN	PITTENDREICH BARON	1982	HO	-10.97
EVC	ERNLO CHAIRMAN VALIANT	1984	HO	-10.78
KVB	KIN-VALE JO BELL LUCAS-ET	1982	HO	-10.04
LES	LESTER	1991	HO	-10.03
CSL	CLASH STERLING 2 ET	1989	HO	-9.92
ACC	A CARNATION COUNSELOR ET	1982	HO	-9.4
SKG	STRICKLER MGM GAMBLER ET	1980	HO	-9.39
DAS	DUREGAL ASTRE STARBUCK ET	1986	HO	-9.32
HHK	HANOVERHILL STARBUCK	1979	HO	-8.93
BVN	BOIS LE VIN	1986	MO	-8.06
BJN	BROEKS JOMAN	1993	HO	-8.06
CCE	CASABIANCA CLEITUS ODEON	1988	HO	-8.06
AHW	A HILLTOPPER WARDEN	1977	HO	-7.97

What’s next

- Continue validation of HV correction with MTT
    - This adjusts (slightly) proofs where there is difference in variance.
- Ensure previously work here is ok
- Submit again to Interbull Jan 2015

ICBF.com

IRISH CATTLE BREEDING FEDERATION

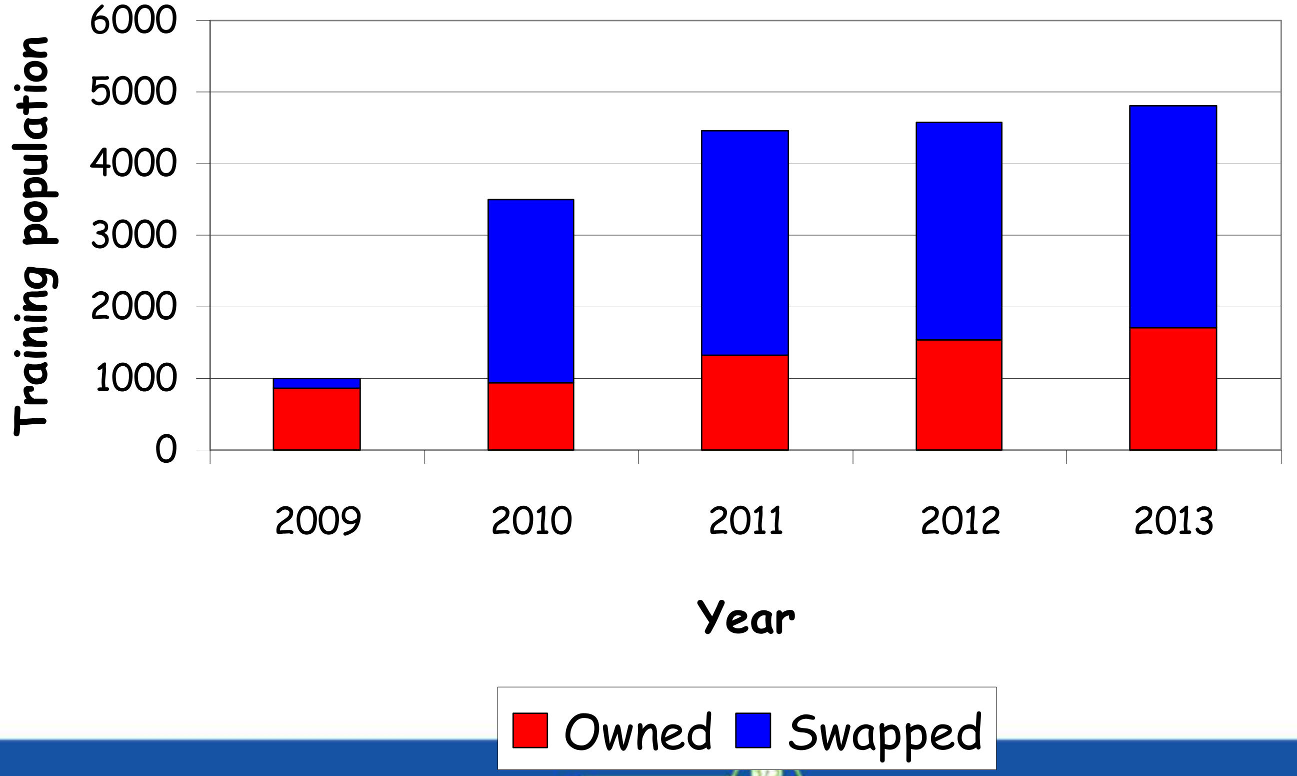
Review of Genomic Evaluation

14th October 2014.

NDP
National Development Plan
Transforming Ireland

Genomic Evaluations

- Introduced in Feb 2009 with ~1000 bulls in the reference (training) population for production
- Less animals in ref. population for most other traits



Genomic Evaluations

- Main method of validating how well genomics is working is to look at the original genomic proof versus the current daughter proof
- 2011 an adjustment was made to the milk production sub-index – overestimate was €9
- Genomic proof is an estimate of what an animal's genetic merit is at 99% reliability, not a bulls first crop proof @80% reliability

Data

- 190 bulls who had a genomic evaluation and now have a progeny based evaluation

Year	No. Bulls
2009	35
2010	39
2011	63
2012	53

Results

- Average PTA (reliabilities in brackets)

	Genomic	Daughter	PA	Genomic Only
Milk	108 (61)	116 (90)	168 (41)	146 (56)
Fat	10.2	10.4	11.9	10
Prot	7.7	7.8	9.6	8.1
CI	-3.7 (46)	-4.5 (71)	-3.1 (30)	-3.23 (45)
SU	1.7	2.01	1.52	1.37
CD	1.9 (50)	2.7 (90)	3.05 (37)	2.44 (45)
Gest	-2.05	-2.7	-1.5	-1.8
Carcase Weight	-3	-1.55	-1.39	-2.6
Carcase Conf	-0.67	-0.64	-0.56	-0.63

Results

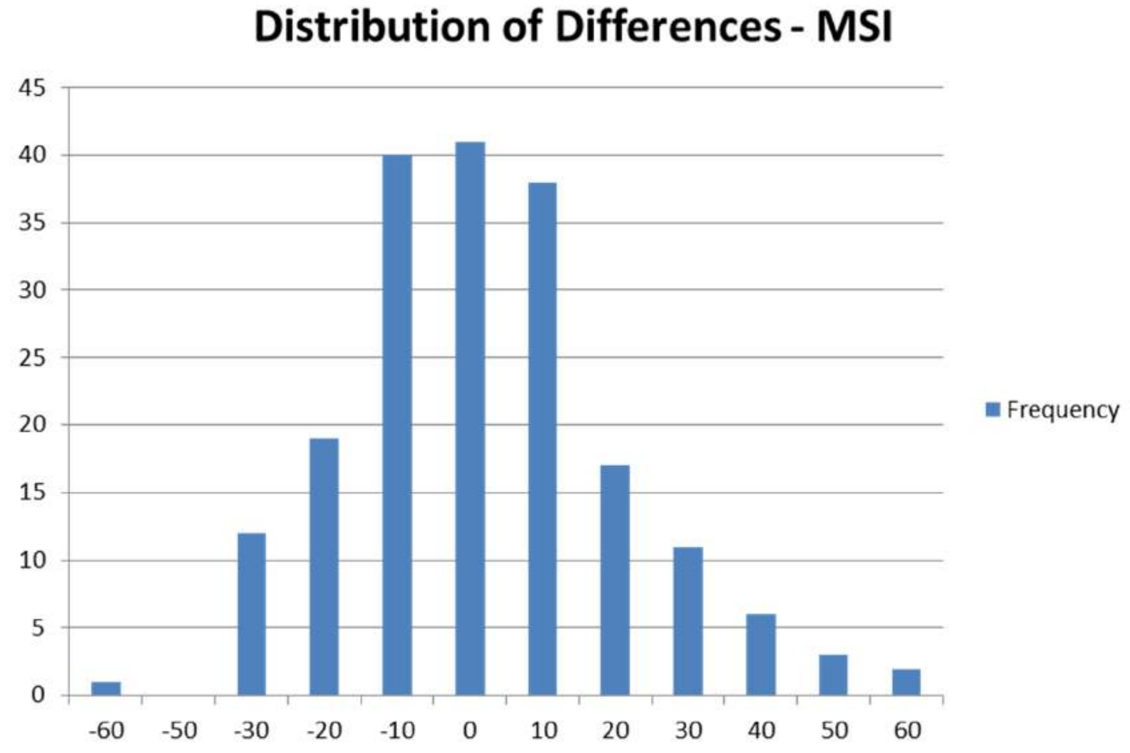
- Correlations to proven proofs

Correlation with DP	Genomic	PA	Genomic Only
Milk	0.79	0.71	0.76
Fat	0.7	0.55	0.68
Prot	0.75	0.63	0.75
CI	0.63	0.6	0.59
SU	0.63	0.41	0.61
CD	0.44	0.36	0.34
Gest	0.6	0.5	0.49
Carcase Weight	0.5	0.5	0.44
Carcase Conf	0.51	0.51	0.49

Results

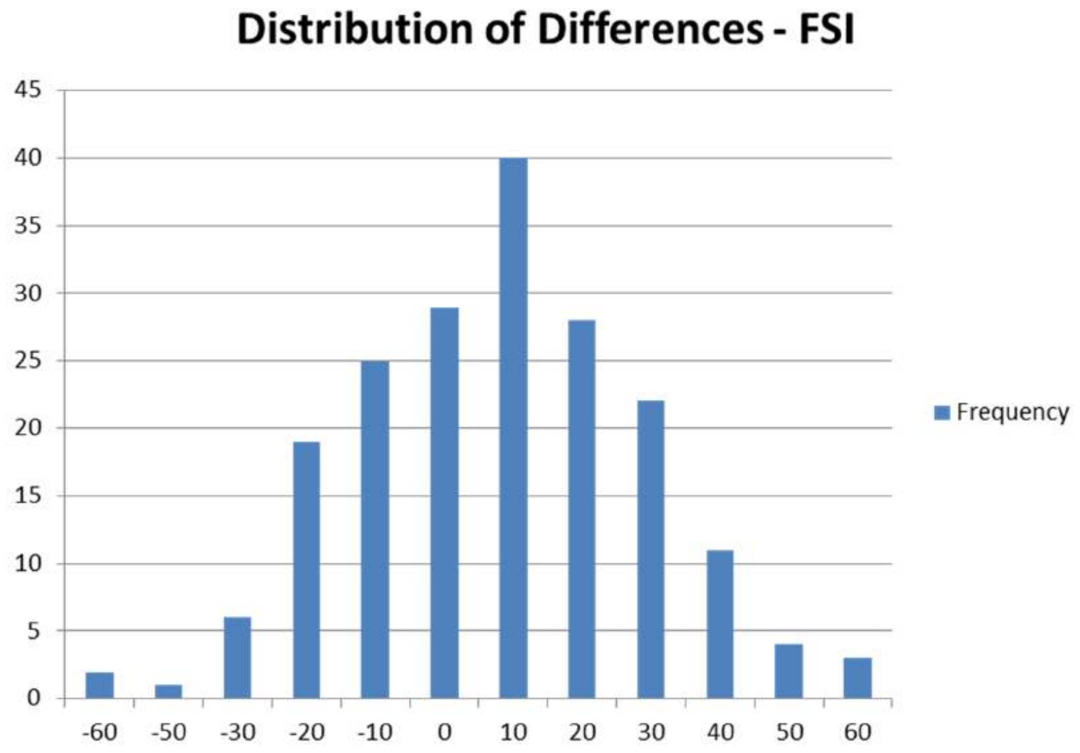
- Expected difference among bulls – average MSI -€3

(daughter proof is greater than genomic proof)



Results

- Expected difference among bulls – average diff FSI of €12 (daughter proof is greater than genomic proof)



Results

- Results are broadly in line with expectations
- Group average is performing as expected
- Some large difference among individual bulls

(can expect ± €75 @ 60% EBI reliability)

- Blended results are proving robust
- Calving may be underestimated (influence of major genes?)
- Use minimum group of 5 genomic bulls and don’t overuse any one bull

Next Steps

- Document and publicise the results of the validation
- Increase the number of animals in the reference population
  - Foreign bulls
  - Cows
- Research on multi breed genomics

GMACE

- GMACE are international evaluations of young bulls
- Published for the first time in August
- Received evaluations for ~9,000 young bulls
  - Production
  - Longevity
  - Fertility
  - Calving
- We did not submit evaluation to GMACE in August run
- Test proof will be made available
- Plan will be to publish them at next official run
- Will still expect a genotype of all foreign bulls before marketing

Next Generation Herd

Update
October 2014

Next Generation Herd - Objective

Genetically elite and diverse research herd

1. Breeding cows compatible to Irish grass based production system
2. To facilitate the monitoring of difficult to measure traits
    - Cow health, greenhouse gas emissions, intake
    - Deleterious consequences of genetic selection?
3. To enhance the development of the EBI
    - Identify new traits

Genetic Potential

	Elite (n=90)	Average (n=45)
EBI	244	133
Milk SI	67	48
Fertility SI	169	63
Calving SI	35	28
Beef SI	-12	-9
Maintenance SI	13	4
Health SI	0	0
Management SI	2	0

Experimental Groups

- All first & second parity animals
- Split across 3 experimental groups
  - Low grass allowance, High concentrate & Control

Feeding Treatments	Control	LGA	HC
Target Post-Grazing Residual (cm)	4.5	3.5	4.5
Annual Concentrates (kg)	300	300	1200

Milk production to date . . .

	National Avg			Elite		
21/09/2014	CON	LGA	HC	CON	LGA	HC
Milk yield	4134	3808	4933	4188	3975	4765
Fat (%)	4.20	4.17	4.10	4.55	4.57	4.36
Protein (%)	3.46	3.43	3.52	3.61	3.61	3.72
Milk solids	316	288	375	341	324	384
Cumulative MS yield	327 (kg/cow)			349 (kg/cow)		

Mature equivalents . . .

	National Avg			Elite		
21/09/2014	CON	LGA	HC	CON	LGA	HC
Milk yield	4611	4247	5502	4671	4434	5315
Fat (%)	4.20	4.17	4.10	4.55	4.57	4.36
Protein (%)	3.46	3.43	3.52	3.61	3.61	3.72
Milk solids	353	323	419	381	363	429
Cumulative MS yield	365 (kg/cow)			391 (kg/cow)		

Fertility to date . . .

	Average	Elite
3 wk submission rate (%)	82	92
6 wk in-calf rate (%)	60	77
12 wk in-calf rate (%)	78	95

Service Sires Used 2014

Cows				Heifers	
Bull	**EBI**	**Bull**	**EBI**	**Bull**	**EBI**
AKZ	279	PHC	337	BGJ	289
DGC	280	WLY	327		
GXY	259	WTC	290	CWJ	251
GZY	376	YAD	342	WAU	257
JRE	312	YKG	317		

Conclusion

- To date . . .
- Higher genetic potential animals (+€111 EBI)
    - Higher milk solids
    - Better fertility

ICBF.com

IRISH CATTLE BREEDING FEDERATION

Calving performance research

NDP
National Development Plan
Transforming Ireland

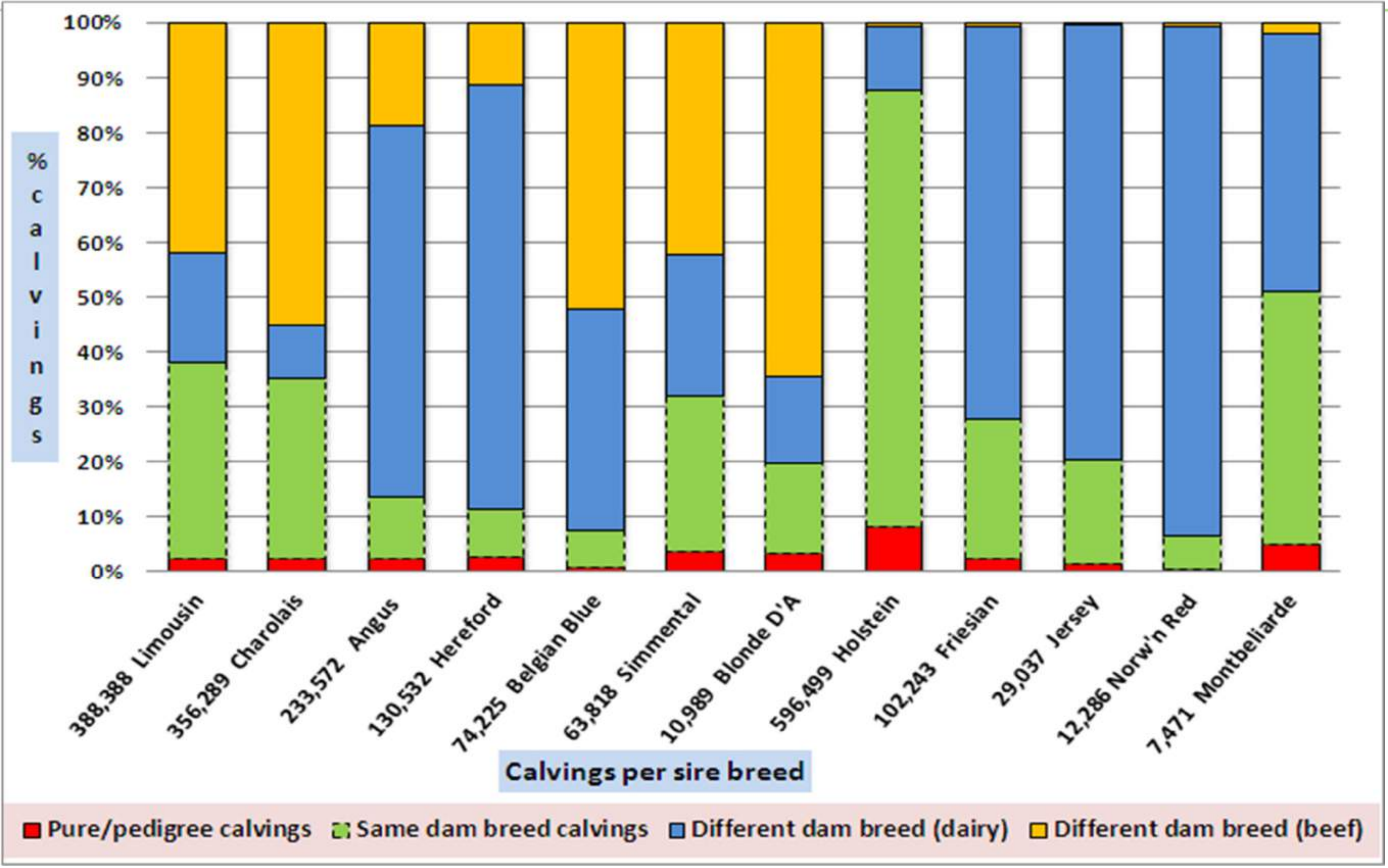
Background

- Current calving evaluation combines data from dairy and beef herds
- A single direct calving difficulty pta and reliability is produced
- Is there evidence to suggest that there needs to be separate dairy herd and suckler herd calving difficulty ptas but also heifer vs mature cow?

New research since May 14

- Transformation from evaluation to % difficult
- Penalty for low reliability in breeds with higher variation in calving difficulty
- Non-linear economic impact of calving difficulty on profitability
- Suitable for heifer recommendation

Sire Breed x Category of dam breed for 2013 born calves



	Angus	B_blue	Charolais	Hereford	Limousine	Simmental
Beef	9%	5%	36%	3%	35%	5%
Dairy	13%	2%	3%	8%	6%	1%

New calving traits

Profile of calving in herds which show variation

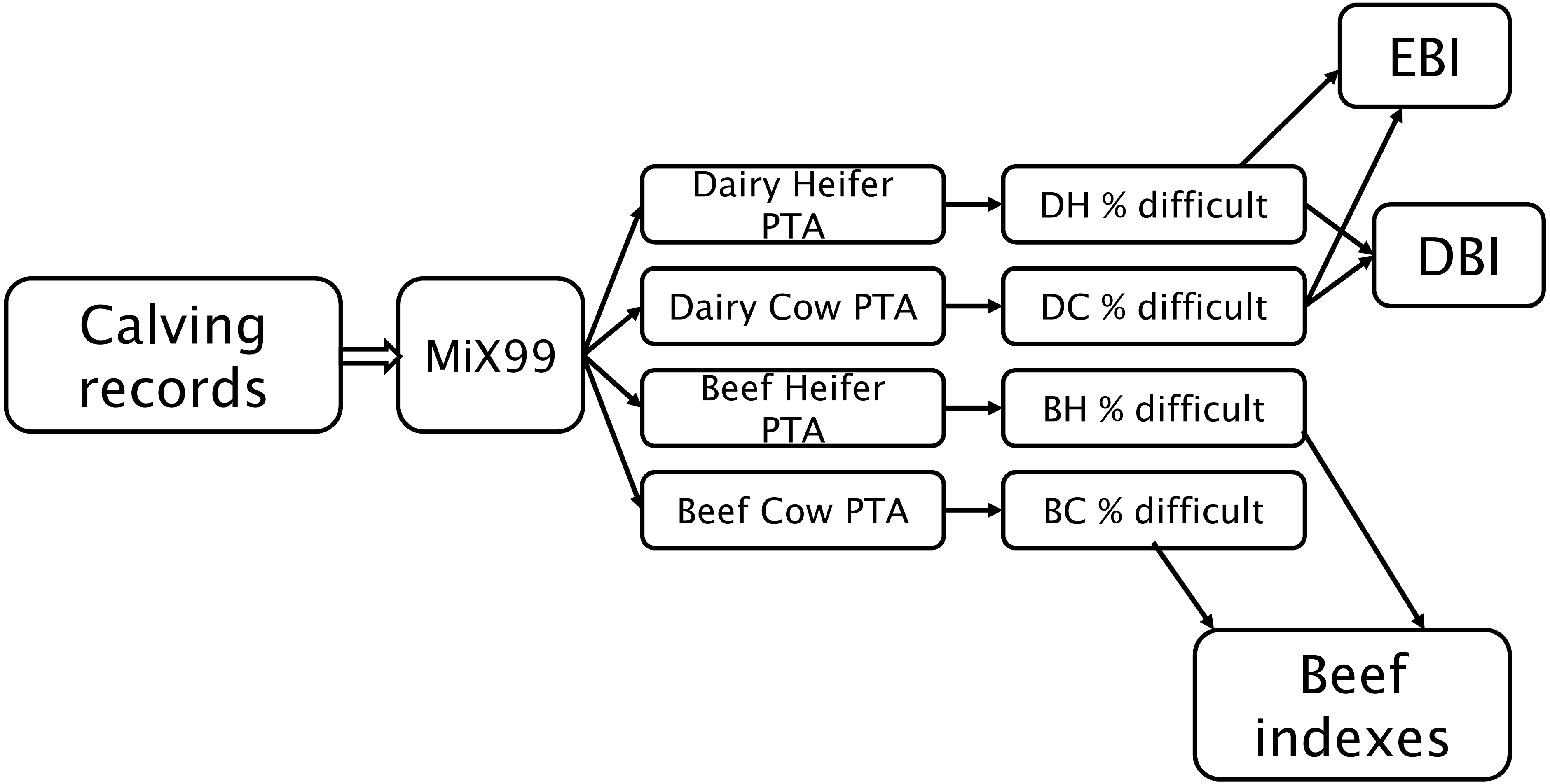
	Dairy heifer	Dairy cow	Beef heifer	Beef cow
Records	604,668	2,139,379	266,420	1,773,389
1	64%	74%	56%	70%
2	29%	22%	32%	24%
3	5.7%	3.2%	6.9%	4.3%
4	1.8%	1.2%	4.9%	1.9%
3 or 4	7.5%	4.4%	11.8%	6.1%
direct h2	0.25	0.15	0.17	0.24
maternal h2	0.06	0.03	0.14	0.09

Economic value

- With a 1% increase in calving difficulty, 74% of the increase in costs comes from scores 3 and 4

Calving difficulty	Description	Calving cost relative to no assistance	Percentage of calvings with 6% difficult	Increase with additional 1% difficult	Cost increase	
2	Slight assistance	€ 101.17	20.28%	1.63%	€ 1.65	26%
3	Severe assistance	€ 286.36	2.52%	0.34%	€ 0.97	74%
3	Veterinary assistance	€ 371.61	2.51%	0.43%	€ 1.60	
4	Caesarean	€ 947.67	0.97%	0.22%	€ 2.08	

Data flow

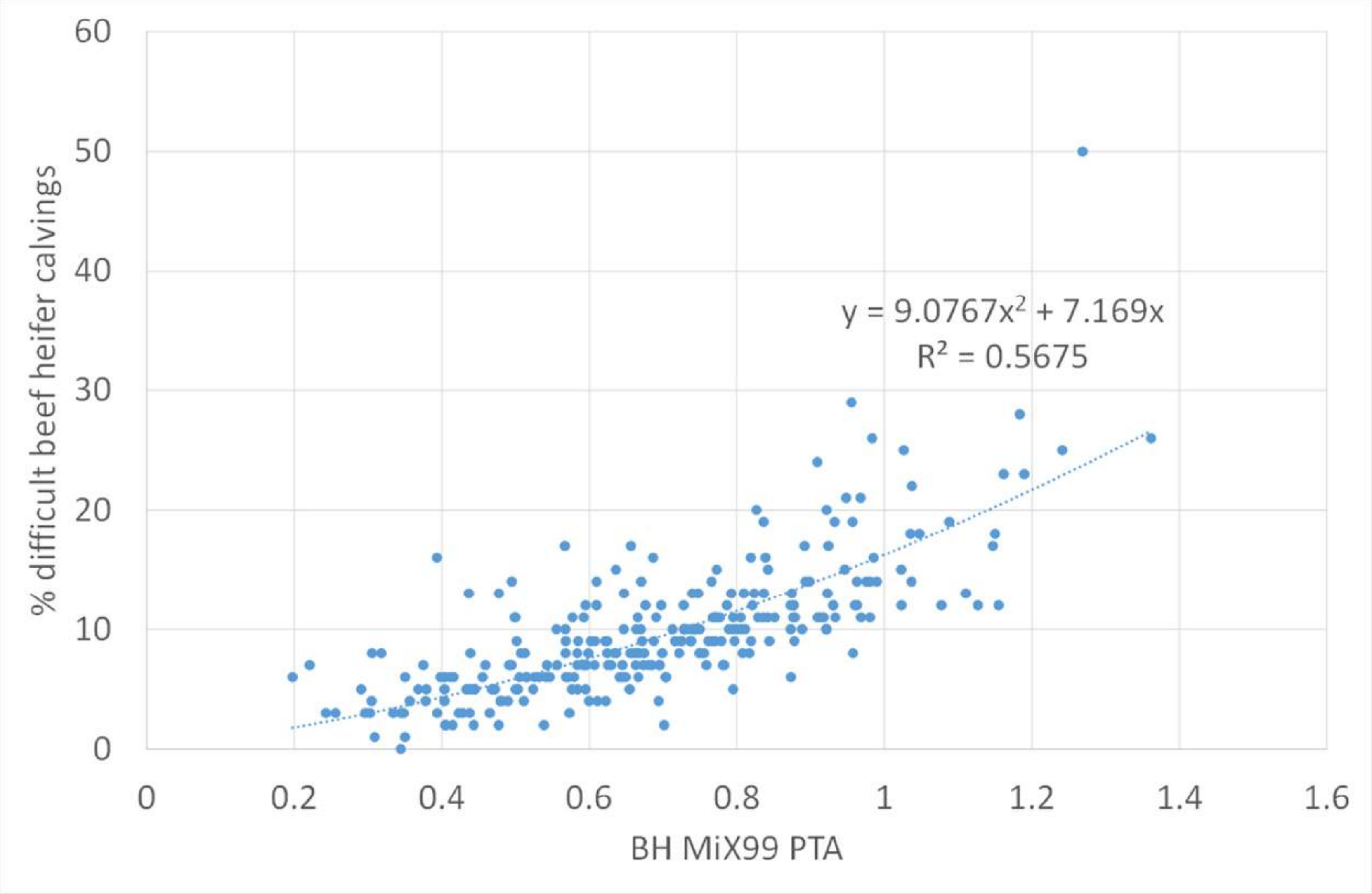

EBI
Dairy Heifer PTA
DH % difficult
DBI
Calving records
MiX99
Dairy Cow PTA
DC % difficult
Beef Heifer PTA
BH % difficult
Beef Cow PTA
BC % difficult
Beef indexes

Relationship between traits

Genetic correlations	Dairy heifer	Dairy cow	Beef Heifer
Dairy heifer			
Dairy cow	0.84		
Beef Heifer	0.76	0.88	
Beef Cow	0.41	0.82	0.92

If no records for DH, maximum reliability = correlation with DC = 0.7

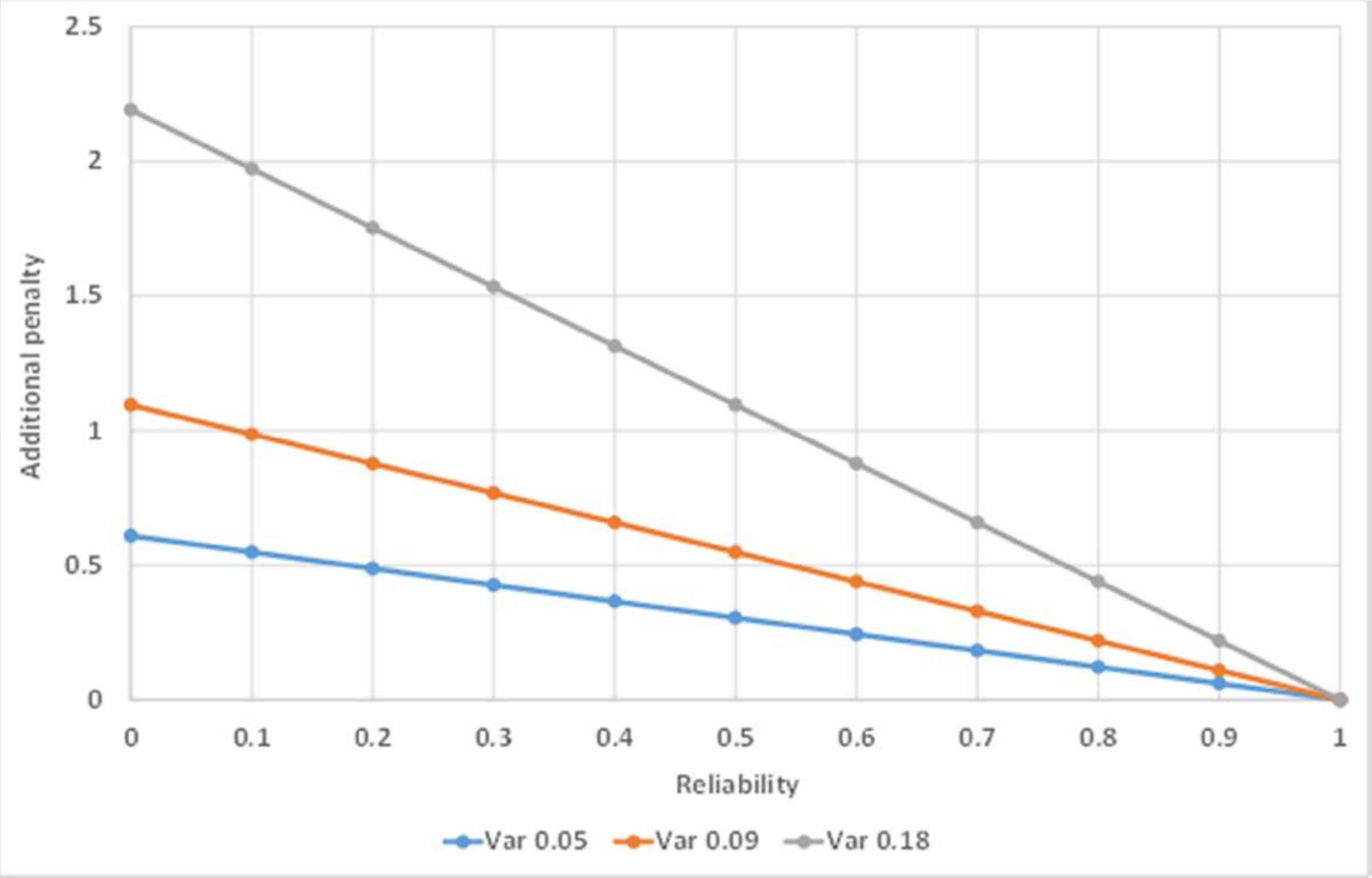
Transforming to % difficult PTAs: BH



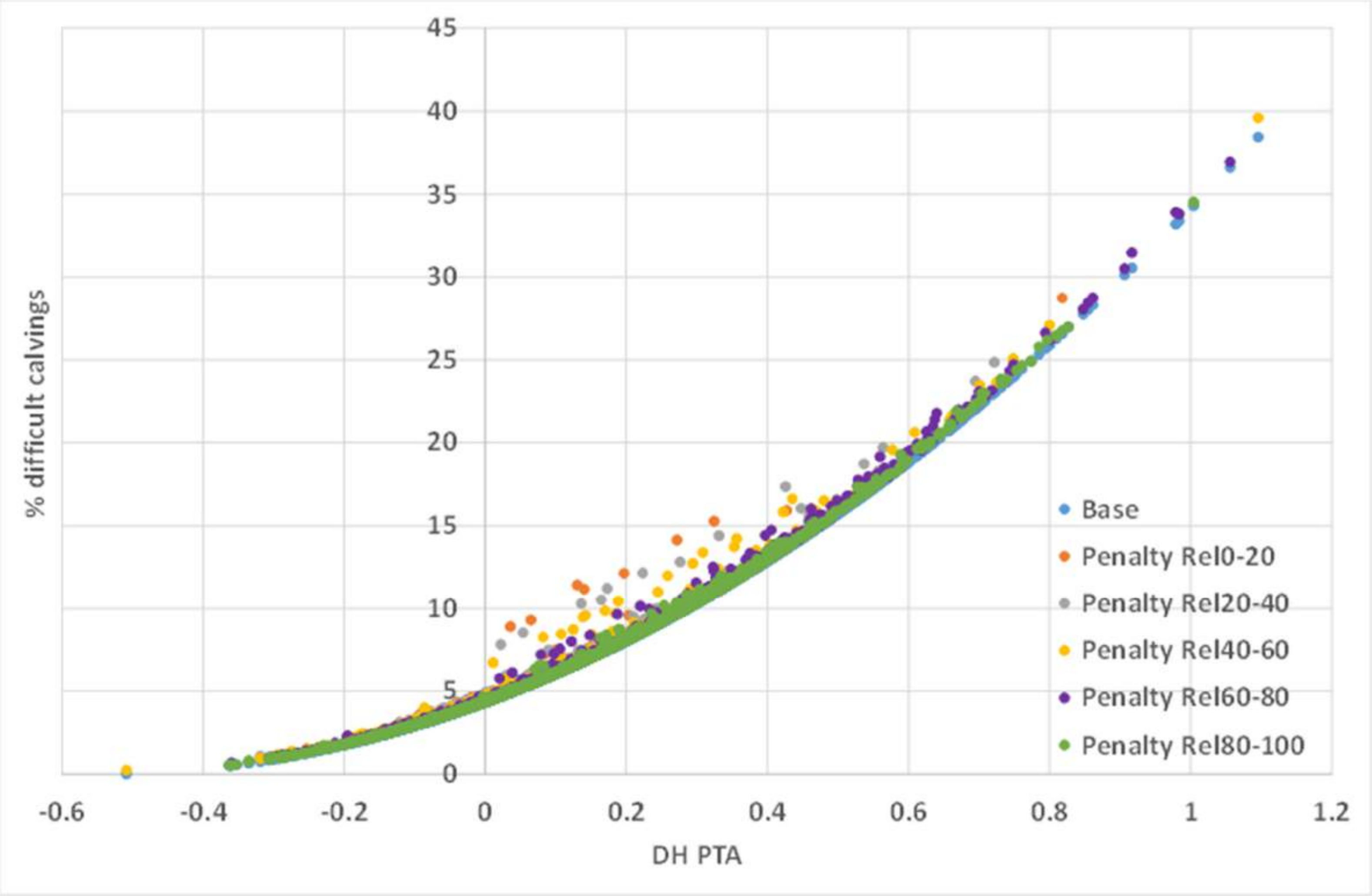
Low reliability adjustment

- Low reliability for MiX99 PTA indicates risk that % difficult calving could be higher than predicted
- This risk is higher in breeds with more variability in the MiX99 PTAs
- Reliability adjustment derived to increase the % difficult calving based on reliability and within breed variance

Low reliability adjustment



Low reliability adjustment



DBI Formulation

- Linear index
  - -€ 6.31 per percentage difficult calvings
  - -€ 3 per additional day of gestation length
  - € 1 per € 1 increase in calf price incorporating mortality [1-((4.29 + mortality PTA)/100)]*calf price

DBI Formulation

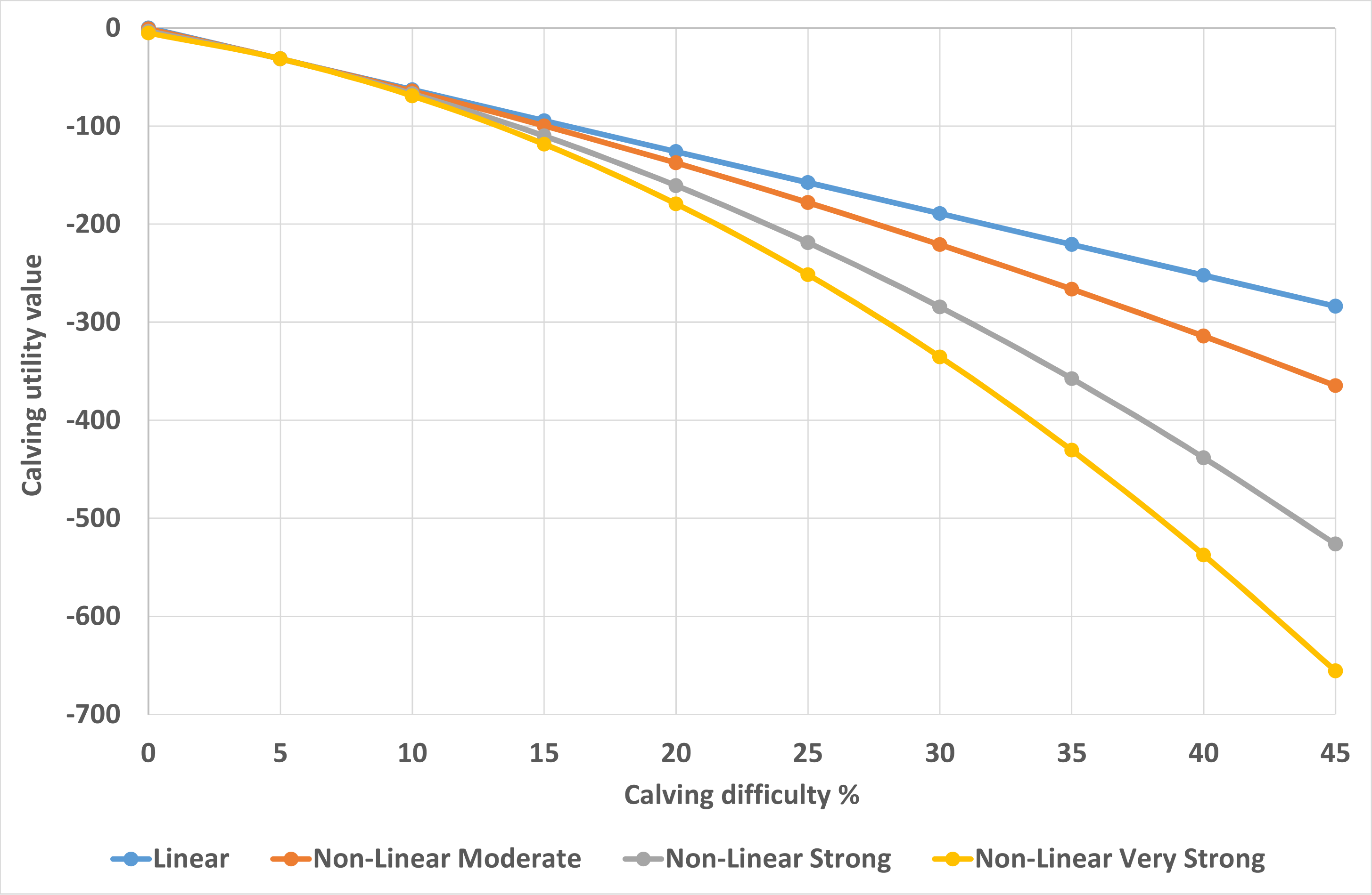
- Ratio 50% DH + 50% DC percentage difficult

Breed	Stock bulls			AI Bulls		
	Number	Total calves	% heifer	Number	Total calves	% heifer
AA	7,070	160,028	49%	288	95,894	53%
CH	2,611	12,661	8%	331	9,049	6%
HE	3,804	77,978	24%	334	33,914	10%
LM	3,710	44,522	19%	307	29,123	43%

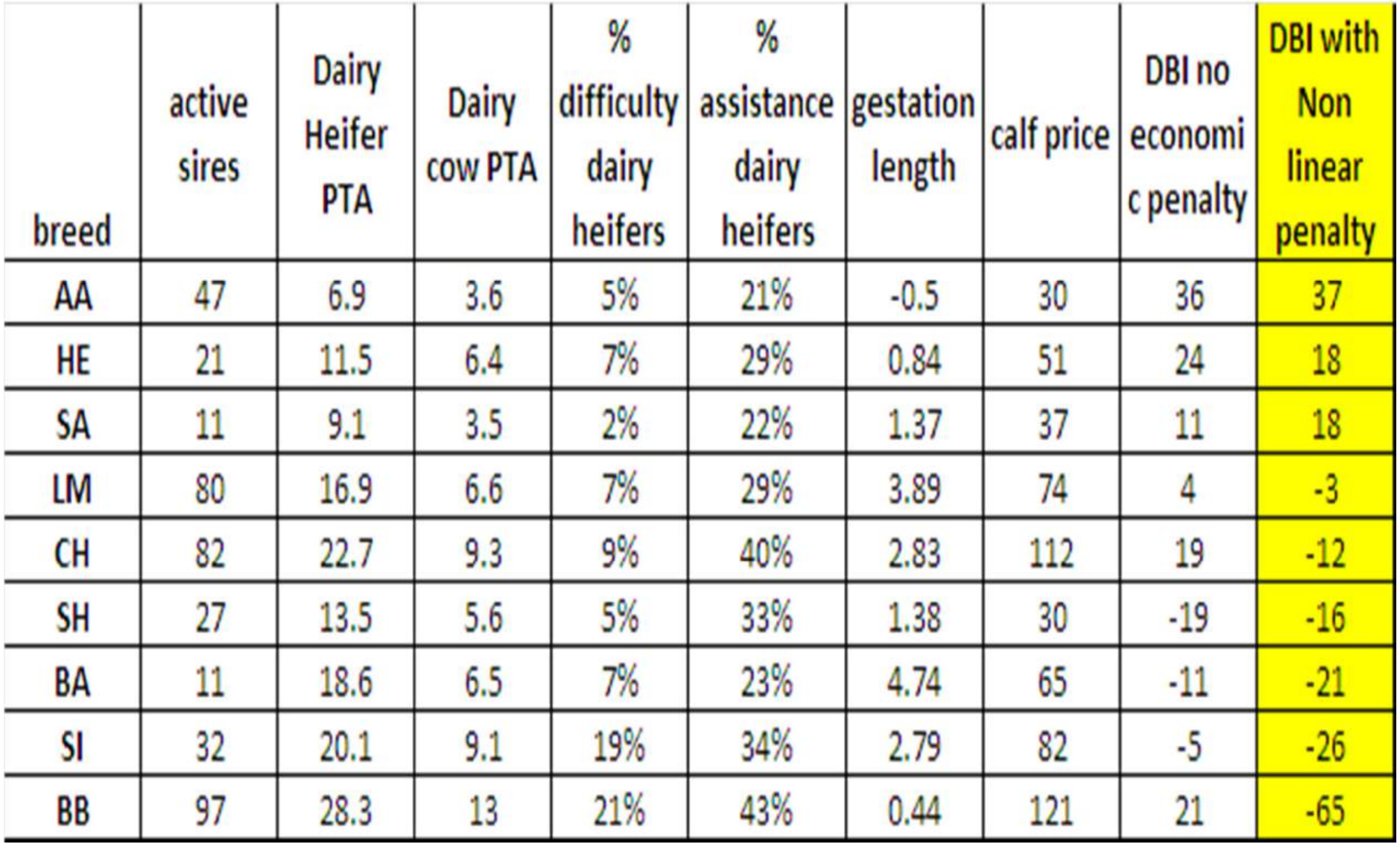
Non-linear calving utility

- Linear index suggests every 1% increase has same negative impact for farmers
- More likely to be adverse to increases when mean level is high
- With high rates of assistance a significant proportion of the herd can be compromised in health

Non-linear calving utility



DBI formulations

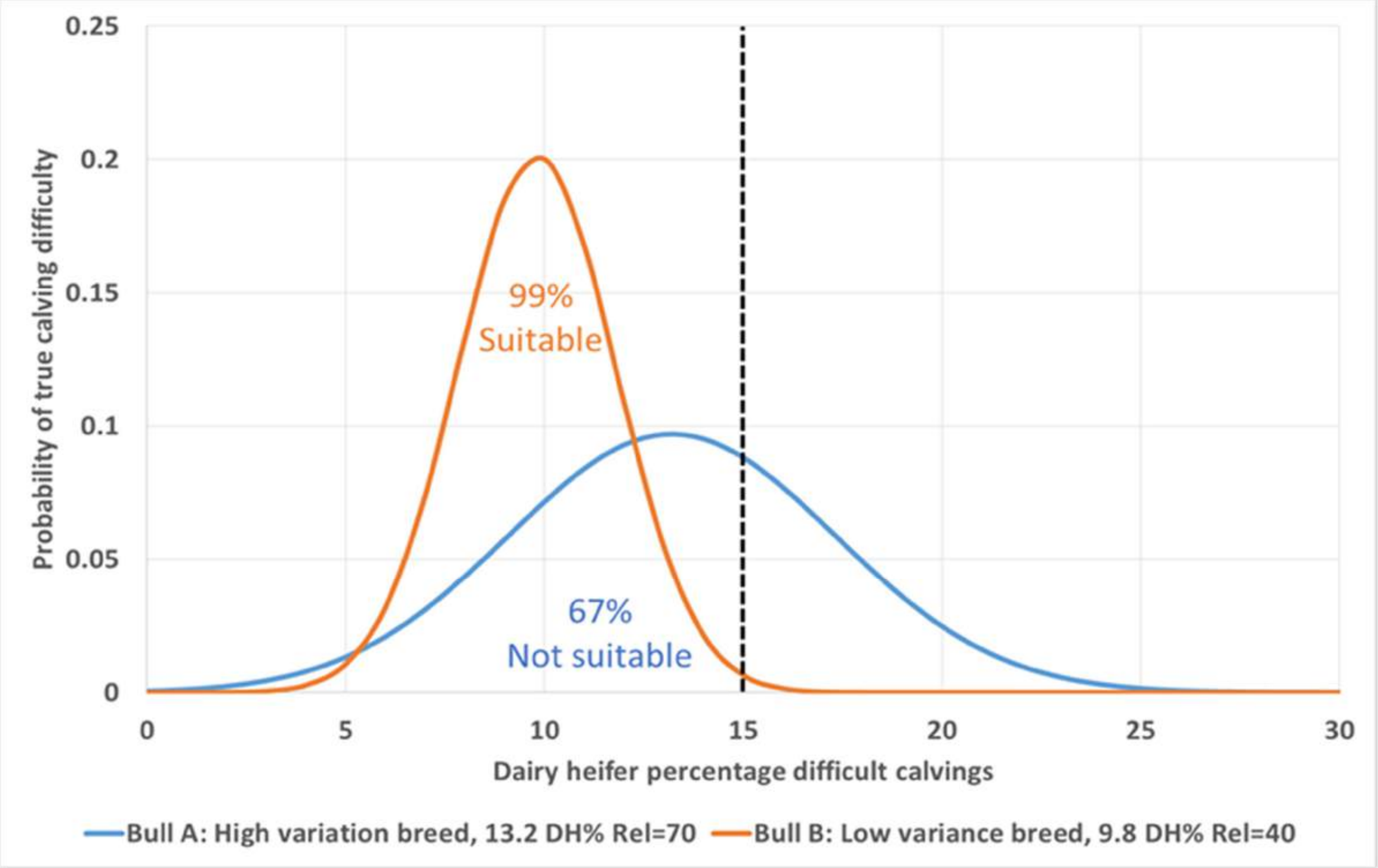


breed	active sires	Dairy Heifer PTA	Dairy cow PTA	% difficulty dairy heifers	% assistance dairy heifers	gestation length	calf price	DBI no economic penalty	DBI with Non linear penalty
AA	47	6.9	3.6	5%	21%	-0.5	30	36	37
HE	21	11.5	6.4	7%	29%	0.84	51	24	18
SA	11	9.1	3.5	2%	22%	1.37	37	11	18
LM	80	16.9	6.6	7%	29%	3.89	74	4	-3
CH	82	22.7	9.3	9%	40%	2.83	112	19	-12
SH	27	13.5	5.6	5%	33%	1.38	30	-19	-16
BA	11	18.6	6.5	7%	23%	4.74	65	-11	-21
SI	32	20.1	9.1	19%	34%	2.79	82	-5	-26
BB	97	28.3	13	21%	43%	0.44	121	21	-65

Proven suitable for heifers

- Undesirable to use bulls with higher calving difficulty % on heifers
- Calculate probability that calving difficulty is less than a threshold
- Only bulls with 90% probability of being under the threshold deemed suitable for heifers

Proven suitable for heifers



Conclusions

- New methodology proposed a non-linear adjustment of calving difficulty
    - Reliability adjustment based on bulls reliability and variation within its breed for that trait
    - Non-linear economic impact of calving difficulty
- These adjustments can be implemented into existing indexes for dairy and beef and new Dairy Beef index
- Lead in time: August 2015 for all changes to web, reports etc.
- Impact of genomics

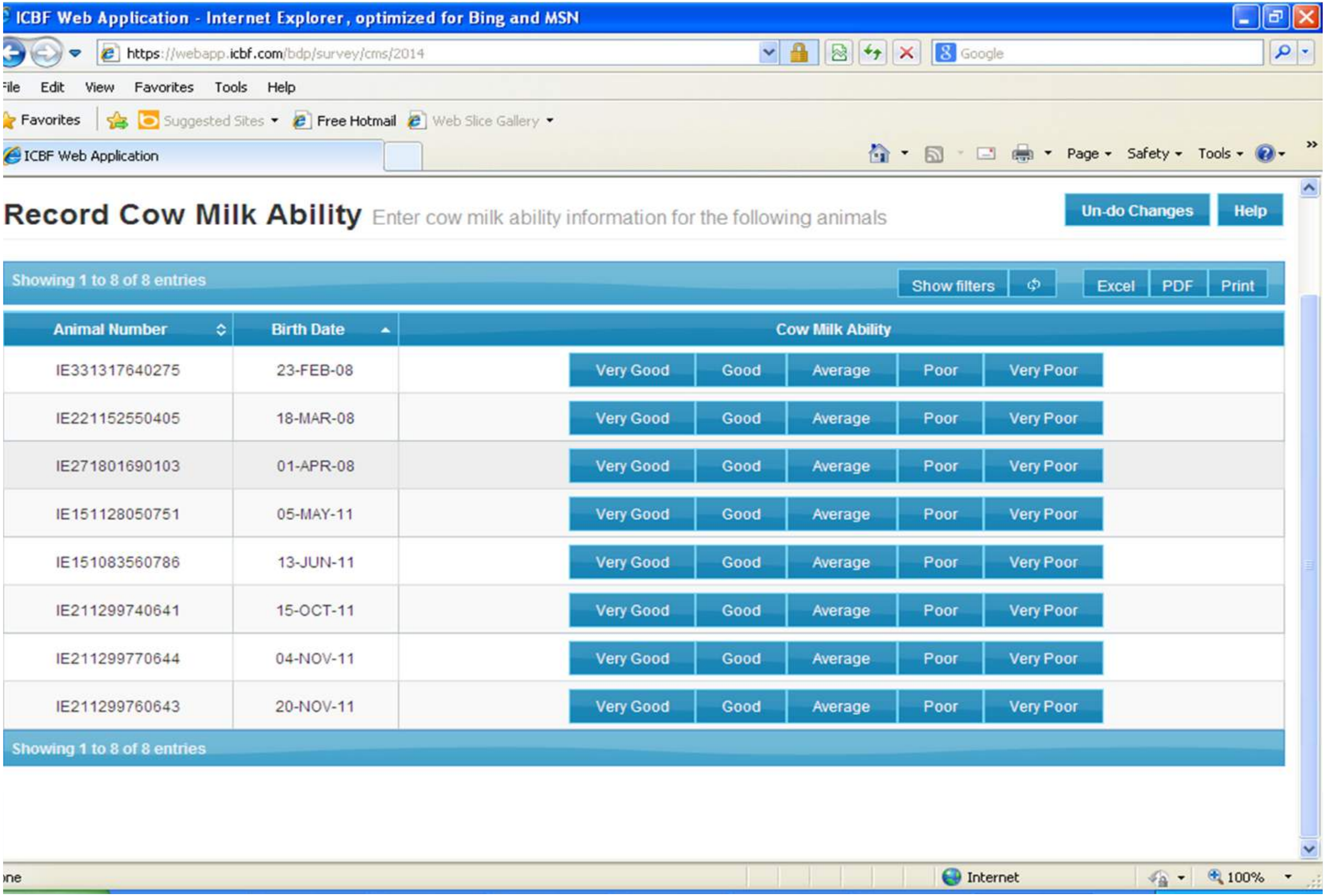
Cow milkability score as a predictor of Maternal weaning weight

Background

- Maternal weaning weight is the goal trait in the evaluation of milkability in suckler cows. <u>However:</u>
  - Need 2 generations of ancestry on calf weighed
  - Low levels of recording: 250,000 records compared to 4 million carcass records
  - Prediction can be inaccurate due un-recorded management i.e. fostering, meal feeding, suckling other cows

Useful predictor trait

- Milkability score has been recorded since 2012 on a voluntary basis (~40,000) heritability of 0.3, correlation of 0.65 with maternal weaning weight
- Now a key requirement for payment under the BDP program
- Multiple records across years on cows
- 666,000 records now collected
- New analysis h2 = 0.3, repeatability = 0.14 correlation of 0.83 with maternal wean wt



Record Cow Milk Ability Enter cow milk ability information for the following animals

Showing 1 to 8 of 8 entries

Animal Number	Birth Date	Cow Milk Ability
IE331317640275	23-FEB-08	Very Good Good Average Poor Very Poor
IE221152550405	18-MAR-08	Very Good Good Average Poor Very Poor
IE271801690103	01-APR-08	Very Good Good Average Poor Very Poor
IE151128050751	05-MAY-11	Very Good Good Average Poor Very Poor
IE151083560786	13-JUN-11	Very Good Good Average Poor Very Poor
IE211299740641	15-OCT-11	Very Good Good Average Poor Very Poor
IE211299770644	04-NOV-11	Very Good Good Average Poor Very Poor
IE211299760643	20-NOV-11	Very Good Good Average Poor Very Poor

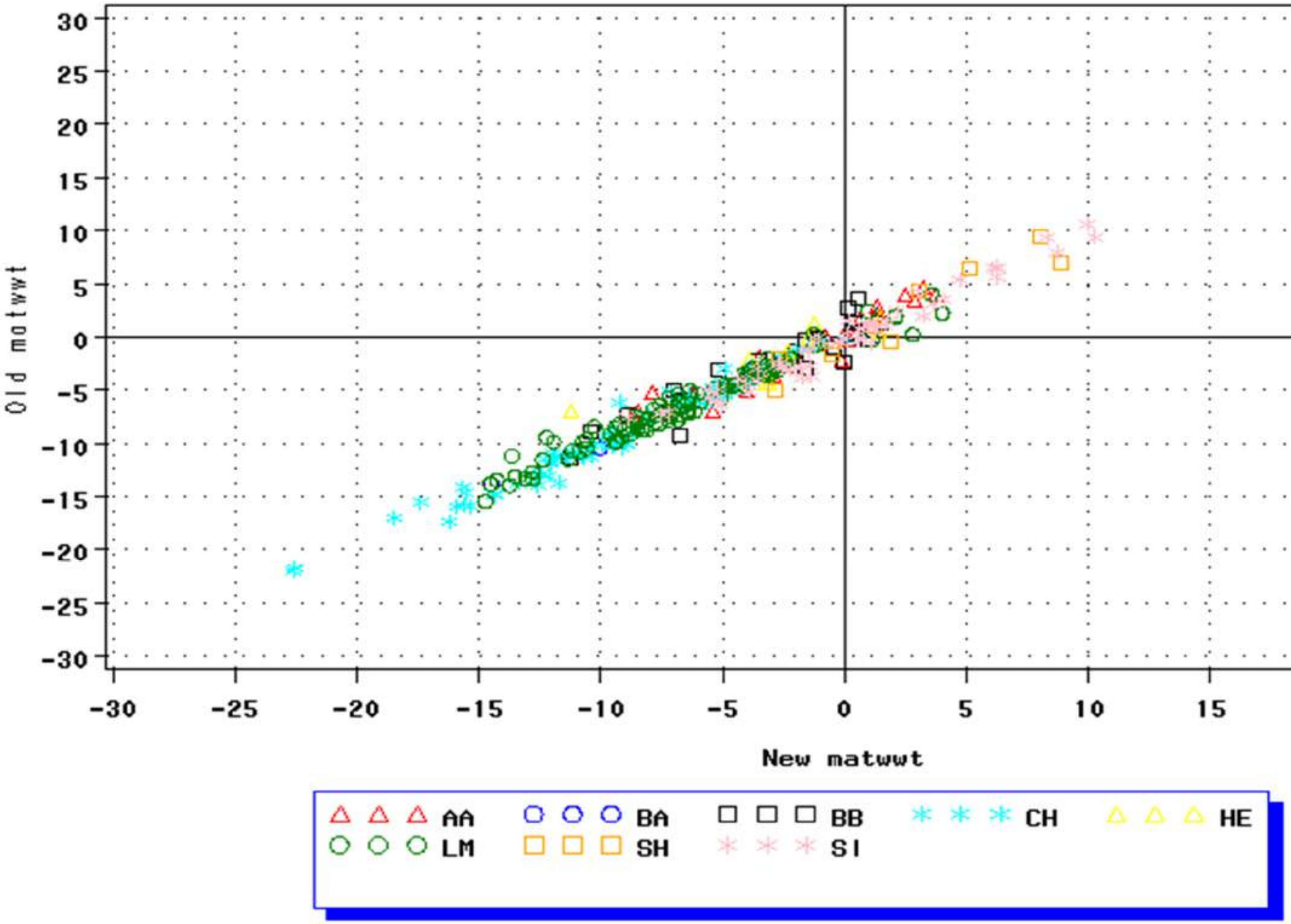
Showing 1 to 8 of 8 entries

AI sires 90% rel compare maternal weaning weight

No of bulls 314 correlation r = 0.984

Oldeval mean = −4.71 {stdev = 5.46}

Neweval mean = −4.88 {stdev = 5.49}

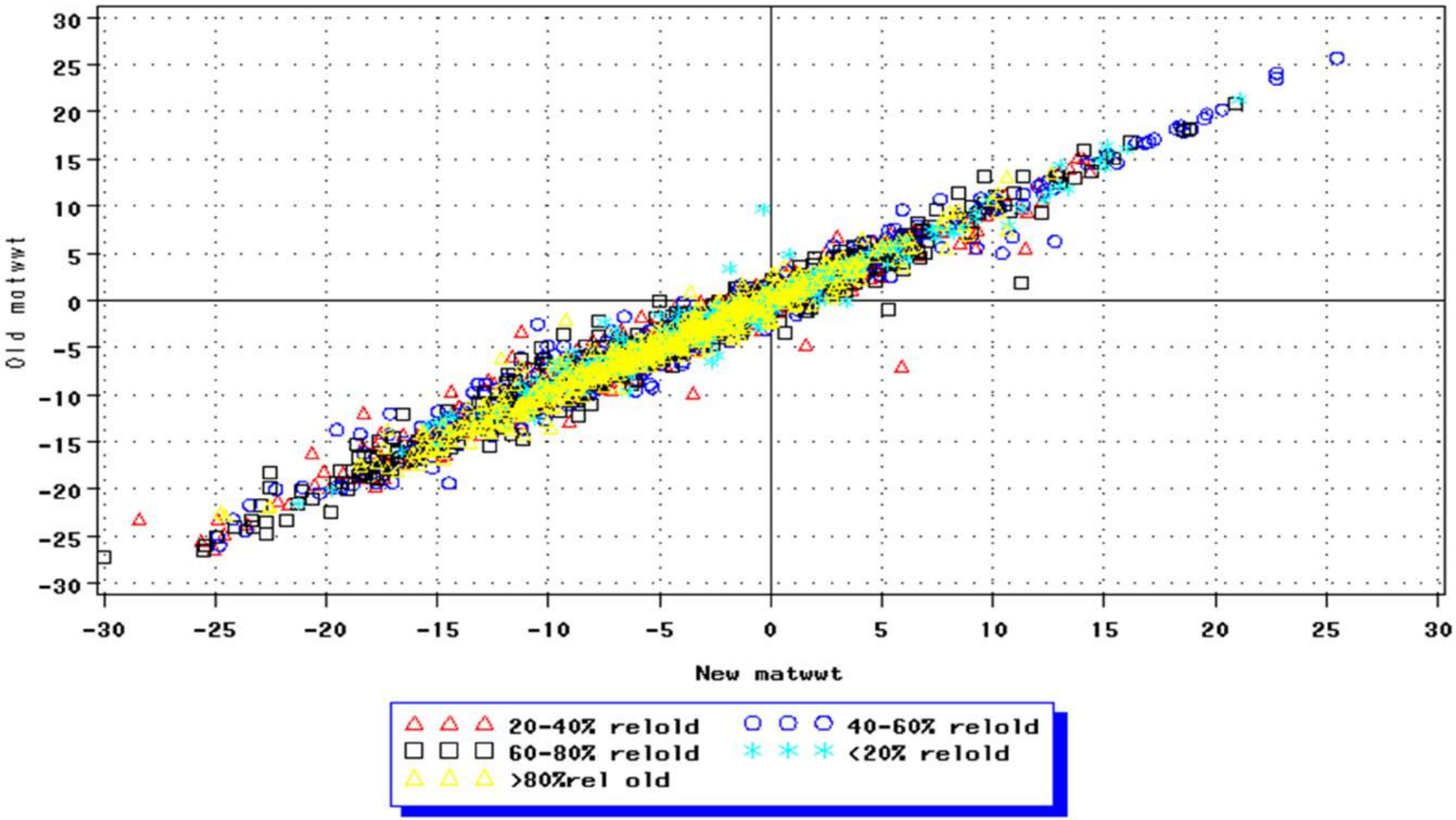


AI sires compare matwwt by previous rel category

No of bulls 3036 correlation r = 0.982

Oldeval mean = −3.7 {stdev = 6.77}

Neweval mean = −3.93 {stdev = 6.92}

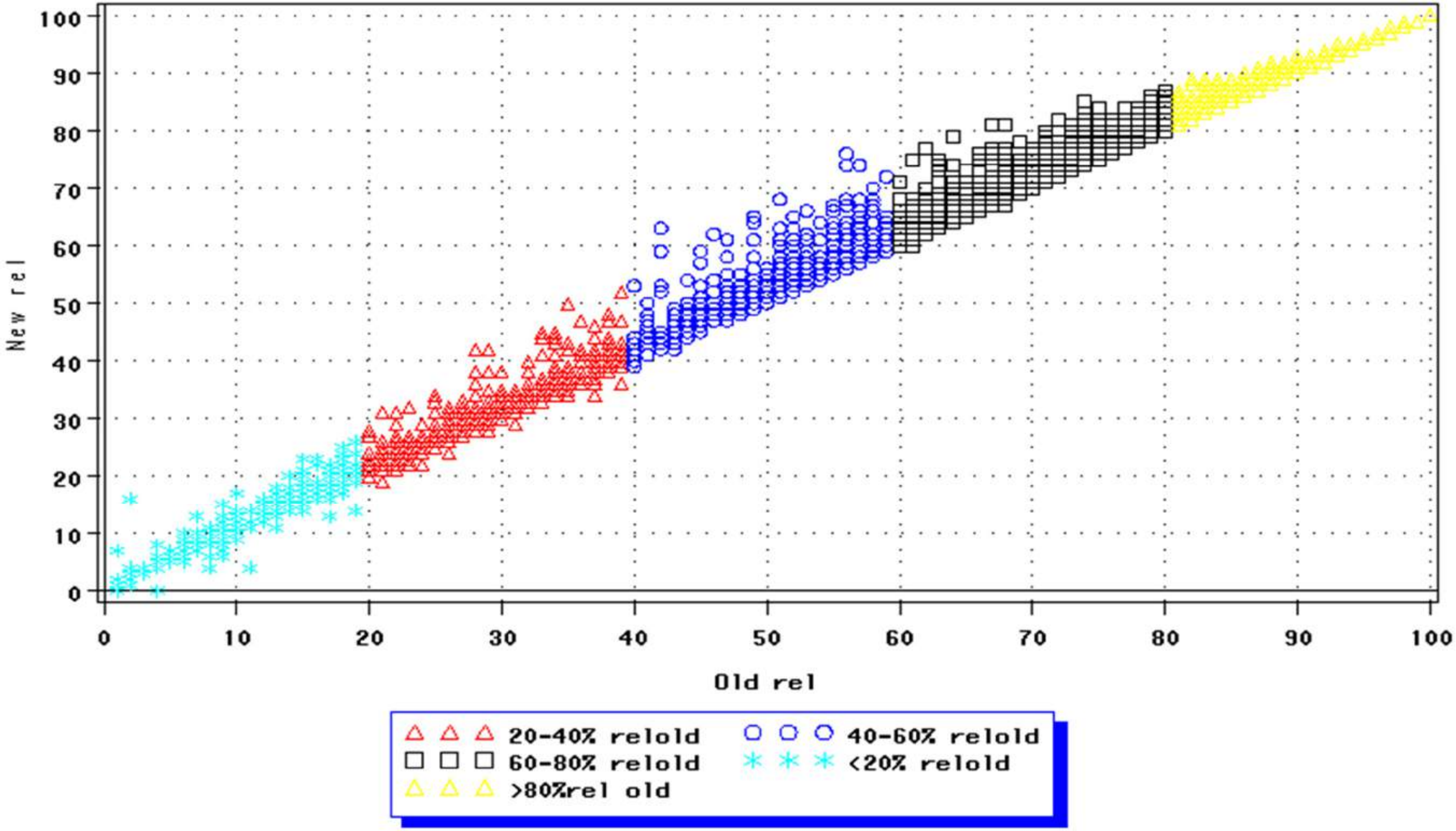


AI sires compare reliability

No of bulls 3036 correlation r = 0.996

Oldeval mean = 48.54 {stdev = 29.17}

Neweval mean = 50.43 {stdev = 29.57}



Conclusion

- Milkability score is a very useful predictor trait for maternal weaning weight
- Evaluates data from herds that don’t weight record
- No effect on well proven sires
- Ready for implementation in December run

IRISH CATTLE BREEDING FEDERATION

On Farm Health and Disease Recording And What Can It Do For You?

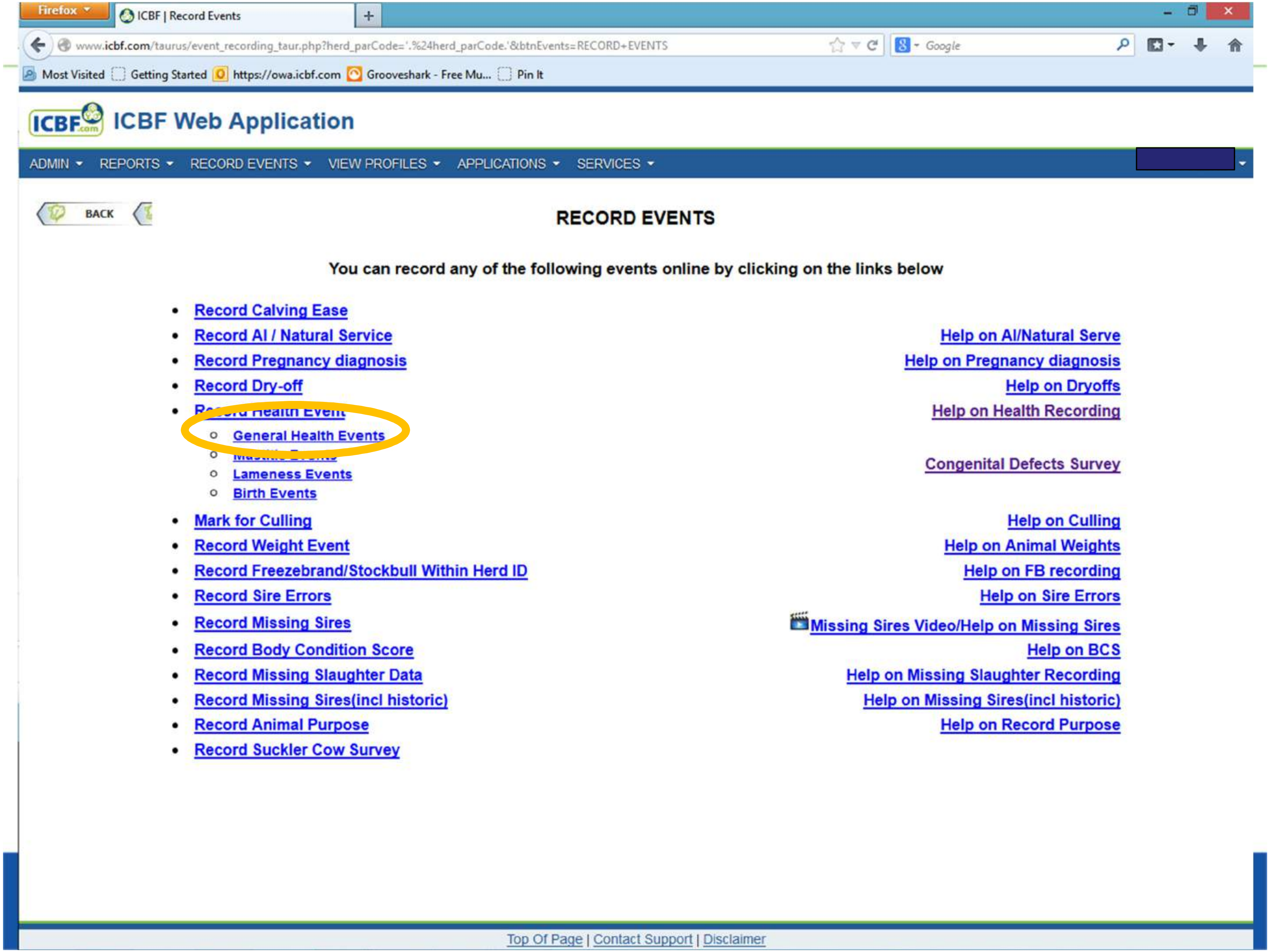
J McClure 2014

National Development Plan

Transforming Ireland

Farmer recorded events

- Pilot program
- You can record events on the ICBF website or farm software
- Why Record?
  - Help keep track of problem animals
    - Multiple mastitis events
    - Multiple pneumonia events
    - Lameness
  - Help with culling decisions
  - Data used to ID superior sires



[redacted]

RECORD EVENTS

You can record any of the following events online by clicking on the links below

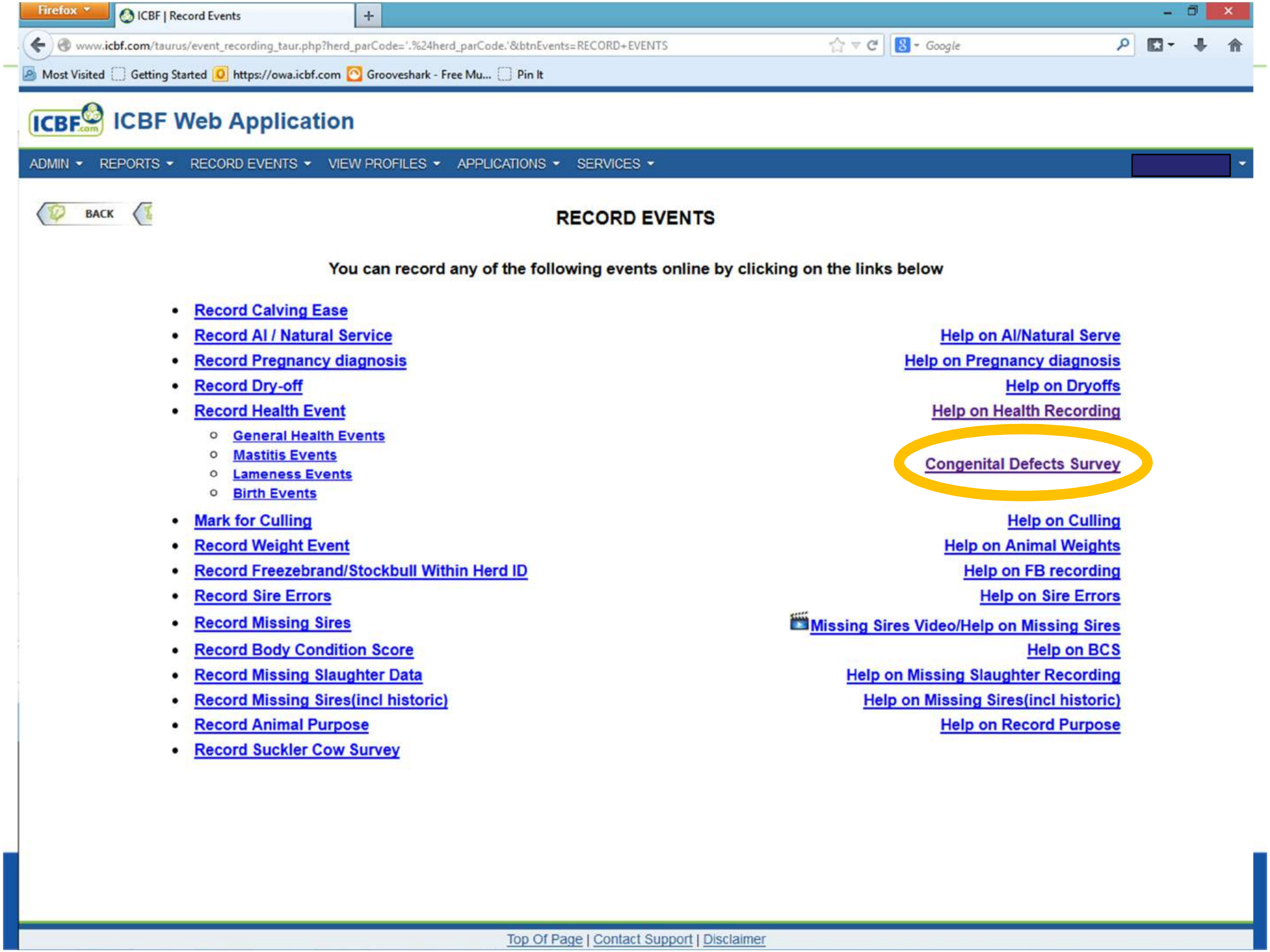
- Record Calving Ease
- Record AI / Natural Service
- Record Pregnancy diagnosis
- Record Dry-off
- Record Health Event
  - General Health Events
  - Mastitis Events
  - Lameness Events
  - Birth Events
- Mark for Culling
- Record Weight Event
- Record Freezebrand/Stockbull Within Herd ID
- Record Sire Errors
- Record Missing Sires
- Record Body Condition Score
- Record Missing Slaughter Data
- Record Missing Sires(incl historic)
- Record Animal Purpose
- Record Suckler Cow Survey

Help on AI/Natural Serve
Help on Pregnancy diagnosis
Help on Dryoffs
Help on Health Recording
Congenital Defects Survey
Help on Culling
Help on Animal Weights
Help on FB recording
Help on Sire Errors
Missing Sires Video/Help on Missing Sires
Help on BCS
Help on Missing Slaughter Recording
Help on Missing Sires(incl historic)
Help on Record Purpose

Top Of Page | Contact Support | Disclaimer

Congenital defects

- Joint effort
  - Data collected from RVL necropsy, **Farmer reporting**, and Vets(?)
- ID sires that produce progeny with deformities
- ID areas in the genome that cause defects (With Teagasc & others)



[redacted]

RECORD EVENTS

You can record any of the following events online by clicking on the links below

• Record Calving Ease	
• Record AI / Natural Service	Help on AI/Natural Serve
• Record Pregnancy diagnosis	Help on Pregnancy diagnosis
• Record Dry-off	Help on Dryoffs
• Record Health Event	Help on Health Recording
○ General Health Events	
○ Mastitis Events	
○ Lameness Events	Congenital Defects Survey
○ Birth Events	
• Mark for Culling	Help on Culling
• Record Weight Event	Help on Animal Weights
• Record Freezebrand/Stockbull Within Herd ID	Help on FB recording
• Record Sire Errors	Help on Sire Errors
• Record Missing Sires	Missing Sires Video/Help on Missing Sires
• Record Body Condition Score	Help on BCS
• Record Missing Slaughter Data	Help on Missing Slaughter Recording
• Record Missing Sires(incl historic)	Help on Missing Sires(incl historic)
• Record Animal Purpose	Help on Record Purpose
• Record Suckler Cow Survey	

Top Of Page | Contact Support | Disclaimer

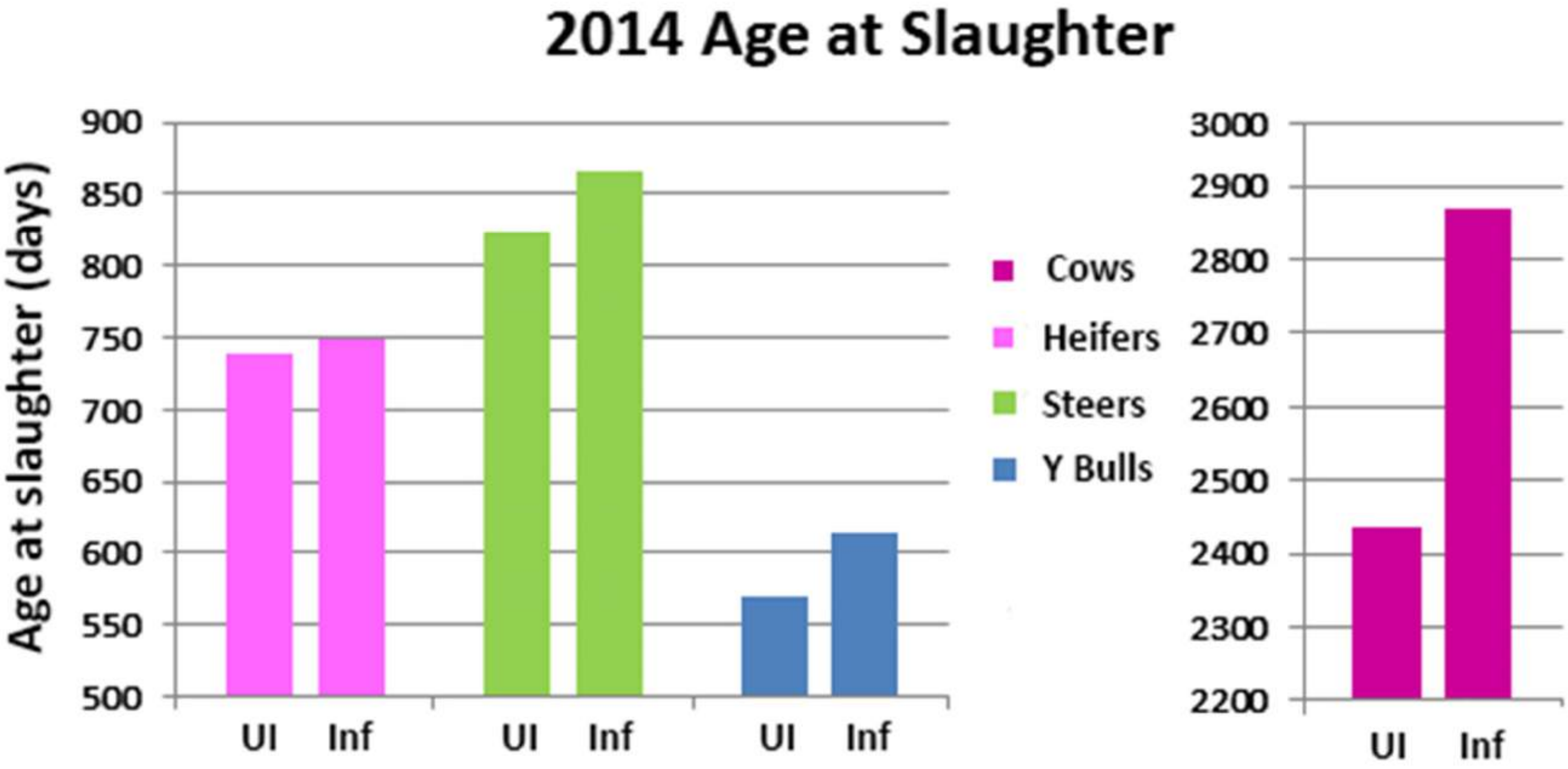
Liver Fluke Stats

- €70-90M cost to industry
- ~73% of livers condemned*

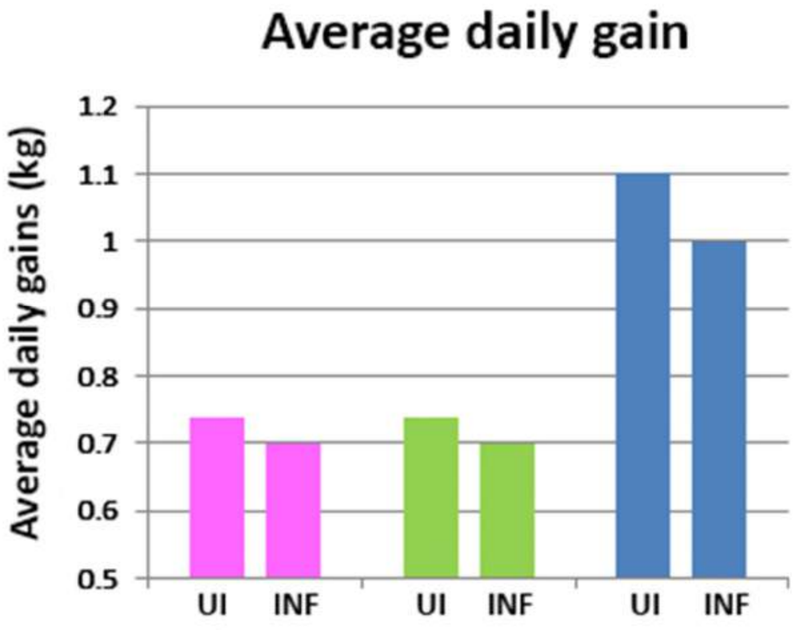
- Infected animals do not:
  - Gain weight as quickly
  - Produce as much
  - May become sicker from infections
  - May not respond as well to vaccines

Vet Parasitol. 2014 Mar 17;201(1-2):31-9. doi: 10.1016/j.vetpar.2014.01.013. Epub 2014 Jan 28.
The effect of Fasciola hepatica infection on respiratory vaccine responsiveness in calves.
Krump L[1], Hamilton CM[2], Sekiya M[2], O'Neill R[3], Mulcahy G[4]

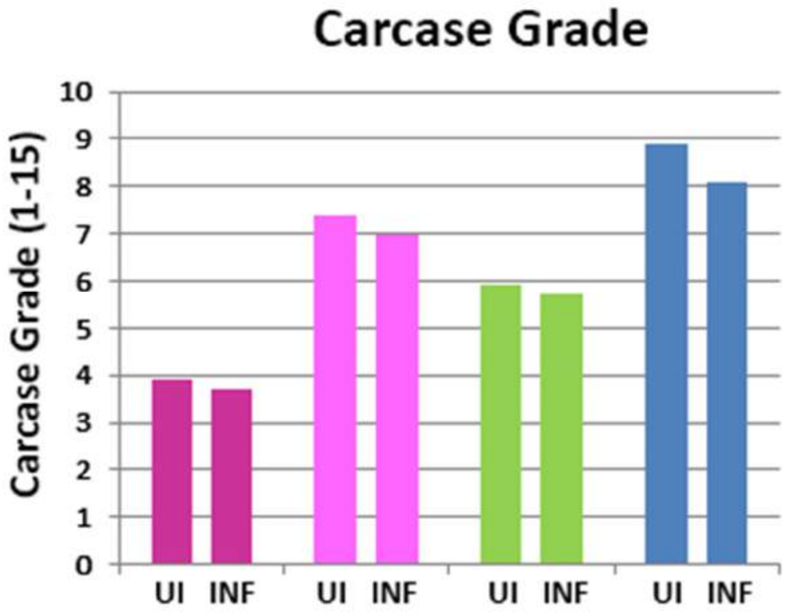
Phenotypic Data from Abattoirs



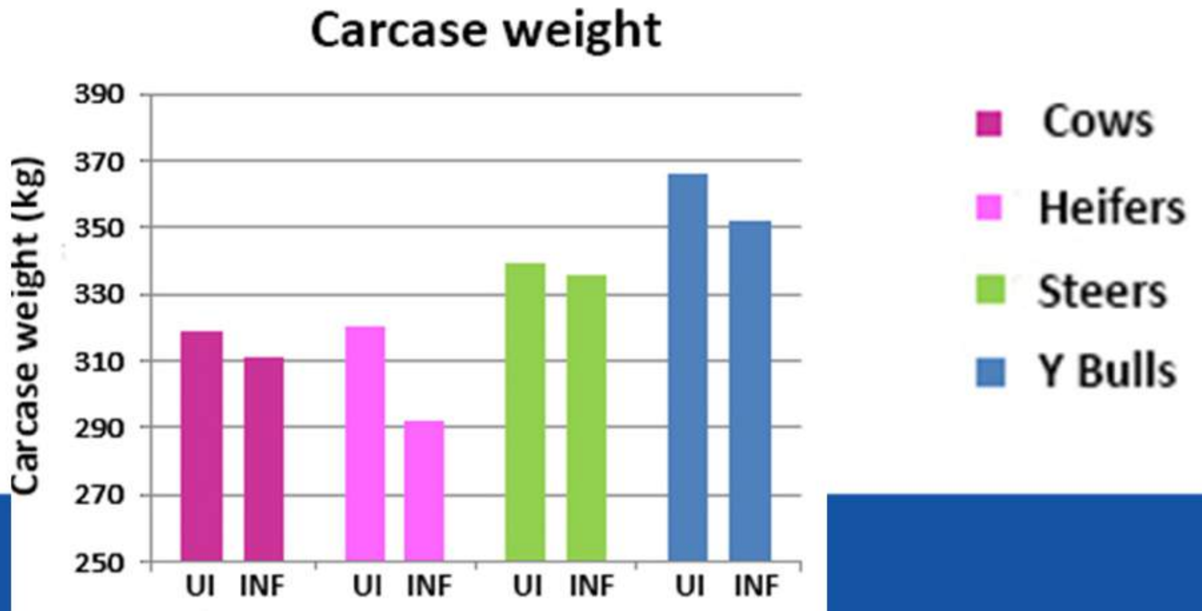
Phenotypic Data from Abattoirs



Average daily gain



Carcase Grade



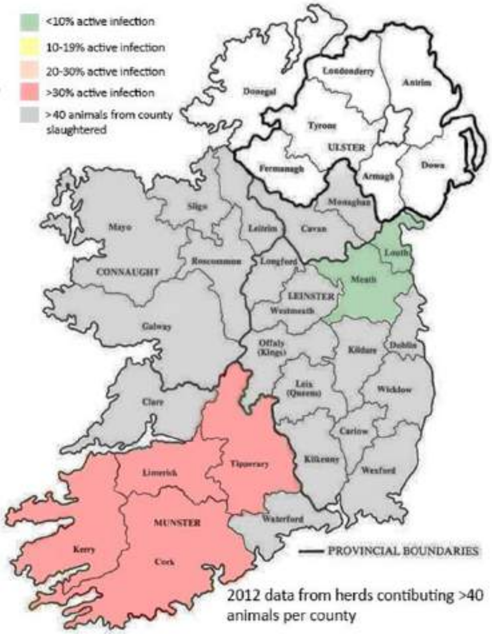
Carcase weight

3 years of data
(2 abattoirs)

Year	Inf+cure (# ani)	Inf (# ani)	Tot # ani	% Inf+cure	% Inf
2012	8,602	**6,003**	20,436	42.1%	**29.4%**
2013	16,231	**12,897**	35,466	45.7%	**36.4%**
2014	47,618	**23,276**	122,143	39%	**19%**

2013: total of ~1.5 million animals slaughtered

Data from animals with active infections based on herd where they spent more than 30 days pre-slaughter



2012 data from herds contibuting >40 animals per county

2013 data from herds contibuting >40 animals per county

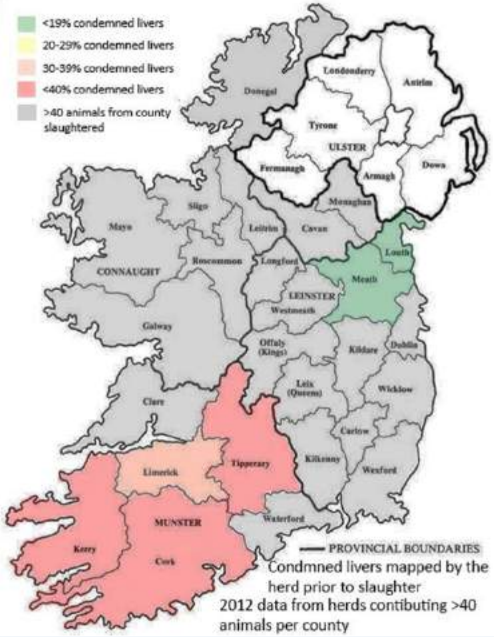
Jan 2014- August 2014 data from counties contributing >100 animals

2012

2013

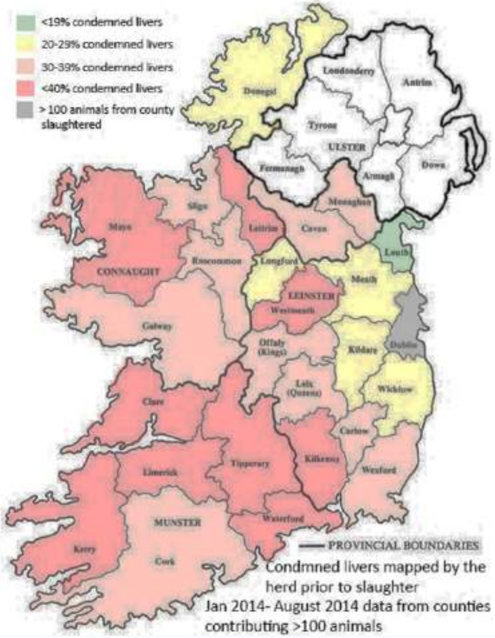
2014

Data from condemned livers (active and previous infection) based on herd where they spent more than 30 days pre-slaughter



Condmned livers mapped by the herd prior to slaughter
2012 data from herds contibuting >40 animals per county

Condmned livers mapped by the herd prior to slaughter
2013 data from herds contibuting >40 animals per county

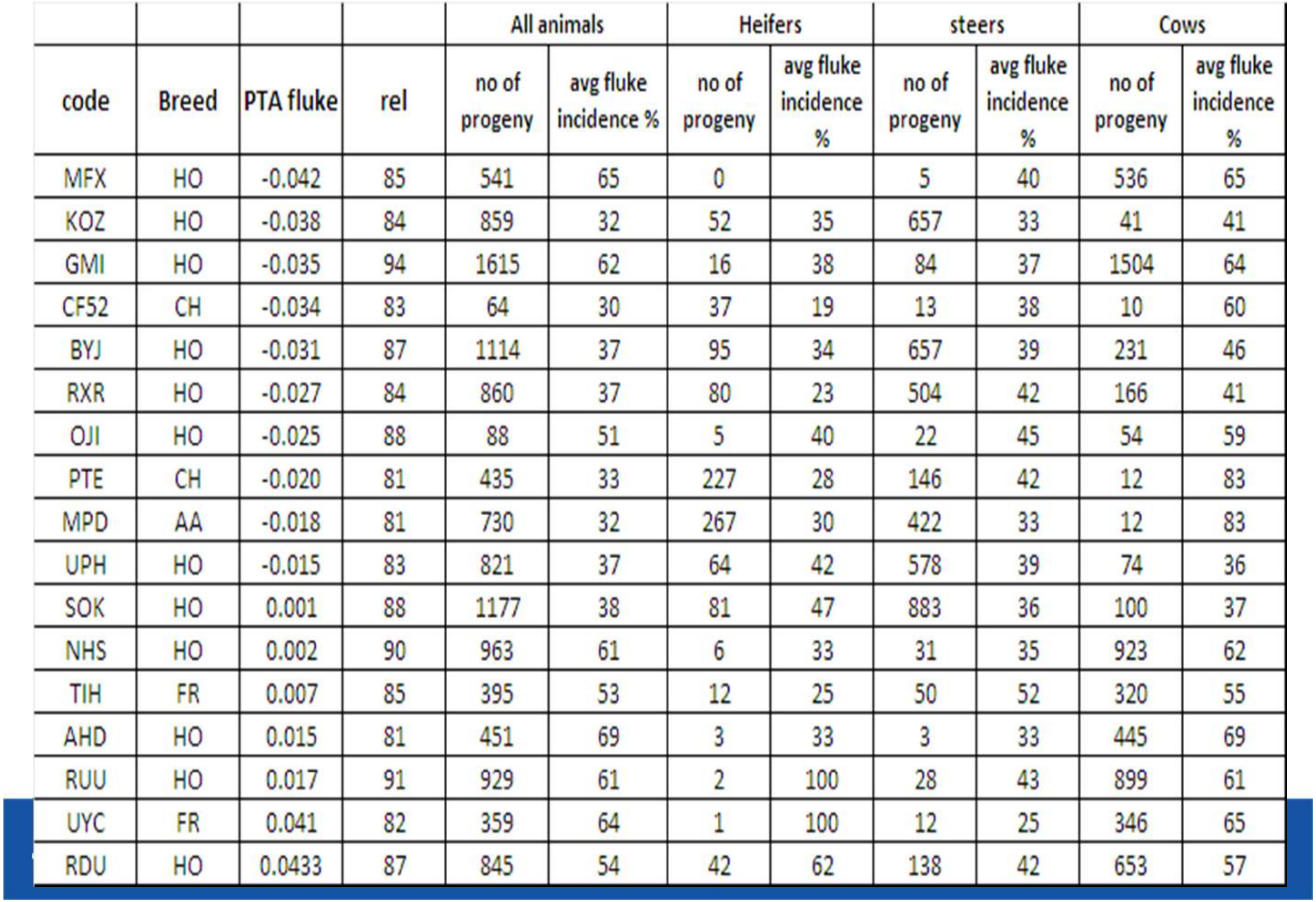


Condmned livers mapped by the herd prior to slaughter
Jan 2014- August 2014 data from counties contributing >100 animals

Genetic analysis

- Subset of data
  - Herd- slaughter days with incidence of fluke kept
  - Maximum of 2 movements
  - Analysis adjusted for factory herd and rearing herd
  - 50k records. Heritability of 2%
- Full evaluation run
  - 163 k records
  - Average fluke incidence 38%

Examples of well proven sires



				All animals		Heifers		steers		Cows	
code	Breed	PTA fluke	rel	no of progeny	avg fluke incidence %	no of progeny	avg fluke incidence %	no of progeny	avg fluke incidence %	no of progeny	avg fluke incidence %
MFX	HO	-0.042	85	541	65	0		5	40	536	65
KOZ	HO	-0.038	84	859	32	52	35	657	33	41	41
GMI	HO	-0.035	94	1615	62	16	38	84	37	1504	64
CF52	CH	-0.034	83	64	30	37	19	13	38	10	60
BYJ	HO	-0.031	87	1114	37	95	34	657	39	231	46
RXR	HO	-0.027	84	860	37	80	23	504	42	166	41
OJI	HO	-0.025	88	88	51	5	40	22	45	54	59
PTE	CH	-0.020	81	435	33	227	28	146	42	12	83
MPD	AA	-0.018	81	730	32	267	30	422	33	12	83
UPH	HO	-0.015	83	821	37	64	42	578	39	74	36
SOK	HO	0.001	88	1177	38	81	47	883	36	100	37
NHS	HO	0.002	90	963	61	6	33	31	35	923	62
TIH	FR	0.007	85	395	53	12	25	50	52	320	55
AHD	HO	0.015	81	451	69	3	33	3	33	445	69
RUU	HO	0.017	91	929	61	2	100	28	43	899	61
UYC	FR	0.041	82	359	64	1	100	12	25	346	65
RDU	HO	0.0433	87	845	54	42	62	138	42	653	57

Next phase

- Continue collecting data
- Expand collection to other factories
- Access to land topography and rainfall as additional environmental factors
- Look at associations with other traits
  - TB, Johne’s, Pneumonia

ICBF.com

IRISH CATTLE BREEDING FEDERATION

AI Codes

NDP
National Development Plan
Transforming Ireland

Backround

- **Three types of AI Codes exist:**

1. 3 letter codes ('Widespread' & 'Test Purposes')
   - E.g. 'SOK', 'DRU','NVI'
   - @150 Codes issued per annum
   - 50 Holstein,12 Friesian,6 Limousin,5 Charolais,3 Angus, 3 Simmental…
2. 'Special Breeding Purposes' (Small quantities/Ped Breeding)
   1. E.g. 'S1623…………'
   2. @140 Codes issued per annum
3. 'On-Farm' collected Bulls
   1. E.g. 'F198………..'
   2. @10 codes issued per annum

- **For 3 letter coded bulls - AI Code generally follows a Bull's name:**
  - Sunnybank Oman = 'SOK'
  - Derrough Samual = 'DRU',
  - Navarin='NVI'.

New AI Code Format

- **Introduce a simple Breed x number Coding system:**
- **2 Breed letters followed by 4 numbers**
- **E.g.CH1075=Charolais Sire, LM1012= Limousin Sire etc**

- **Pros:**
- **Set Length – will never be more than 6 characters in length.**
- **Would be quick and easy to administer.**
- **Tells you something about the Bull's breed.**
- **Would be longlasting.**

- **Cons:**
- **Only slight negative is that it is 6 characters long. Longest current AI Code is 5 characters long.**

Summary

- Preference would be to go with new format in January 2015.
  - Sexed indicator will be added for 2015 again i.e.'-F90'.
  - Separating this away from the code & into a dropdown on the handhelds was looked into for 2015 but was found to be too risky to currently complete without affecting other aspects of the handheld software.

- The barcode on an AI Straw is a separate issue – the AI code will never be able to also cover that function.

- Please think about it again and come back with any suggestions before October 31st .

AI Bulls with Genetic Defects

- **Some CVM positive bulls have recently been proposed for coding.**

- **They were declined as the current ruling is that:**
  - **A CVM positive bull must be ranked in the top 50 on EBI in order to be approved for AI Use.**
  - **This is so as the risk involved in using such a bull is some way balanced with the bulls genetic merit.**
  - **This ruling is in place since CVM was first discovered in 2001**
- **Is the industry still happy with this approach?**

- **If not please come back to ICBF with an alternative suggestion as to how this can be managed before the 31st of October.**

ICBF.com

IRISH CATTLE BREEDING FEDERATION

Data Quality for Genetic Evaluations.

Andrew Cromie

NDP
National Development Plan
Transforming Ireland

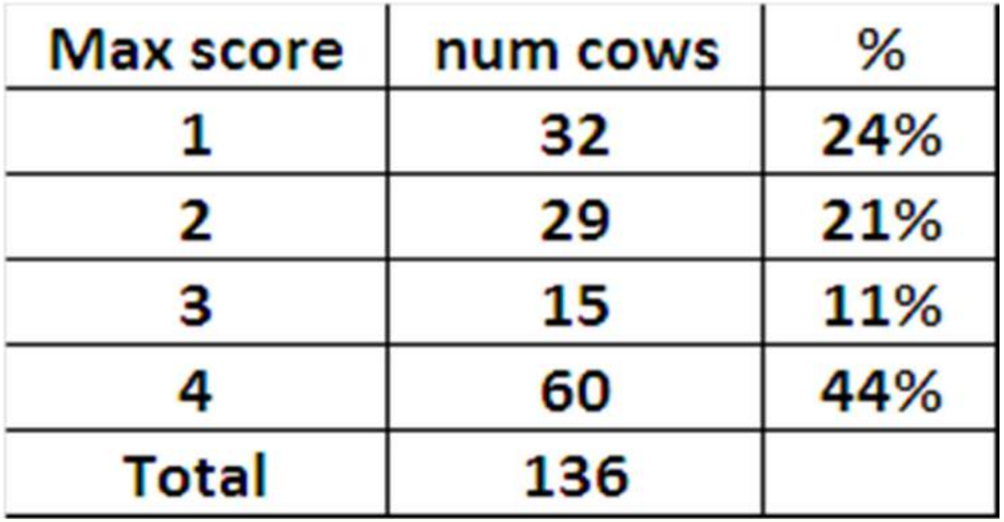
The Issue.

- Genetic evaluations are dependent on good quality data;
  - Calving, live-weights, milk volumes….
- Some recent examples where there is evidence of deliberate miss-recording.
- ICBF are building systems to reward good data recording – Herd Data Quality Index.
- To fairly reward good data recording, we must also penalise deliberate miss-recording.

Data Edits for new evaluations

- Deliberate mis-recording: Reasons:
  - Pedigree herd:
    - To avoid young bulls calving difficulty figure increasing
    - To make herd sire look good against AI sires
  - Commercial herd: Box ticking exercise

Cows on maternal bull breeder program with evidence of a C-section scored by linear scorers



Max score	num cows	%
1	32	24%
2	29	21%
3	15	11%
4	60	44%
Total	136	

Plan for 2015+

- To make HDQI's available for all herds (beef & dairy).
- To introduce new "terms & conditions" under which herd-owners receive genetic evaluations.
  - Compare against other data sources (e.g., milk co-op and beef quality assurance).
- Establish an across service provider approach
- Target implementation; August 2015.

Department of Agriculture, Food and the Marine
An Roinn Talmhaíochta, Bia agus Mara

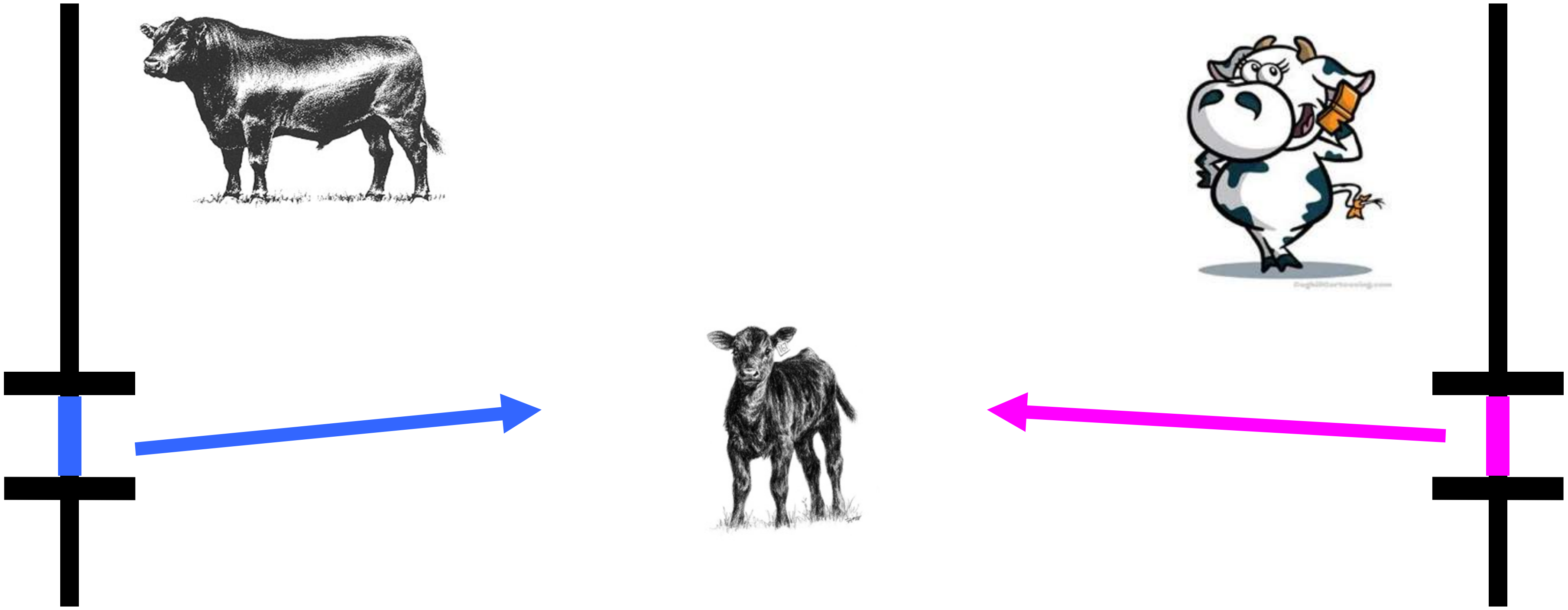
Multi-breed beef genomics

D.P. Berry[1], F. Kearney[2], R.D. Evans[2], T. Pabiou[2], M. McClure[2], J. McCarthy[2], D. Purfield[1], M. Judge[1], P. Flynn[3], R. Weld[3], M. Mullen[1], A. Bouwman[4], A.R. Cromie[2]

[1] Teagasc, Moorepark, [2] Irish Cattle Breeding Federation
[3] Weatherbys, [4] Wageningen

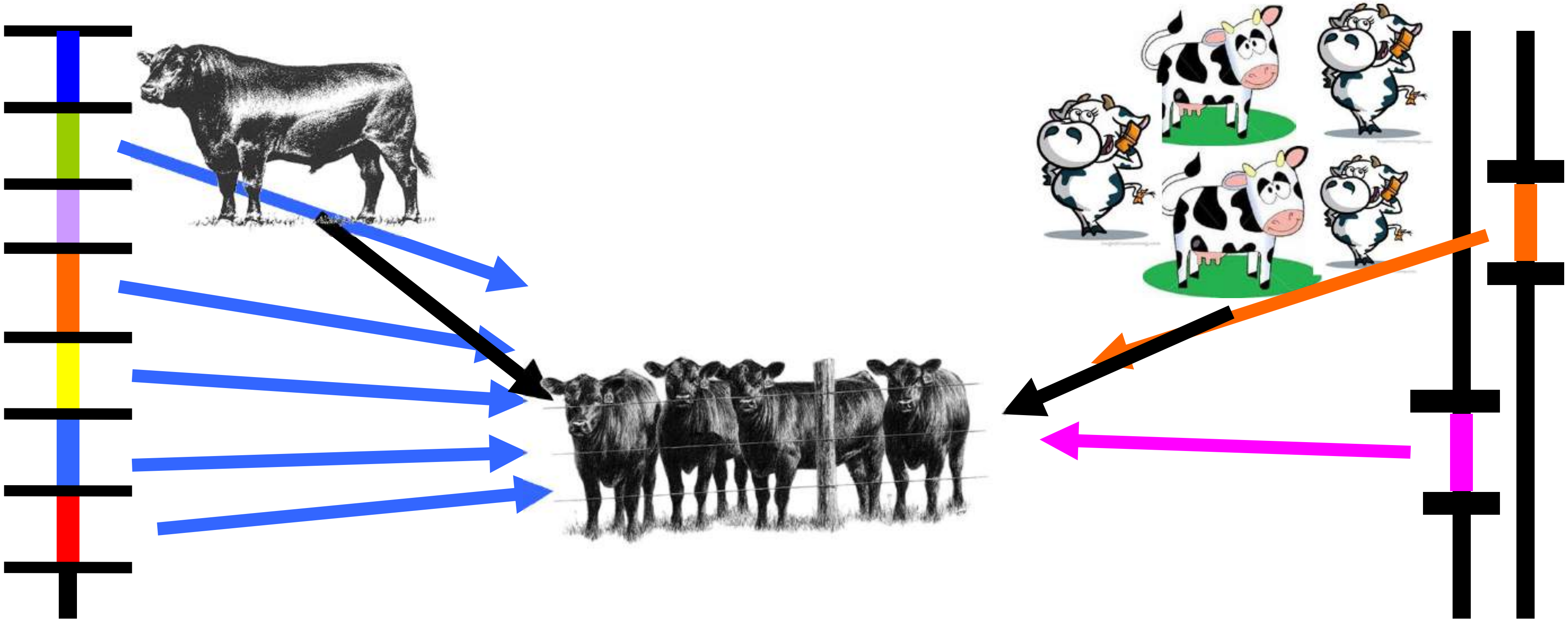
ICBF Industry Meeting, Portlaois, Oct 2014

Traditional Animal Breeding



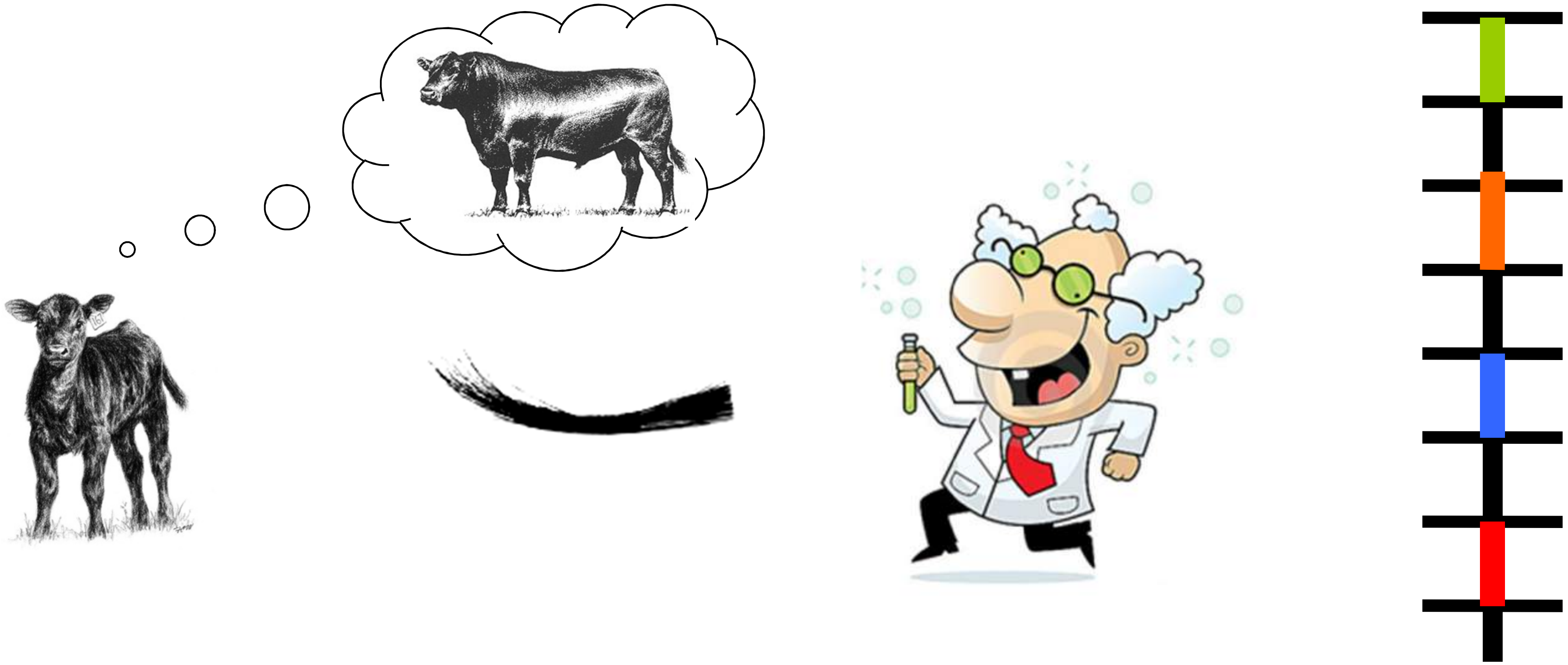
- Calf produces 320 kg carcass
- Bull reliability ~30%

Bull completes his progeny test



- Bull has 100 progeny slaughtered
- More of his DNA expressed in the population
- Bull reliability for carcass traits ~80%

Using genomics



- At birth we know about parts of the calf DNA
- Calf EBV reliability increases to ~ 55% (dairy)
  - Equivalent of 45 daughters milking for EBI

Genomics

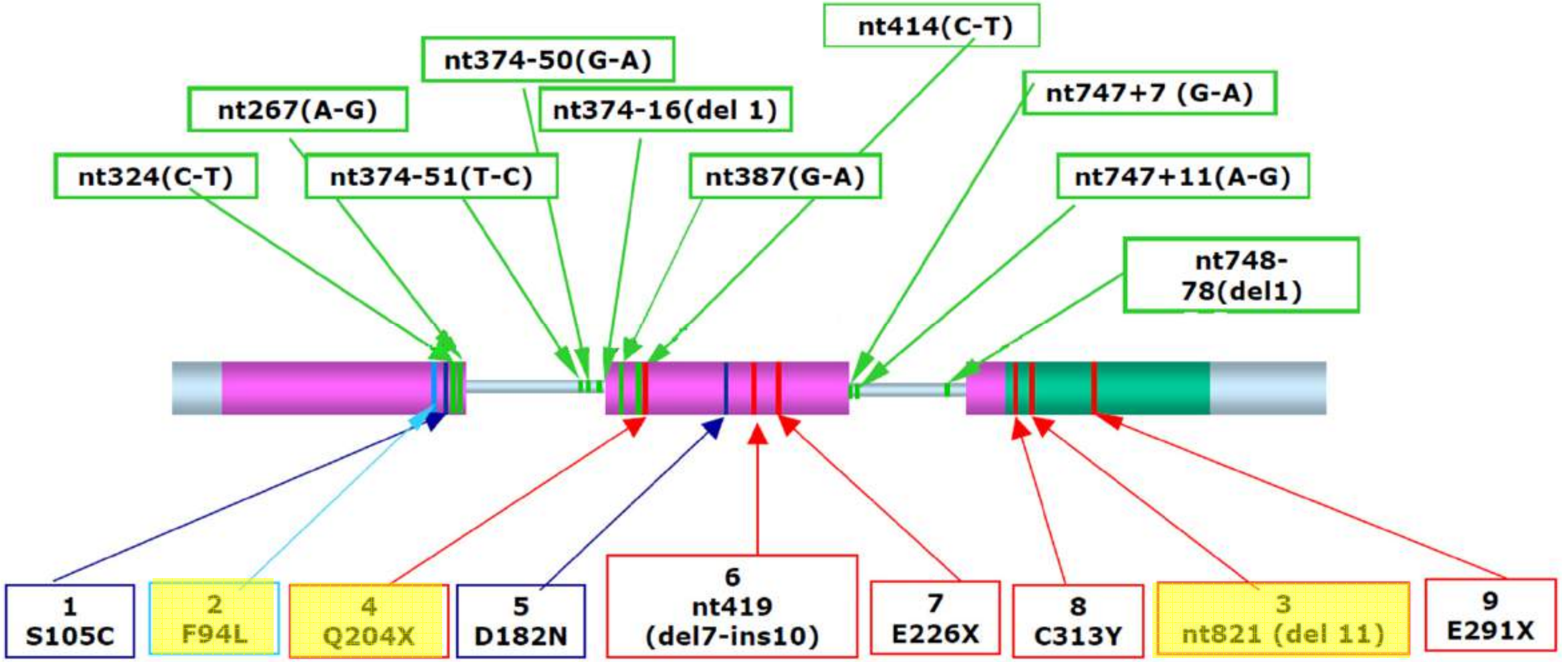
1. Parentage
2. Major genes (e.g., myostatin)
3. Genomic selection

Beef genomics scheme

- >5000 high reliability influential sires with high density genotypes
- Informative cows representing ~15% of national herd plus stock bulls

- Pedigree male calves genotyped by breed societies
- Genotypes shared (LM with UK)

Myostatin



nt414(C-T)

nt374-50(G-A)

nt267(A-G)

nt374-16(del 1)

nt747+7 (G-A)

nt324(C-T)

nt374-51(T-C)

nt387(G-A)

nt747+11(A-G)

nt748-78(del1)

1 S105C

2 F94L

4 Q204X

5 D182N

6 nt419 (del7-ins10)

7 E226X

8 C313Y

3 nt821 (del 11)

9 E291X

Résultat :

Culard

Génotype :	C313Y	E226X	E291X	F94L	NT419
	+ / +	+ / +	+ / +	MH / MH	+ / +
	NT821	Q204X	S105C	D182N	
	+ / +	+ / +	+ / +	+ / +	

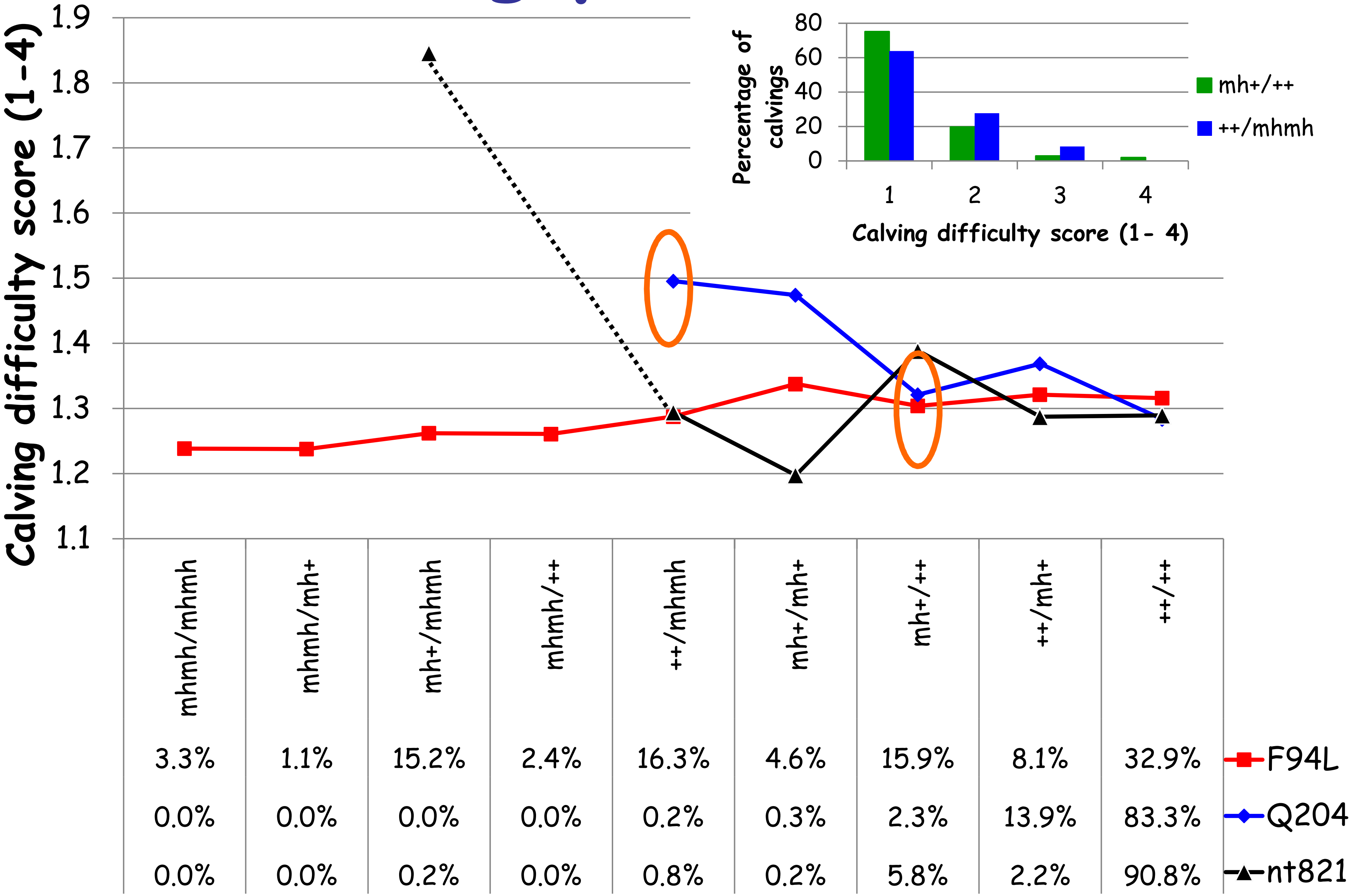
Incidence (n≈93,000)

	Males			Females		
	+/+	+/mh	mh/mh	+/+	+/mh	mh/mh
F94L	61.6	12.02	26.38	66.92	26.83	6.25
Q204	89.7	10.10	0.17	97.60	2.38	0.02
nt821	95.5	2.82	1.70	93.80	5.98	0.22

Incidence per breed (≥87.5 purity)

		F94L			Q204X			nt821		
	N	+/+	+/mh	mh/mh	+/+	+/mh	mh/mh	+/+	+/mh	mh/mh
AA	3396	98.85	0.85	0.29	99.91	0.09	0.00	95.52	4.42	0.06
BB	530	98.68	1.32	0.00	100.00	0.00	0.00	0.06	2.26	97.17
CH	12980	74.94	23.33	1.74	73.48	26.03	0.49	99.86	0.14	0.00
HE	2268	99.60	0.18	0.22	99.82	0.18	0.00	99.69	0.31	0.00
LM	12596	0.94	12.51	86.55	95.02	4.93	0.05	94.97	5.02	0.02
SI	2329	98.75	1.16	0.09	99.79	0.21	0.00	99.87	0.13	0.00

Calving performance



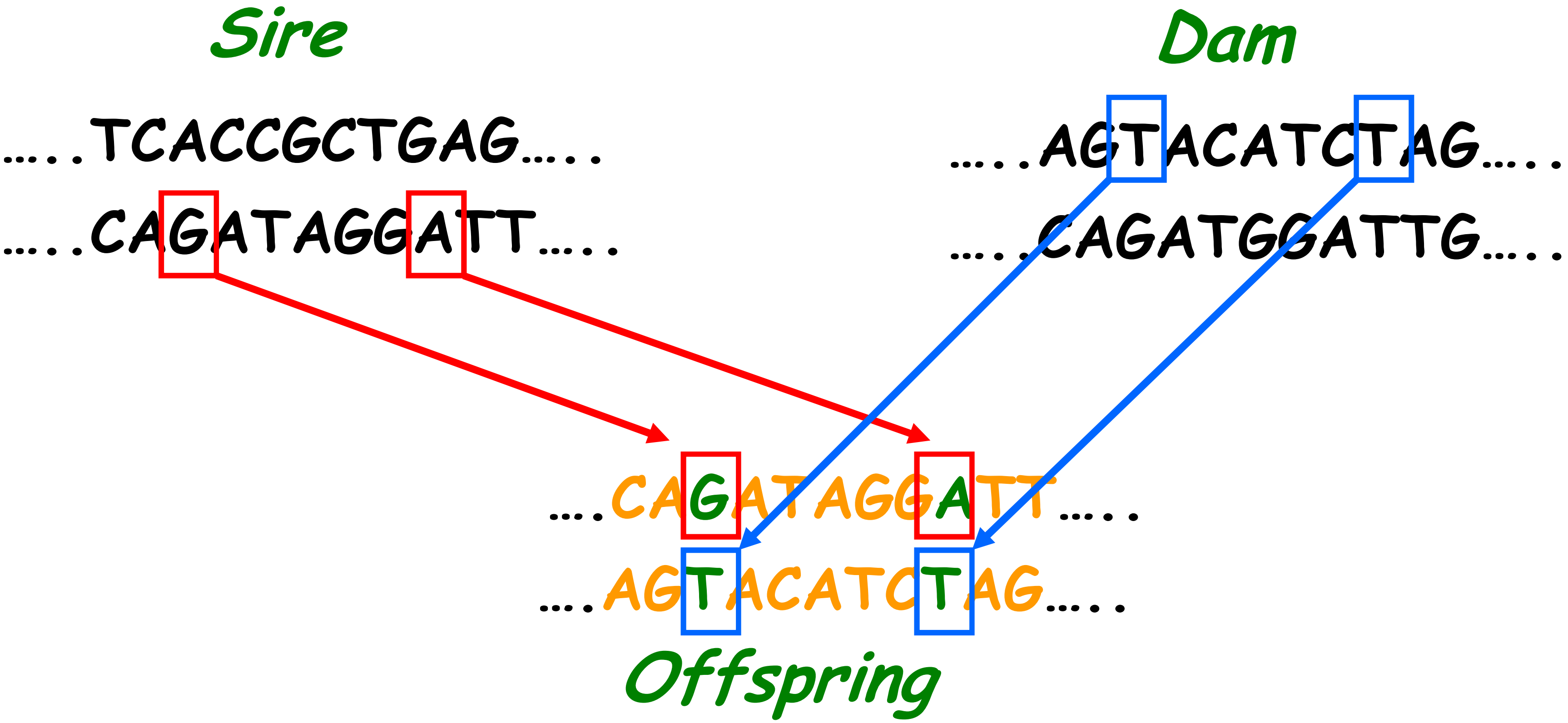
	mhmh/mhmh	mhmh/mh+	mh+/mhmh	mhmh/++	++/mhmh	mh+/mh+	mh+/++	++/mh+	++/++
F94L	3.3%	1.1%	15.2%	2.4%	16.3%	4.6%	15.9%	8.1%	32.9%
Q204	0.0%	0.0%	0.0%	0.0%	0.2%	0.3%	2.3%	13.9%	83.3%
nt821	0.0%	0.0%	0.2%	0.0%	0.8%	0.2%	5.8%	2.2%	90.8%

Imputation

- Genomic selection in dairy uses 54,000 DNA markers
- IDB genotype chip has ~12,500 for genomic selection
    - ~33% of the cost

- Predict (impute) 54,000 DNA markers from 12,500
    - 5,194 animals with "54,000" markers

Imputation



Sire

…..TCACCGCTGAG…..

…..CAGATAGGATT…..

Dam

…..AGTACATCTAG…..

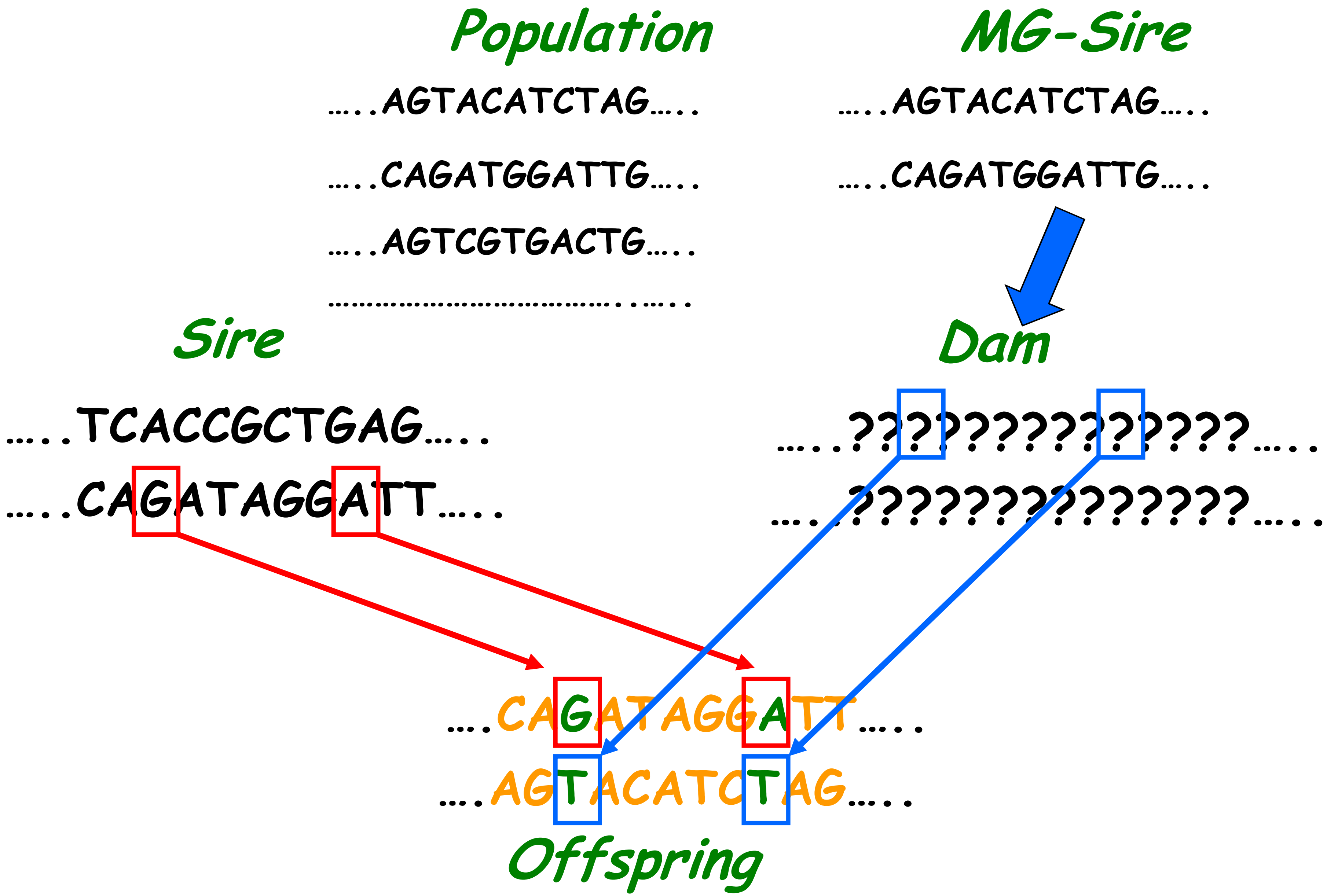
…..CAGATGGATTG…..

….CAGATAGGATT…..

….AGTACATCTAG…..

Offspring

Imputation



Population

…..AGTACATCTAG…..

…..CAGATGGATTG…..

…..AGTCGTGACTG…..

……………………………….…..

MG-Sire

…..AGTACATCTAG…..

…..CAGATGGATTG…..

Sire

…..TCACCGCTGAG…..

…..CAGATAGGATT…..

Dam

…..??????????????…..

…..??????????????…..

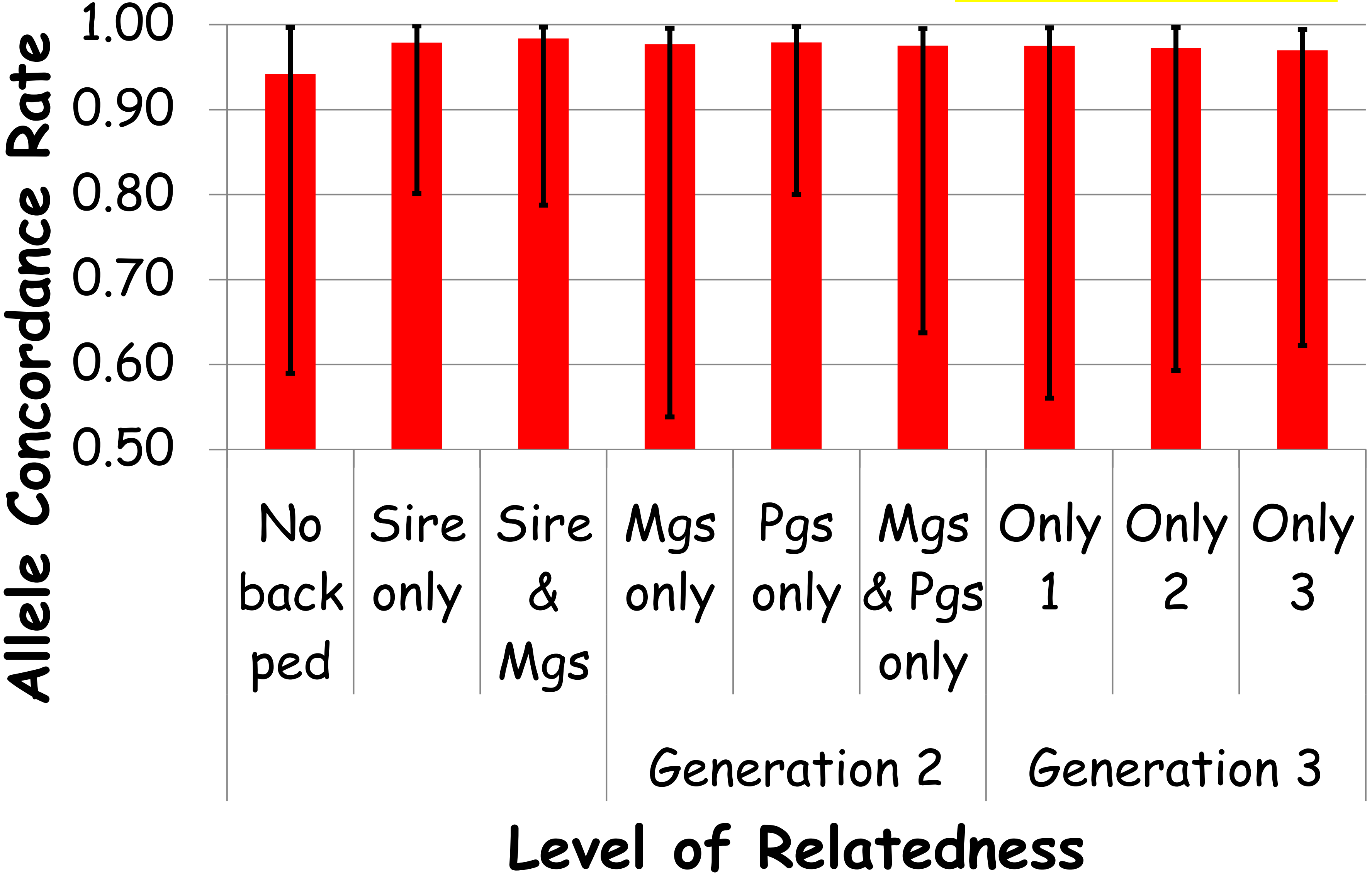
….CAGATAGGATT…..

….AGTACATCTAG…..

Offspring

Imputation

97.3%
(54%-100%)

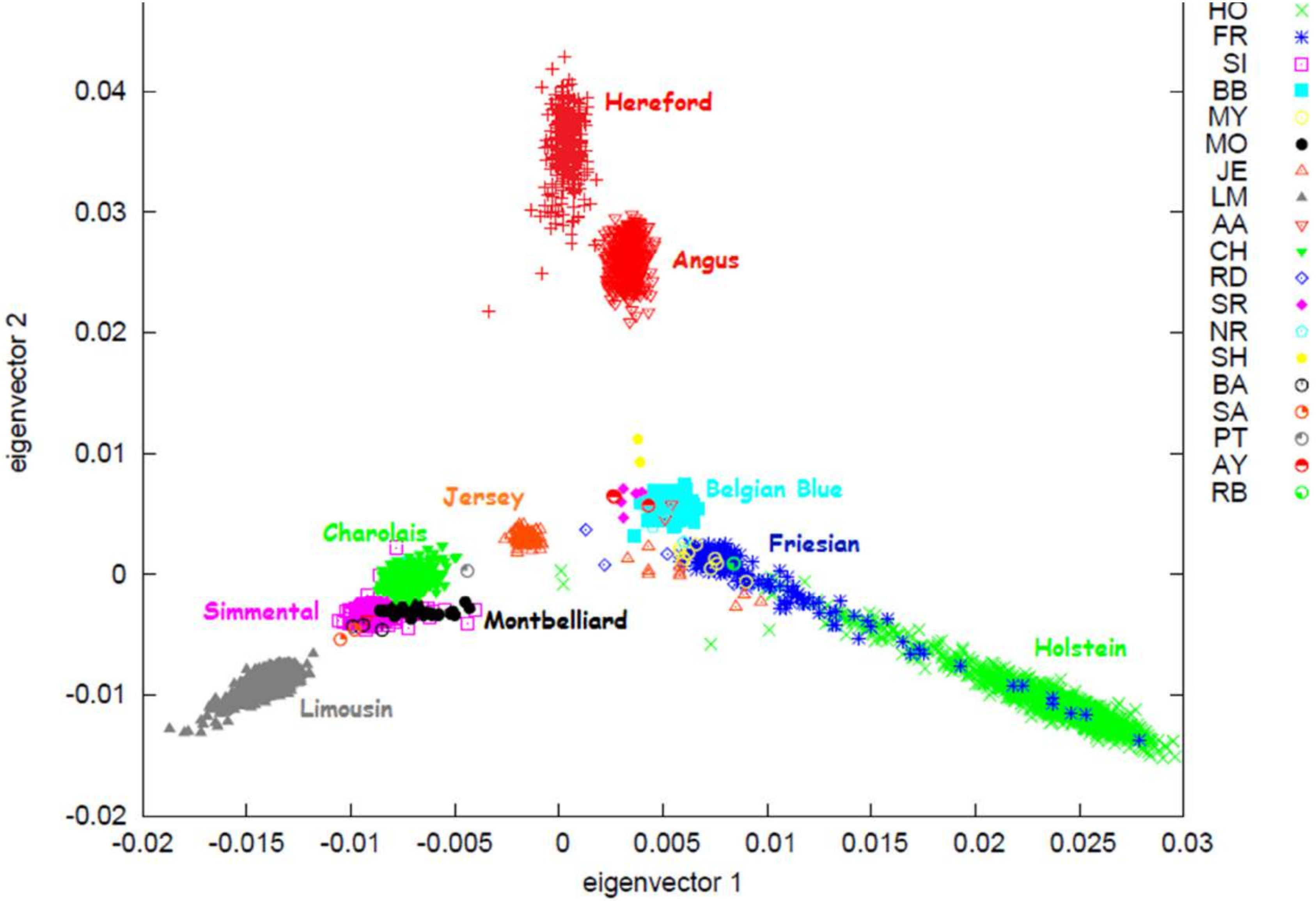


Genomics predictions

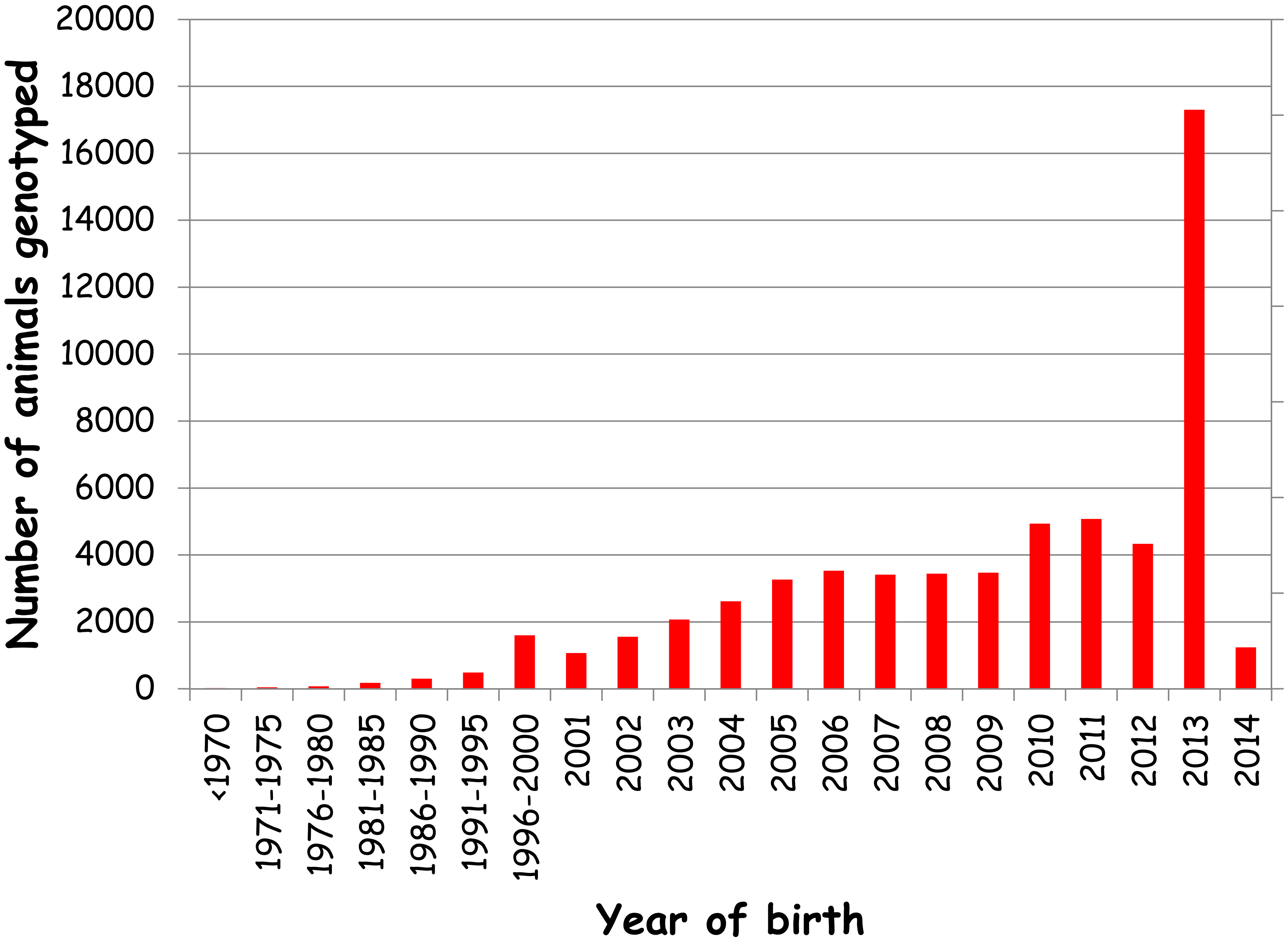
- Use the DNA profile of animals with performance to predict the genetic merit of young animals
- High reliability >> low reliability

- Develop predictions based on PTAs of older bulls
  - More recent data deleted from genetic evaluations
- Apply prediction equations to younger bulls with progeny in Ireland and compare predictions versus progeny proof

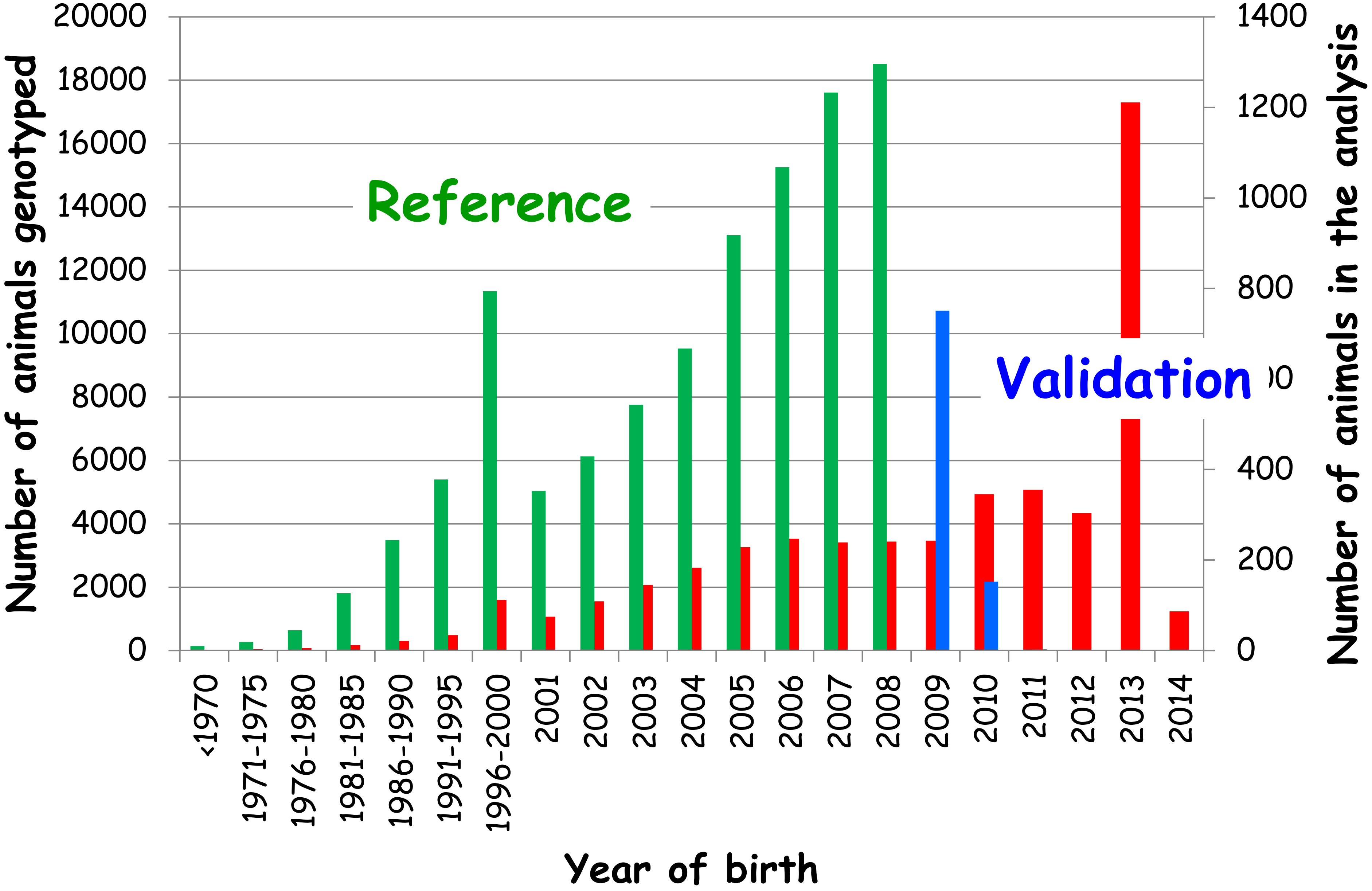
Population structure



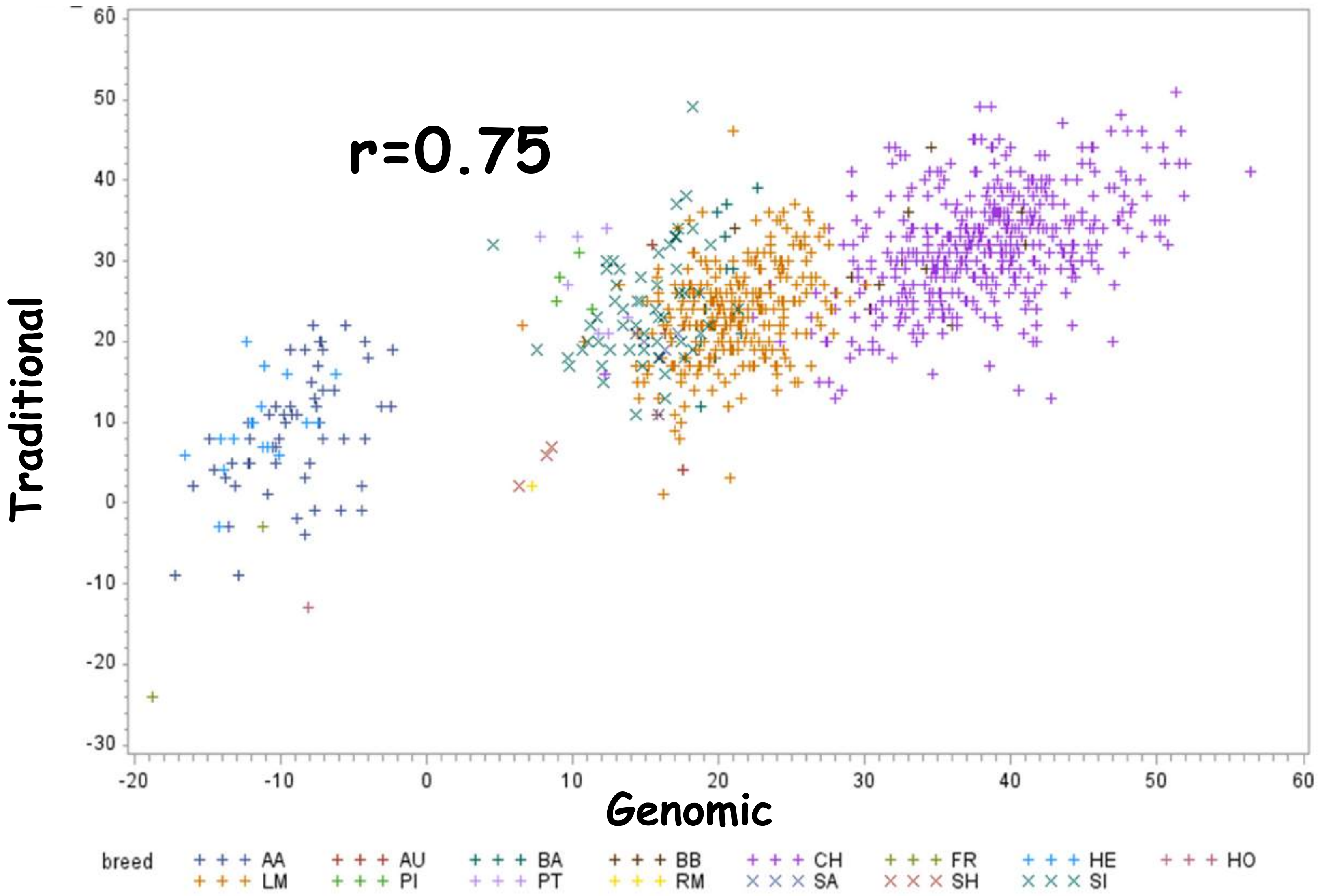
Genotyped animals



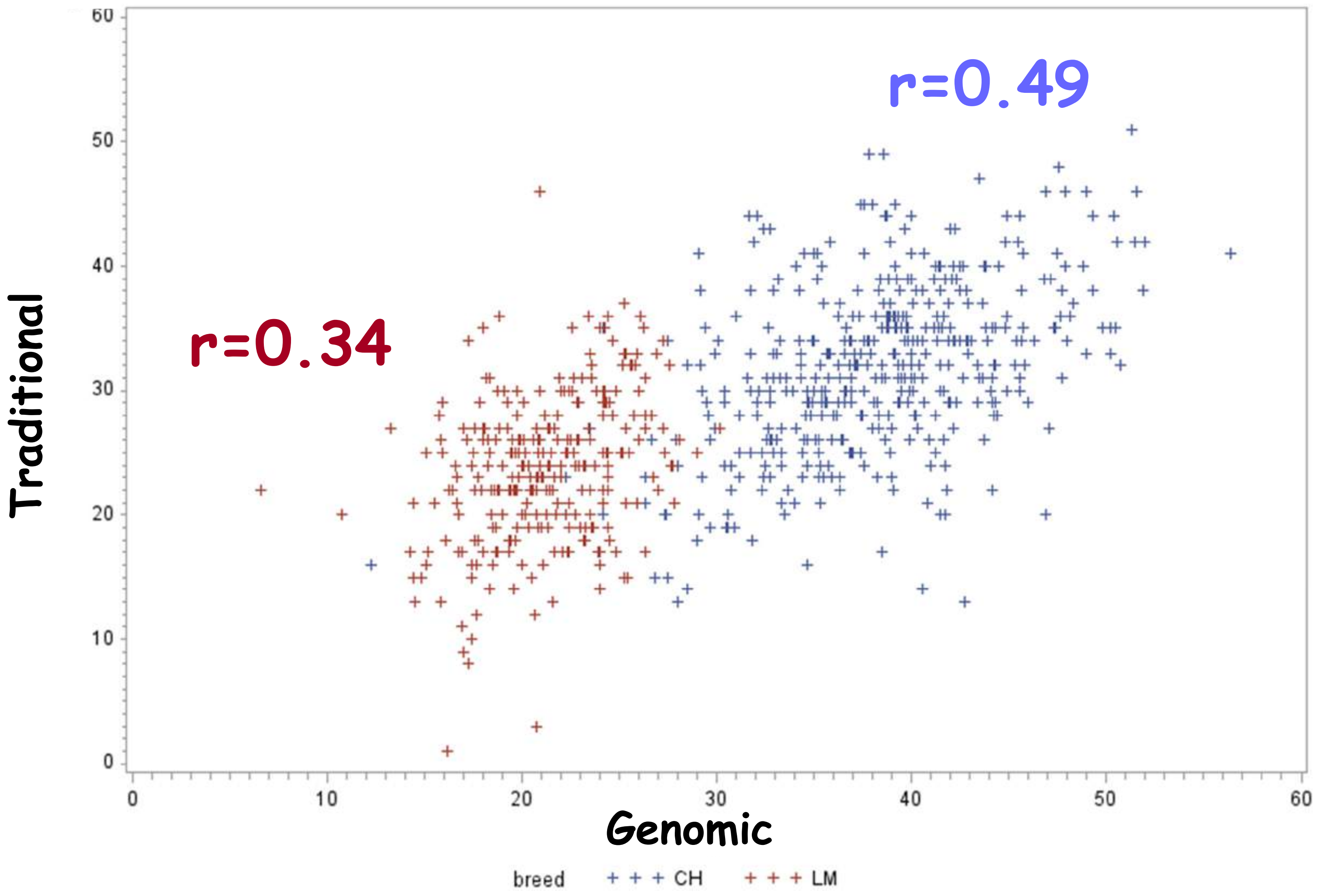
Genotyped animals



Carcass weight

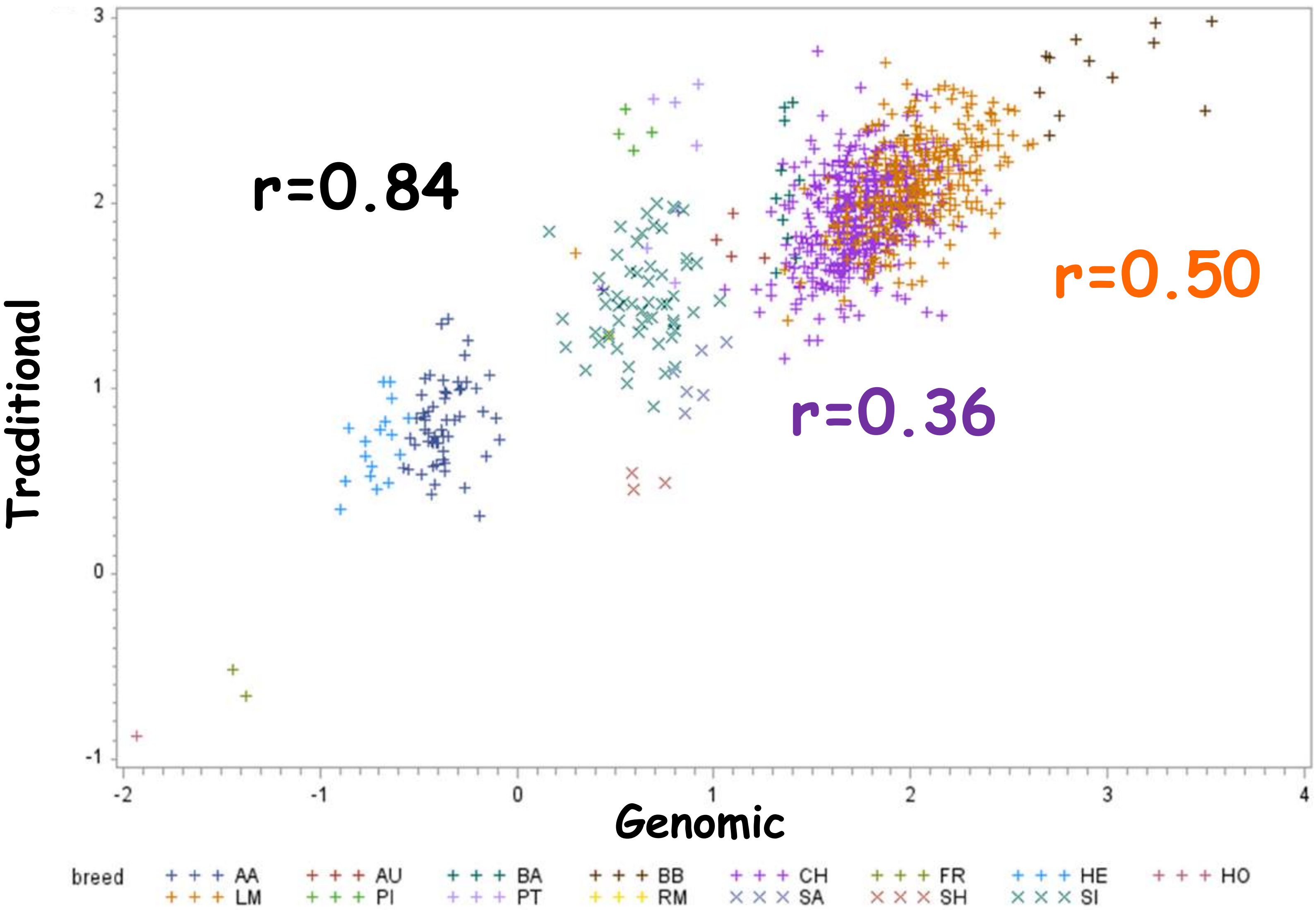


Carcass weight

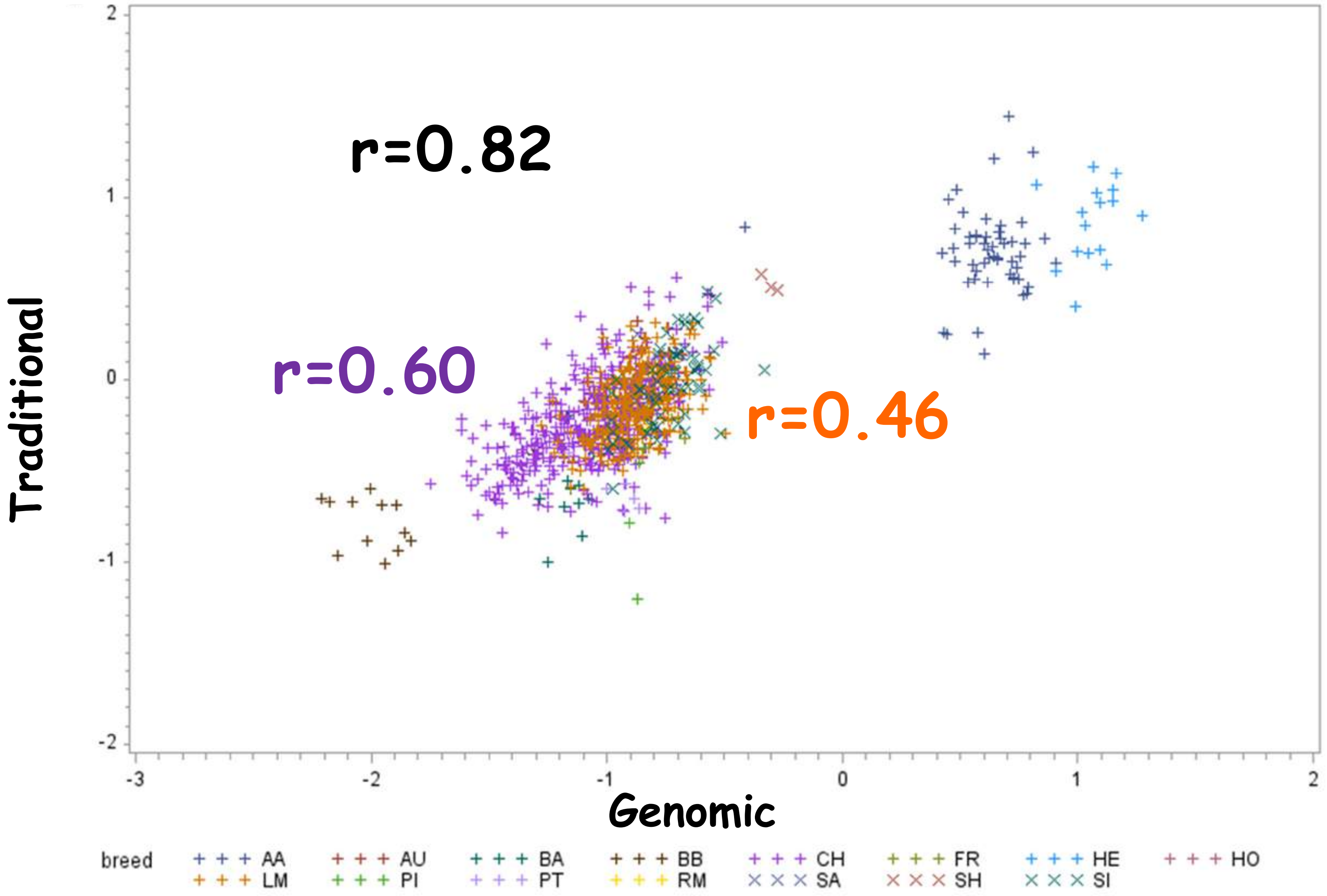

r=0.49

r=0.34

Carcass conformation



Carcass fat

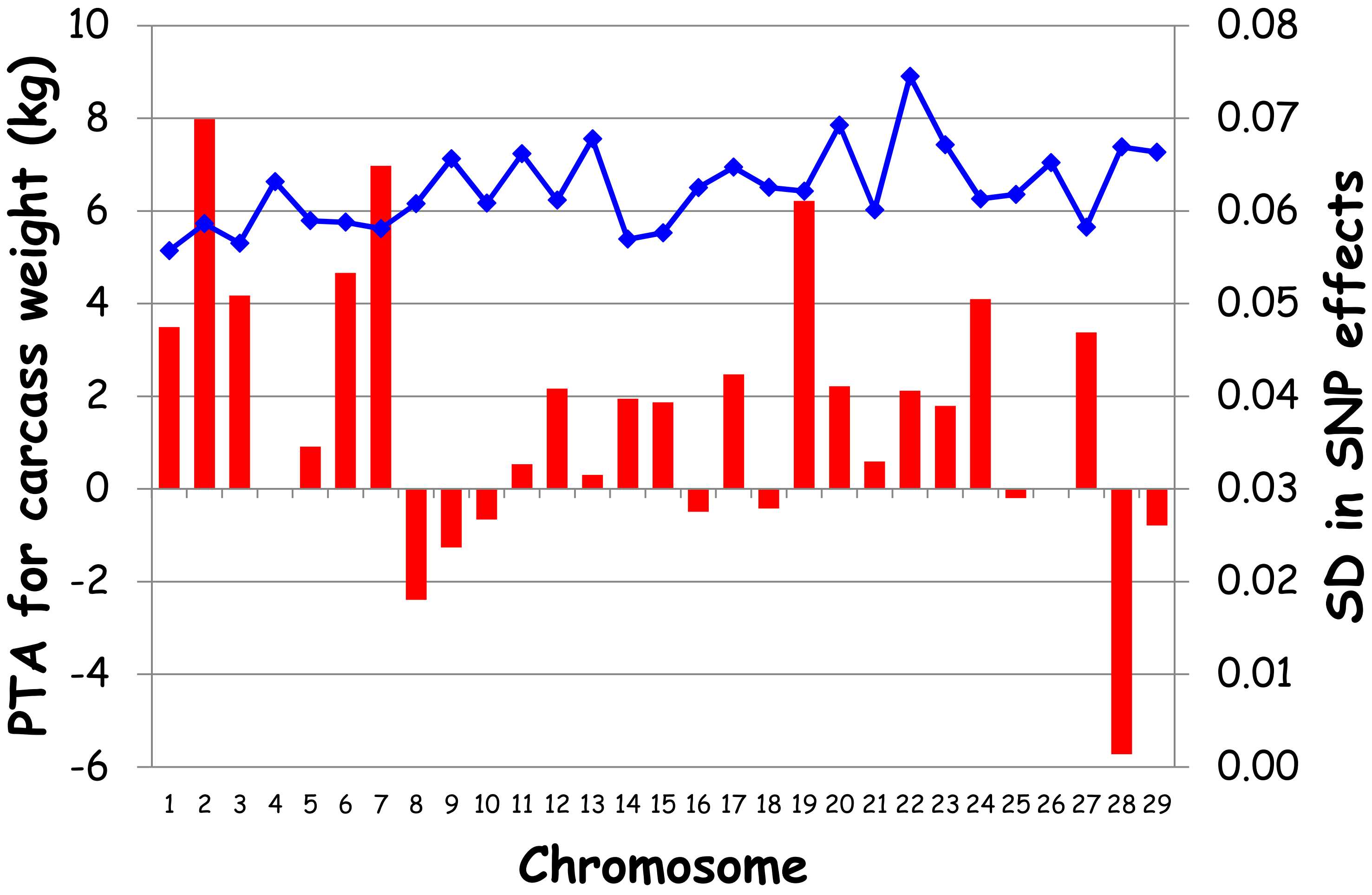


r=0.82

r=0.60

r=0.46

CF52 – chromosomal PTAs



Next steps

1. More complicated (i.e., accurate) genomic prediction algorithms
2. All traits (e.g., calving interval)
3. Including all animals in reference population
4. Blending of genetic & genomic evaluations
5. Calculation of accuracy
6. Speeding up evaluations

Acknowledgements

- Research Stimulus Fund (11/S/112 & 13 F 403)
- Irish farmers
- Breed Societies
- AI stations
- Raph Mrode (SRUC), Esa Mantysaari & Ismo Stranden (MTT)
- Scientific advisory group

Department of Agriculture, Food and the Marine
An Roinn Talmhaíochta, Bia agus Mara

IRISH CATTLE BREEDING FEDERATION

Beef Genomics Workshop.

Andrew Cromie

NDP
National Development Plan
Transforming Ireland

Genomics Workshop.

- Scientific advisory group re: suckler beef genomics project visiting Ireland on Monday 24 November.
- Interbeef genomics workshop on 25 (all day) & 26 November (AM only).
- *Beef genomics workshop for Irish industry on Wednesday 26 November, Roganstown Hotel, Swords, 2 PM – 5.00 PM.*

How Genetic Differences in Beef Terminal Traits are Reflected in Phenotypic Performance Differences

Stephen Connolly BAgrSC
Msc Student Teagasc Moorepark

Teagasc
Agriculture and Food Development Authority

The Irish Agriculture and Food Develo

ICBF.com

Motivation

- Do calf differences in terminal index values manifest themselves as differences in on-farm performance as older animals?
- Is performance differences in animals divergent for terminal index consistent between **young bulls, heifers and steers**?
- Is performance differences in animals divergent for terminal index consistent between **bucket-reared calves or suckled calves**?

Study Overview

- Animals born in 2009/2010
  - Genetic merit from evaluations in 2010
- Animals slaughtered from 2010 to 2013
- Animals split into 4 groups based on terminal index
- 159,097 animals from 7,303 herds

Top 20% v. Bottom 20% on Terminal Index

	Elite EBV	Low EBV	Difference
Age (days)	744	750	**6 (20)**
Cwt (kg)	369	330	**39**
Conformation	8.51(R+)	6.3 (O+)	**2.21**
Value (€)	1409	1222	**187**
Feed intake EBV	-0.170	0.203	**0.373**
HVC (kg)	68	57	**11kg (16%)**
Tot meat yield (kg)	253	218	**35kg (14%)**

Cost - Benefit

- **Farmer finishing 50 cattle**
- **Revenue**
  - **50 cattle x €187 = €9,350 in carcass value**
- **Costs**
  - **6 days you**
  - **Assumi 2 kg DM @ €290/ tonne (kg x 6 days x 50 animals) €1**
  - **Also eating 0.373 kg less per day x 50 animals x 84 days = 1.75 tonnes x €290 = €454**

€10,848 profit!!!

eagasc
Agriculture and Food Development Authority

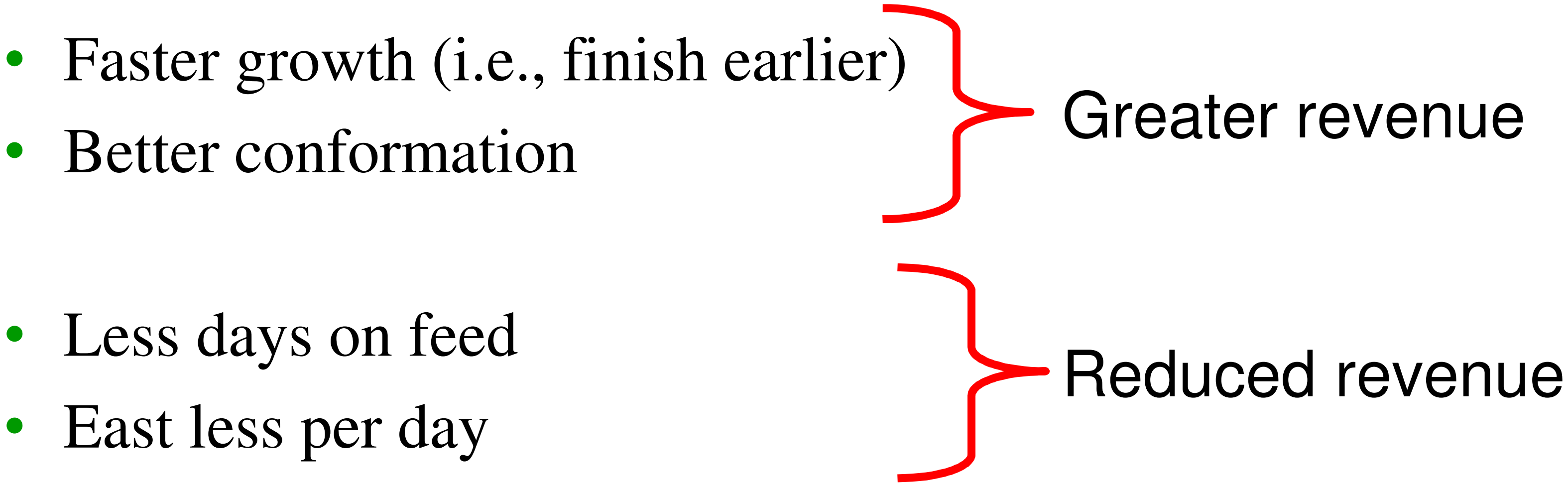
Terminal Index robustness

- Differences between divergent terminal index groups was similar irrespective of whether calves were suckled or bucked-reared

- Differences between divergent terminal index groups was similar irrespective of whether the animal was a bull, steer or heifer
    - Slightly greater performance difference between genetically divergent young bulls

Conclusion

- Terminal index is working at farm level and robust across contrasting production systems
- Selecting for more profitable animals through



  - Faster growth (i.e., finish earlier)
  - Better conformation

Greater revenue

  - Less days on feed
  - East less per day

Reduced revenue

Funding from ABP

If there are any questions I would be happy to answer them

IRISH CATTLE BREEDING FEDERATION

Phenotypic and Genetic Analysis of Meat Eating Quality Traits in Irish Cattle

Francis Kearney, ICBF.

NDP
National Development Plan
Transforming Ireland

Background

- Huge improvements in meat eating quality over past 10 years (e.g., slow-chilling, hip-hanging & dry-age process).

- Processes account for ~80% of improvements in meat eating quality. Now “standard” procedures
- Can genetics influence the last 20%?
- What if last 20% is having a 50% impact on value of higher value meat cuts?

Partners involved in the research

GENE IRELAND®
Breeding future Profits

Teagasc
Agriculture and Food Development Authority

Slaney
FOODS

EOLAS
INTERNATIONAL RESEARCH

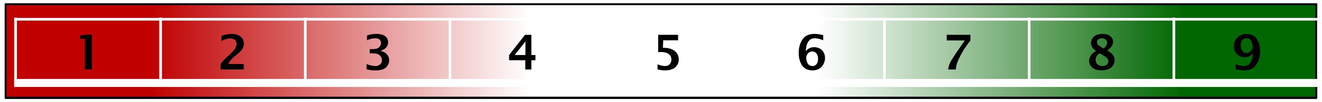
abp

Outline of Sensory analysis

- Eolas International, Co. Cork
- 7-10 trained panellists
- http://www.eolasinternational.com

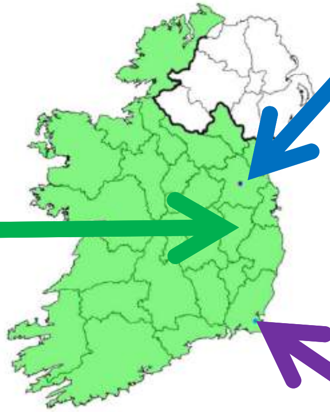
- *longissimus thoracis* muscle from right side of each carcass
- 2.5cm steaks which were thawed at 4℃ at 24 hours before analysis
- grilled to a ‘medium’ cooking finish, allowed to rest for two minutes

Measurement Scale



“Extremely Tough” “Not at all Juicy” “Off-note”	**<u>Tenderness</u>** **<u>Juiciness</u>** **<u>Flavour</u>**	“Extremely Tender” “Extremely Juicy” “Extremely flavoursome”

Datasets available



Dataset 1

- ICBF performance test centre Tully Co. Kildare
- Animals are purchased from commercial farms at 10-12 months and evaluated for 90 days following 1 month of acclimatisation
- Ad-lib concentrate diets
- Genotyped, Weight gain, Feed intake, linear classification, carcass
- 507 crossbred progeny from 127 AI sires
- 4,578 sensory observations

Dataset 2

- Teagasc research Centre, Grange, Co. Meath
- Primary suckler beef cattle research centre
- Systems and breed comparison trials
- 129 crossbred suckler progeny from 75 sires
- 141 sensory observations

Dataset 3

- Teagasc research centre, Johnstown castle, Co. Wexford
- Dairy and dairy x beef research centre
- Systems and environment al research
- 151 dairy and dairy x beef progeny, 48 AI sires
- 874 sensory observations

Datasets available

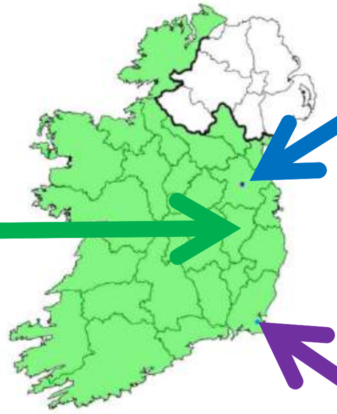
Dataset 1

- 91% Bulls, 9% steers
- Breed composition: Limousine (32%), Charolais (14%), Simmental (14%), Belgian Blue (11%), Angus (6%),
- Holstein (7%),
- Hereford (2%)
- 13 slaughter dates from 2012 – 2014

4 sires in common

Dataset 2

- 100% bulls
- Breed composition: Charolais (41%), Limousine (24%), Holstein (8%), Simmental (6%), Hereford (5%) Belgian Blue (2%), Angus (2%)
- 7 slaughter dates from 2011



Dataset 3

- 32% Bulls, 26% steers, 42% heifers,
- Breed composition : Holstein (44%), Angus (18%), Hereford (14%), Friesian (9%)
- 11 slaughter dates from 2011 to 2103

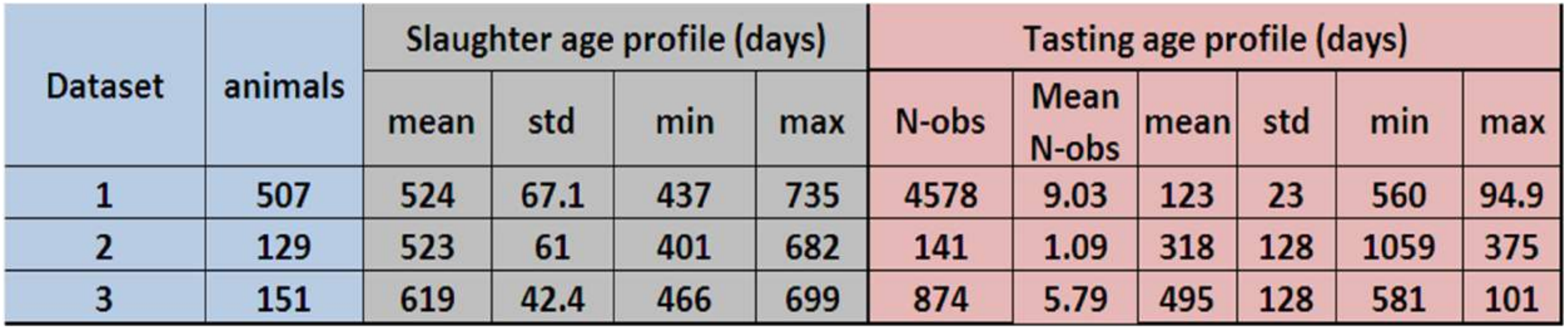
Datasets have weak sire links but strong connections to national population

Dataset 1 sires: 306,961 recorded progeny slaughtered

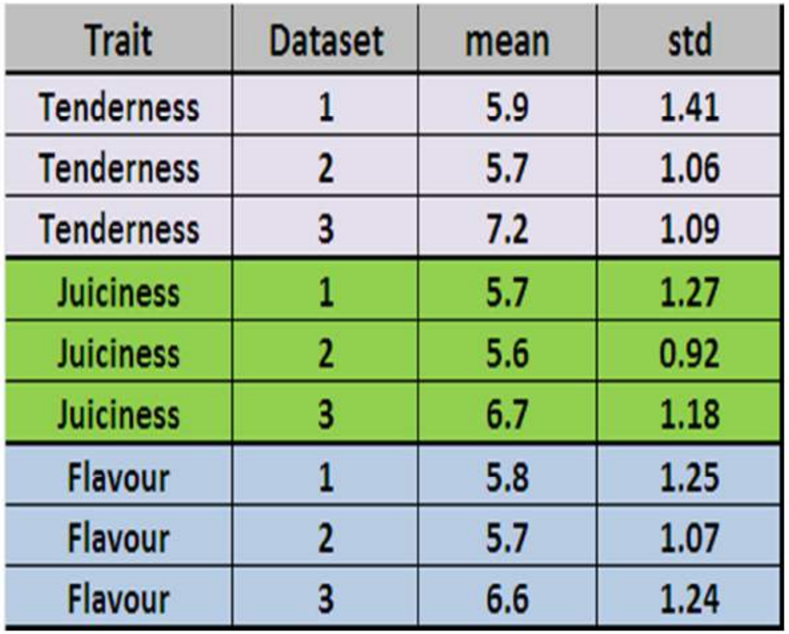
Dataset 2 sires: 94,036 recorded progeny slaughtered

Dataset 3 sires: 49,554 recorded progeny slaughtered

Dataset statistics



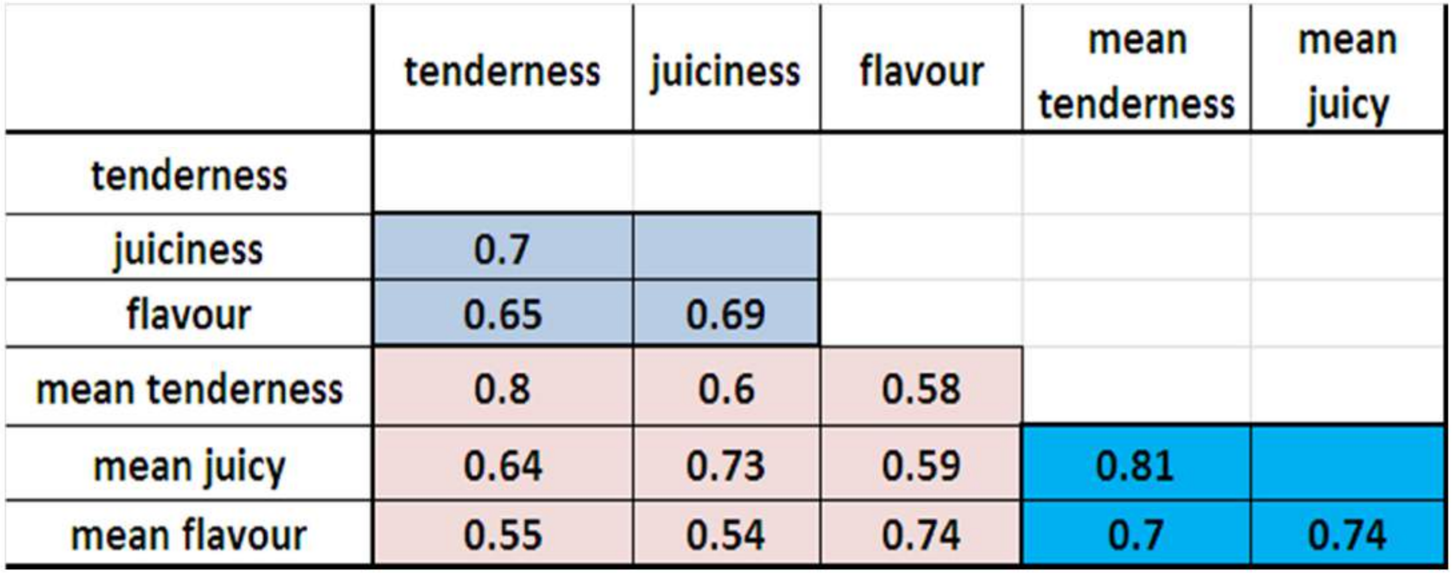
Dataset	animals	Slaughter age profile (days)				Tasting age profile (days)					
		mean	std	min	max	N-obs	Mean N-obs	mean	std	min	max
1	507	524	67.1	437	735	4578	9.03	123	23	560	94.9
2	129	523	61	401	682	141	1.09	318	128	1059	375
3	151	619	42.4	466	699	874	5.79	495	128	581	101



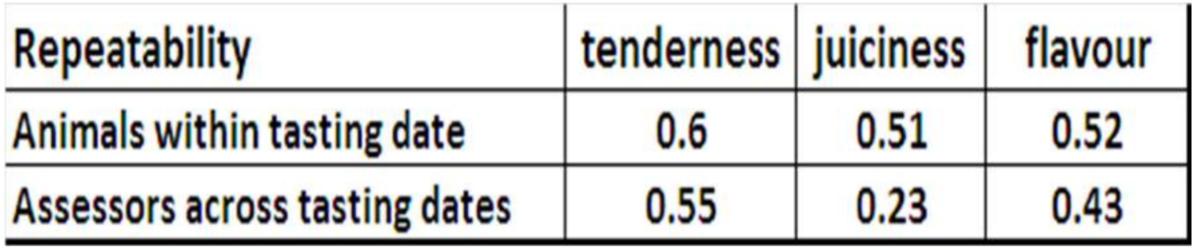
Trait	Dataset	mean	std
Tenderness	1	5.9	1.41
Tenderness	2	5.7	1.06
Tenderness	3	7.2	1.09
Juiciness	1	5.7	1.27
Juiciness	2	5.6	0.92
Juiciness	3	6.7	1.18
Flavour	1	5.8	1.25
Flavour	2	5.7	1.07
Flavour	3	6.6	1.24

- **87 animals (16%) in dataset 1 had repeated sensory analysis on different days**
- **39 tasting dates in total**
- **27 are bulls only, 2 are steers only,**
- **4 have a mixture of steers and heifers**
- **6 have a mixture of bulls, steers and heifers**

Phenotypic results



	tenderness	juiciness	flavour	mean tenderness	mean juicy
tenderness					
juiciness	0.7				
flavour	0.65	0.69			
mean tenderness	0.8	0.6	0.58		
mean juicy	0.64	0.73	0.59	0.81	
mean flavour	0.55	0.54	0.74	0.7	0.74



Repeatability	tenderness	juiciness	flavour
Animals within tasting date	0.6	0.51	0.52
Assessors across tasting dates	0.55	0.23	0.43

Edits & model applied for genetic analysis

Edits applied to data
Minimum contemporary group of slaughter and tasting day of 10 animals
5,510 observation on 751 animals remaining, 9653 animals in pedigree file

Fixed effects
- Dataset x slaughter date
- Date of sensory tasting
- Sensory assessor

Covariates
- Covariate of age at slaughter (days)
- Covariate of time from slaughter to tasting (days)
- Covariate of breed fraction (n = 8)

Random effects
- Random animal genetic effect
- Random animal x date of sensory test effect
- Random animal x scorer effect
- Random residual effect

Genetic parameters

Trait	heritability	permanent environment	
		animal x tasting date	animal x assessor
Tenderness	0.27	0.25	0.01
Juiciness	0.07	0.36	0.02
Flavour	0.16	0.27	0.06

	genetic correlations	
	Tenderness	Juiciness
Juiciness	0.79 (0.019)	
Flavour	0.69 (0.026)	0.72 (0.025)

Fixed effects (BLUEs)

Fixed effect of carcass type

Carcass type	Tenderness		Juiciness		Flavour	
	Estimate	se	Estimate	se	Estimate	se
Heifer	0.00	0.000	0.00	0.000	0.00	0.000
Steer	-0.05	0.254	0.09	0.209	-0.06	0.225
Bull	-1.87	0.532	-1.71	0.439	-1.90	0.473

Fixed effects (BLUEs)

Regression co-efficients

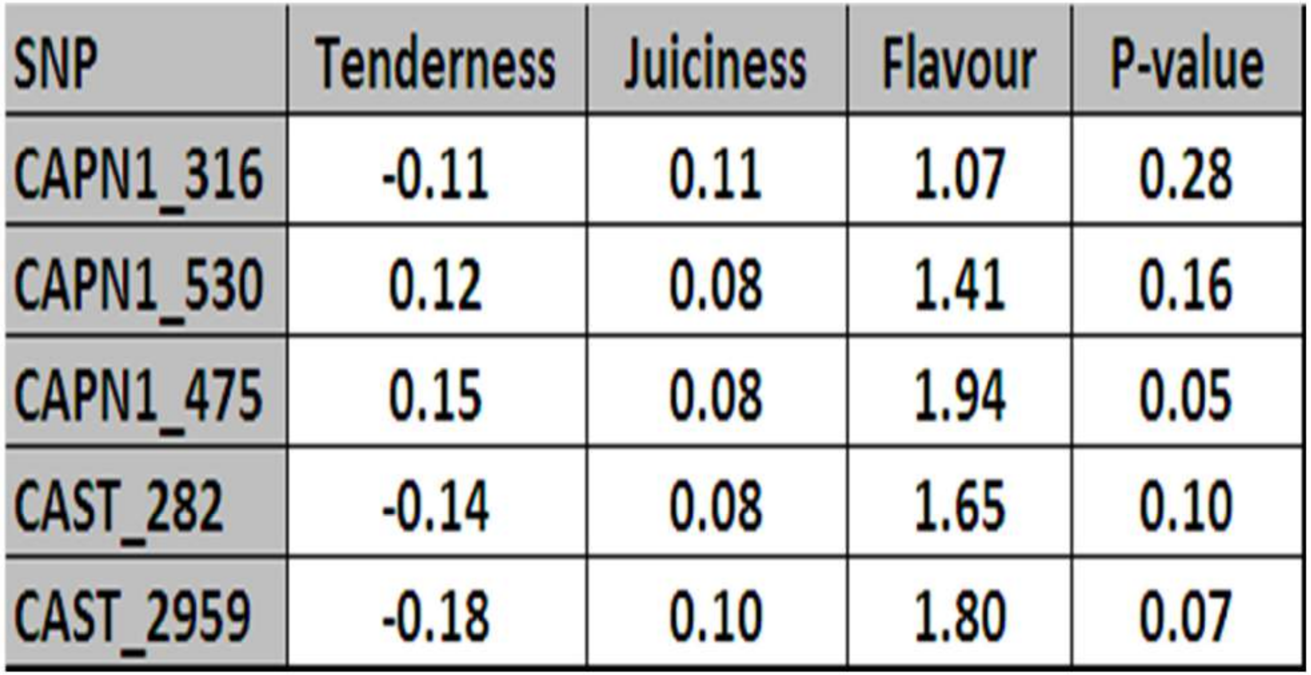
Regression variable	Tenderness		Juiciness		Flavour	
	Estimate	se	Estimate	se	Estimate	se
slaughter age (days)	-0.002	0.002	-0.001	0.002	-0.002	0.002
slaughter to taste (days)	-0.012	0.005	-0.009	0.004	-0.004	0.004
Hereford	0.79	0.482	0.68	0.384	1.08	0.423
Angus	0.16	0.393	0.29	0.300	0.11	0.339
Limousine	0.14	0.299	-0.01	0.222	-0.02	0.256
Belgian Blue	0.07	0.359	0.03	0.265	0.01	0.306
Charolais	-0.14	0.318	-0.13	0.238	-0.32	0.273
Holstein	-0.38	0.639	-0.51	0.539	-0.05	0.580
Friesian	-0.47	0.853	-0.04	0.701	-0.51	0.759
Simmental	-0.57	0.353	-0.47	0.257	-0.44	0.300
Beef x beef heterosis	0.02	0.153	-0.04	0.127	-0.02	0.137
Beef x dairy heterosis	0.20	0.330	0.12	0.274	0.17	0.297

Potentially useful predictor traits

	genetic correlations					
	Warner Bratzel Shear Force	pH: 24 hr post slaughter	Temperament score in feedlot	Carcass traits		
				weight	grade score	fat score
Records available	331	524	481	698		
Source	dataset 1	dataset 1 & 3	dataset 1	dataset 1, 2 & 3		
Tenderness	-0.86 (0.125)	-0.19 (0.051)	0.10 (0.146)	-0.12 (0.075)	-0.14 (0.099)	0.02 (0.102)
Juiciness	-0.51 (0.102)	-0.18 (0.052)	0.19 (0.171)	-0.31 (0.145)	-0.25 (0.182)	-0.11 (0.178)
Flavour	-0.53 (0.104)	-0.48 (0.070)	0.05 (0.146)	-0.08 (0.081)	-0.16 (0.109)	0.11 (0.113)

Major gene search

- *498 animals with IDB 19K genotypes from dataset 1*
- *Model based on average score, adjusts for date of tasting and pedigree structure*



SNP	Tenderness	Juiciness	Flavour	P-value
CAPN1_316	-0.11	0.11	1.07	0.28
CAPN1_530	0.12	0.08	1.41	0.16
CAPN1_475	0.15	0.08	1.94	0.05
CAST_282	-0.14	0.08	1.65	0.10
CAST_2959	-0.18	0.10	1.80	0.07

Conclusions

- **Meat eating quality as assessed by trained scorers exhibits additive genetic variation**

- **No significant differences between breeds based on current small dataset**

- **Potential useful relationships with traits collected routinely e.g. temperament and pH at factory post slaughter**
- **No indication yet of major genes at play**

- **Need to collect larger volumes of data and run validation studies with consumers to confirm results**

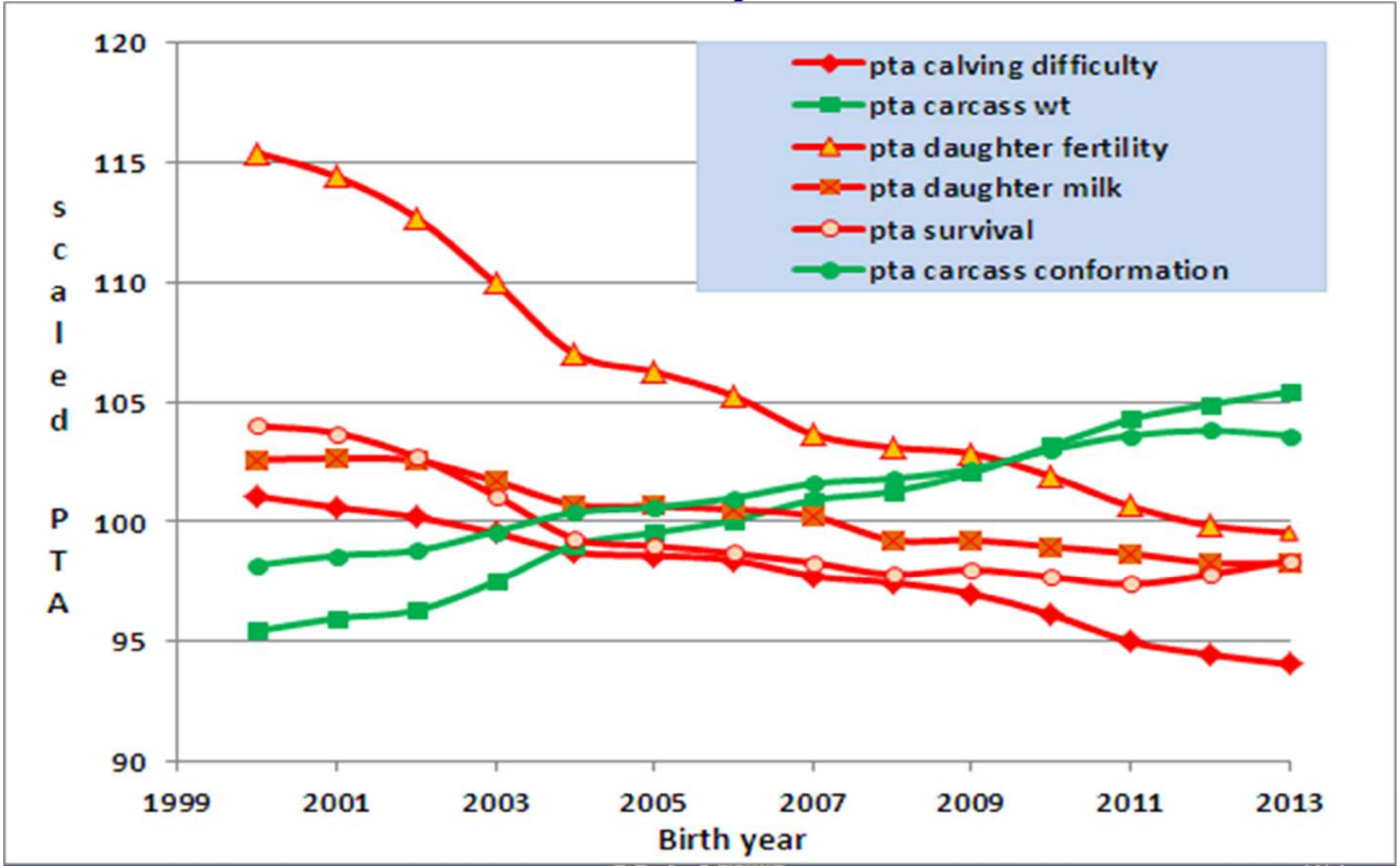
IRISH CATTLE BREEDING FEDERATION

G€N€ IR€LAND Maternal Beef breeding program

14th October 2014

NDP
National Development Plan
Transforming Ireland

Why?


120
115
110
105
100
95
90
scaled PTA
1999
2001
2003
2005
2007
2009
2011
2013
Birth year
pta calving difficulty
pta carcass wt
pta daughter fertility
pta daughter milk
pta survival
pta carcass conformation

GI bulls purchased to date

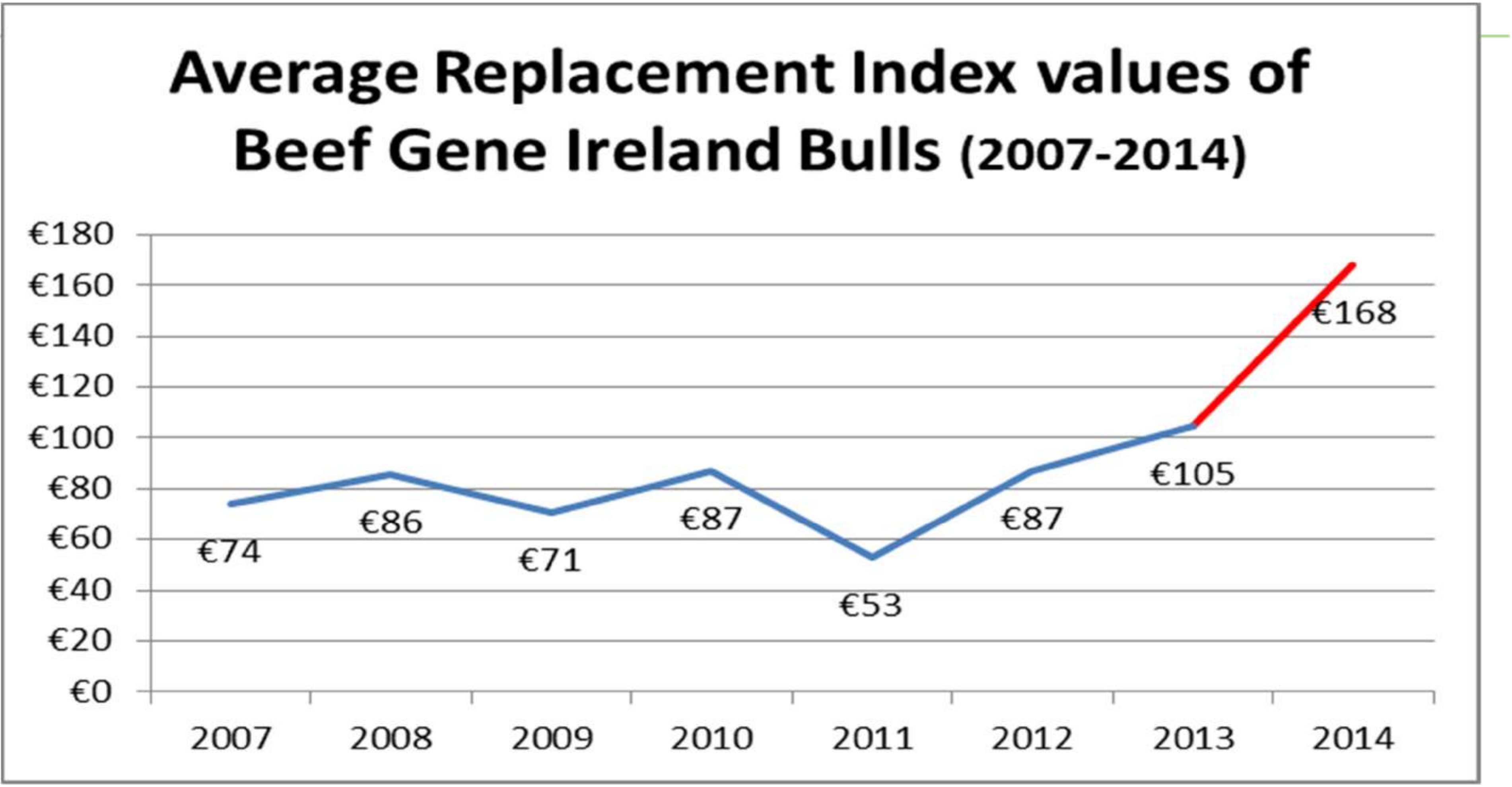
- 40 bulls purchased to date (2013 =15) (2014 =25)

Breed	AA	AU	BB	SA	CH	HE	LM	PT	BA	SH	SI
Pedigree females	6	1	2	2	7	3	7	3	2	1	6*

* Semen from XDM included

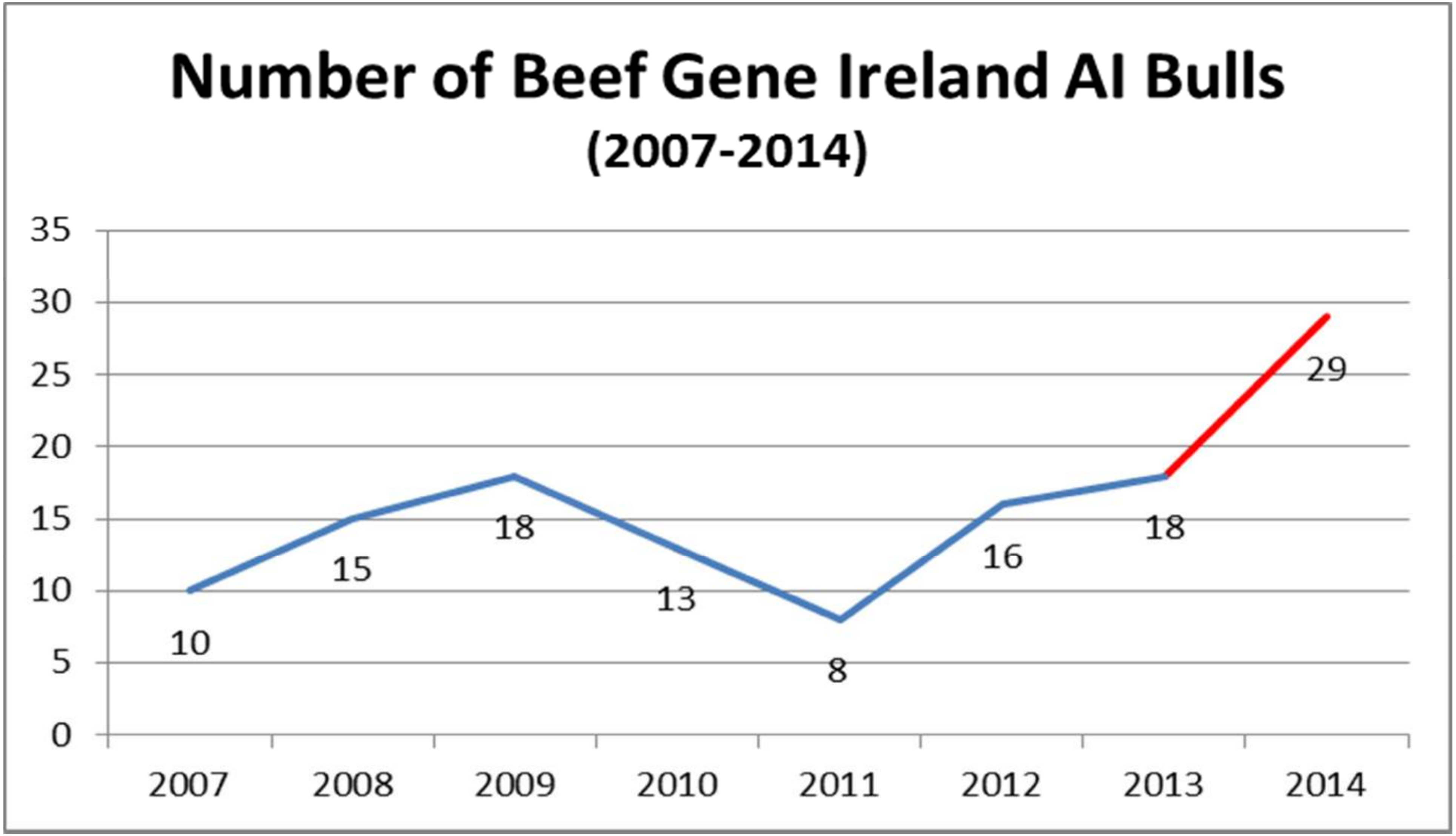
Autumn 2014 - Gene Ireland Young Bull Panel

Bulls				€uro-Star			
Identification			Ancestry	Replacement Index			Owner
ID	Breed	Name	Sire	€-val	Rel %	Stars Within	
JBS	Angus	Steil Jacob	Aynho Rossiter Eric	**€233**	**27%**	**5**	Gene Ireland
VEZ	Aubrac	Balinclea Iveco	Dreylands Fred	**€241**	**21%**	**5**	Gene Ireland
SGA	Blonde	Scaughmolin G Mail	Blackwater Ainsley	**€140**	**20%**	**5**	Gene Ireland
AGY	Belgian Blue	Rosemount Giga ET	Boherard Cantona ET	**€41**	**24%**	**4**	Gene Ireland
RFF	Belgian Blue	Ringfort Goulu	Maserati Van De Vloeikenshoeve	**€29**	**19%**	**3.5**	Dovea
YCM	Charolais	Clewbay High-Master	Repair	**€92**	**27%**	**4.5**	Gene Ireland
GEZ	Charolais	Gedeon	Dany	**n/a**	**n/a**	**Outcross (n/a)**	NCBC
YKM	Hereford	Moyclare Lucky	Brocca Saviour	**€113**	**22%**	**5**	Gene Ireland
ZCH	Limousin	Carrowreagh Honduras	On-Dit	**€246**	**30%**	**5**	NCBC
OHT	Limousin	Roundhill Hunter	Vivaldi	**€198**	**32%**	**5**	Gene Ireland
OKH	Limousin	Keltic Handsome	Ampertaine Commander	**€198**	**24%**	**5**	NCBC
XGL	Limousin	Glorieux	Chaton	**€172**	**5%**	**4.5**	NCBC
AYH	Parthenaise	Lisnagranchy Hulio	Lisnagranchy Carlo	**€246**	**29%**	**5**	Gene Ireland
ZYH	Parthenaise	Alamira Harry	Ti Lapin	**€163**	**22%**	**4**	Gene Ireland
KTM	Saler	Knottown Michael	Knottown Hermes	**€302**	**28%**	**5**	Gene Ireland
ZBZ	Saler	Breffni Muzz	Ecrin	**€215**	**11%**	**1**	Gene Ireland
EMS	Shorthorn	Doon Erasmus	Alta Cedar Perfect Storm	**€177**	**18%**	**4**	Gene Ireland
LZZ	Simmental	Lisnacrann Demertios	Kilbride Farm Newry	**€200**	**33%**	**4.5**	Gene Ireland



Average Replacement Index values of Beef Gene Ireland Bulls (2007-2014)

- Average replacement index from 2007-2013 was **€80**
- Average replacement index for the 29 bulls available in 2014 is **€168**



- Average of **14 bulls** tested each year from 2007-2013
- **29 maternal bulls** available through the GI program in 2014

Data collection

- 230 herds
- Complimentary second visit in year two of the program

Herd Liaison Officers

Name	Mobile	Email	Counties
James Mc'Enroe	086-3542213	james.mcenroe@hotmail.com	Cavan, Monagahan, Louth, Longford, Westmeath, Meath, Dublin
Sean Crummy	085-7222797	crummy.sean@gmail.com	Roscommon, Mayo, Sligo, Leitrim, Galway, Donegal
Alan Rigney	087-1700778	rigneyalan@hotmail.com	Offaly, Laois, Kildare,Carlow, Wicklow, Wexford
Padraig Ryan	087-9710071	pauseryan@yahoo.co.uk	Tipperary, Limerick, Clare, Kilkenny
Noel McSweeney	086-1242847	noelmc92@gmail.com	Cork, Kerry, Waterford

- Educating farmers about €uro-Star ratings of the herd.
- Recording of data online
- HDQI (Herd Data Quality Index) of the herd.
- Selection of sires for future matings.
- Encouraging the recording of calf birthweights in the herd.
- Weighing calves in the herd to calibrate the birthweights that are being recorded.

Data collection cont'd

- First calved heifers and stockbulls are eligible for free linear scoring and weight recording (where possible) in year 2 of the GI program

- Promoting HDQI stamp is a priority at the moment

- Recommended sire list has being distributed to all herds in the program

ICBF GENE IRELAND ICBF
Breeding future Profits

Maternal Beef Breeding Program

Recommended Beef AI Sire list - 2014

Next round of GI Committee meetings

Provisional dates:

- Tuesday 13th November
  - HE, AU & SH

- Wednesday 14th November
  - SA, BA & PI

- Tuesday 18th November
  - SI, CH & LM

- Thursday 20th November
  - BB, AA & PT

Educating farmers on the GI program

Tully open days:

- 4 BTAP events were held where over 500 farmers attended.
- Various other farmer groups visited the centre both Irish and from abroad.
- Industry groups also visited the centre e.g. ASA, Bord Bia, AI Technicians, Meat processors etc

Ploughing championships:

- Focus on ideal female replacement

Teagasc Beef 2014:

- Information available on all aspects of the GI maternal program