Genomic Selection in Dairy Cattle

Sander de Roos

Head Breeding & Support

EAAP Stavanger 2011

PhD thesis

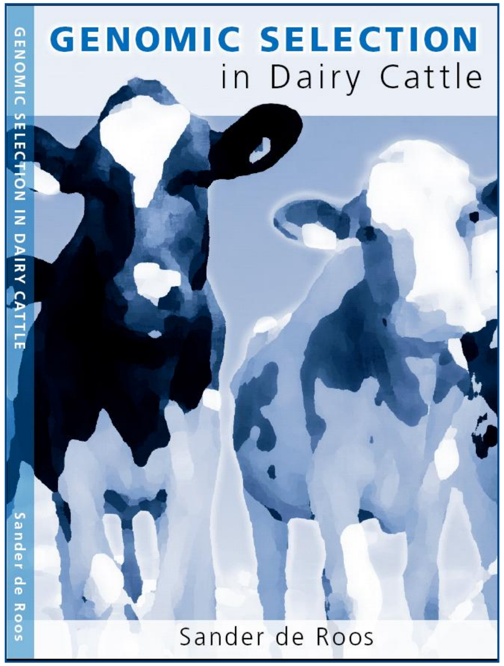
Models & reliabilities

High density & sequence

Cow reference populations

Multiple breed

Inbreeding



Genomic prediction models & reliability

Meuwissen *et al.* (2001)

- use genome-wide dense markers
- fit all markers simultaneously

$$\mathbf{y} = \mu + \Sigma_i \mathbf{X}_i \mathbf{g}_i + \mathbf{e}$$

RR-BLUP

- all markers have same variance

Bayesian

- many small, few large variance

Genomic prediction models & reliability

G-BLUP

$\mathbf{y} = \mu + \mathbf{u} + \mathbf{e}$

$\mathbf{u} \sim N(0, \mathbf{G}\sigma^2)$

G = genomic relationship matrix

- all markers evenly important
- similar genotype ⇒ similar EBV
- G-BLUP is equivalent to RR-BLUP

Genomic prediction models & reliability

Many small QTL → RR-BLUP, G-BLUP

Few large QTL → Bayesian (or similar)

RR-BLUP

- easy to implement, fast

G-BLUP

- allows integration of **G** and **A**

Bayesian

- higher reliability when QTL can be detected

Genomic prediction models & reliability

Reliability not same for everyone

RR-BLUP & G-BLUP

- many, close family in reference pop. $\Rightarrow$ higher r^2
- higher correlation with phenotypes
- large chromosome segments

Bayesian

- more robust
- markers in LD with QTL

Genomic prediction models & reliability

Bayesian > RR-BLUP & G-BLUP when enough power

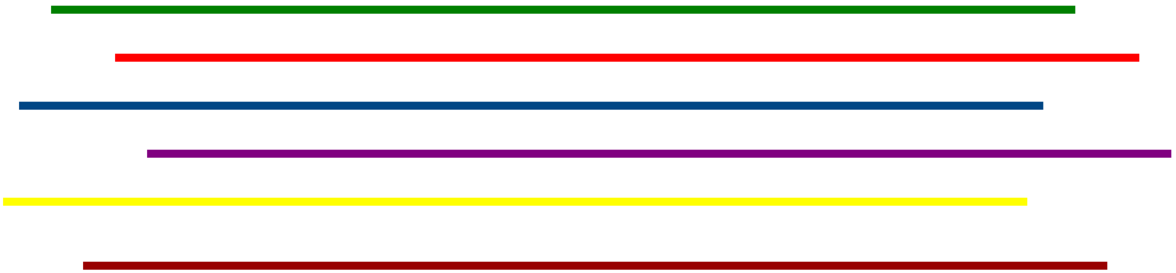
- very dense markers
- large Nh^2
- large QTL

More persistent genomic predictions

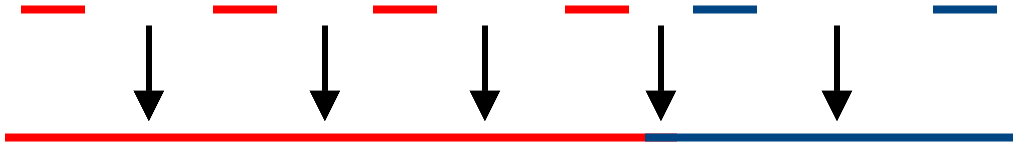
- across families
- across generations
- across breeds

High density SNP & genome sequence

HD genotyping / sequence only key ancestors:



Impute missing genotypes on others:



low density

high density

Cow reference populations

h^2 cow	h^2 bull	1 bull ~
0.10	0.72	7 cows
0.30	0.89	3 cows
0.50	0.93	2 cows

$r^2 \sim Nh^2$

Cow reference populations

h^2 cow	h^2 bull	1 bull ~
0.10	0.72	7 cows
0.30	0.89	3 cows
0.50	0.93	2 cows

- # bulls is limited
- lower h^2 so need large N
- genotyping gets cheaper
- novel traits
- direct value for farmer

Cow reference populations

What is value of a GEBV?

- genotype all heifer calves
- select best 50%

Break-even when genotyping < € 27

Genomic selection across breeds

Combine favourable traits

- e.g. Holstein production x Jersey fertility

Cross-breds have lot of variation

- detect best cross-breds using genomics

Combine reference populations

- increase reliability

Genomic selection across breeds

Relationships across breeds very weak

- RR-BLUP & G-BLUP don’t work

Marker - QTL phase may be reverse in other breed

LD persist across breeds only for pairs <10 kb

Genomic selection across breeds

May work if:

- $\geq$1 marker per 10 kb $\Rightarrow$ >300,000 markers
- use Bayesian method to capture marker - QTL LD
- large QTL and/or very large Nh^2

But, even then:

- different breeds, different QTL
- QTL effects may differ between breeds
- Nh^2 too small for most QTL

Waiting for results...

Inbreeding in genomic selection schemes

1. Select on GEBV (versus PA)
2. Reduce generation interval
   - double ΔG
   - same ΔF per generation
   - but ΔF per year almost tripled!

Inbreeding in genomic selection schemes

1. Select on GEBV (versus PA)
2. Reduce generation interval
   - double ΔG
   - same ΔF per generation
   - but ΔF per year almost tripled!

3. Restrict ΔF per year
   - almost double ΔG

Inbreeding in genomic selection schemes

Some inbreeding is OK

- selection of favourable QTL alleles

Currently, however

- selection of favourable, long haplotypes

Selected haplo's may include unfavourable QTL alleles

Unselected haplo's may include favourable QTL alleles

Need for applications that better capture QTL

Conclusions

RR-BLUP & G-BLUP work well

Future: capture individual QTL

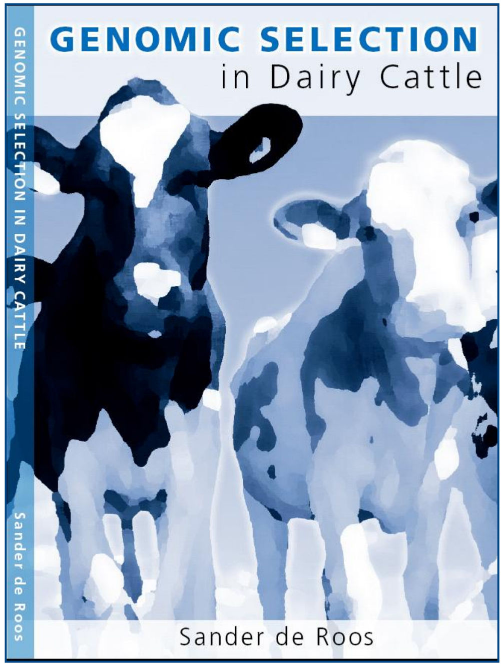
- persistent across generations, families, breeds
- multi-breed, very high density, very large Nh^2

Cow reference populations

- increase Nh^2, novel traits, direct value for farmer

ΔG may double, but ΔF needs attention

Thank you for your attention



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