

A decorative graphic consisting of a dark brown arrow pointing right, a light blue arrow pointing down, and a solid brown rectangle in the top right corner.

Across-breed genomic evaluation based on BovineHD genotypes, and phenotypes of bulls and cows

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Genomic evaluation New Zealand

- Currently, no national genomic evaluation
 - Performed in-house, by breeding organisations
 - CRV Ambreed, LIC
- Genomic evaluation CRV Ambreed
 - Started in 2007/2008
 - Using 50k SNP data
 - customCRV v1 and v2, BovineSNP50 v1 and v2
 - Single breed evaluations
 - Friesians
 - Jerseys

Reference populations CRV Ambreed

- Size by Feb. 2008 (protein):
 - Friesians: 1,050
 - Jerseys: 420
- Size by Dec. 2012 (protein):
 - Friesians: 2,350
 - Jerseys: 1,200
- Growth through
 - Yearly expansion: waiting bulls becoming daughter proven bulls
 - Exchange between CRV Ambreed and LIC
- Note: Eurogenomics reference population: > 25,000

How to increase size of reference?

- Multi-breed evaluation
 - Combine reference populations for Friesians, Jerseys and Crossbreds into one genomic evaluation
 - LD between SNP and mutations affecting the trait
 - Linkage phase the same in each breed
 - At least 300k SNP needed (de Roos et al, 2008)
 - Use BovineHD
- Expand reference population with cow phenotypes
 - Phenotypic info of cows is less reliable than phenotypic info of bulls
 - Therefore, relatively more cows are needed

Objective

to study the effect on the reliability of genomic ebv when combining single-breed reference populations into one multi-breed reference population, and using HD genotypes and cow genotypes and phenotypes

Material & Methods

- BovineHD (777k) genotypes
 - 463 Friesians
 - 229 Jerseys
 - 57 crossbreds
- Custom CRV 50K chip / BovineSNP50
 - 3,550 reference bulls
 - 4,500 cows, 10 herds
 - removed cows with pedigree inconsistencies
 - → approx. 3,600 cows left

Processing genotypes

- Imputation of 50k genotypes to BovineHD
 - approx. 623k SNP
 - Beagle 3.3
 - allelic imputation error rate dependent on chip and breed
 - 0.44% for Jersey, BovineSNP50 v2
 - 1.13% for Friesian, custom CRV chip v1
- Determine haplotype id based on Beagle output
 - at each BovineHD locus
- Select 1 out of 10 loci for further analyses
 - reduce computer requirements
 - omit redundant information

Validation study

- Subset of 7 traits in NZMI with moderate to high reliability
 - Prot., milk, livew., somatic cells, capacity, rump angle, udder
- Phenotype: deregressed proofs
 - of bulls
 - of cows, reliability of proof > threshold
 - # cows: 2,000 – 2,700
- weights: EDC
- youngest bull cohort considered as validation bulls
 - Friesians: 350
 - Jerseys: 160
 - Crossbred: 60
 - phenotype omitted from analyses
 - phenotype of their daughters omitted from analyses

Genomic evaluation model

- Estimation of GBV with Bayes SSVS (Calus et al, 2008)

$$y_i = \mu + u_i + \sum_j^n (q_{ij1} + q_{ij2})v_j + e_i$$

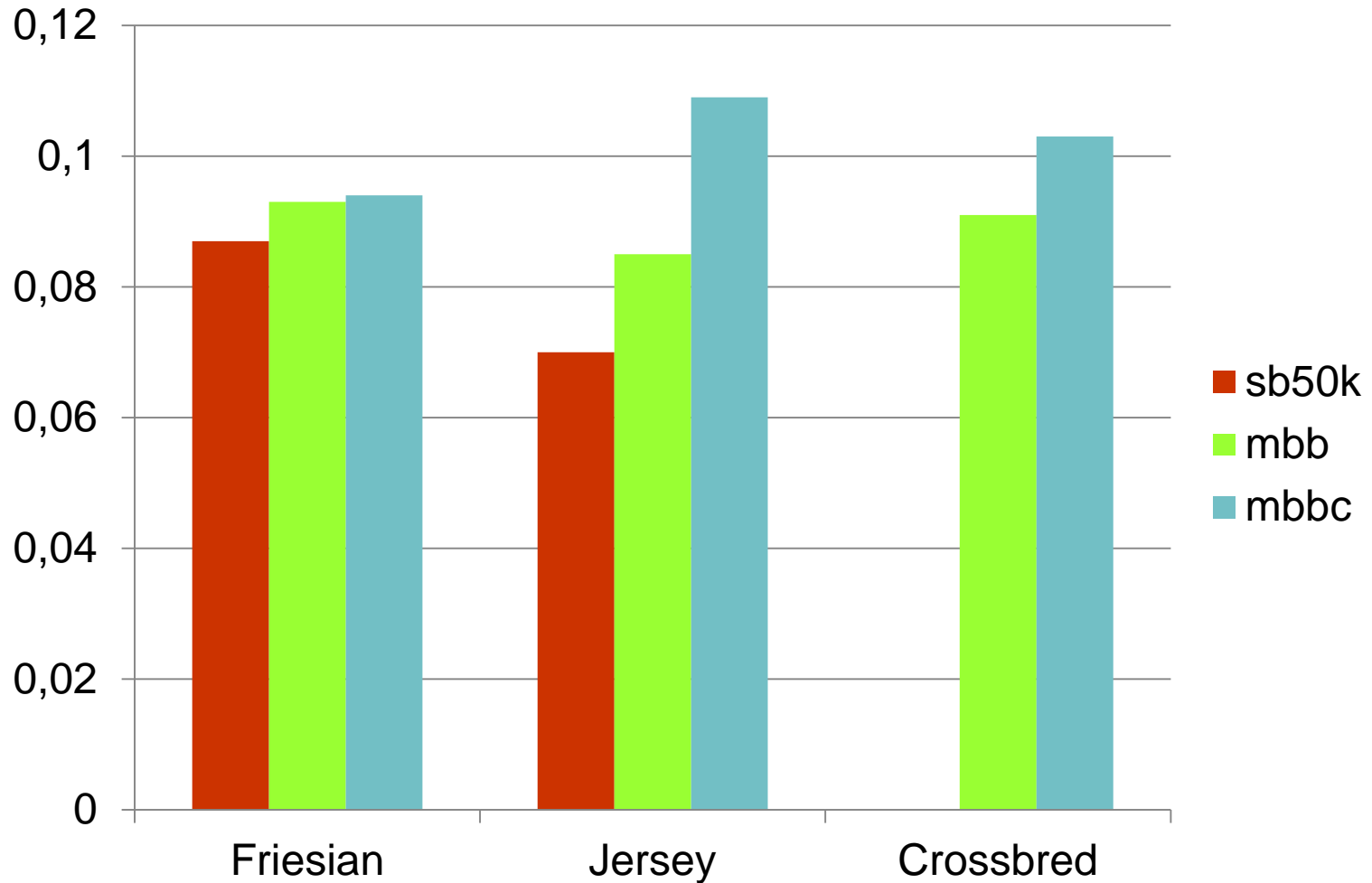
- where y_i : deregressed proof
 - μ : overall mean
 - u_i : random polygenic effect of animal i
 - $q_{ij1(2)}$: size of effect for haplotype 1 (2) of animal i at locus j
 - v_j : direction vector of effects at locus j
 - e_i : residual
- Separate runs on same data without genomic component: ➔ PBV
 - 4 replicates per trait

Validation

- Compare genomic (GBV) and polygenic breeding values (PBV) with daughter based phenotype (DRP)

$$\Delta R^2 = \frac{R_{GBV,DRP}^2 - R_{PBV,DRP}^2}{REL_{DRP}}$$

Results – average ΔR^2 across 7 traits



Results: ΔR^2 per trait per breed per ref. set

Trait	Friesian			Jersey			Crossbred	
	sb50k	mbb	mbbc	sb50k	mbb	mbbc	mbb	mbbc
Protein	.117	.104	.054	.047	.092	.070	.047	.122
Milk	.154	.158	.116	.204	.135	.070	.023	.098
Livew.	.035	.068	.078	.049	.116	.164	.075	.077
Som. Cells	.069	.024	.088	.051	.106	.185	.224	.125
Capac.	.095	.130	.103	.040	.036	.087		
Rump angle	.119	.108	.129	.013	.061	.112	.121	.111
Udder	.021	.062	.093	.084	.051	.072	.055	.085
Avg.	.087	.093	.094	.070	.085	.109	.091	.103

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Summary / implications

- Squared correlations between genomic prediction and daughter based breeding value increased by using HD-genotypes, cow phenotypes in addition to bull phenotypes, and multi-breed evaluation
- Increase in R^2 varied from 0.007 (Friesian) to 0.039 (Jersey)
 - R^2 did not increase for all trait-breed combinations
- No need for further HD-genotyping
- Recommendation
 - Make use of HD- and cow-info for traits for traits where it is beneficial
 - Genotype more females if genotyping cost are sufficiently low

Thank you for your attention

