IRISH CATTLE BREEDING FEDERATION

ICBF Dairy & Beef Industry Meetings – Dairy Session and Joint Dairy & Beef Session.

Killeshin Hotel, Portlaoise.
14th April 2011.

Dairy traits & dairy breeding programs (10am – 12 mid)

- Genomics research – *Donagh Berry.*
- Genomics operational – *Francis Kearney.*
- Female fertility evaluations – *Ross Evans.*
- Teagasc breeding initiative in North East – *George Ramsbottom.*
- AOB.

Dairy & beef. Common agenda items (12-1 pm)

- Calving evaluations (1st & later lactations) – *Francis Kearney.*
- Carcass evaluations (Use of VIA data) – *Thierry Pabiou.*
- DNA archive (operational plan) – *Pat Donnellan.*
- ICAR Meeting 2012 – *Brian Wickham.*
- ICBF & Weatherby's initiative – *Andrew Cromie.*
- AOB.

Beef traits & beef breeding programs (2 – 4.30 pm).

- Female fertility evaluations – *Ross Evans*
- Maternal weaning evaluations – *Ross Evans.*
- Beef genomics research – *Donagh.*
- Developments in beef breeding, incorporating GROW review preliminary report – *ICBF Team.*
- Developments in breeding indexes – *Andrew Cromie.*
- AOB.

Dairy genomics

Donagh Berry

Topics

1. Genomic evaluations for Friesians
2. Genomic evaluations for type traits
3. Technologies for genomic selection and future research

Genomic selection in Friesians

- Success of genomic selection is based on recognising the DNA signature from a large number proven animal
- Holstein ≠ Friesian
- In 2010
  - 575 animals ≥50% Friesian incl.
  - 228 animals ≥81.25% & incl.
  - 122 animals 100% FR
- In 2011
  - 635 animals ≥50% FR incl.
  - 267 animals ≥81.25% incl.
  - 148 animals 100% FR

Research

1. Not very easy because want to maximise the number of Friesians in the training and validation (esp. for non-milk traits)
   - *Correlations, regressions, mean bias and variation in bias*
2. Inappropriateness of GS in Friesians originally identified by observing huge outliers
   - *Search for large outliers in young bulls & compare to parental average*

1. Forward prediction

Genomically predict more recently progeny evaluated bulls and compare to traditional proof

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Research ≥81.25% Friesian

- **Milk:** Training=205; Validation=62; young bulls=188
- **CIV:** Training=139; Validation=45; young bulls=271
- **SUR:** Training=83; Validation=41; young bulls=331
- SNP effects estimated using Training Friesians (plus all Holsteins) and genomic proofs estimated on validation bulls *(who have daughters but that info. is ignored)*

Validation of genomic proofs with daughter proofs

	Friesian			
	N	r	Mean bias	SD bias
Milk yield	62	0.32	-25.1	167
Fat yield	62	0.24	0.01	5.98
Prot. yield	62	0.31	-0.53	4.43
SCC	60	0.64	0.02	0.08
Calv. Int.	45	0.45	0.88	2.26
Survival	41	0.62	-0.08	0.94

Not all bulls are high reliability for traditional evaluation

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Validation of genomic proofs with daughter proofs

	Friesian				Holstein			
	N	r	Mean bias	SD bias	N	r	Mean bias	SD bias
Milk yield	62	0.32	-25.1	167	1786	0.64	10.9	125
Fat yield	62	0.24	0.01	5.98	1786	0.61	0.67	4.31
Prot. yield	62	0.31	-0.53	4.43	1786	0.64	0.77	3.59
SCC	60	0.64	0.02	0.08	2029	0.55	-0.01	0.08
Calv. Int.	45	0.45	0.88	2.26	499	0.81	-0.56	2.10
Survival	41	0.62	-0.08	0.94	345	0.73	0.31	1.35

Not all bulls are high reliability for traditional evaluation

2. Evaluate proof spread

Graphically evaluate the spread of genomic proofs from unproven bulls (i.e., no traditional proof to compare to) and investigate for outliers

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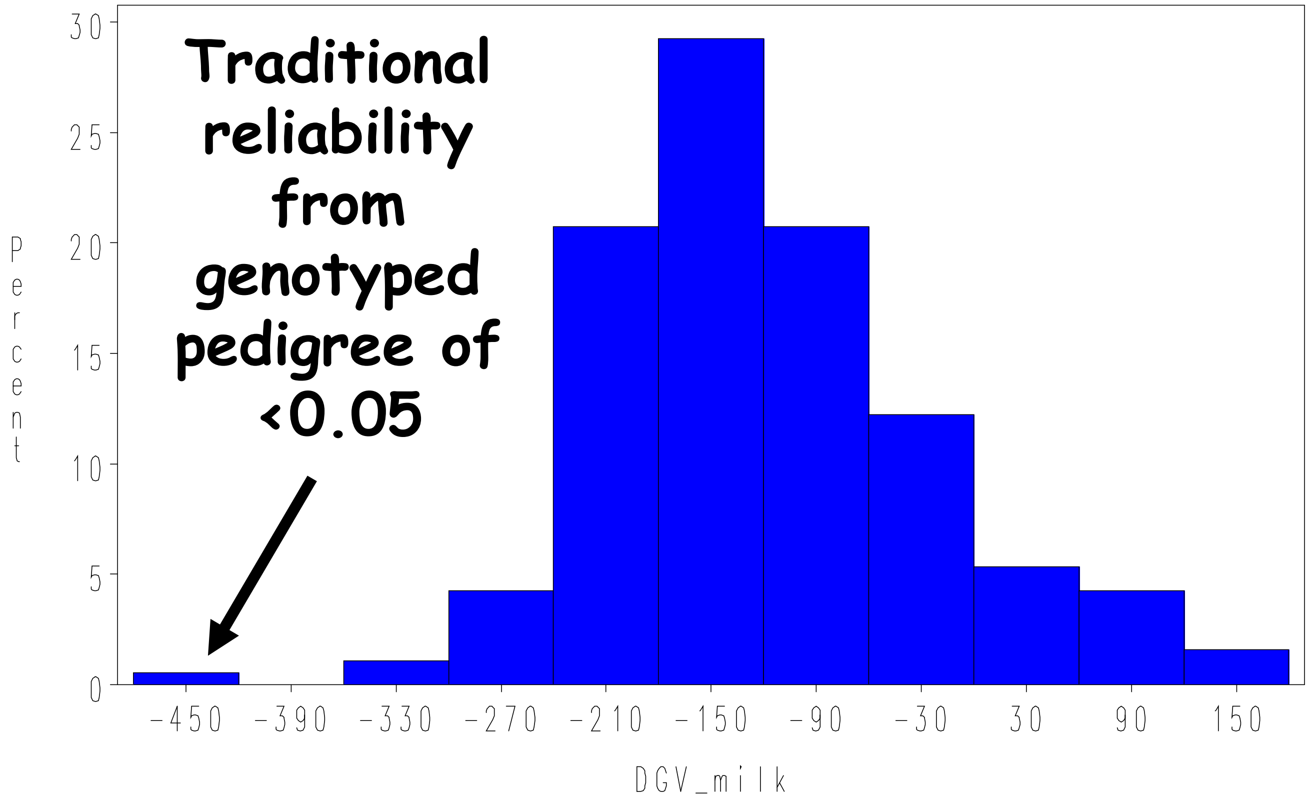
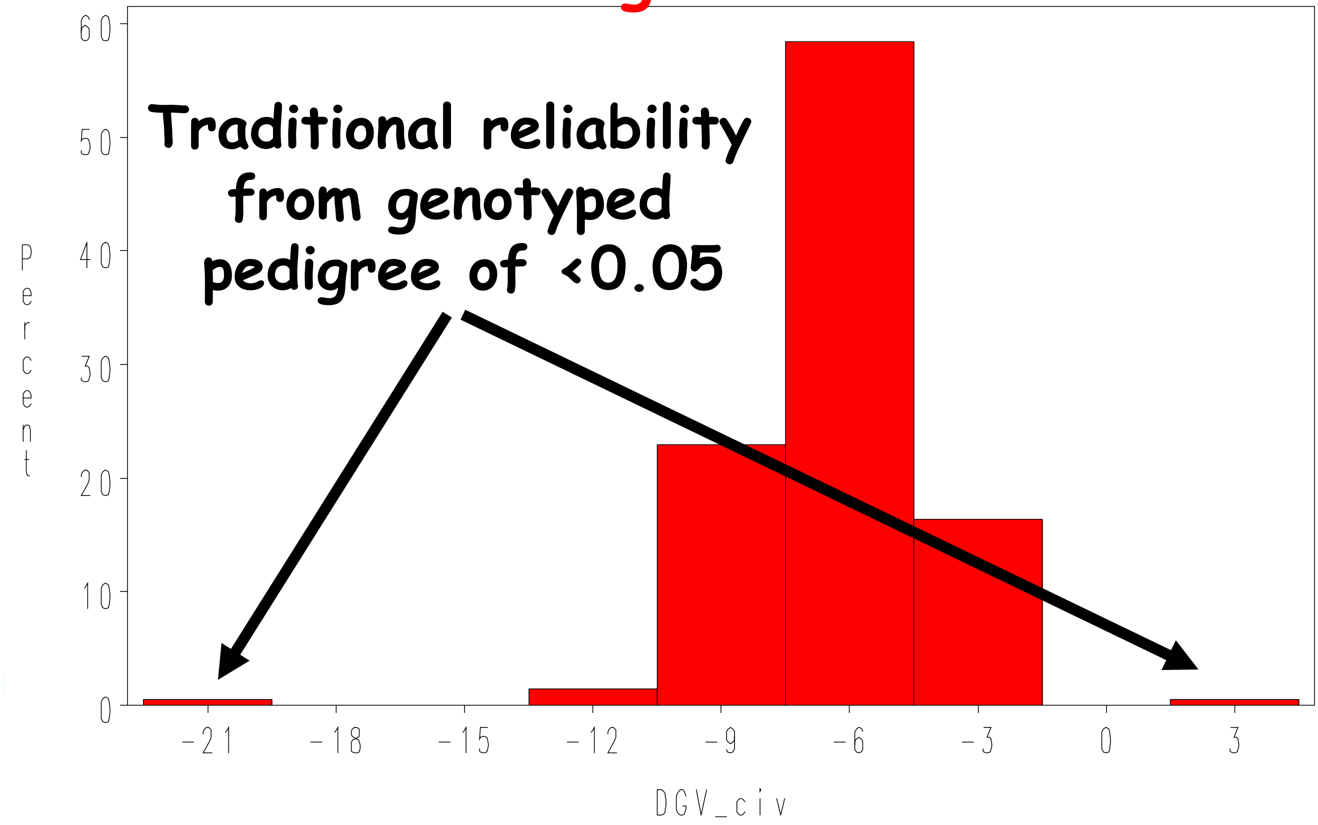
Genomic values of young bulls – Milk



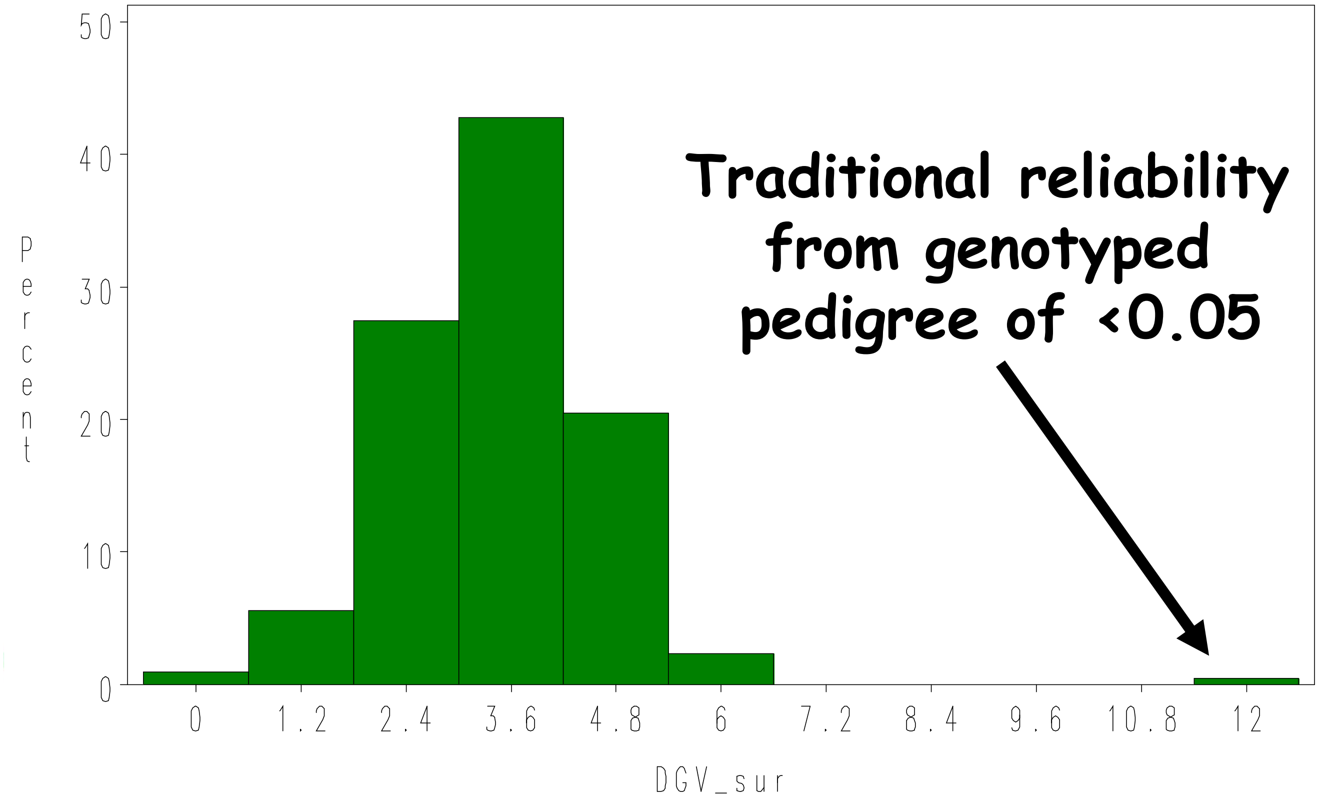
Traditional reliability from genotyped pedigree of <0.05

Genomic values of young bulls – Calving interval



Traditional reliability from genotyped pedigree of <0.05

Genomic values of young bulls – Survival



Traditional reliability from genotyped pedigree of <0.05

Reliability of "young bulls"

	Friesians			Holsteins		
	Milk	CIV	SUR	Milk	CIV	SUR
Parental average	0.20	0.13	0.12	0.30	0.19	0.18
Genomic	0.36	0.28	0.23	0.47	0.39	0.37
Blended	0.39	0.27	0.22	0.49	0.36	0.34
Weight on genomics	0.22	0.16	0.12	0.27	0.22	0.19

Holsteins includes all bulls (n=4,026) so expect reliability to be higher for Irish young bulls

GS in Friesians - conclusions

- Analysis of a relatively small dataset suggests more accurate predictions for most bulls
- Doubling of reliability using genomics
- Generate genomic values for animals with a traditional reliability coming from genotyped pedigree >5%
- Monitor closely over next few years and revise decision
- Need more Friesian semen
- Need to discuss presentation of proofs for bulls with genomic proof for milk but not fertility

Genomic selection for type traits

Testing approach

- All animals>40% reliability after removing parental contribution
- Test dataset: animals born prior to 1994
  - 523 to 1106 animals; average=806
- Validation dataset: animals born post 1993 *(not all high reliability from traditional)*
  - 31 to 285 animals; average=161
- SNP effects estimated using training dataset and genomic proofs estimated on validation bulls

Accuracy of cross validation - 1

Type trait	No. Train	No. Valid	r	Bias	RMSE
STA	803	286	0.78	0.24	1.06
ANG	730	206	0.68	0.19	1.32
BCS	687	129	0.11	-0.08	0.88
CW	803	285	0.59	0.01	0.88
BD	744	212	0.59	0.24	1.05
RA	803	286	0.59	-0.07	0.90
RW	803	285	0.67	0.15	0.86
FUA	799	287	0.59	0.43	0.93
RUH	799	287	0.71	0.35	1.05
UD	739	210	0.56	0.29	0.84
US	746	212	0.62	0.21	1.07
TL	739	210	0.40	-0.18	1.12
TPR	803	287	0.66	0.15	0.89
TPS	607	104	0.49	-0.05	0.97
RLS	797	275	0.52	-0.04	0.95
FA	923	196	0.49	0.06	0.99

Accuracy of cross validation - 2

Type trait	No. Train	No. Valid	r	Bias	RMSE
RLS	797	275	0.52	-0.04	0.95
FA	923	196	0.49	0.06	0.99
TEMP	523	94	0.08	0.72	1.75
EOM	607	104	0.47	-0.12	0.91
Overall Mam	680	104	0.82	0.15	0.52
Overall Legs	680	104	0.57	0.16	1.36
Overall type	680	104	0.81	0.16	0.98

Reliabilities

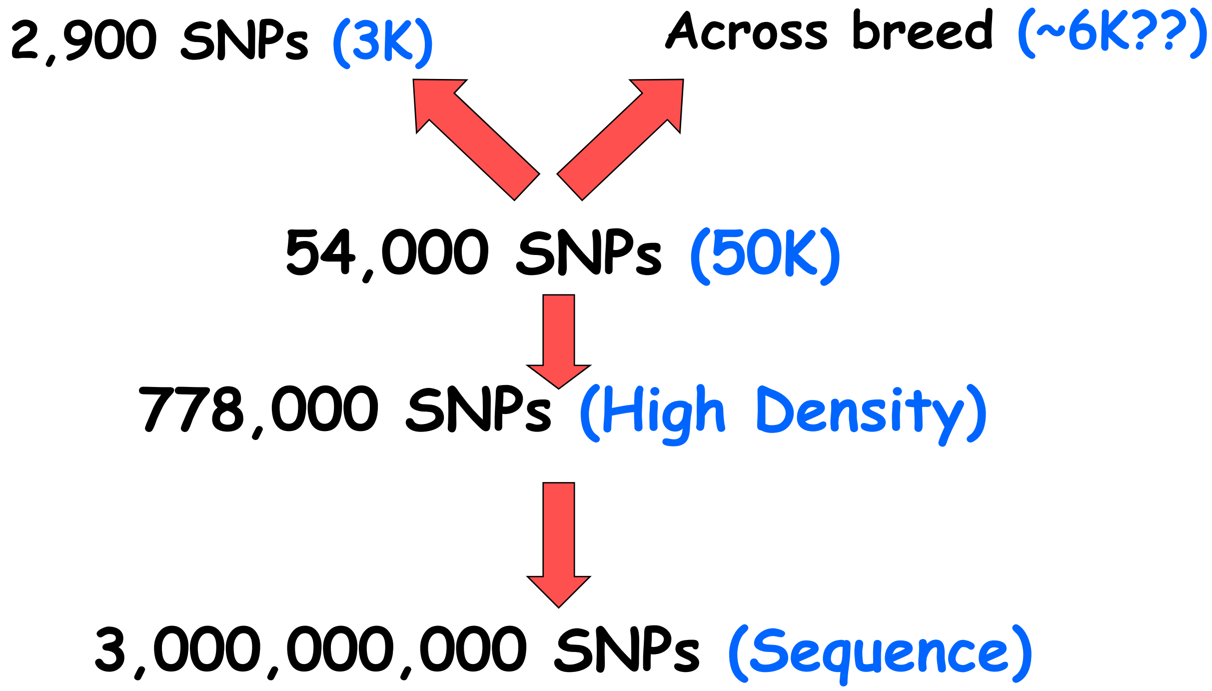
- Individual type traits
  - Parental average: 0.22
  - Genomic proof: 0.36
  - Weighting on genomics: 0.18
- Composite type traits
  - Parental average: 0.18
  - Genomic proof: 0.28
  - Weighting on genomics: 0.16

Type traits - conclusions

- Good correlations between genomic proofs and traditional proofs even for small training dataset
  - Increased reliability of proofs
  - Training dataset will increase by 26% in official run (i.e., includes validation bulls)
- Implement genomic selection for type traits if resources are available
- Handling of coding of proofs?

Genomic selection technologies and future research

Technologies



2,900 SNPs (3K)

Across breed (~6K??)

54,000 SNPs (50K)

778,000 SNPs (High Density)

3,000,000,000 SNPs (Sequence)

On-going genomic research

- Improving speed and efficiency of algorithms *(Mario Calus)*
- Multi-breed evaluation (HO & FR)
- Improving imputation speed
- Dealing with sequence data
- One-step genomic evaluation

The Irish Agriculture and Food Development Authority

IRISH CATTLE BREEDING FEDERATION

Genomics Operational Update.

Francis Kearney.
Killeshin Hotel, Portlaoise.
14th April 2011.

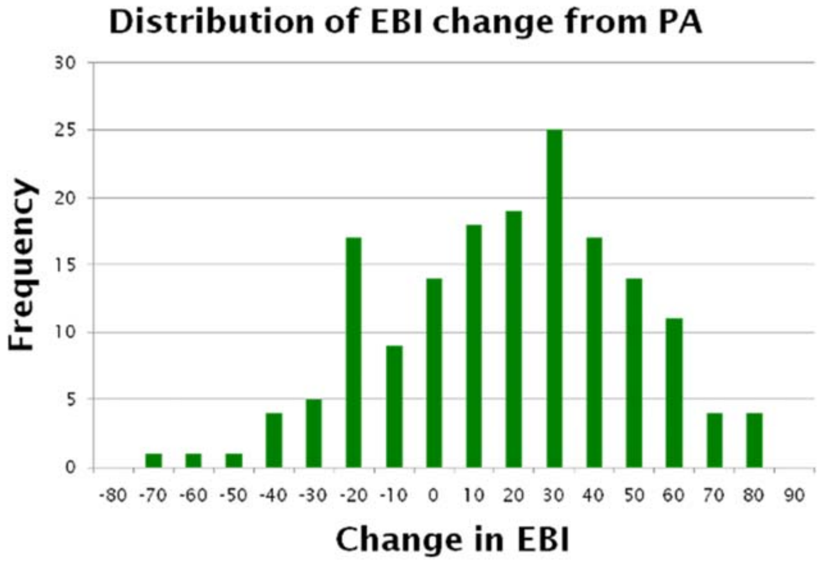
Genomics – 3k

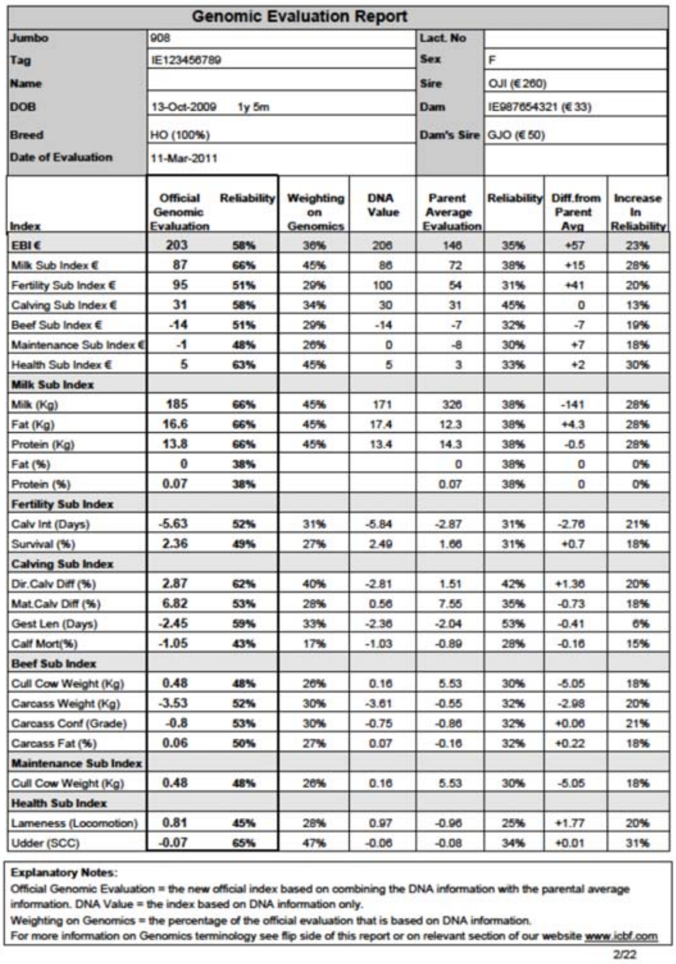
- Service based on 3k or 50k chip is available (not cows)
- Orders through website or phone
- No issues with ordering process to date
  - Issue with invalid IDs where samples are not bar-coded
- Reports have been generated for pilot project heifers
  - Feedback has been good
- Defined schedule – dispatch middle of month, results middle of following month
  - Will try to facilitate more runs in busy season

Genomics

- Technical Issues
  - Lab delay – samples back in middle of routine run
  - Imputation – computer specify issues and also availability of space
  - Parentage issue – all animals of some sires showing up with wrong sires
  - Genomic Software – need to optimise to cope with increasing numbers
- Solutions
  - More than one lab being used
  - More PCs now available for imputation/Testing new procedure
  - Genomic Software currently being updated
  - Parentage issues currently under investigation

GEBI - What to Expect?





Genomic Evaluation Report

Jumbo	908	**Lact. No**	
Tag	IE123456789	**Sex**	F
Name		**Sire**	OJI (€ 260)
DOB	13-Oct-2009 1y 5m	**Dam**	IE987654321 (€ 33)
Breed	HO (100%)	**Dam's Sire**	GJO (€ 50)
Date of Evaluation	11-Mar-2011		

Index	**Official Genomic Evaluation**	**Reliability**	**Weighting on Genomics**	**DNA Value**	**Parent Average Evaluation**	**Reliability**	**Diff.from Parent Avg**	**Increase In Reliability**
EBI €	203	58%	36%	206	146	35%	+57	23%
Milk Sub Index €	87	66%	45%	86	72	38%	+15	28%
Fertility Sub Index €	95	51%	29%	100	54	31%	+41	20%
Calving Sub Index €	31	58%	34%	30	31	45%	0	13%
Beef Sub Index €	-14	51%	29%	-14	-7	32%	-7	19%
Maintenance Sub Index €	-1	48%	26%	0	-8	30%	+7	18%
Health Sub Index €	5	63%	45%	5	3	33%	+2	30%
Milk Sub Index								
Milk (Kg)	185	66%	45%	171	326	38%	-141	28%
Fat (Kg)	16.6	66%	45%	17.4	12.3	38%	+4.3	28%
Protein (Kg)	13.8	66%	45%	13.4	14.3	38%	-0.5	28%
Fat (%)	0	38%			0	38%	0	0%
Protein (%)	0.07	38%			0.07	38%	0	0%
Fertility Sub Index								
Calv Int (Days)	-5.63	52%	31%	-5.84	-2.87	31%	-2.76	21%
Survival (%)	2.36	49%	27%	2.49	1.66	31%	+0.7	18%
Calving Sub Index								
Dir.Calv Diff (%)	2.87	62%	40%	-2.81	1.51	42%	+1.36	20%
Mat.Calv Diff (%)	6.82	53%	28%	0.56	7.55	35%	-0.73	18%
Gest Len (Days)	-2.45	59%	33%	-2.36	-2.04	53%	-0.41	6%
Calf Mort(%)	-1.05	43%	17%	-1.03	-0.89	28%	-0.16	15%
Beef Sub Index								
Cull Cow Weight (Kg)	0.48	48%	26%	0.16	5.53	30%	-5.05	18%
Carcass Weight (Kg)	-3.53	52%	30%	-3.61	-0.55	32%	-2.98	20%
Carcass Conf (Grade)	-0.8	53%	30%	-0.75	-0.86	32%	+0.06	21%
Carcass Fat (%)	0.06	50%	27%	0.07	-0.16	32%	+0.22	18%
Maintenance Sub Index								
Cull Cow Weight (Kg)	0.48	48%	26%	0.16	5.53	30%	-5.05	18%
Health Sub Index								
Lameness (Locomotion)	0.81	45%	28%	0.97	-0.96	25%	+1.77	20%
Udder (SCC)	-0.07	65%	47%	-0.06	-0.08	34%	+0.01	31%

Explanatory Notes:

Official Genomic Evaluation = the new official index based on combining the DNA information with the parental average information. DNA Value = the index based on DNA information only.

Weighting on Genomics = the percentage of the official evaluation that is based on DNA information.

For more information on Genomics terminology see flip side of this report or on relevant section of our website www.icbf.com

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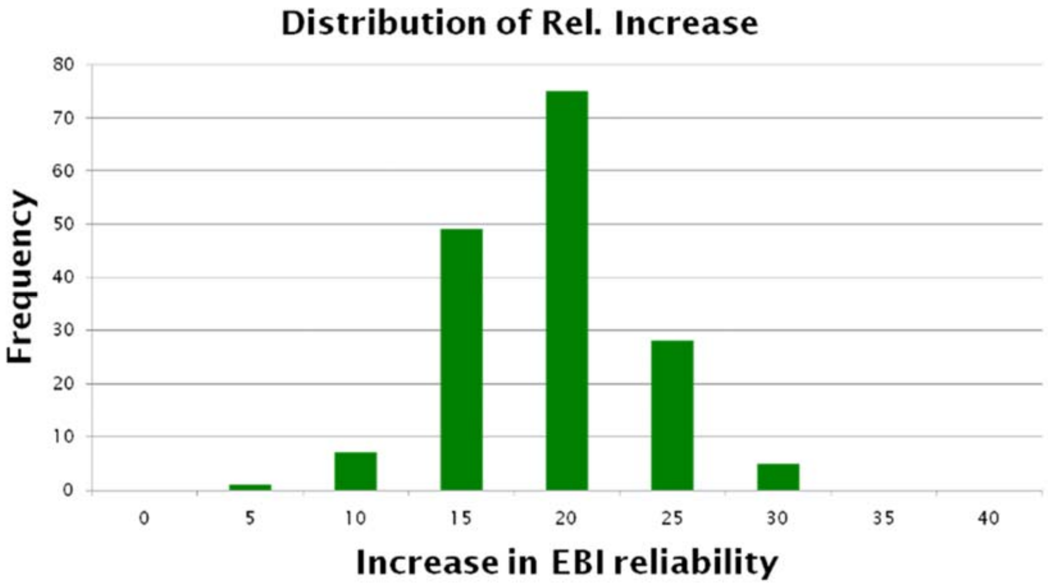
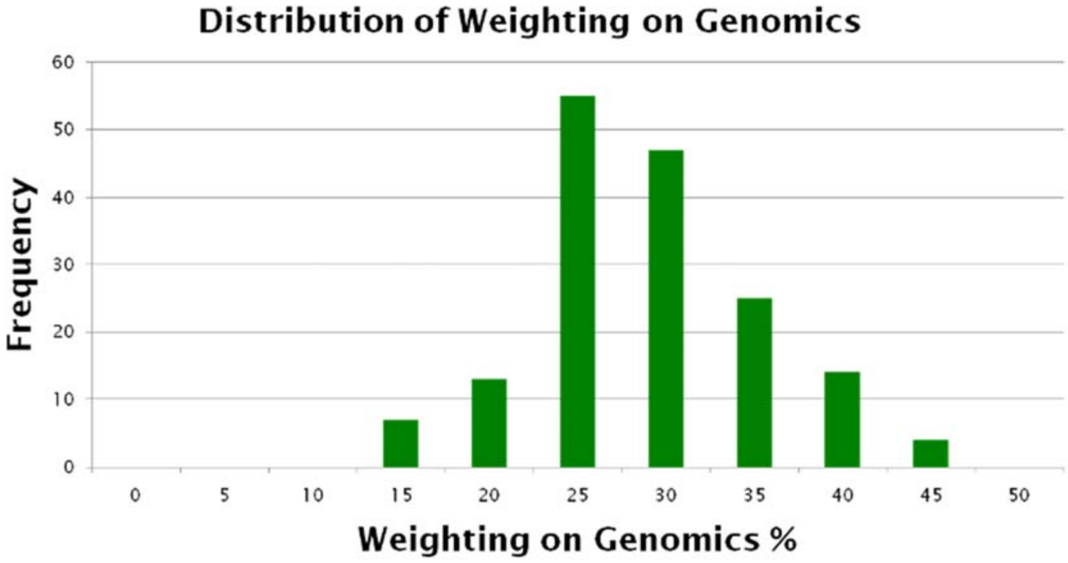
GEBI - What to Expect?



GEBI - What to Expect?



Summary

- Service is up and running
- Improvements currently underway to improve the turnaround time of genomic evaluations
  - Software for analysis and imputation
  - More hardware to run jobs
  - Invalid ID need to be eliminated!
- Monthly evaluations as per schedule with extra in busy periods
- Cows not included currently
- Expand to include FR

IRISH CATTLE BREEDING FEDERATION

New dairy fertility evaluations.

Ross Evans
Killeshin Hotel, Portlaoise.
14th April 2011.

National Development Plan
Transforming Ireland

Background.

- Previous meeting
  - Re-ranking required further investigation
- Increased variation of proofs: reasons?
  - New capacity in MIX99 to test existence of heterogenous variation: already accounted for in Milk evaluations

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Current Fertility evaluations: lactations 1-3 for CIV and Survival

Cow A

	1st Calving → 2nd Calving	2nd Calving → 3rd Calving	3rd Calving → 4th Calving
CIV	**370 days**	**365 days**	**380 days** ← **Lowly heritable!**
Milk	**4,900kg**	**5,100kg**	**5,300kg** ← **Good heritability!**

Cow B

Current parameters have strong negative link between milk and fertility BUT parameters now 7 years old: need re-estimating

	1st Calving → 2nd Calving	2nd Calving → 3rd Calving	3rd Calving → 4th Calving
CIV	**410 days**	**390 days**	**400 days** ← **Lowly heritable!**
Milk	**6,700kg**	**7,200kg**	**9,000kg** ← **Good heritability!**

Cow A

New Fertility evaluations

1st Calving | 2nd Calving | 3rd Calving | 4th Calving | 5th Calving | 6th Calving

CIV	370	365	380	370	350
Milk	4,900kg	5,100kg	5,300kg	5,400kg	5,200kg
CFS	85 days	75 days	83 days	63 days	80 days
NS	1 insem	1 insem	2 insem	1 insem	1 insem

Cow B

1st Calving | 2nd Calving | 3rd Calving | 4th Calving | 5th Calving

CIV	410	390	420	600	culled
Milk	6,700kg	7,200kg	9,000kg	9,200kg	8,500kg
CFS	95 days	93 days	110 days	88 days	105 days
NS	2 insem	3 insem	2 insem	2 insem	5 insem

Negative link between milk and fertility is reduced with CFS and NS

Insemination traits are better biological predictors of calving interval

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Compare old v new parameters

	survival 1		survival 2		survival 3	
	old	new	old	new	old	new
civ 1	-0.20	-0.58	-0.03	-0.62	0.00	-0.45
civ 2	-0.24	-0.61	-0.12	-0.70	-0.09	-0.61
civ 3	0.02	-0.26	0.06	-0.53	0.13	-0.55

	civ 1		civ 2		civ 3	
	old	new	old	new	old	new
milk1	0.51	0.36	0.50	0.39	0.64	0.41
milk2	0.51	0.25	0.49	0.35	0.62	0.36
milk3	0.44	0.28	0.47	0.40	0.67	0.42

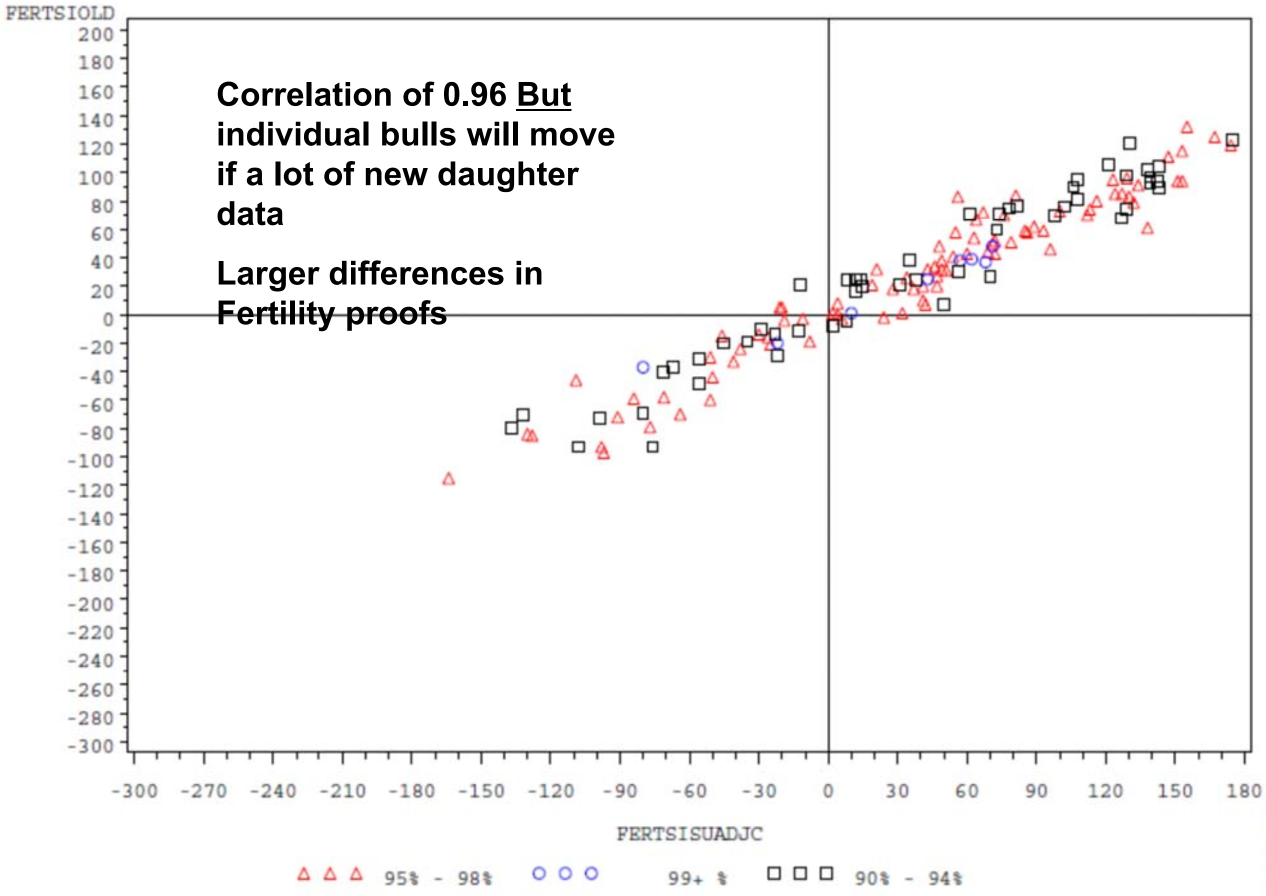
	survival 1		survival 2		survival 3	
	old	new	old	new	old	new
milk1	0.25	0.00	0.55	-0.11	0.43	-0.19
milk2	0.13	0.04	0.48	-0.16	0.39	-0.20
milk3	0.32	0.06	0.42	-0.09	0.47	-0.14

- Increase in genetic correlation between CIV and survival
- Reduction in genetic correlation between milk and CIV
- Reversal of correlation between milk and survival

Other additional changes

- **Increase CIV cut-off limit 600-800 day**
  - Where an insemination is recorded
- **Specific heterosis effects included**
  - Differing heterosis for FRxHO, HOxJE, HOxMO
- **Cows with no milk recording but with fert**
  - 250,000 cows
- **Tighter definition of a contemporary group**
  - 180 days to 70 day period for grouping of cows
- **New software: actual reliabilities for cows**
- Age at first calving evaluated

Comparing AI sires old versus new Fertility Sub-index



Correlation of 0.96 <u>But</u> individual bulls will move if a lot of new daughter data

Larger differences in Fertility proofs

Heterogeneity of variance

All year round calving, high input herds

Herd A
CIV CG σ^2 400 d
Sires A, B

Min	Average	Max
CIV	CIV	CIV
350	395	750

Relaxed Spring Calving, medium input herds

Herd B
CIV CG σ^2 150 d
Sires C, D, E

Min	Average	Max
CIV	CIV	CIV
350	385	500

Herd C
CIV CG σ^2 140 d
Sires D, E, F

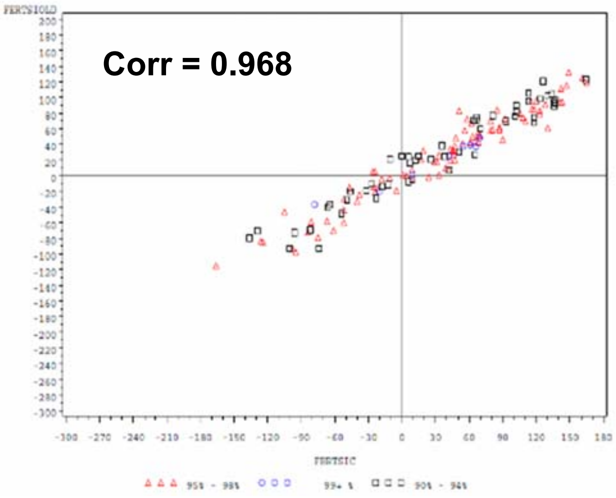
Min	Average	Max
CIV	CIV	CIV
350	380	490

Strict Spring Calving, low input herds

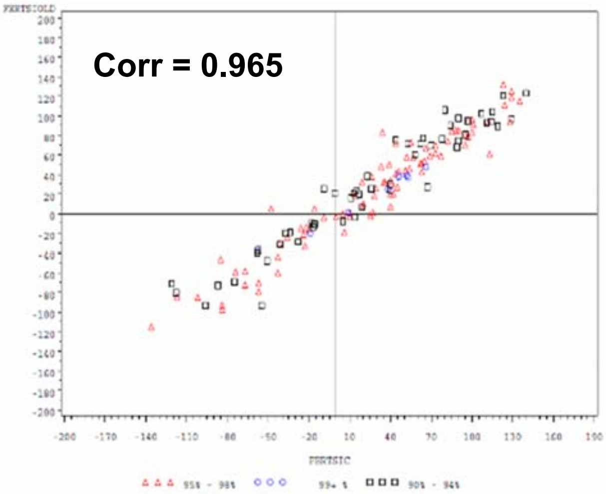
Herd D
CIV CG σ^2 80 d
Sires G,H

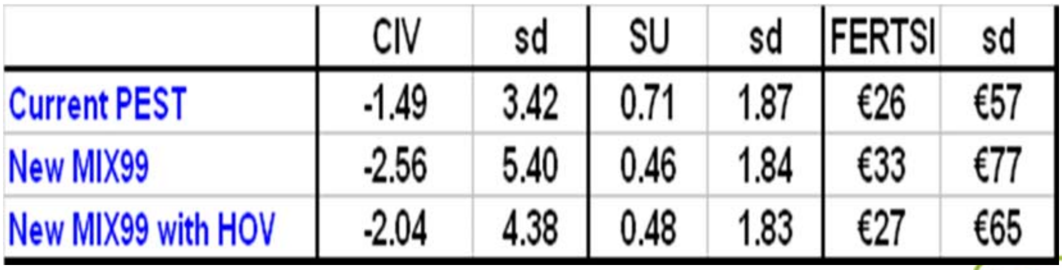
Min	Average	Max
CIV	CIV	CIV
350	370	430

Without adjustment



With adjustment





	CIV	sd	SU	sd	FERTSI	sd
Current PEST	-1.49	3.42	0.71	1.87	€26	€57
New MIX99	-2.56	5.40	0.46	1.84	€33	€77
New MIX99 with HOV	-2.04	4.38	0.48	1.83	€27	€65

Movement in sire proofs

Reliability category	Num sires	min diff FERTSI	avg diff FERTSI	max diff FERTSI
99+ %	8	-24	8	20
90% - 94%	147	-52	4	63
75% - 90%	441	-76	3	80
60% - 75%	685	-99	2	86

Reliability category	Num sires	min diff civ	avg diff civ	max diff civ
99+ %	8	-1.72	-0.6	1.97
90% - 94%	147	-6.17	-0.6	4.66
75% - 90%	441	-5.58	-0.4	6.26
60% - 75%	685	-6.57	-0.3	6.52

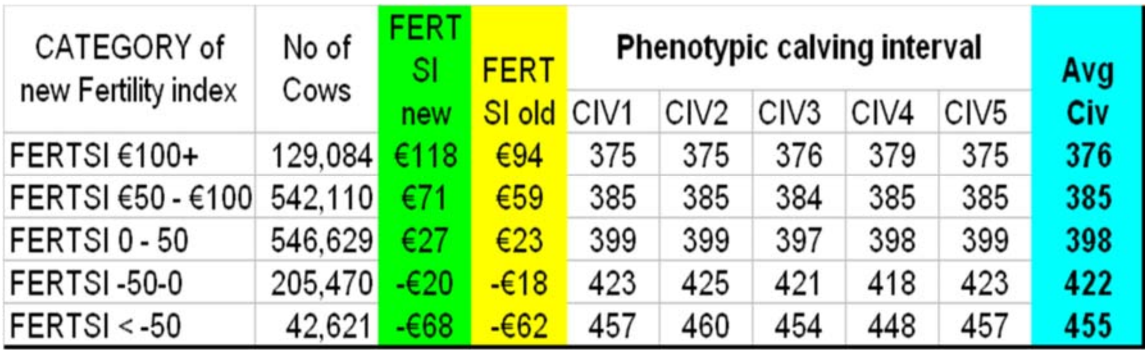
Reliability category	Num sires	min diff SU	avg diff SU	max diff SU
99+ %	8	-0.65	0.05	0.85
90% - 94%	147	-3.07	-0.36	1.71
75% - 90%	441	-3.72	-0.22	2.25
60% - 75%	685	-3.66	-0.23	2.79

Breed effects using AI sires with 60% reliability on new indexes

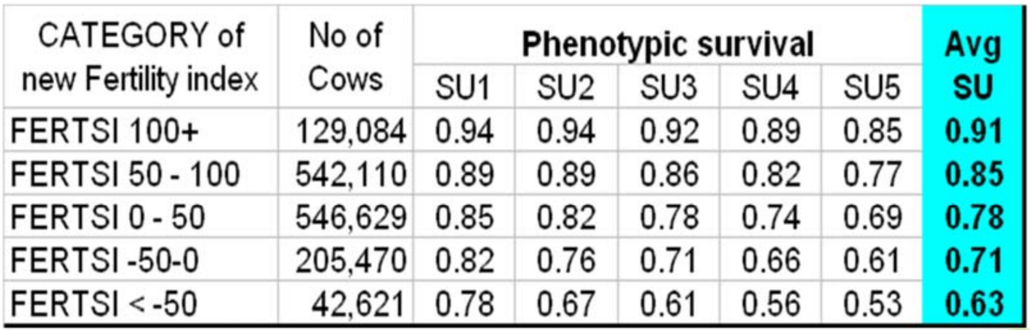
Breed	No of sires	Fertility SI old	Fertility SI new	Age 1st Calving (days)
FR	213	€83	€94	-2
HO	870	-€6	-€5	0
JE	14	€85	€72	2
MO	29	€78	€94	14
NR	4	€89	€112	1
SR	2	€85	€90	7

- **Rise for FR and MO sires**
- **Reduction in JE sires due to better handle on specific heterosis**
- **Age at 1st calving not factored into FERTSI yet**

Comparison of index to phenotype



CATEGORY of new Fertility index	No of Cows	FERT SI new	FERT SI old	Phenotypic calving interval					Avg Civ
				CIV1	CIV2	CIV3	CIV4	CIV5	
FERTSI €100+	129,084	€118	€94	375	375	376	379	375	**376**
FERTSI €50 - €100	542,110	€71	€59	385	385	384	385	385	**385**
FERTSI 0 - 50	546,629	€27	€23	399	399	397	398	399	**398**
FERTSI -50-0	205,470	-€20	-€18	423	425	421	418	423	**422**
FERTSI < -50	42,621	-€68	-€62	457	460	454	448	457	**455**



CATEGORY of new Fertility index	No of Cows	Phenotypic survival					Avg SU
		SU1	SU2	SU3	SU4	SU5	
FERTSI 100+	129,084	0.94	0.94	0.92	0.89	0.85	**0.91**
FERTSI 50 - 100	542,110	0.89	0.89	0.86	0.82	0.77	**0.85**
FERTSI 0 - 50	546,629	0.85	0.82	0.78	0.74	0.69	**0.78**
FERTSI -50-0	205,470	0.82	0.76	0.71	0.66	0.61	**0.71**
FERTSI < -50	42,621	0.78	0.67	0.61	0.56	0.53	**0.63**

Conclusions

- Research close to completion
- New evaluation should give a more accurate picture of a cow’s fertility
  - More parities, insemination data and more relevant genetic parameters to today’s herds
  - More reward for cows with better own and progeny fertility history
- Larger differences in sire fertility proofs
- Test proofs released: end June.
- Interbull test run: end August
- Implementation in December 2011

North East Breeding Initiative.

George Ramsbottom.

Program Partners.

Initiated by Ballyhaise research farm steering committee.

Includes;

Co-op personnel and farmer representatives from Connacht Gold, Town Monaghan, Donegal Creameries and Lakeland

Teagasc research & advisory staff.

Why?

Quantity of heifers.

Quality of heifers.

Rearing heifer replacements.

Trends in number of dairy herds, total dairy cows, replacement rates and EBI nationally and for ‘northern’ counties (Source: ICBF Dairy Cattle Statistics, ICBF, December 2010).

	National	**‘Northern’ counties***
Number of Active Dairy Herds, 2010	17,071	4,002 (23%)
Total dairy cows, 2010	961,389	197,645 (21%)
Number 0 – 1 year old dairy heifers, 2008 2009 2010	203,186 242,056 (+19.1%) 250,007 (+ 3.3%)	41,471 50,307 (+21.3%) 51,038 (+1.5%)
Number 1st lactation dairy cows, 2010	177,917 (18.5% of dairy cows)	36,575 (18.5% of dairy cows)
Herd EBI, 2010	€64	€54

* Cavan, Donegal, Dublin, Galway, Leitrim, Longford, Louth, Mayo, Meath, Monaghan, Offaly, Roscommon, Sligo, Westmeath

How?

Sub-group formed.

Four main outcomes.

Standard technical messages across co-op newsletters.

Farmer profiles in co-op newsletters.

Walk in each co-op area.

Sire Advice initiative with ICBF & AI companies.,

Progress.

Technical messages and farmer profiles continuing.

Farm walks under way.

- Cavan, Mayo & Monaghan (350 attending).
- Donegal – tomorrow.

Bull teams being finalised based on latest proof run.

- ~10 bulls across AI companies.

IRISH CATTLE BREEDING FEDERATION

Calving Evaluations.

Killeshin Hotel, Portlaoise.
14th April 2011.

National Development Plan
Transforming Ireland

Update

- Results presented at previous meeting to show that calving in heifer is a different trait to calving in later parity
- Lower heritability, therefore less weight given to an individual records
- Pedigree animals will be closer to the parent average evaluation when their own calving record is taken into account
- In process of incorporating foreign breeding values – changes to software

Update

- Considerations:
  - Update of economic models
  - Update of genetic expressions
  - Consideration given to how information is presented

The economics of CD

- Cost of death in heifer and cow CD
  - Higher cost of replacement if heifer dies
  - 1 extra replacement required (€1533) if heifer dies
  - 0.44 extra replacement required (€675) if average cow dies

The economics of CD

- Higher probability of a dead calf in heifer CD?
- Reduced reproductive success in heifer CD?
- Cost of heifer CD will be higher than cost of cow CD

Calving difficulty

- Separation of maternal heifer and cow CD will lower the weighting on the current trait
  - Because currently the trait include bulls’ daughters calving as heifers
- Possibility of new trait for CD in heifers (both direct and maternal)

Presentation of CD traits

- Heifer calving evaluations very important, but
  - Will have lower reliabilities for young bulls/ bulls not mated to heifers
- One trait weighted for both heifer and cow CD?
- In addition to existing CD (all parities) present a "heifer CD"?

Presentation of CD traits

- Economically the impact on heifers will be more significant – therefore weighting would be more towards heifer breeding values
- Reliability would depend on number of records on heifers
- But some bulls may never have many calvings on heifer
- Bull with many records on later parities with low reliability for heifer calving

Issues

- Would need to create a separate contemporary group to divide heifer vs older cows
- Some small herds may have very little calvings on heifers - potential loss of information

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Summary

- Close to having new evaluations with foreign (French) data included
- Peter Amer is doing work on the economics and impact on the indexes/subindexes
- CG needs a closer look to see how much data will be lost
- Test proofs available by the end of May
- Industry feedback welcomed

Finally…

- Bull mated to all pedigree CH cows

Average % in Dams by Breed

BB	CH	LM	HO	SI	AA
0	100	0	0	0	0

Finally…

- Bull Mated to 150 cows
- 50 Ped CH;50 ½ LM* ½ SI;50 ¾ BB* ¼ HO

Average % in Dams by Breed

BB	CH	LM	HO	SI	AA
25	33	17	8	17	0

- 150*32=4800 Total Breed fractions
- (50*32/4800)*100 = 33% CH in dams
- (50*16/4800)*100 = 17% LM & SI in dams
- (50*24/4800)*100 = 25% BB in dams
- (50*8/4800)*100 = 8% HO in dams

IRISH CATTLE BREEDING FEDERATION

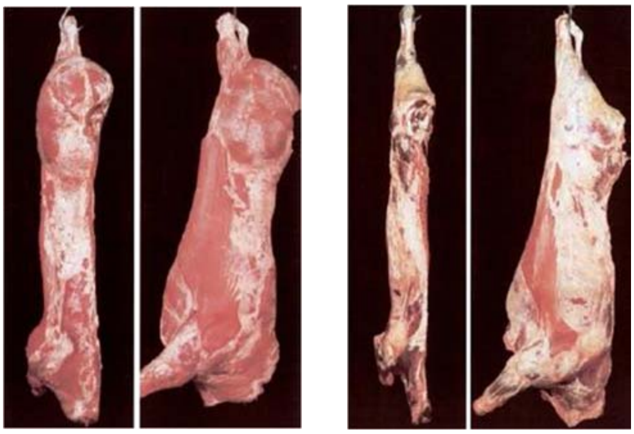
Using digital images from factories.

Killeshin Hotel, Portlaoise.
14th April 2011.

National Development Plan
Transforming Ireland

Background: on the farm

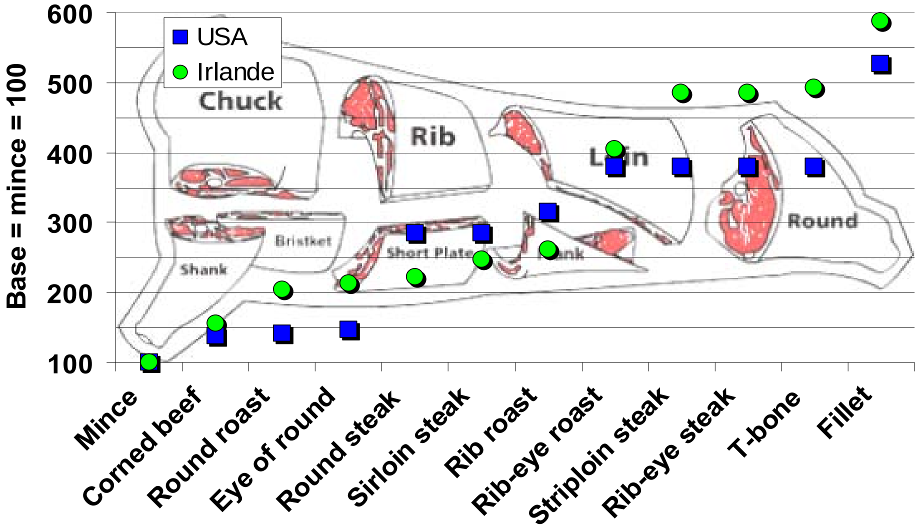
- The EUROP carcass classification
  - Assessment of conformation (6 grades) & fat (5 grades) by Experts / machines



Payment on carcass weight, conformation grading & fat grading.

Background: on the shelves

- Different cuts, different prices

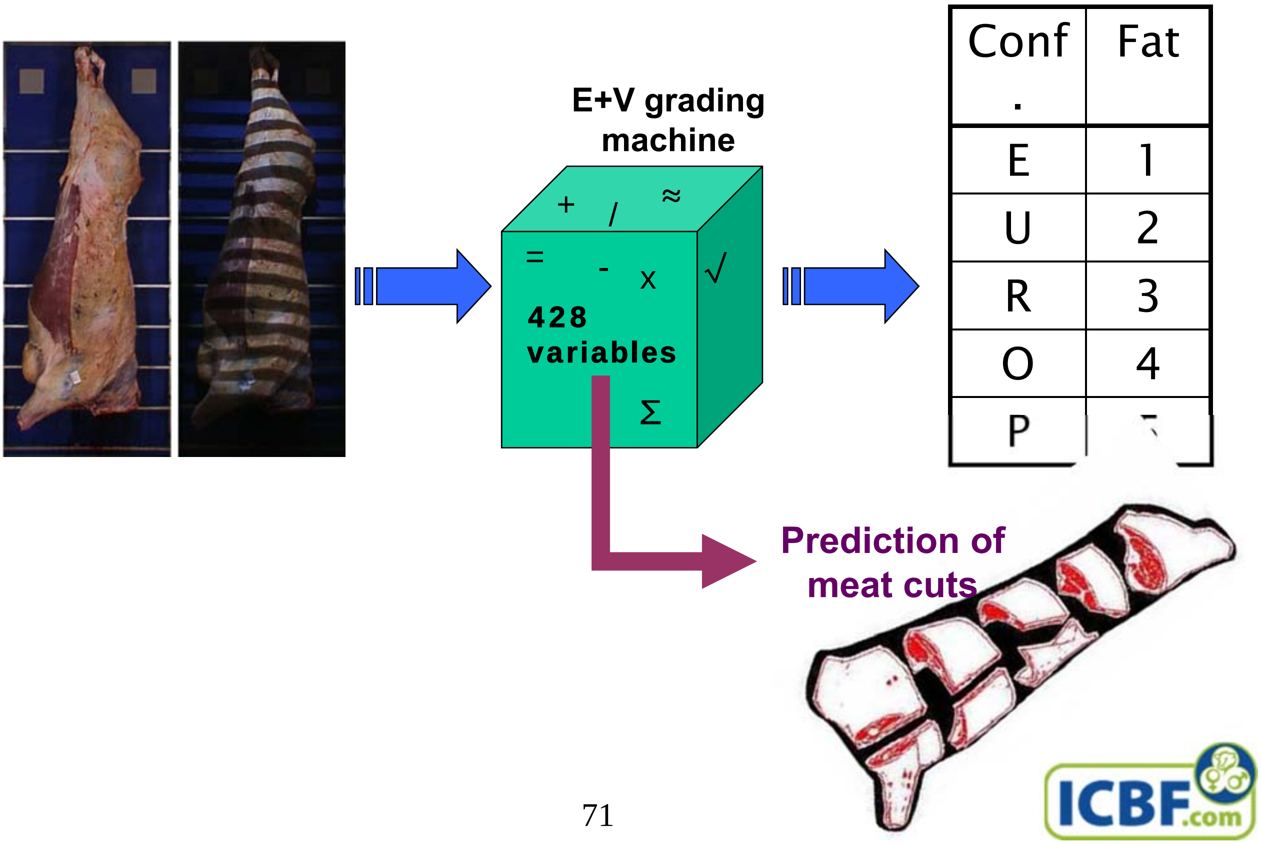


Source: 2 commercial butcher price list downloaded April 2011

Mechanical grading

- Mechanical grading machine VBS2000 (EplusV, Germany)
  - Approved since 2001 for grading beef carcasses
  - 2 images / carcass
  - Fed into Irish database on a regular basis since 2005

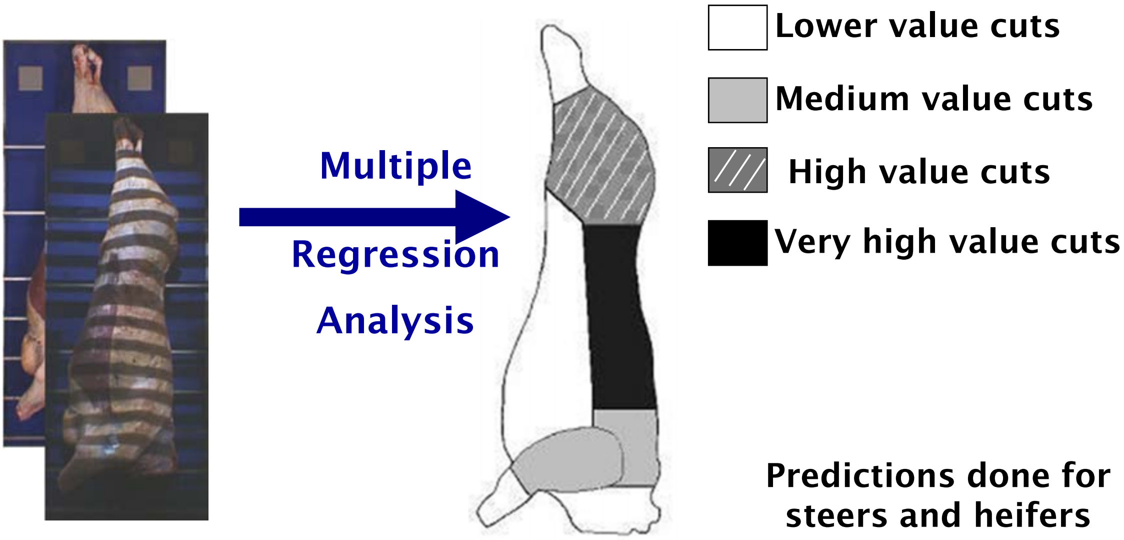
Principle



Conf.	Fat
E	1
U	2
R	3
O	4
P	5

Predicted cuts

- Converting images into cut weights



☐ Lower value cuts
▒ Medium value cuts
▨ High value cuts
■ Very high value cuts

Predictions done for steers and heifers

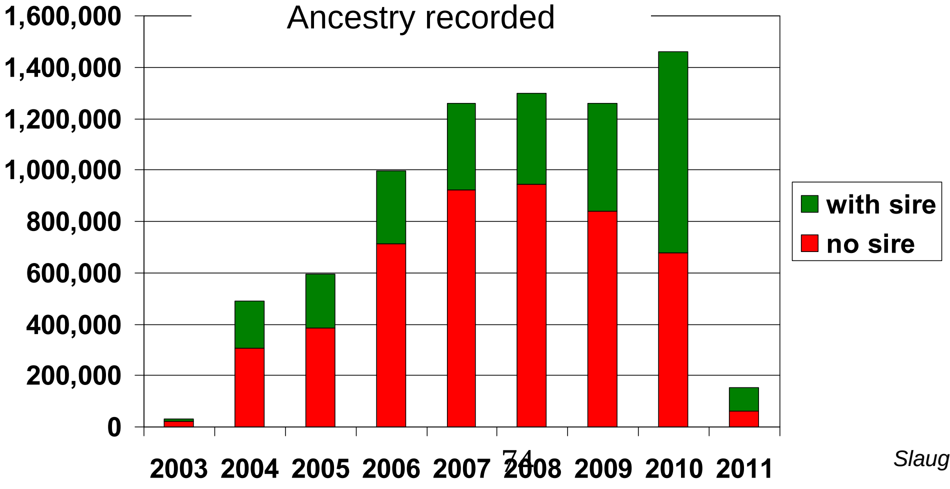
Accuracy of prediction

- **R^2 of regressions**

Wholesale Cut Weight	Dataset	
	Heifer	Steer
Lower Value Cuts	0.65	0.92
Medium Value Cuts	0.70	0.86
High Value Cuts	0.85	0.93
Very High Value Cuts	0.72	0.84

Data

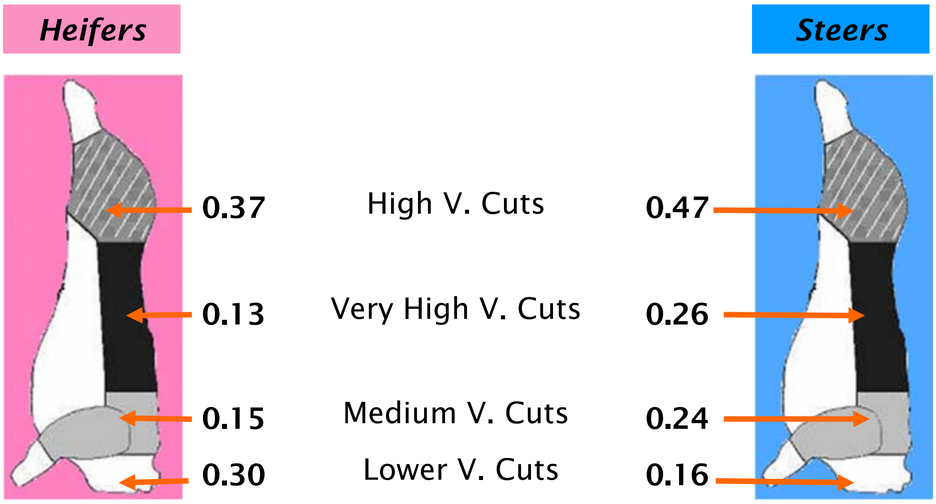
- Digital images processed
  - –Animals slaughtered between 07/2005 and 06/2010
  - –Across 22 slaughter houses in Ireland
  - –Raw data = 1,300,000 carcasses with x 2 images
    - 600,000 steers & 370.000 heifers



Slaughter extract 03/2011

Results

- Heritability



Heifers		Steers
0.37	High V. Cuts	0.47
0.13	Very High V. Cuts	0.26
0.15	Medium V. Cuts	0.24
0.30	Lower V. Cuts	0.16
s.e. < 0.06		*s.e. < 0.03*

Results

- Genetic correlations

Steers **Heifers**	**Carc. Weight**	**Low. V. cuts**	**Med. V. cuts**	**High V. cuts**	**Very H. V. cuts**
Carcass weight		0.4	0.32	0.43	0.45
Lower V. cuts	0.26		0.45	0.66	0.57
Medium V. cuts	0.10	0.47		0.79	0.86
High V. cuts	0.26	0.80	0.82		0.89
Very H. V. cuts	0.38	0.69	0.82	0.82	

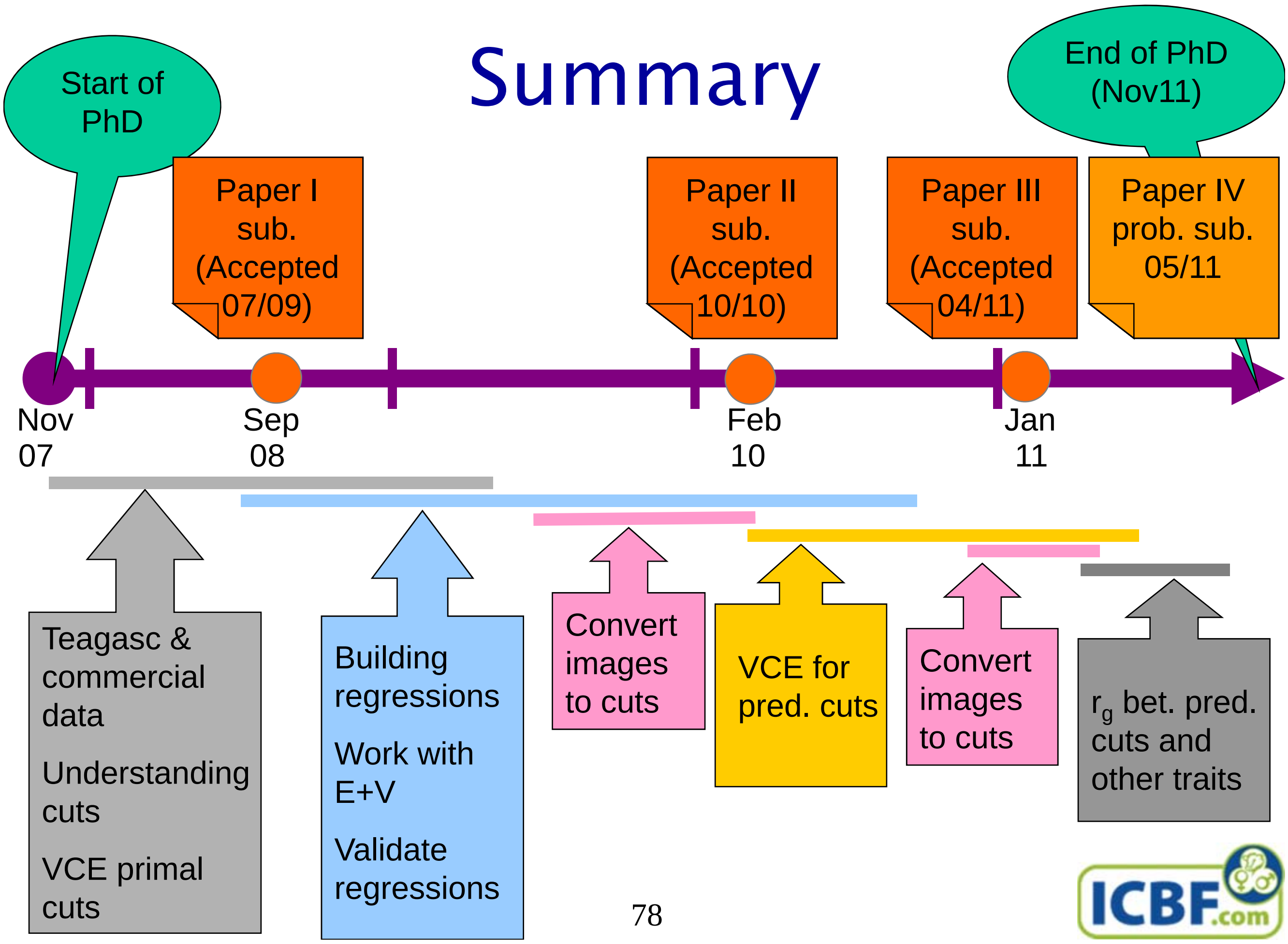
Results in progress

- More genetic correlations between carcass cuts &

Trait	Status	r_g
Carcass value (€/kg)	Done	0.35 (MVC) ; 0.69 (VHVC)
Mart prices x3 (€/kg)	UNDER CONSTRUCTION	
Calf quality (1-5)	Done	0.12 (MVC) ; 0.49 (VHVC)
Live weight weaning (kg)	Done	-0.13 (MVC) ; 0.23 (LVC)
Live weight post-weaning (kg)	UNDER CONSTRUCTION	
Linear weaning x7 (1-10 [15])	Done	-0.06 (MVC) ; 0.46 (VHVC)[1]
Linear post-weaning x7 (1-10 [15])	Done	0.23 (MVC) ; 0.44 (VHVC)[1]

[1] r_g between cuts and hindquarter development

Summary



Teagasc & commercial data

Understanding cuts

VCE primal cuts

Building regressions

Work with E+V

Validate regressions

Convert images to cuts

VCE for pred. cuts

Convert images to cuts

r_g bet. pred. cuts and other traits

Next

- Streamlining the process of cut conversion
- Integrating the new traits in the current genetic evaluation
  - Test proofs by mid summer.
  - New economic weights to reflect use of carcass cut data.
- Finish up PhD!

AI Sire DNA Archiving for Research

15th April 2011

DNA Archiving for Research Purposes

- **Backround:**
  - Lack of a readily available DNA archive for bulls that have been used in AI in Ireland.
  - Ireland is at a competitive disadvantage compared to other countries that have established such archives.
- **Objectives:**
  - Increase the accuracy of genetic evaluations that incorporate genomic data.
  - Facilitate parentage & identification testing.
  - Facilitate the detection of major genes (desirable & undesirable) controlling traits of importance to Irish Farmers.
  - Improve quality control in genotyping & genetic evaluations using genomic data.

DNA Archiving

- **Procedure:**
  - A DNA sample (tissue, semen, blood) is supplied to ICBF by the Organisation seeking AI Approval for every Bull entering AI.
  - Proposed Timeframe:
    - 2 Straws of each new AI Bull coded.
    - Bulls coded Jan – July: collected in **July**.
    - Bulls coded Aug – Dec: collected in **December**.
  - The sample supplied becomes the property of ICBF for the purpose of achieving the 4 objectives.
  - ICBF will not use the sample for any other purposes.

Semen Availability

2011 New AI Sires		
	Farmer	AI Company
Special	36	-
Test	-	34
Widespread	-	23
Total	**36**	**57**

- 93 AI Sires coded so far in 2011.
- 57 Bulls (60%) of Bulls straws owned by AI Companies.
- 36 Bulls (40%) of Bulls straws owned by Farmers.
- 32 of all Bulls (34%) collected in Ireland.

Major Genes

- Numerous Genome wide association studies underway to locate & determine ‘Major Gene’ carrier status.
- Some tests are currently Breed Specific. Others require licensing & royalty payments.
- Some tests require specialized typing as they are not SNP’s but rather large insertions/deletions.
- These could not be included in a SNP chip but could be run in parallel as part of a comprehensive product.
- Parentage, Genomics & Major Gene tests completed at same time not available yet but possibly will be in the future.

Major Genes

Major Gene		AA	BB	BS	CH	HE	HO	LM	SA	SH	SI
Crooked Tail Syndrom	SQT		Y								
Dwarfism	GMC	Y	Y								
Prolonged Gestation	GP		Y								
Hamarthoma (Vascular prolif under jaw)	HAM		Y								
Arthrogryposis (Curly Calf)	ARTH	Y	Y		Y						
Heterochromia Irides (White Eye)		Y									
Tibial Hemimelia	TH									Y	Y
BLAD	BL						Y				
CVM	CV						Y				
Weaver	W			Y							
SMA	M			Y							
SDM	D			Y							
SAA (Spiderleg)	A			Y							
Osteopetrosis (Marble Bone Disease)		Y									
Double Muscling		Y	Y								
Mule Foot		Y					Y				
Pulmonary Hypoplasia	PHA									Y	Y
Beta Mannosidosis										Y	
Fawn Calf Syndrome or Contractural Arachnodactylyl	FCS or CA	Y									
Neuropathic Hydrocephalus	NH	Y									
Hypotrichosis						Y					
Idiopathic Epilepsy	IE					Y					
Protoporphyria (Photosensitization)								Y			

- **At least 23 Major Genes found across 10 breeds**

Major Genes

- **All known Major Genes must be recorded in database at time of AI Coding**
    - Certain Bulls have known ‘Major Genes’ but these are not recorded at time of coding.
    - ICBF will create new categories for ‘Major Genes’ as required.
    - Breed Societies must ensure all know ‘Major Genes’ are recorded.
    - Possibility that for web link to AI Sire’s web info displayed on ICBF.com.
- **Farmer recording:**
    - System to be developed to allow farmers record ‘Major Genes’.
    - Scan data – early embryo loss also has possible uses.

Summary

- Important that DNA of AI Sires is collected & stored for research purposes.
- Important that any known gene based information is made available.

€uro-Star Rating (ICBF, Apr 2011)

STK — **Breed:** RM (100%)

STERLING CLINKER — **Owner:** DEPARTMENT OF AGRICULTURE

01-JAN-1985 — **Date of Evaluation:** Apr 2011

- New Tab for Gene Test Results or Bull's Organisation website link is possible.
- Building of a DNA Archive must be established as an ongoing process.

IRISH CATTLE BREEDING FEDERATION

ICAR Meeting

Brian Wickham
Killeshin hotel, Portlaoise.
14th April 2011.

National Development Plan
Transforming Ireland

ICAR 2012

- Dates: Monday 28th May to Friday 1st June
- Theme: Recording to Increase Animal Profitability
- Location: Rochestown Park Hotel, Cork
- Attendees: ca 450 from 40 countries, animal recording, genetic evaluations, manufacturers, laboratories
- Target Irish audience: All involved in, using the results of, who business depends on - animal recording and /or genetic evaluations to increase profitability of farming in Ireland

ICAR 2012

CONFERENCE

CORK
IRELAND

Mon 28th May
- Fri 1st June 2012

www.icar2012.ie

IRISH CATTLE BREEDING FEDERATION

ICBF & Weatherby's Initiative

Andrew Cromie
14th April 2011.

National Development Plan
Transforming Ireland

Program of work.

- Weatherbys took delivery of an Ilumina platform last October.
- Quality Assurance program put in place with ICBF (Nov-Feb).
  - Samples; blood, hair semen, nasal.
  - Platforms; 3k & 54k.
- Excellent results obtained.
- ICBF now using Weatherby's for routine work on 3k and 54k platforms.

Going forward.

- Additional "Quality Assurance" work underway.
  - Parentage testing using SNP's – HO breed.
  - Testing on HD platform (for beef breeds).
- Establishing "live link" to ICBF database for accessing genotypes.
- Additional project work being scoped.
  - Stored DNA (~10k stock bulls with hair samples that would be of value to genomics research & for future parentage verification.
  - 3k genotype work with bull breeder herds.
- Excellent development for Irish cattle breeding industry. Well done.

WEATHERBYS IRELAND

DNA LABORATORY

Genotyping Service Provider for Genome Wide Studies and Parentage Verification.