Reliable genomic evaluations across breeds and borders

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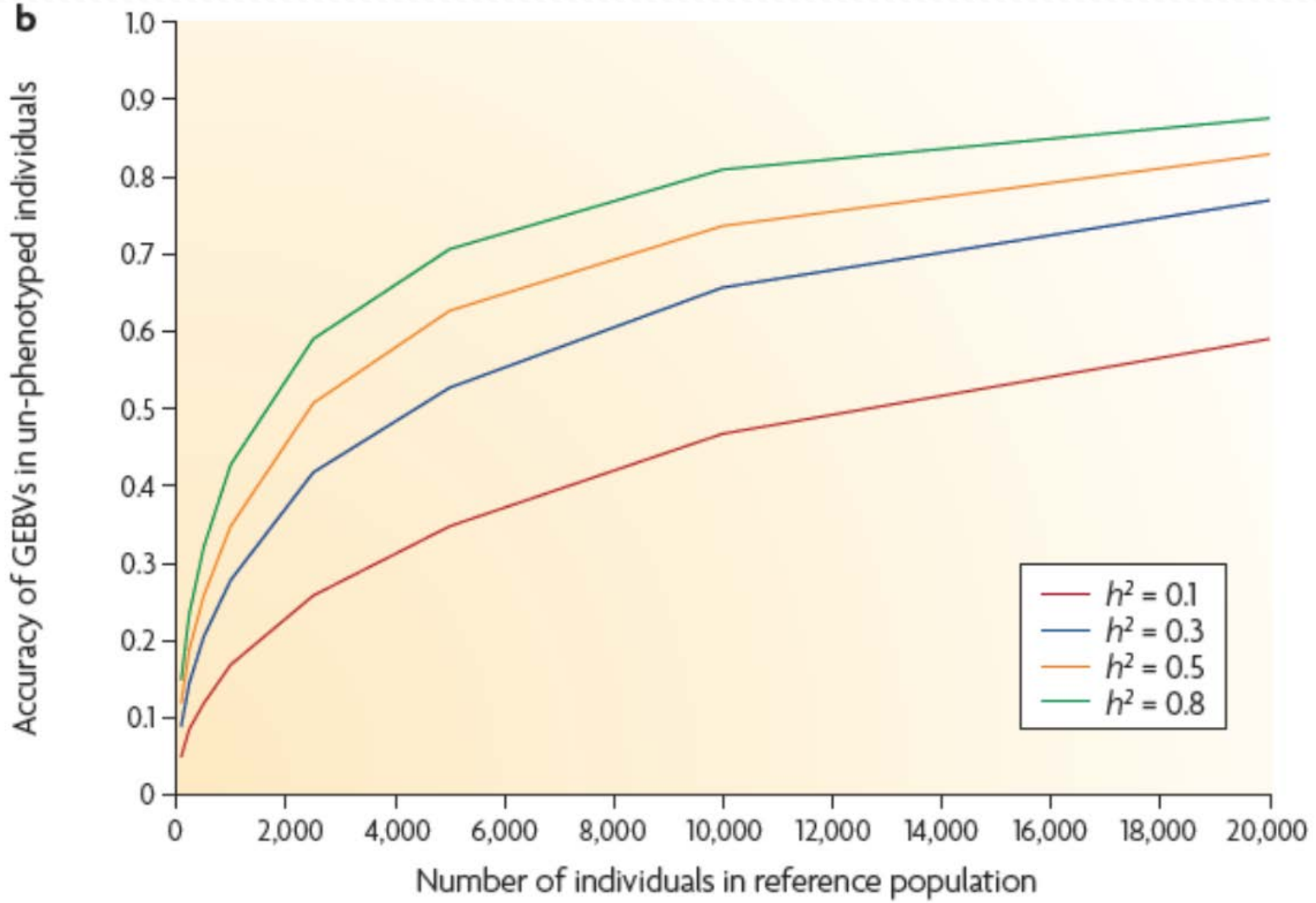
Reliable Genomic Estimated Breeding Values (GEBVs)

- We all want more reliable GEBVs
  - more accurate selection
  - use young bulls with confidence

- REL (GEBV) ~ N * h^2
  - N = size of reference population
  - h^2 = heritability of phenotypes

Daetwyler *et al.* 2008

Goddard 2009



Goddard & Hayes 2009

Reliable GEBVs

- International exchange
  - higher N
  - but h^2 is lower ($r_G < 1$)
- *e.g.* EuroGenomics (N = 4,000 $\rightarrow$ N = 16,000)
  - udder depth +15 % Reliability
  - somatic cell +11 %
  - fertility +7 %
  - protein yield +6 %

Lund *et al.* 2011

What else can we do?

- Cows
- Other breeds

- Aim = outline the opportunities & challenges

Why use cows?

- Increase reference (ref.) population
  - 100,000 ref. cows ≅ 24,000 ref. bulls ($h^2 = 0.2$)
- Unlimited numbers
- Small breeds
- New countries or environments (GxE)
- New traits
- Selection of females

Costs

- Cost for genotyping € 40
  - 100,000 cows x € 40 (BovineLD) = € 4,000,000

- Commercial value to farmer € 10 – 30
  - select best heifer calves
  - beef / conventional / sexed / flush
  - Highest Return On Investment (ROI) when selection intensity is high

De Roos 2011

Pryce & Hayes 2012

Dassonneville 2012

Bias

- GEBV = conventional EBV + genomic info
  - bias due to preferential treatment
  - bias due to selective genotyping

- Strategies
  - adjust cow phenotypes
  - omit cow phenotypes
  - use only complete herds

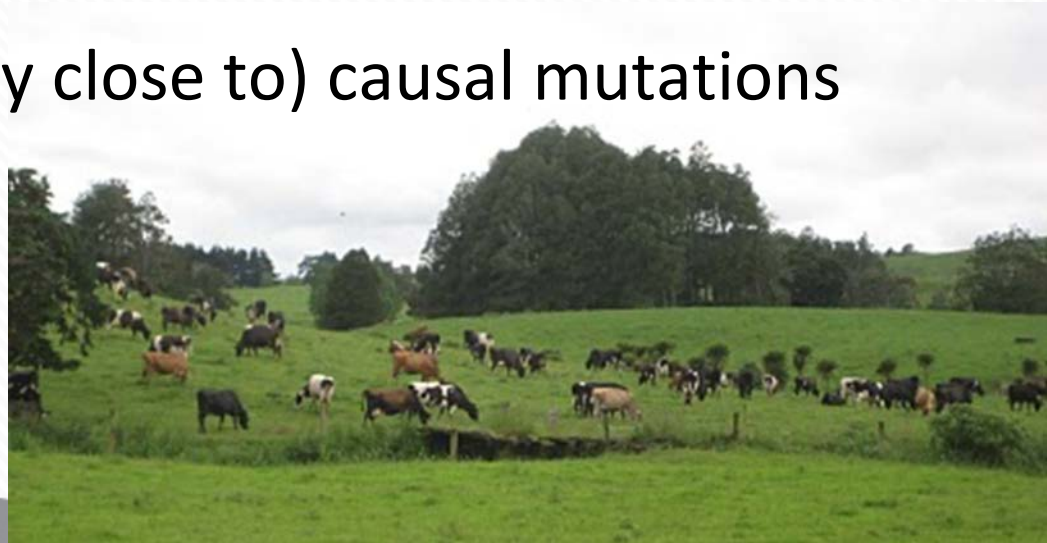
Wiggans *et al.* 2011; 2012

CRV reference herds

- Herds with excellent recording
  - milk production, conformation, fertility, …
  - claw health, milk composition, (health treatment)
- Genotype all females
  - farmer pays € 15 for calves, € 0 for cows
- Now : 20 herds, 4,000 females
- Aim : 600 herds, 120,000 females

Why use other breeds?

- Predict GEBVs of crossbreds
  - crossbreds exhibit more genetic variation
  - *e.g.* Holstein production + Jersey fertility
- Use crossbreds in ref. population
- Use breed A to improve GEBVs of breed B
  - exploiting (SNPs very close to) causal mutations



Crossbreds

- Crossbreds have large chromosome segments from purebred ancestors
  - SNPs trace inheritance across generations

Crossbreds

- Crossbreds have large chromosome segments from purebred ancestors
  - SNPs trace inheritance across generations
- Phenotypes of crossbreds are useful
  - estimate effect of ancestral chromosome segment
- GEBVs of crossbreds
  - sum of effects of ancestral chromosome segments

Use breed A to predict in breed B

- QTL must exist in both breeds
  - requires whole genome sequence, or
  - BovineHD (777K), for SNP-QTL phase to persist
- Individual QTL have very small effects
  - requires extremely large ref. population and Bayesian modeling to distinguish QTL from noise
- Maybe some medium QTL can be captured

Examples

- New Zealand Holstein & Jersey — Harris *et al.* 2011
  - accurate GEBVs for crossbreds
- Nordic Red Breeds — Brøndum *et al.* 2011
  - +7% Rel. multi-breed vs. single-breed
- Australian Holstein & Jersey — Erbe *et al.* 2012
  - +4% Rel. in Jersey by adding Holstein ref. bulls
  - +0% Rel. in Holstein by adding Jersey ref. bulls

Computation

- Assume 160,000 ref. animals, 777,000 SNPs
  - 8x more animals, 15x more SNPs = 120x more
  - 3 years computing
- Also consider imputation from LD to HD
- Also consider whole genome sequence

Conclusions

- Cows attractive to expand ref. population
  - higher rel., new traits, new breeds, new countries
  - costs still too high for large scale uptake
  - potential biases needs to addressed
- Multi-breed ref. population
  - straightforward in crossbred populations
  - many animals x dense SNPs in Bayesian modeling
  - computationally challenging