Animal genomics in breeding – opportunities and challenges

Donagh Berry

Teagasc, Moorepark
Captured opportunities

Genetic gain = Intensity of selection + Accuracy of selection + Genetic variability

- 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
Global phenomenon
Bias in genomic predictions for populations under selection

Z. G. Vitezica, I. Aguilar, I. Misztal, and A. Legarra

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

Clotilde Patry and Vincent Ducrocq

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

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

M. Koivula, I. Strandén, G.P. Aamand, and E.A. Mäntysaari
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