IRISH CATTLE BREEDING FEDERATION

# Multi-breed Genomic Evaluations for 1 million Beef Cattle in Ireland.

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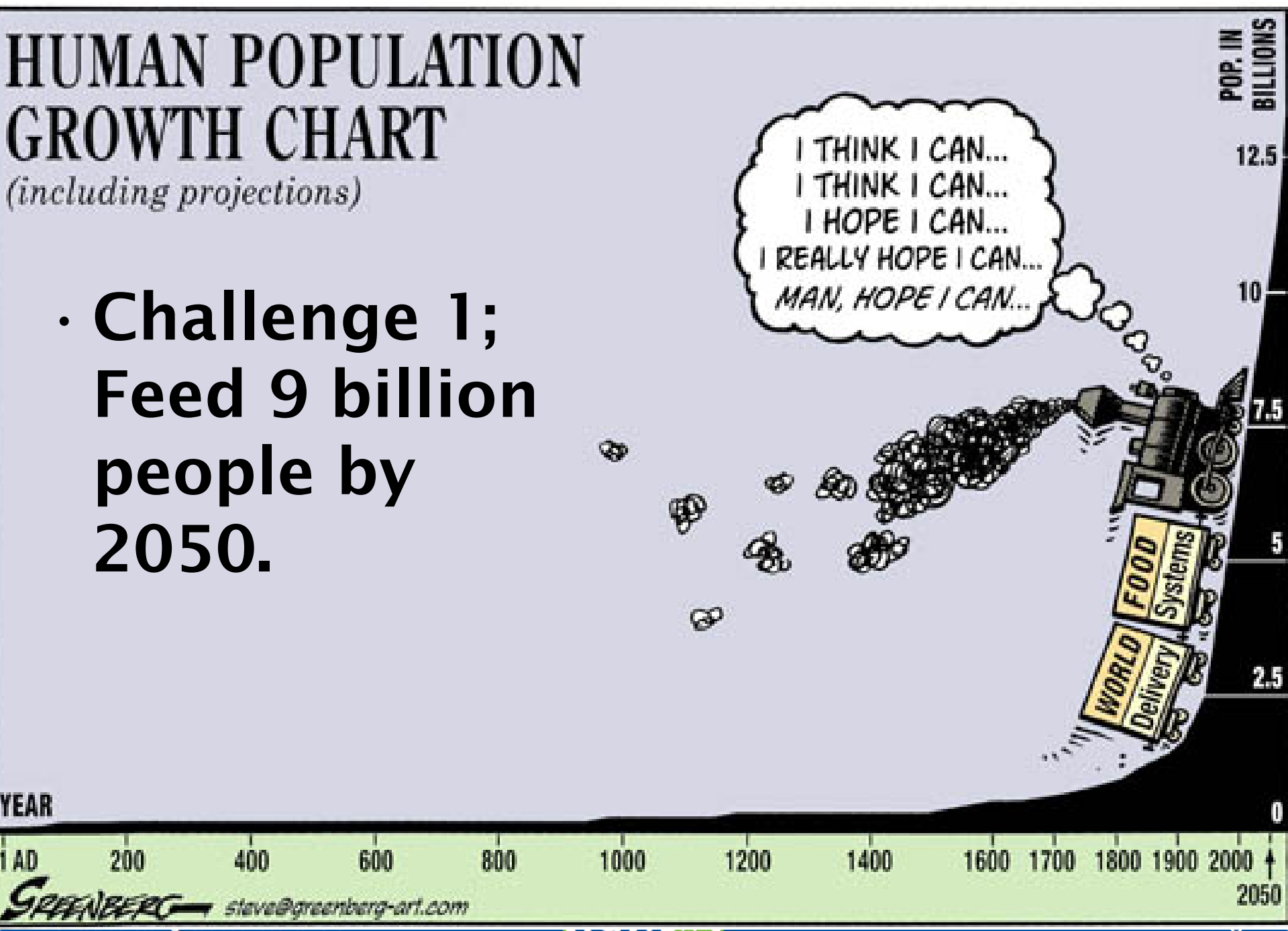
An Roinn Talmhaíochta, Bia agus Mara

# Overview of Talk.

- Challenges and Opportunities.
- Using to genomics/genetics to address GHG efficiency.
- The Irish Beef Data and Genomics Program.
  - Specific challenges being encountered.
- Summary.

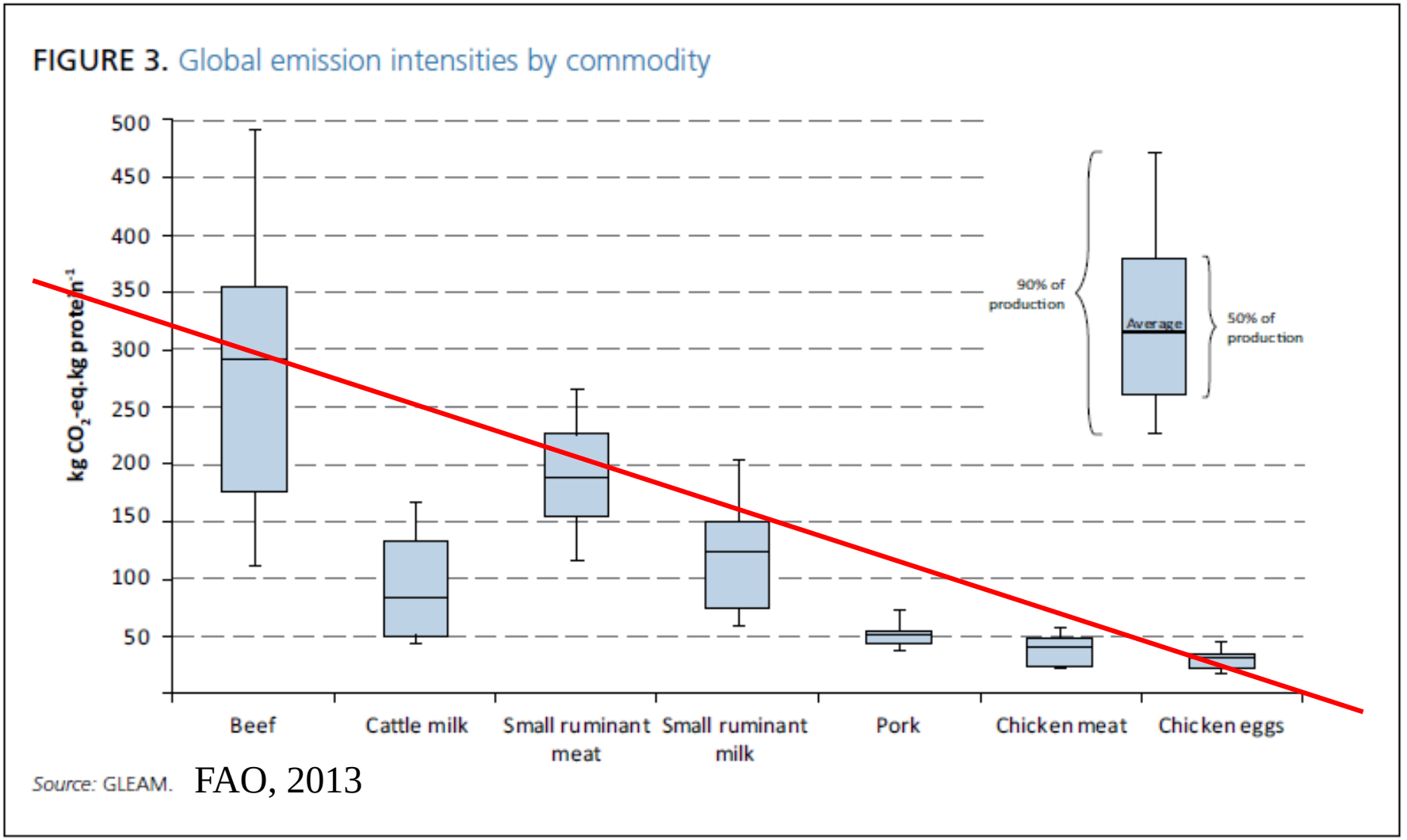



- **Challenge 1; Feed 9 billion people by 2050.**

# Challenge 2; Protect Climate & Environment.


- Ireland; To cut carbon emissions by 20%.
  - Agriculture currently responsible for almost 50% of total GHG emissions.

# Challenge 3; The Beef Cow!

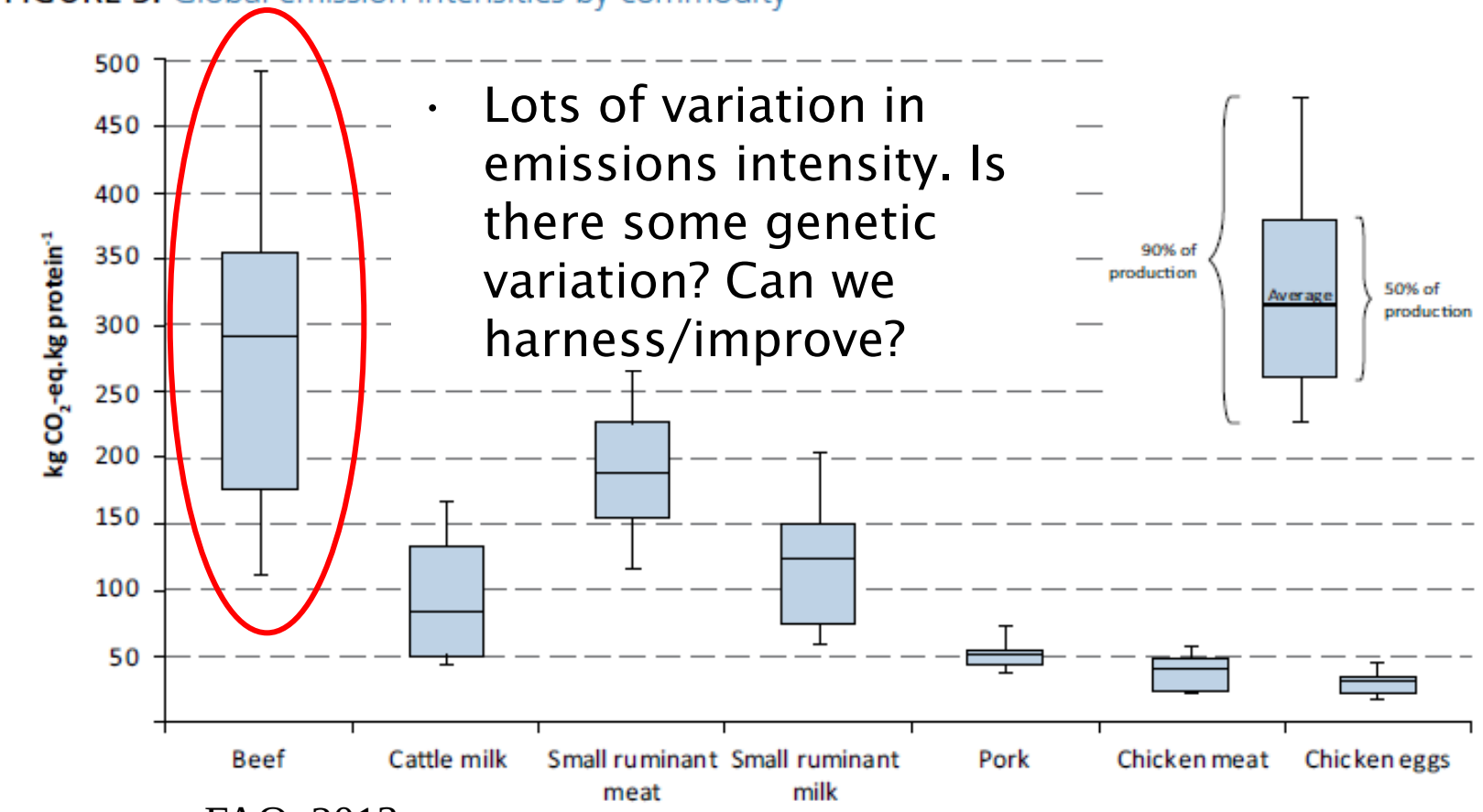



FAO, 2013

# Challenge 4; Rural Infrastructure.

- Suckler cows & beef cattle are a key part of Irelands rural infra-structure.
  - Small fragmented farms, marginal land etc.
- *"In the context of the food versus climate challenge, there is a requirement on countries such as Ireland to become even more efficient in their beef production*". Searchinger 2016.

# Opportunity; The Beef Cow!




- Lots of variation in emissions intensity. Is there some genetic variation? Can we harness/improve?

FAO, 2013

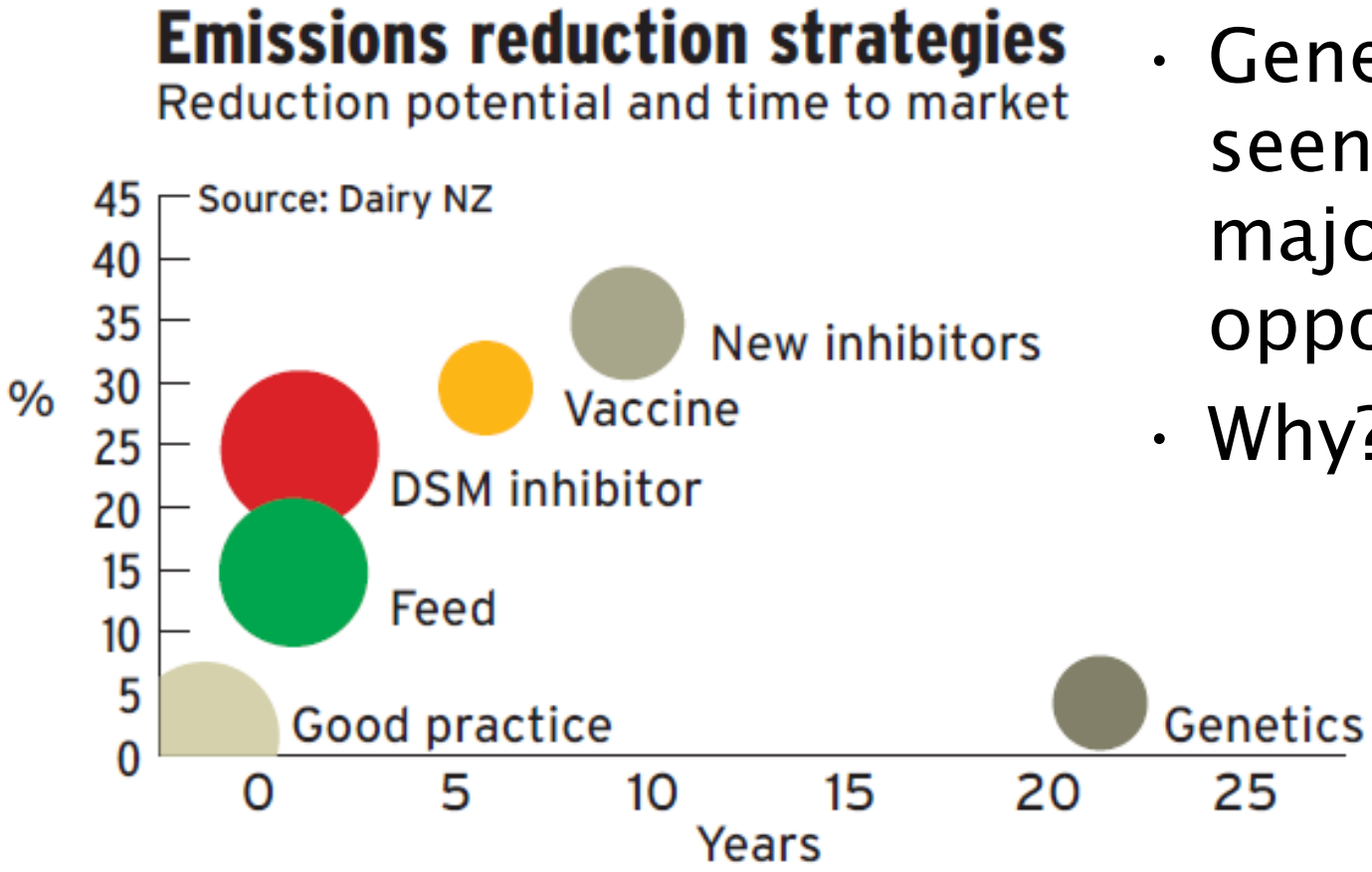
# Genetic parameters in Australian Beef Cattle (de Haas et al., JAM 2016)

| Trait | $\sigma^2a$ | $\sigma^2p$ | MeP | RPM | RGM | DMI | WT |
|---|---|---|---|---|---|---|---|
| **MeP** | 49.7 | 166.9 | **0.30** | 0.65 | 0.55 | 0.83 | 0.80 |
| | | | **(0.06)** | (0.11) | (0.14) | (0.05) | (0.06) |
| **RPM** | 12.9 | 84.7 | 0.71 | **0.19** | 0.98 | 0.04 | -0.01 |
| | | | (0.02) | **(0.05)** | (0.02) | (0.17) | (0.17) |
| **RGM** | 11.8 | 96.7 | 0.62 | 0.94 | **0.15** | 0.00 | 0.00 |
| | | | (0.02) | (0.00) | **(0.05)** | (0.18) | (0.18) |
| **DMI** | 0.1 | 0.2 | 0.70 | 0.00 | -0.10 | **0.39** | 0.98 |
| | | | (0.02) | (0.04) | (0.03) | **(0.06)** | (0.01) |
| **WT** | 415.4 | 1010.6 | 0.67 | 0.00 | 0.03 | 0.93 | **0.41** |
| | | | (0.02) | (0.04) | (0.03) | (0.01) | **(0.06)** |

* Heritabilities on diagonal, genetic correlations above diagonal, phenotypic correlations below diagonal

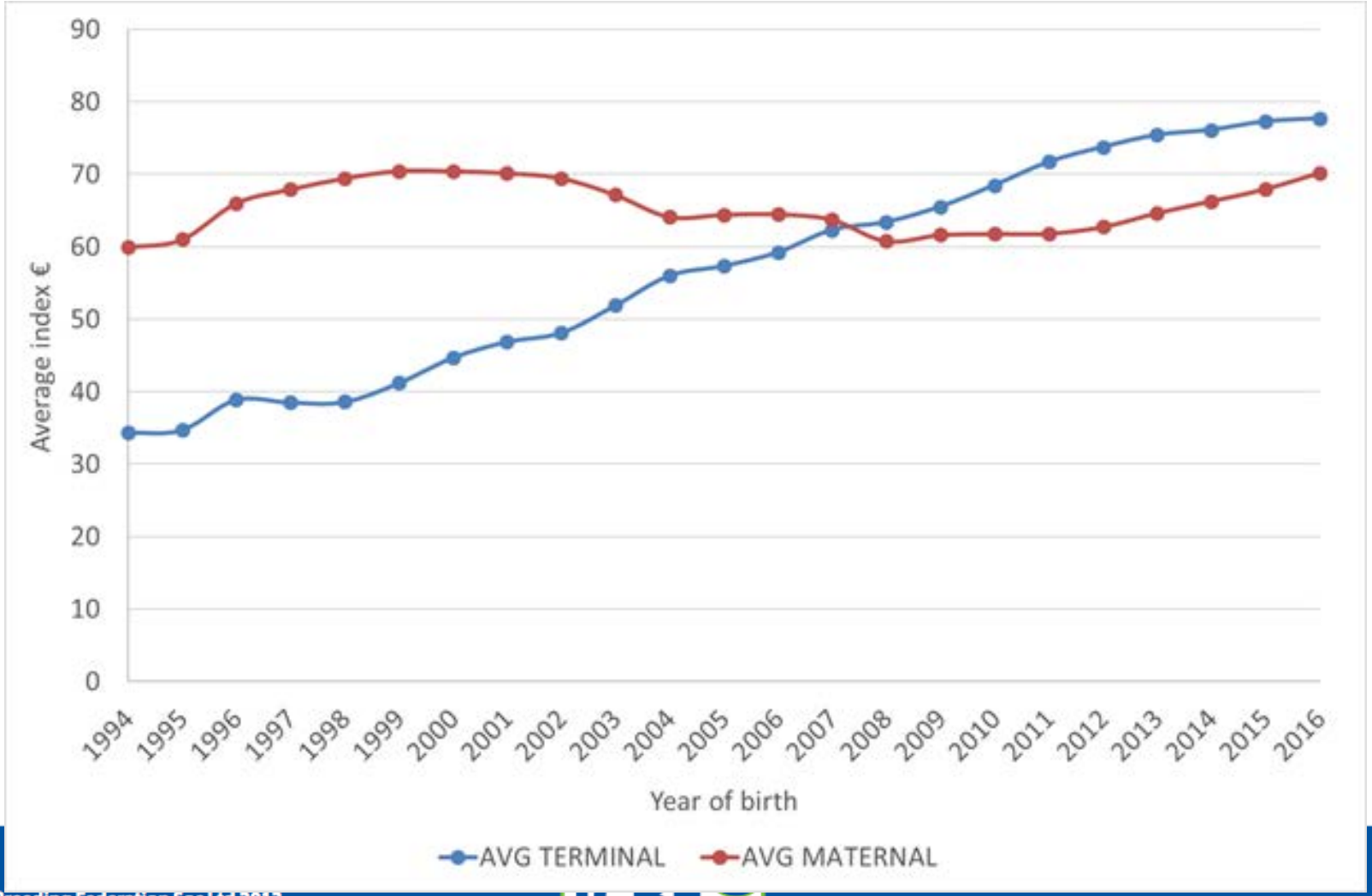
- *Session 50, today starting 14.00, Corallia Manzanilla-Pech.*

# Can we harness/improve?




- Genetics is not seen as a major opportunity?
- Why?

# We are only now starting to focus on cost of production traits.



# €uro-Star Replacement Index.

| Trait | Goal | Relative wt |
|---|---|---|
| Calvi | | 16% |
| Feed | | % |
| Carca | | % |
| Mater | | % |
| Femal | More | 29% |
| Docility | More | 4% |

Emphasis:

Cow traits 71%

Calf traits 29%

# 5 Star Cows Leaving More Profit....

## All Suckler Cows

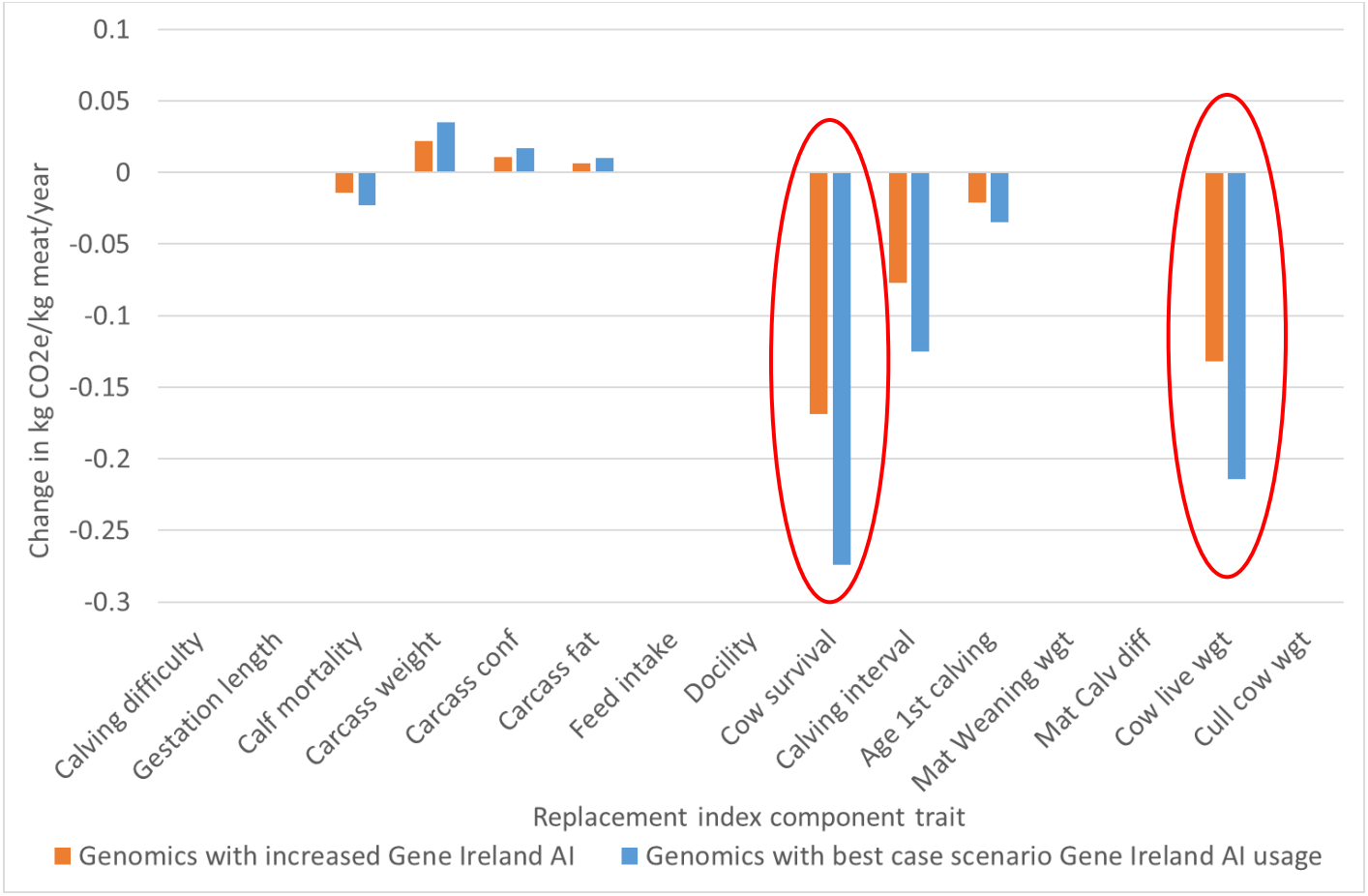
| Cow Details | | | | Milk Performance | | Fertility Performance | | | Progeny Carcass Performance | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Star Rating | No. of Cows | Replacement Index | % Still Alive | Calf Weaning Weight (kg) | Cow Milk Score (1-5) | Age 1st Calving (months) | Calving Interval (days) | No. of Calvings | Carcass Weight (kg) | Carcass Value | Age at Slaughter (days) |
| ★★★★★ | 33,493 | €108 | 83% | 336 | 4.08 | 30.2 | 403 | 2.69 | 358 | €1,474 | 697 |
| ★★★★ | 24,317 | €76 | 80% | 324 | 3.87 | 30.9 | 407 | 2.56 | 356 | €1,469 | 712 |
| ★★★ | 21,644 | €60 | 79% | 319 | 3.74 | 31.3 | 411 | 2.47 | 356 | €1,470 | 715 |
| ★★ | 20,908 | €43 | 76% | 315 | 3.61 | 31.5 | 416 | 2.40 | 357 | €1,475 | 721 |
| ★ | 23,911 | €12 | 72% | 309 | 3.36 | 32.1 | 423 | 2.25 | 357 | €1,477 | 726 |
| **Difference 5 Star V's 1 Star** | | **+€96** | **11%** | **27kg** | **0.72** | **-1.9 months** | **-20 days** | **0.44 calves** | **0kg** | **€-2** | **-29 days** |

*Performance of all suckler females born in 2011, when ranked on new generation test proofs*

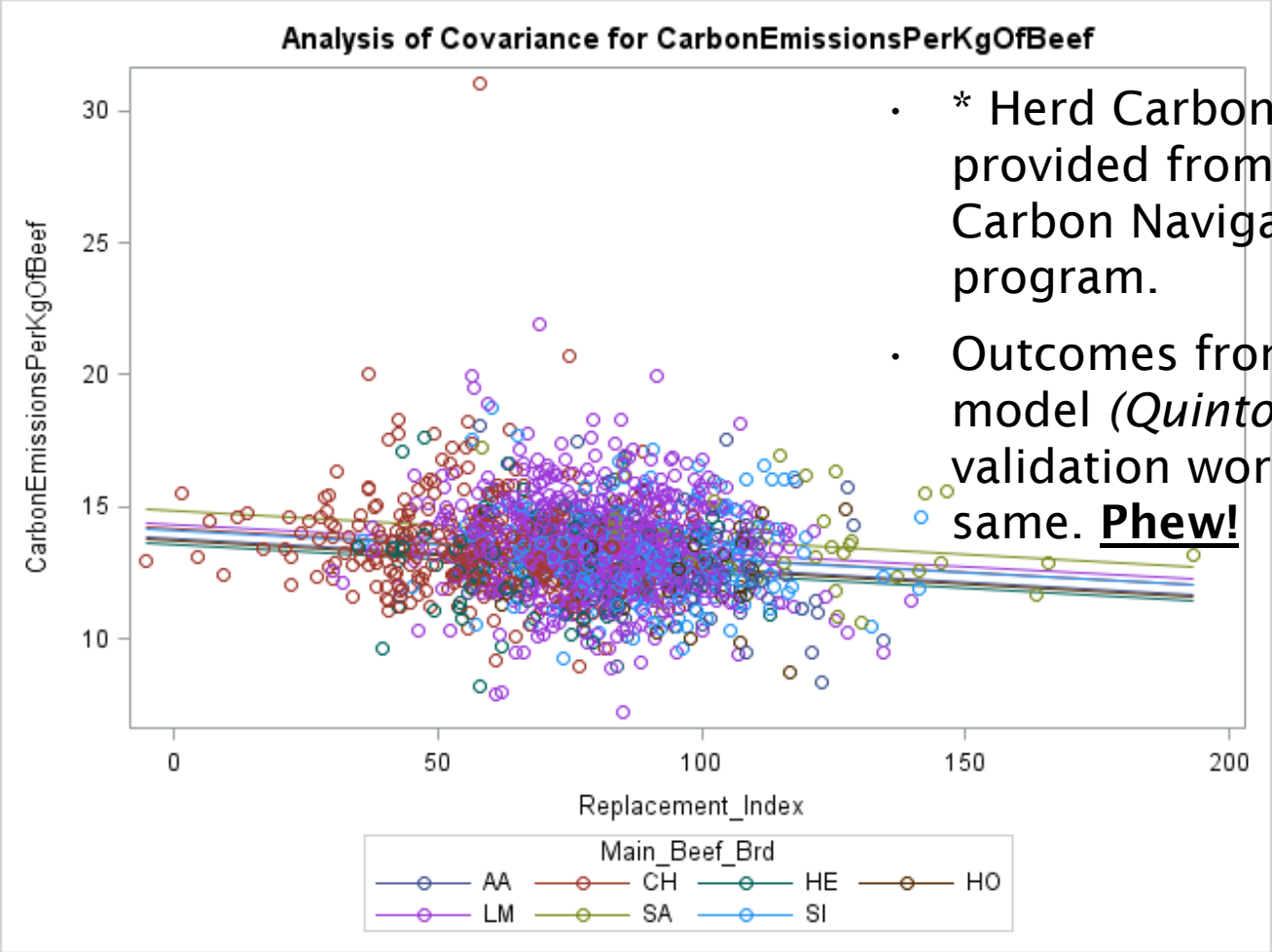
# Expected Reductions in Emissions from Genomics (Abacus Bio, NZ).

- Part 1. Impact of changes to the breeding program; genomics, increased AI, more Irish bred animals *(Fiona Hely, EAAP 2016, Abs 1193*).
  - 4-fold increase in rates genetic gain => €20m/cow/yr.
- Part 2. System model developed to estimate kg $CO_2$ emissions produced by average breeding cow *(Cheryl Quinton, ICAR Chile, 2016).*
  - Consequences of genetic gain on DMI for all traits in the Replacement & Terminal Indexes => Emissions.
  - Estimated reduction -0.009kg $CO_2$/kg meat per breeding cow per year for a €1 increase in replacement index

# Changes in Emissions from Selection on Replacement Index; Key Traits.



# Validation; High Genetic Merit Herds are More Carbon Efficient*




- * Herd Carbon data provided from Bord Bia Carbon Navigator program.
- Outcomes from system model *(Quinton et al)* and validation work were same. **Phew!**

*Breeds with at least 40 herds in data set

# Results; Expected Reductions in Emissions from Genetics/genomics.

| | 2020 | | | 2030 | | |
|---|---|---|---|---|---|---|
| Suckler beef breeding strategy | kT of CO2e | % reduction Agri | % reduction All | kT of CO2e | % reduction Agri | % reduction All |
| Current replacement index trend | -66.14 | 0.4% | 0.2% | -529.1 | 2.8% | 1.2% |
| Genomics with increased Gene Ireland AI | -261.56 | 1.4% | 0.6% | -1,442.1 | 7.8% | 3.3% |
| Genomics with best case Gene Ireland AI | -385.02 | 2.1% | 0.9% | -2,270.2 | 12.2% | 5.2% |

- Genomics, including improvements to the breeding program (more AI & G€N€ IR€) has potential to increase rates of genetic gain by 400% (Hely, EAAP 2016).
- If we can achieve this rate of gain, then genetics/genomics can reduce KT CO2e by 5.2% (IRE).

# The Irish Beef Data and Genomics Program

- Focused on breeding more profitable , sustainable and carbon efficient cows.
- Funded from EU Rural Development Program.
  - Under article 28 (Climate + Environment).
  - Co-funded by Irish government (DAFM).
- €300m total funding 6 years (2015-2020)
  - Farmers paid ~€90/cow/year to complete key actions re: the scheme.
  - ~500k animals genotyped to-date. ~2.5m animals will be genotyped during period of scheme.

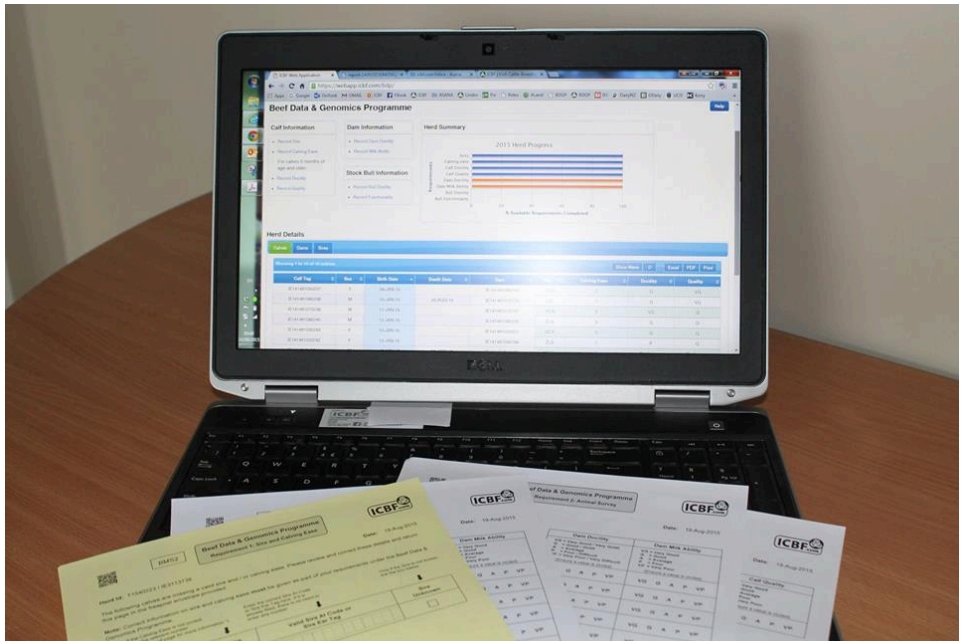
# Key Project partners.

- **DAFM/EU**; Scheme "owners" and responsible for scheme delivery.
- **ICBF**; Data collection, genotyping, delivery of genetic/genomic evaluations & reports.
  - Role of Scientific Advisory Committee (Amer, Garrick, Mantysaari, Meuwissen & Veerkamp).
- **Teagasc**; Research, extension & training.
- **Illumina**; Delivery of IDB 54k cust chip.
- **Weatherby's/Eurofins**; Lab services.
- **Bord Bia;** Carbon Navigator.

# Key Actions; Tagging


- Started with tagging cows (for reference population), now moving more toward female calves => potential female replacements.
- Pedigree males prioritised.

# Key Actions; Data Recording


- Farmers receive forms regularly re: data recording (including any animals that are missing data).
- Paper based and electronic recording.

# Key Actions; Data recording

## Beef Data & Genomics Programme

### Calf Information

- Record Sire
- Record Calving Ease
- Record Birth Size
- Record Vigour

For calves 5 months of age and older:

- Record Docility
- Record Quality
- Record Scour
- Record Pneumonia

### Dam Information

- Record Dam Docility
- Record Milk Ability
- Record Culling Reasons

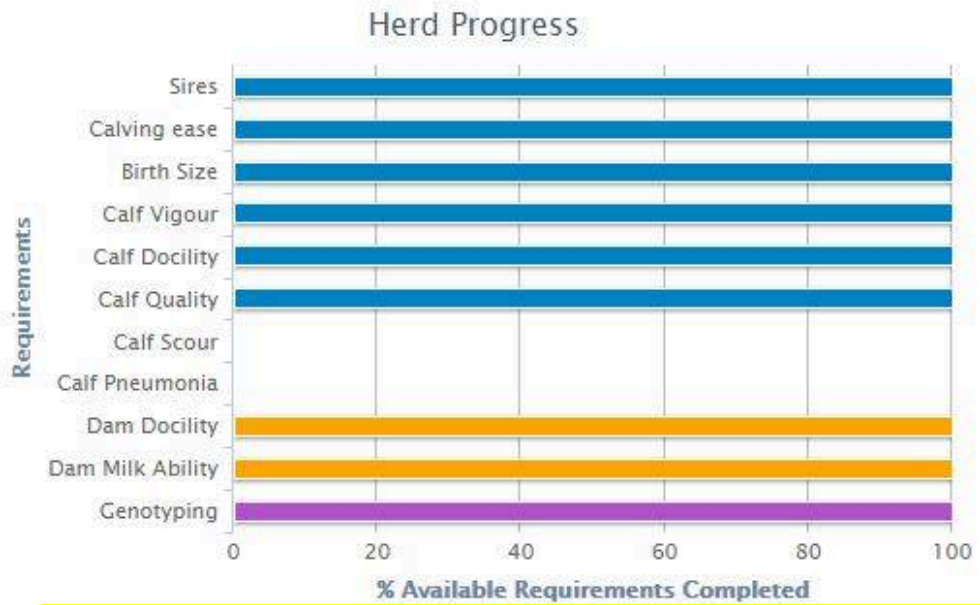
### Stock Bull Information

- Record Bull Docility
- Record Functionality
- Record Culling Reasons

### Genotype Information

- View Genotype Details

### Herd Summary




Very good h2 estimates for farmer recorded traits, e.g., 0.25 for cow milk score with an rg of 0.8 with maternal weaning weight

# Key Actions; % 4 & 5 star females.

## Commercial Females

**Report Date:** 18-May-16 (May 2016 Evaluation)
**Herd:** T1560143 / IE3113852
**Herd Owner:** THOMAS MCGOWAN JNR

All commercial females are listed here, by order of Replacement Index.
A commercial female is a female not recorded as purebred in the ICBF database.

| Jumbo | Tag | Date of Birth | Calvings | Breed (Blue Card) | Dam | Sire | Replacement Index | | Genomic Eval. |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | Index | Euro-Stars Across Breed | |
| 2496 | IE311338662496 | 21-May-15 | | HEX | IE311338632007 | IE251141240404 | €115 | ★ ★ ★ ★ ★ | Yes |
| 106 | IE311385230106 | 11-Feb-09 | 5 | BBX | IE311385280060 | TZA | €65 | ★ ★ ★ | Yes |
| 183 | IE311385270183 | 04-Apr-15 | | LMX | IE311385230147 | EBY | €63 | ★ ★ ★ | |
| 184 | IE311385280184 | 04-Apr-15 | | LMX | IE311385210145 | EBY | €50 | ★ ★ | |
| 200 | IE311385270200 | 17-Feb-16 | | LMX | IE231226920126 | ZGM | €34 | ★ ★ | |

Farmers must have a minimum of 20% of breeding females as 4 or 5 stars by 2018 and 50% by 2020.
At least one breeding male must be 4 or 5 star by 2019.

# Evolution of ICBF Beef Evaluations.

| 2005 | 2007 | 2010 | 2013 | 2015 |
|---|---|---|---|---|
| Within breed muscle and skeletal for LM, CH, SI (40k) | Across breed. New calving (200k recs) and carcass evaluations (100k recs) | New fertility and cow milk-ability evaluations First overall beef profit indexes | 39 million pedigrees Calving 10m recs Live-weight 4m recs Calf Quality 2m recs Carcass 7m recs Fertility 4m recs 50,000 foreign ebvs | 530,000 genotypes |

# Range of breeds & cross-breeds.

| Breed Sire * Breed Dam | Num animals |
|---|---|
| HO_FR | 55,258 |
| LM_ | 28,943 |
| CH_ | 26,777 |
| LM_HO | 25,212 |
| LM_CH | 23,346 |
| CH_LM | 21,569 |
| LM_SI | 19,408 |
| AA_HO | 14,619 |
| LM_AA | 14,246 |
| LM_HE | 14,235 |
| AA_ | 13,908 |
| HO_ | 11,627 |
| CH_SI | 11,617 |
| HE_HO | 10,715 |
| LM_BB | 10,385 |

- 533,093 animals with genotypes.
- 30 different breeds.
- 791 different sire breed * dam breed combinations.
- ~68% of data is from cross-bred animals.

# Approach to Genomic Evaluations.

- Two step (SNP BLUP with blending) applied successfully in dairy cattle since 2009.
- Mix99 software used (Luke, Finland).
- Preference to use Single Step (SS) GBLUP.
  - Multiple breeds including cross-breds, cows & calves.
- "Hard" deadline of August 2016 for delivery of "official" genomic evaluations.
- After ~12 months intensive R&D, took a decision in May 2016 to proceed with 2-step, NOT 1-step.
- **Farmers needed proofs to make decisions ahead of 2018 and 2020 replacement deadlines.**

# Experience with ssGBLUP.

- Existing evaluations were developed to utilise all available data.
  - Beef performance evaluation was a 29 trait model with 7m records, to predict 6 goal traits.
  - Models needed to be simplified to incorporate genomics.
- Some traits were not converging as well as others, e.g. cow survival & maternal weaning weight.
- Computer resource quickly became a problem
  - RAM (Random Access Memory) to create H-Inv
  - Hard disk space: huge temporary files

# Solutions investigated.

- Short term.
  - Purchase more computer resource.
    - Running SSGBLUP with up to 200k genotyped animals. Needed 500k. Considered splitting evaluation into multiple runs with core group of genotypes in each run. NOT a satisfactory technical solution.
- Medium to long term
  - Use the SAC to investigate other options.
    - LUKE: Application of APY method.
    - WUR and Iowa State University: Variations of Single Step Bayesian Regression.
    - NMBU: ssGBLUP by genotype imputation.

# Computer requirements for ICBF evaluations

I phone 5
1 GB RAM

Cerus x **2**
Ram 6,000 GB
Disk 40,000 GB

lgen2
Ram 760 GB
Disk 4,000 GB

198
Ram 356 GB
Disk 1,500 GB

151
Ram 120GB
Disk 1,800GB

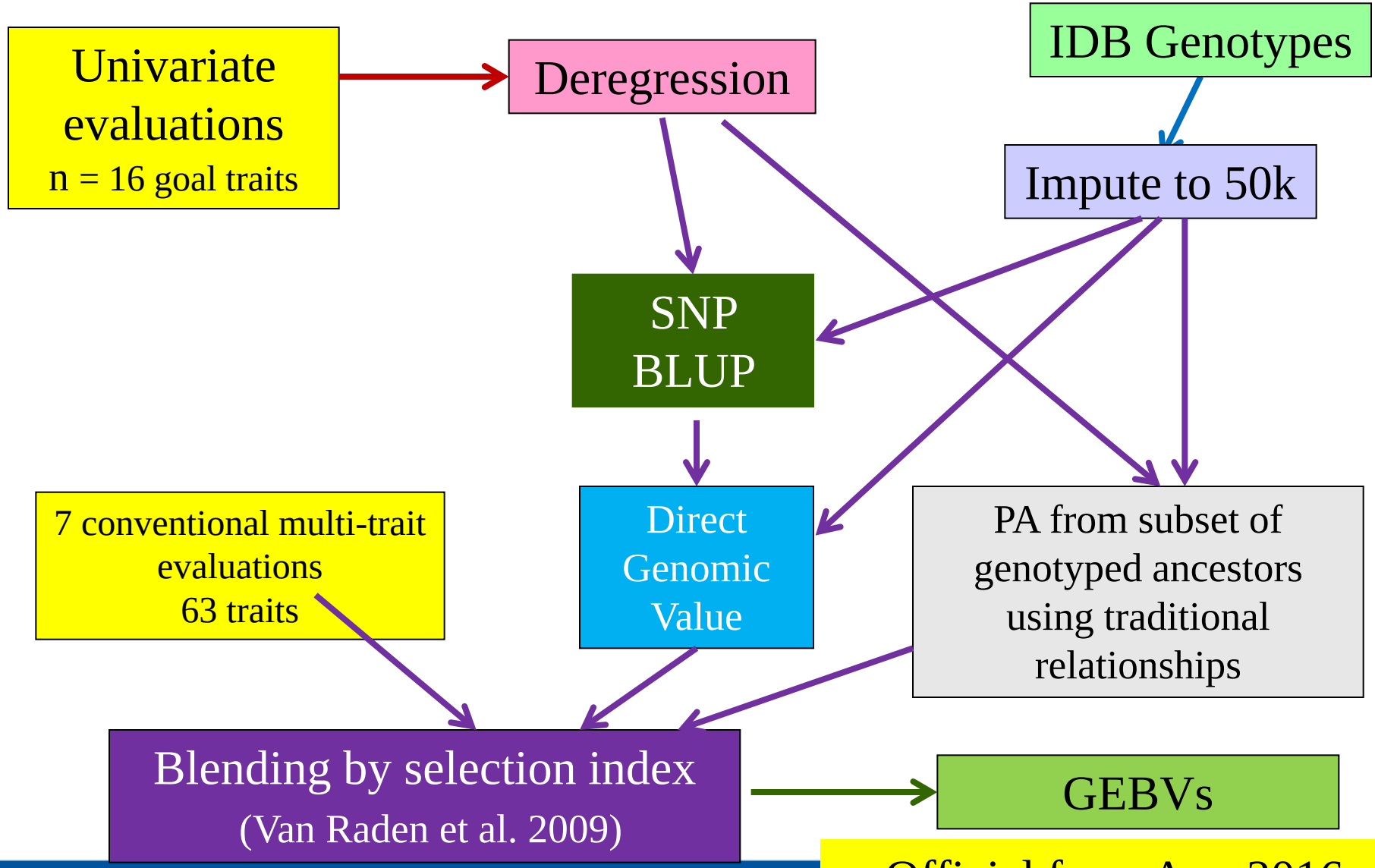
143
Ram 64GB
Disk 698GB

109
Ram 16GB
Disk 279GB

163
Ram 2GB
Disk 80GB

| 2005 | 2007 | 2010 | 2013 | 2015 |
|---|---|---|---|---|

# 2-Step Genomic Evaluation



# Validation; Docility as an example.

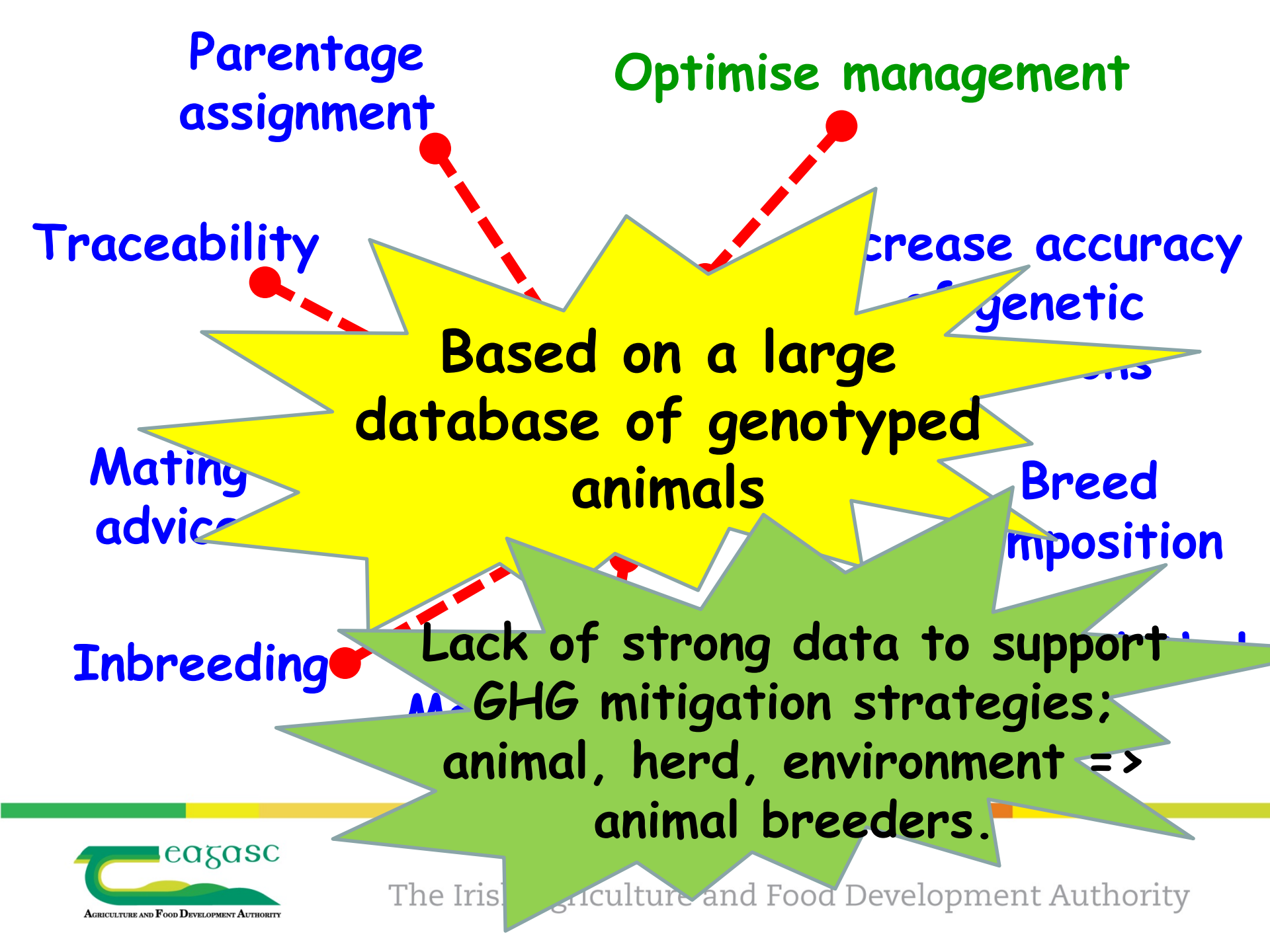
- Based on 48k animals with phenotypes & genotypes from more recent years.
- Regression of phenotype on different evaluations.
  - "Single trait" conventional evaluation = 0.62 (0.03).
  - Direct Genomic Value = 0.77 (0.03).
  - "Blended" genomic/genetic evaluation = 0.86 (0.03).
- Genomics is moving us in right direction.
- Should we derive genomic predictions from univariate or multivariate analysis?
  - "True" biological trait, versus the benefits of predictors.
- Using validation to inform switch to SS GBLUP.

# Can we use information from one breed to predict another breed?

- "Test" evaluations based on 218k in SNP BLUP (all breeds + cross-breds).
- Drop all LM animals from the "Test" evaluation => 100k in SNP BLUP.
- Correlate the DGV's => Correlation with remaining breeds?
- Correlation with pure-bred LM breed (28k animals)??

| Breed | Calving | Docility | Carcass Weight | Calving Interval |
|---|---|---|---|---|
| Angus | 0.95 | 0.89 | 0.95 | 0.98 |
| Charolais | 0.99 | 0.94 | 0.98 | 0.99 |
| Hereford | 0.95 | 0.94 | 0.94 | 0.96 |
| Simmental | 0.96 | 0.94 | 0.97 | 0.98 |
| Limousin | 0.33 | 0.25 | 0.47 | 0.27 |

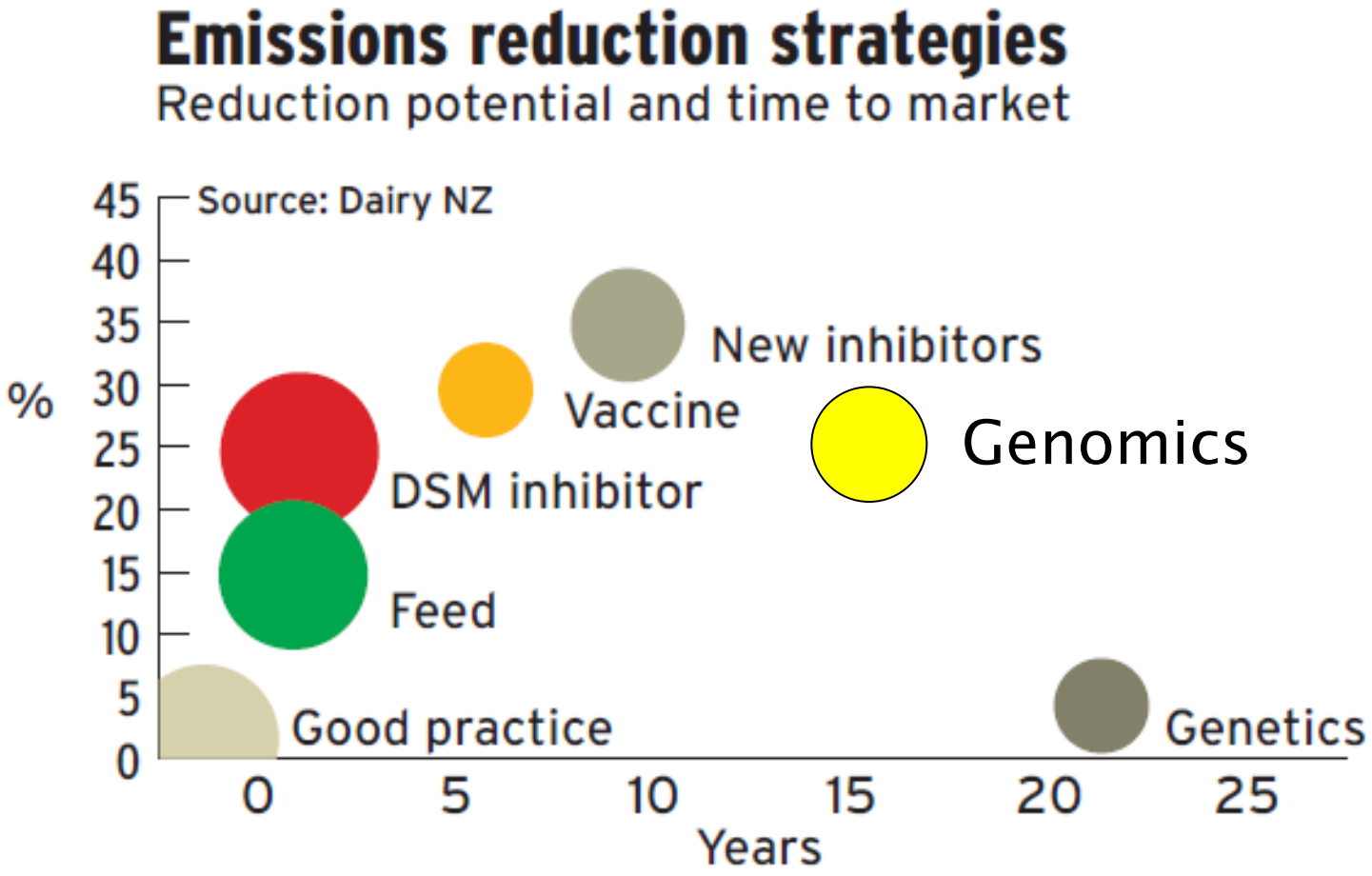
- Evidence that we can use one breed to predict a second breed.
  - ~10-15% genes in common across main cattle breeds.


Parentage assignment
Optimise management
Traceability
crease accuracy
genetic
Based on a large database of genotyped animals
Mating advic
Breed
mposition
Inbreeding
Lack of strong data to support GHG mitigation strategies; animal, herd, environment => animal breeders.

# 5. Conclusions.

- Genomics/genetics can contribute positively to profitability and GHG efficiency.
  - A significant "tool in the box" to address GHG mitigation.
- At present, 2-step methods are best to deliver a stable genomic evaluation service.
  - 1-step methods are better. How soon? The focus of the remainder of this session and others during EAAP.
- The BDGP has had a huge impact on the uptake/interest in genetic gain in Ireland.
- Strongly encourage ALL other countries to consider such programs for their countries, e.g., future RDP's.
  - Will help address GHG, but many other long term benefits.

# We can use Genomics to address GHG efficiency.



# Acknowledgement.


- Irish Department of Agriculture, Food and Marine (DAFM) & EU for the “Beef Data and Genomics Program”.
  - For more information, please see ICBF and DAFM websites.
  - Contact myself acromie@icbf.com.
- All partners involved in the Irish Beef Data and Genomics Project.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