



# Animal genomics in breeding – opportunities and challenges

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*Teagasc, Moorepark*

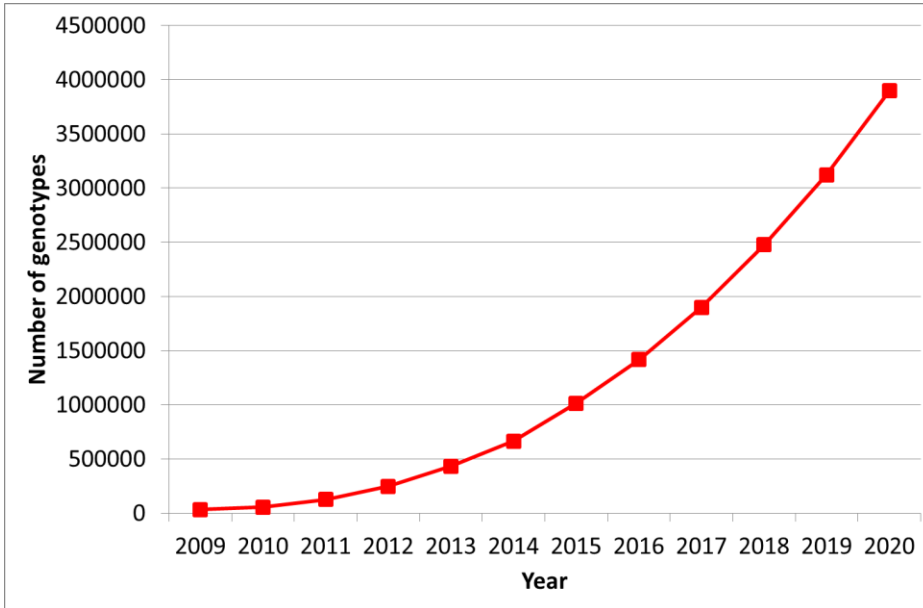
# Captured opportunities

$$\text{Genetic gain} = \frac{\text{Intensity of selection} + \text{Accuracy of selection} + \text{Genetic variability}}{\text{Generation interval}}$$

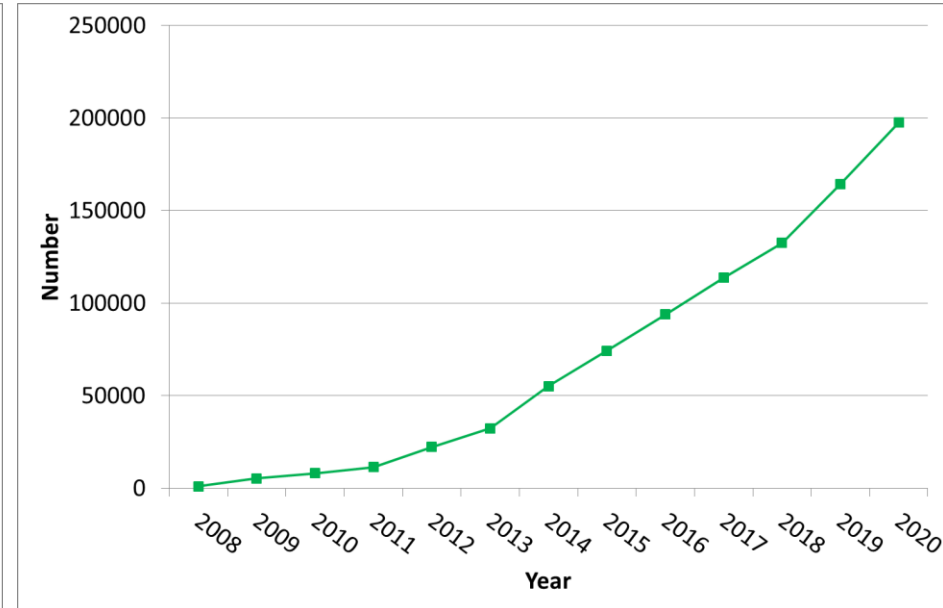
- Correction of parentage
  - More precise EBIs and mating plans
- Breed prediction
  - More precise EBIs

# Uptake of genotyping

US



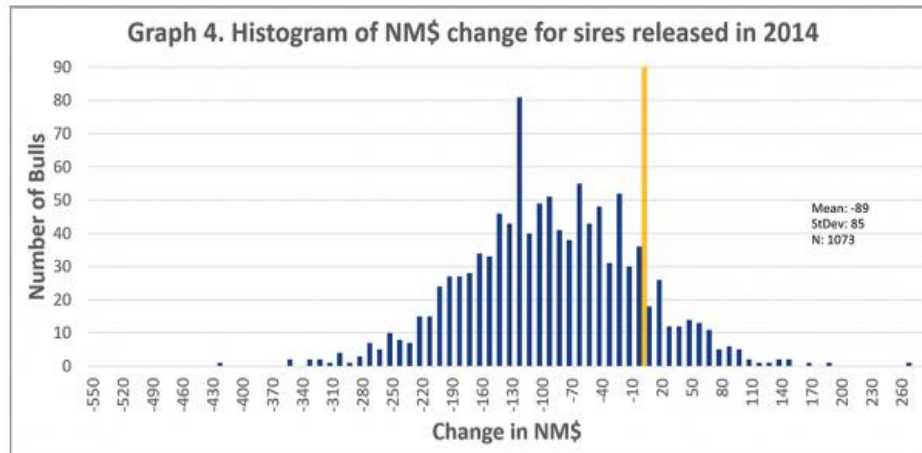
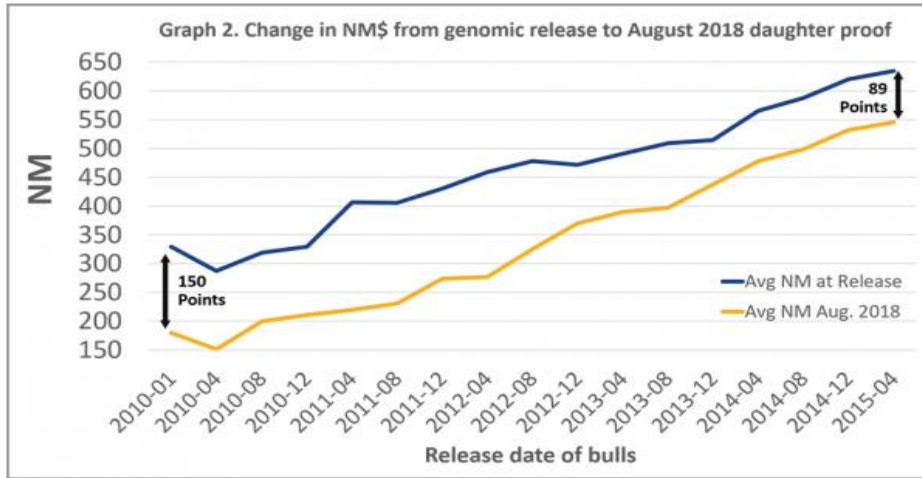
Ireland



# Challenges

- Exhaustion of sire genotype information
  - Inclusion of genotyped females in training populations
- Rate of generation turnover has increased dramatically
  - Candidate sires off grand-sires with no progeny information
  - Blending parentage average with genomic proof but now only a low reliability parental average
- Single-step evaluations & very large datasets and models
- **Genomic bias**

# United States



**HOARD'S DAIRYMAN**

NEWS  BUZZ  E-SOURCES  IN HOARD'S  BLOGS  YOUTH  BOOKSTORE  WEBINA

ome - All Articles - Features - Features - Bias remains a challenge for genomic evaluations

**FEATURES** May 25 2014 08:01 AM

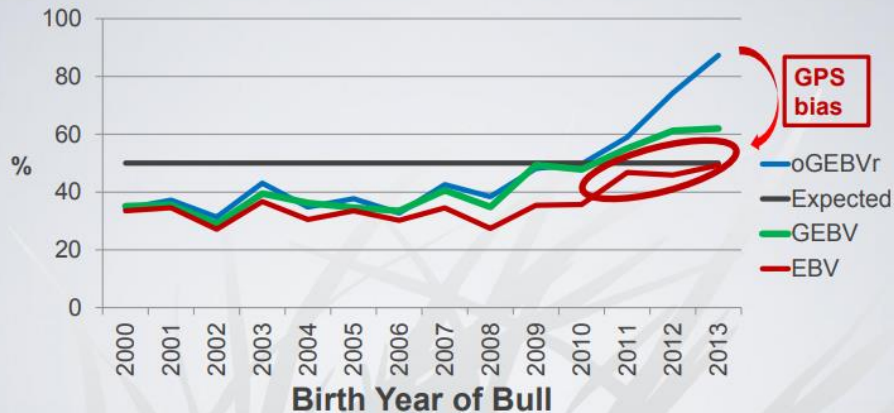
## Bias remains a challenge for genomic evaluations

BY CHAD DECHOW

# Global phenomenon

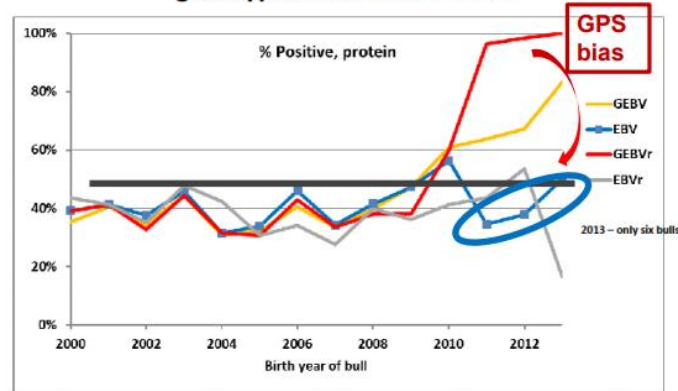


## %Positive MS: **Conformation** bull+sire+dam proven in **Canada**



## %Positive MS: **Protein** bull proven in **DFS**

RDC bull mendelian percentage  
genotyped bulls with  $r^2 > 0.79$



GEBV - from full data EBV - from full data  
GEBVr - from reduced data EBVr - from reduced data

# Global Research

*Genet. Res., Camb.* (2011), **93**, pp. 357–366. © Cambridge University Press 2011  
doi:10.1017/S001667231100022X

357

## Bias in genomic predictions for populations under selection

Z. G. VITEZICA<sup>1\*</sup>, I. AGUILAR<sup>2</sup>, I. MISZTAL<sup>3</sup> AND A. LEGARRA<sup>4</sup>

Patry and Ducrocq *Genetics Selection Evolution* 2011, **43**:30  
<http://www.gsejournal.org/content/43/1/30>

**GSE** Genetics  
Selection  
Evolution

RESEARCH

Open Access

## Accounting for genomic pre-selection in national BLUP evaluations in dairy cattle

Clotilde Patry<sup>1,2\*</sup> and Vincent Ducrocq<sup>1</sup>

## A Simple Method for Correcting the Bias Caused by Genomic Pre-Selection in Conventional Genetic Evaluation

Z. Liu, F. Seefried, F. Reinhardt and R. Reents  
*vit w.V., Heideweg 1, 27283 Verden, Germany*

Received: 13 July 2017 | Accepted: 22 January 2018

DOI: 10.1111/jbg.12318

ORIGINAL ARTICLE

WILEY Journal of Animal Breeding and Genetics

## Reducing bias in the dairy cattle single-step genomic evaluation by ignoring bulls without progeny

M. Koivula<sup>1</sup> | I. Strandén<sup>1</sup> | G.P. Aamand<sup>2</sup> | E.A. Mäntysaari<sup>1</sup>

# Potential sources of bias

1. Always was bias!
2. Selective genotyping of animals
  - What would happen if you only linear classified the good daughters of a bull?
3. Preferential treatment of females in the training population
4. Culmination of a little bias per generation but now over multiple generations before self-correction
  - 10 years ago 90% of the genotyped candidates had sires in the training population
  - Now only 12% of the young animals have sires in training pop



# So what are people doing?

- Minimising the bias
  - Simple subtraction of bias
  - Shrink estimates of genetic merit
    - By trait
    - By distance from training population

# Summary

- Genomics is making even traditional evaluations more precise
- Providing more information than just genomic EBIs
- Bias was always an issue
  - Adjustments made for milk traits since 2013
  - Countries are now applying a shrinkage factor