

#### IRISH CATTLE BREEDING FEDERATION

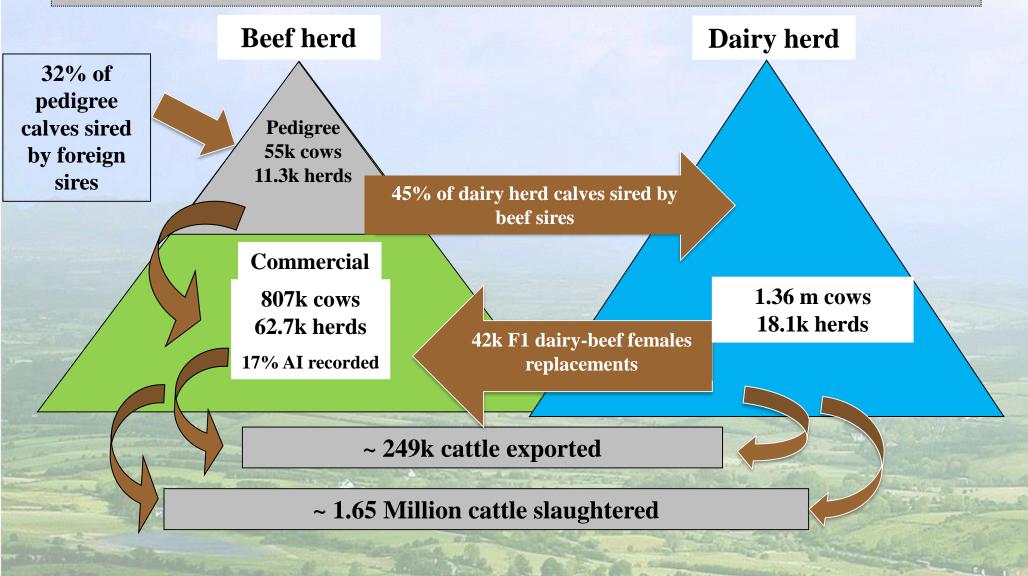
#### Genomic selection in Irish beef cattle



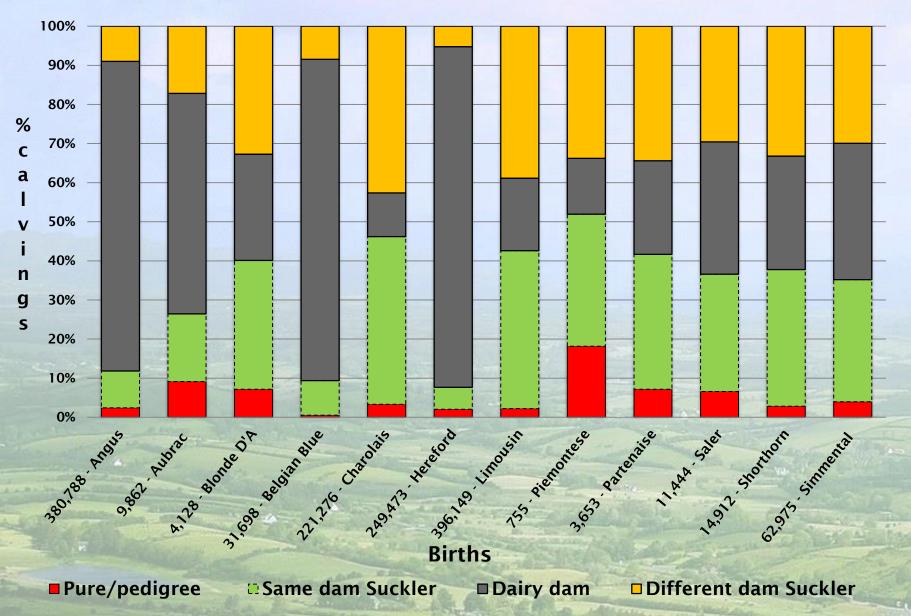
Ross Evans ICBF World Charolais Conference - Kilkenny – 08/08/2019



#### Overview of the different layers in the Irish beef Industry 2018



#### **Breed Profile of Calves Born 2018**





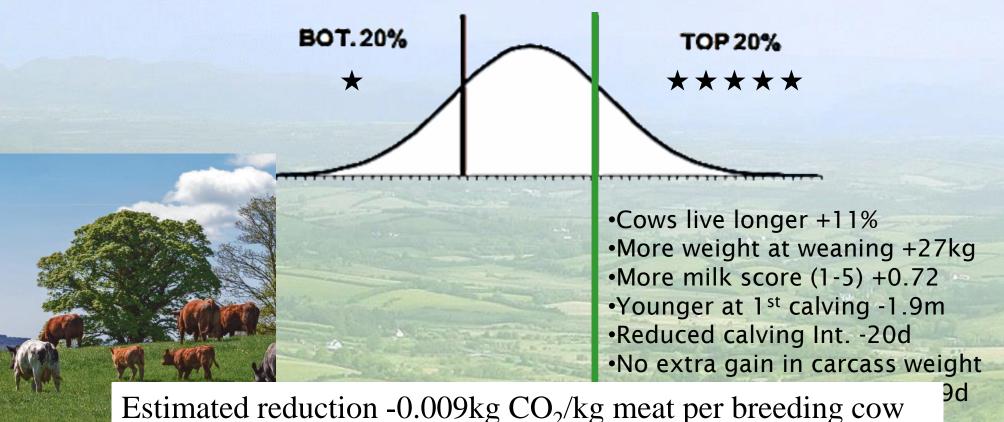
## The Beef Genomics Journey

- · 2006 +: Genotyping of AI straws (AI, Herdbooks, breeders)
- 2008-2012: Animal Welfare Recording and Breeding Scheme (Govt funded)
  - Sire recording, calving & weanling trait recording & weanling welfare
- · 2013-2014: Beef Data Programme (BDP) (Govt funded)
  - Extension of BDP to cow traits
- · 2014: Beef Genomics Scheme (BGS) Govt funded
  - 15% of herd genotype requirement
- · 2015 2020: Beef Data and Genomics Program
  - Co-Funded by Irish Government and EU Rural Development program
  - Breeding Profitable, Sustainable, Carbon efficient cows
  - Farmers paid ~€80/cow/year to complete actions (Reference yr 2014)
- 2017 2020: Beef Data and Genomics Program II



## Breeding More Efficient Cows

REPLACEMENT INDEX



per year for a €1 increase in replacement index

W



## Main Requirements

- 1. Commitment to stay for duration of scheme
- 2. Calf surveys: calving difficulty, calf size
- 3. Cow surveys: docility, milk
- 4. Genotyping 60% of animals / year
- 5. Replacement strategy: 50% females indexed 4 or 5 stars + (if any) 1 bull 4 or 5 stars
- 6. Carbon navigator
- 7. Training









## **Participation**

- Total signups BDGP 1: 29,889 herds
- Currently Active BDGP 1: 22,944 herds (77%)
- Total signups BDGP 2: 1,811 herds
- Currently Active BDGP 2: 1,489 herds (82%)
- · Circa 400 herds merged into farm partnerships





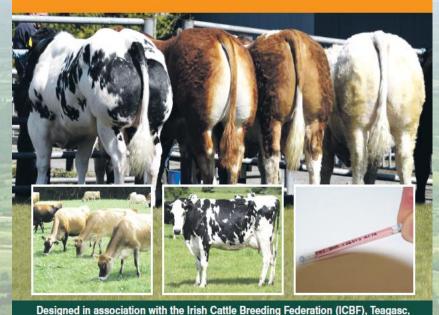


#### **Genotyping Chip**

- BDGP scheme: public EU tenders for
  - ✓ SNP chip provision
  - ✓ Lab services: DNA extraction, genotype reporting

#### **IDB SNP CHIP**

INTERNATIONAL DAIRY & BEEF SNP CHIP



Weatherbys and USDA's Agricultural Research Service.



- Developed in Ireland
- 54,000 SNPs
- 160 Major genes/defects
- Imputation SNPs
- Microsatellite imputation SNPs
- 800 Parentage SNPs
- V1 to V3 Illumina platform
- V4 Thermofisher platform
- Lab services
  - Weatherbys Ireland
  - > Eurofins Denmark

# Choice of DNA sampling method Biological sample failure rates





Sample type	Count	% Fail (Call rate <90%)
Ear punch	92,868	2.46%
Tail Hair	15,518	4.18%
Semen	309	16.80%
BVD diluent	341	20.50%

<sup>\*</sup> The overall call rate of a sample is equal to the number of SNPs receiving an AA, AB, or BB genotype call divided by the total number of SNPs on the chip.

#### Selection of animals in BGS

- Farmers were required to genotype 15% of cows (100k)
- Algorithm developed to identify most informative animals to develop genomic selection
- Based on quantity of data and divergence

$$\begin{aligned} \text{Data Quantity} &= WT_{CIV} \\ &\cdot \sum_{i=1}^{3} \text{Info\_CIV}_i + \ WT_{MILK} \cdot \sum_{i=1}^{3} \text{Info\_MILK}_i + WT_{CALVING} \\ &\cdot \sum_{i=1}^{3} \text{Info\_CALVING}_i + WT_{CARCASS} \cdot \sum_{i=1}^{3} \text{Info\_CARCASS}_i \end{aligned}$$

$$\begin{aligned} \text{Divergence} &= WT_{CIV} \cdot |\text{Diverge}_{\text{CIV}}| + WT_{MILK} \cdot |\text{Diverge}_{\text{MILK}}| + WT_{CALVING} \cdot |\text{Diverge}_{\text{CALVING}}| \\ &+ WT_{CARCASS} \cdot |\text{Diverge}_{\text{CARCASS}}| \end{aligned}$$

$$Sire_{LIMIT} = 10 + \left(\frac{(1 - reliability)}{2} * 100\right)$$

#### **BDGP** Genotyping process

#### Genotypes

020100200011102222111101110100010

**Priority based** on urgency of sample e.g. AI, pedigree



**Empty** sample: hair card

> Barcode tracks sample

> > 3-4 week

turnaround

Lists sent to TAG

**Selection algorithm:** identify and prioritise animals for genotyping

within herd

Farmer option to change

online

providers

Mullinahone Co-op

DATAMARS









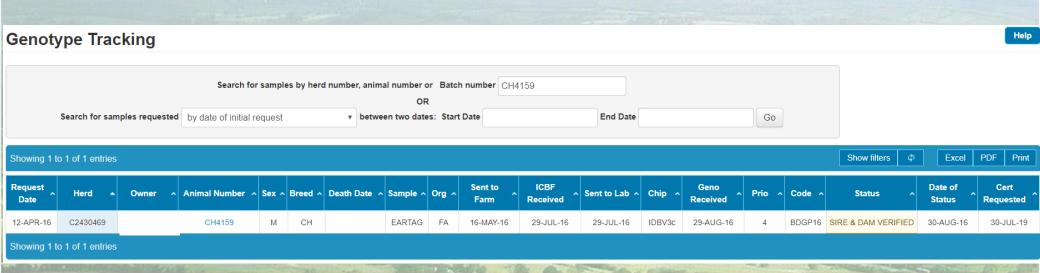




SMS TEXT

#### ICBF genotype QC process

- Genotype call rate check (>90%)
- Sex check
- Breed composition check
- Duplicate check
- Parentage check (ISAG 200 parentage SNPs + 600 ICBF)
- Checks complete: Genotype is validated for further use

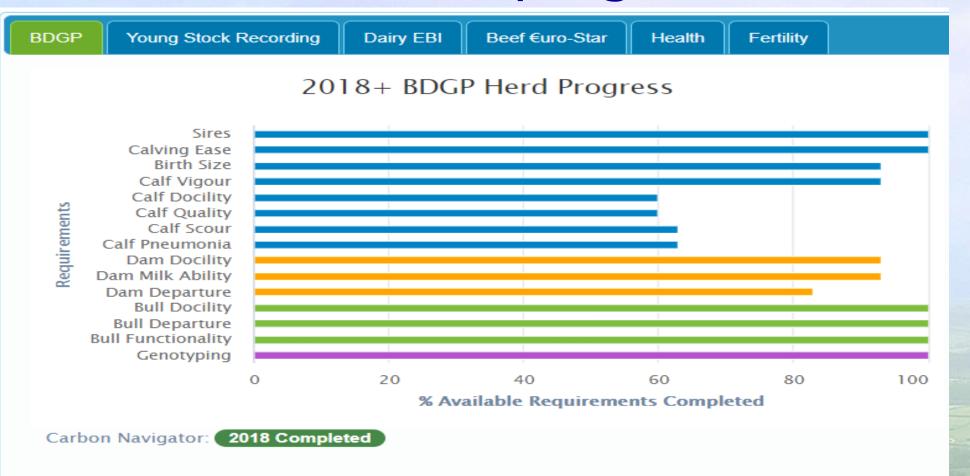


#### Parentage verification/prediction

Categories	Commercial	Pedigree	Ped Charolais
Number	1,499,259	277,328	48,186
Genotyped sire	68%	84%	87%
Sire to offspring conflict	14%	5%	5%
Sire changed	15%	6%	6%
Predicted sire where unknown	6%	1%	1%
Genotyped dam	51%	42%	42%
Dam to offspring conflict	6%	2%	2%

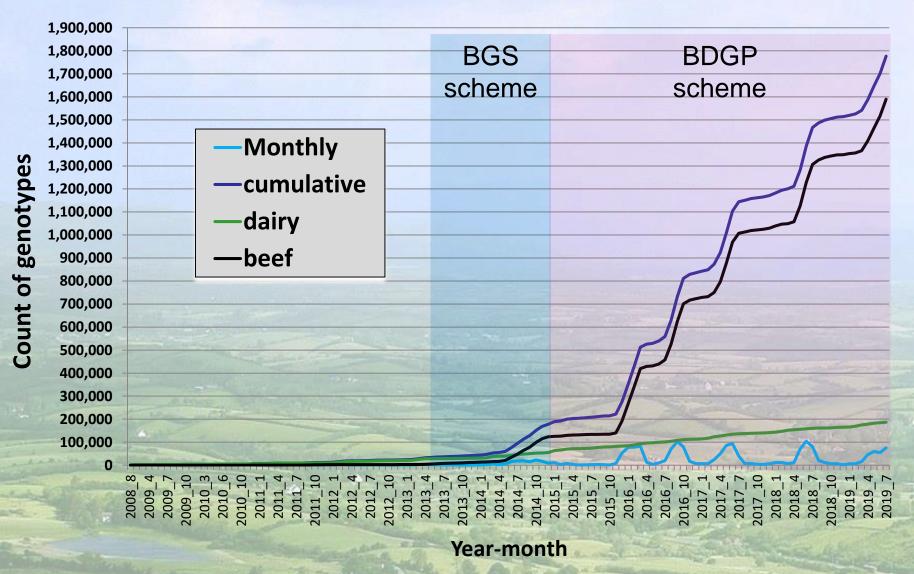
\*Stats July 2019

#### **BDGP** Herd progress



BDGP Replacement Strategy Requirements							
1. Fer	nales	2. Stock Bulls		3. Al Requirement			
2018	2020	2019	2020	2017/2018	2018/2019	2019/2020	
✓	✓	✓	✓	✓	✓		

#### Genotype levels



#### Characteristics of Genotyped animals

5,646

53,494

8,026

27,765

20,389

3,707

71,036

23,115

73,010

50,676

23,417

11,852

66,982

60,370

16,703

24,702

5,415

128,507

114,324

136,052

121,996

34,672

21,024

277,302

29,535

215,352

63,328

37,238

443,134

151,985

477,897

391,426

285,794

3,713

83,289

6,320

30,694

16,769

11,897

95,660

35,788

104,832

78,886

53,742

7,206

78,530

14,938

33,200

23,451

8,245

103,507

45,778

115,904

84,600

59,119

Characteristics of denotyped annihilas								
Main Breed	Angus	Belgian Blue	Charolais	Hereford	Holstein	Limousin	Simmental	Other
Total	169,617	57,070	367,998	95,132	158,624	543,700	124,326	135,203
Al sires	306	313	506	223	2,904	509	378	1,465

20,797

146,905

24,236

175,572

51,624

27,328

289,046

82,962

324,791

270,393

200,372

**Natural service sires** 

**Non parent Males** 

**Non Parent Females** 

**Pedigree registered** 

Single Breed Non ped

Sire is also genotyped

Dam is also genotyped

Multi-breed

Sired by AI

**Known sire** 

Cows

10,029

83,180

13,577

62,556

34,010

4,914

130,693

53,470

143,162

105,033

68,374

1,294

34,542

2,083

18,862

2,608

1,474

52,988

36,967

50,226

45,468

18,516

### Development of genomic evaluations

Scientific Advisory Committee established



Esa Maantasari Ismo Stranden



Peter Amer



Roel Veerkamp Jeremie Vandeplas Jan te Napel



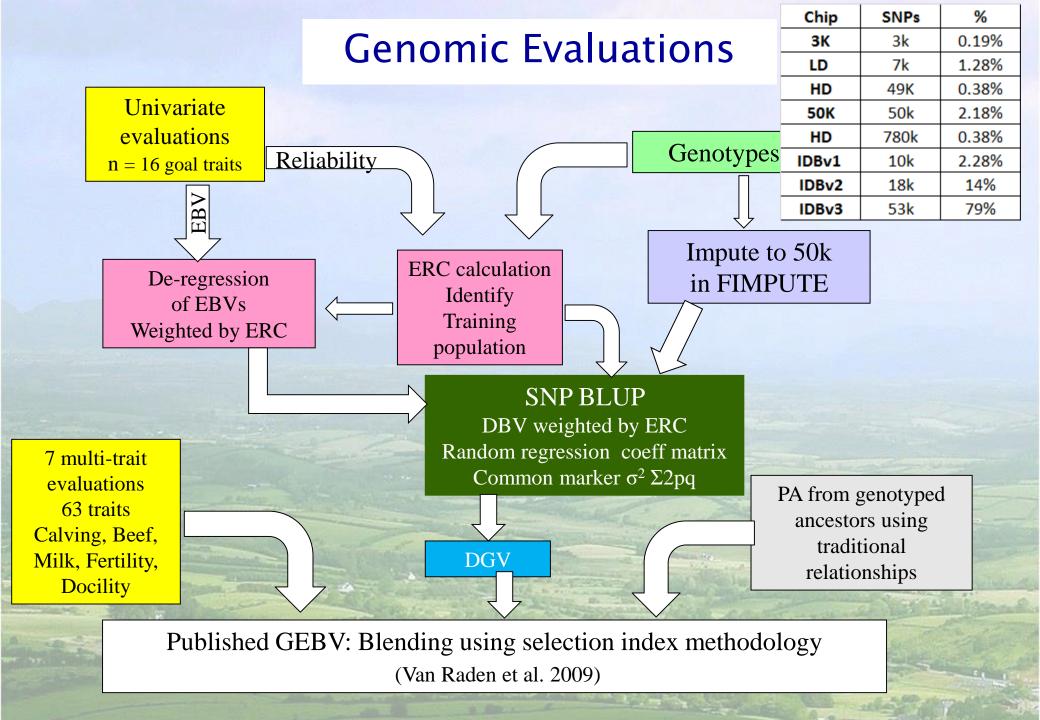


Theo Meuwissen



Donagh Berry

- Tasked with guidance in the rollout of genomic selection
  - Computation Methods: GBLUP, SNPBLUP, Single step
  - > Validation

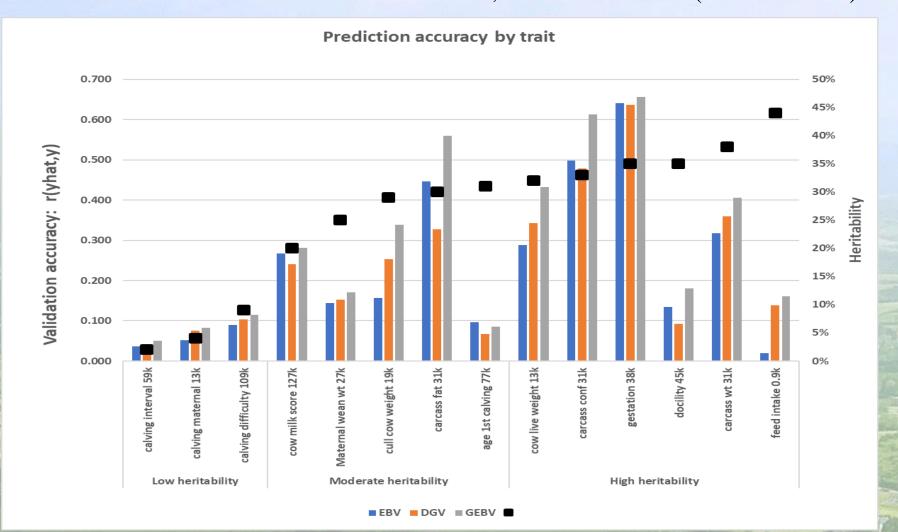


## Influence in SNP training: CH

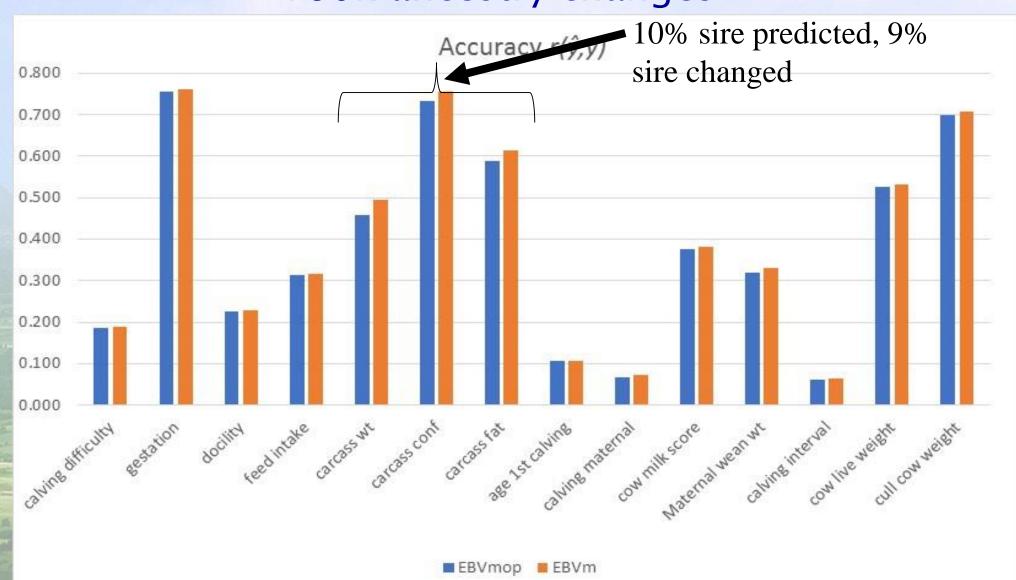
Trait	Category	count	avg_ERC	max_ERC	Total ERC
calving difficulty	Al sires	421	322	9,420	135,543
calving difficulty	Natural service sires	16,372	16	134	261,461
calving difficulty	Cows	17,979	3.5	11	64,234
carcass weight	Al sires	405	164	4,668	66,232
carcass weight	Natural service sires	14,942	8	74	118,229
carcass weight	Cows	32,338	1.1	6.6	33,925
maternal weaning wt	Al sires	250	34	877	8,497
maternal weaning wt	Natural service sires	378	2.0	11.5	754
maternal weaning wt	Cows	43,126	4.0	10	173,374
calving interval	Al sires	282	193	5,036	54,402
calving interval	Natural service sires	950	6.7	95	6,341
calving interval	Cows	69,383	5.9	18	411,081

## Does genomics work?

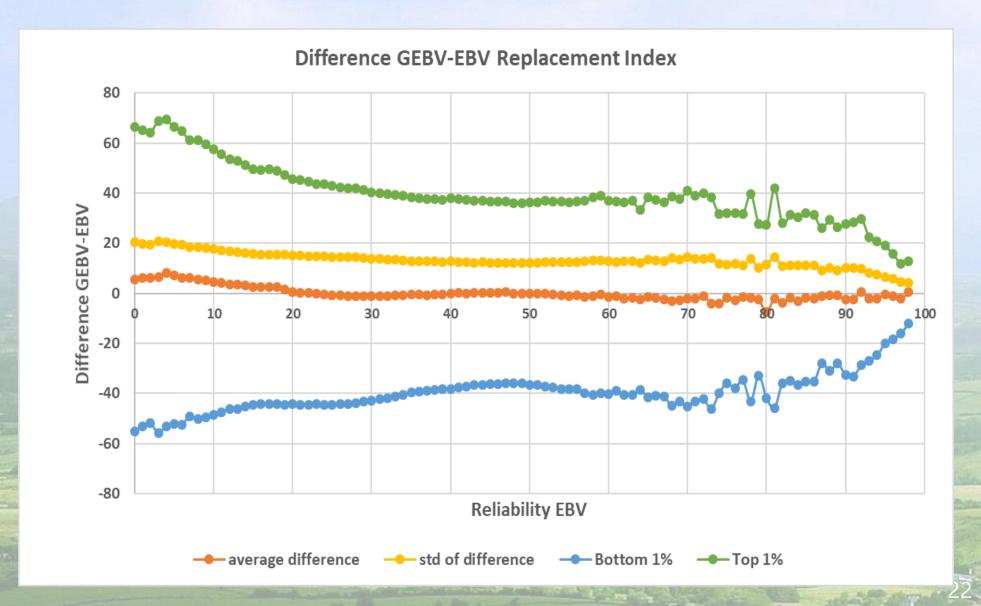
- Forward prediction: 33% of phenotypes from animals with genotypes omitted
- Phenotype corrected for breed and evaluation fixed effects
- Then correlated with validation EBV, DGV and GEBV (without breed)



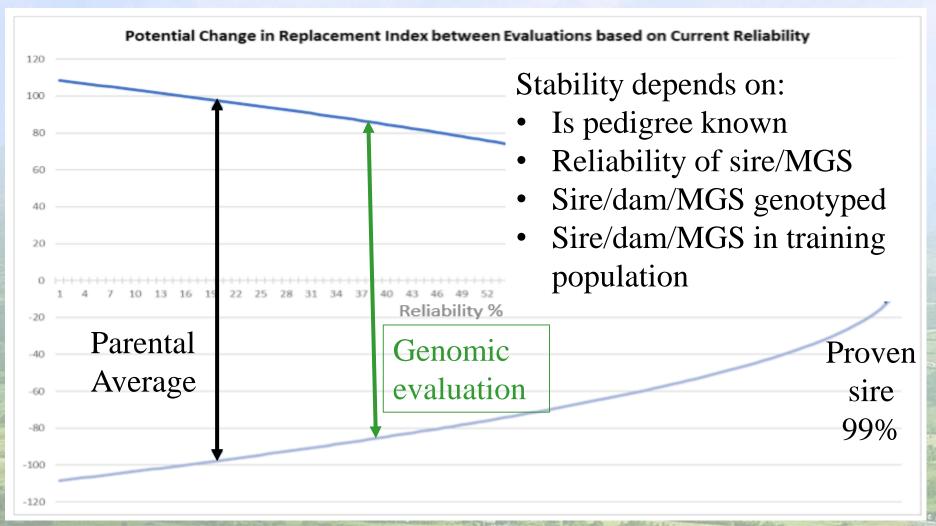
## Benefit of correcting pedigree 160k ancestry changes



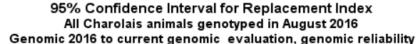
## Impact of genomics by reliability

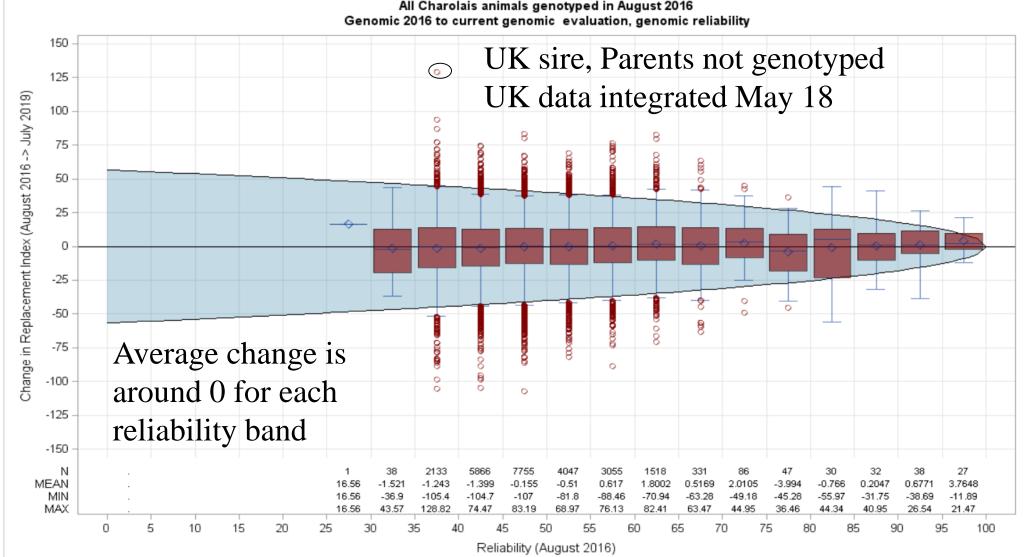


## Stability of first GEBV



### In Reality





#### Current research

- Single step evaluations
  - > Algorithms and knowledge have developed in last 2 years
  - Currently testing on new calving evaluation with SAC partners
- Interbeef
  - > 8 countries participating: currently calving, weaning
  - Integration of data into Irish evaluations
- New traits/indexes
  - Dairy Beef index
    - > Specific calving traits: Dairy heifer, Dairy Cow, Beef heifer, Beef cow
    - > Specific beef traits: Dairy herd carcass, Beef herd carcass
  - > Meat Eating Quality
  - > Whole Herd Performance cow traits: udder, functionality, skeletal
  - > Cow intake: Greenbreed on farm project
  - > Carbon emissions: Greenfeed boxes in Tully performance centre
- Sire advice
  - Genomic inbreeding, genetic defects, major genes (myostatin)
  - > Beef on the Dairy herd: expanding market





#### **Our Farmer & Government Representation**







#### **Our AI & Milk Recording Organisations**









#### Our Herdbooks









































#### **Acknowledging Our Members**