



Experiences with genomic evaluation in numerically smaller breeds

Chris Schrooten - Breed4Food SEMINAR
12 July 2018

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CRV GS – Reference populations

Breed	Country	Start GS	# ref. bulls 2018
Holstein Friesian	NLD/FLA	2007	37,923
MRY	NLD	2016	444
Friesian	NZL	2008	3,199
Jersey	NZL	2008	1,851
Crossbred	NZL	2011	5,582
Fleckvieh	DEU/CZE	2012	~7,000
Nelore	BRA	2016	
Girolando	BRA	2016	

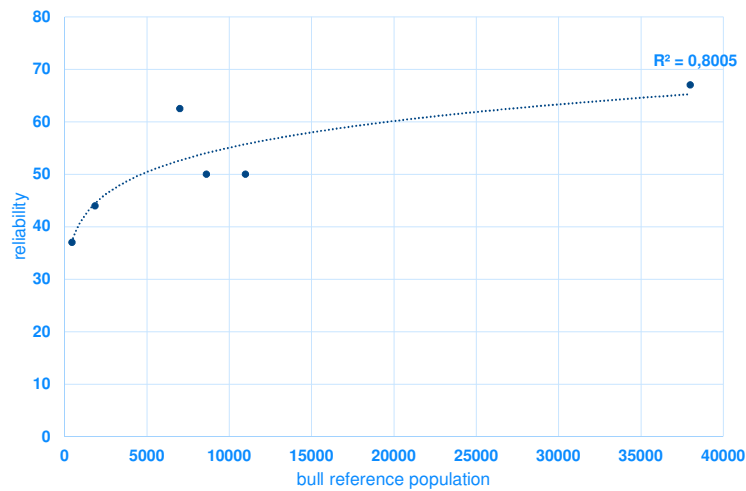
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CRV GS – Reliabilities

Breed	Country	Start GS	# ref. bulls 2018	rel. prod.
Holstein Friesian	NLD/FLA	2007	37,923	67
MRY	NLD	2016	444	37
Friesian	NZL	2008	8,599	50
Jersey	NZL	2008	1,851	44
Crossbred	NZL	2011	10,982	50
Fleckvieh	DEU/CZE	2012	7,000	62.5
Nelore	BRA	2016		
Girolando	BRA	2016		

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CRV GS – reliability vs. size of reference



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Factors affecting reliability of GS

- Size of the reference population
- Reliability of the phenotype
 - Heritability of the trait
 - Number of observations
 - Number of daughters
- Effective population size
- Evaluation model
- Method for calculating reliability

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GS in numerically small populations - implications

- Relatively low reliability, affects:
 - Genetic progress
 - Competitiveness of breed
 - Confidence of customers in GS bulls
 - Ability to provide management solutions based on genomic info
 - → Need solutions to increase reliability
- Difficult to determine reliability in a validation study
 - Correlate “realized” and predicted breeding value to estimate genomic reliability
 - Correlation affected by sampling due to (very) small validation set

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How to increase reliability?

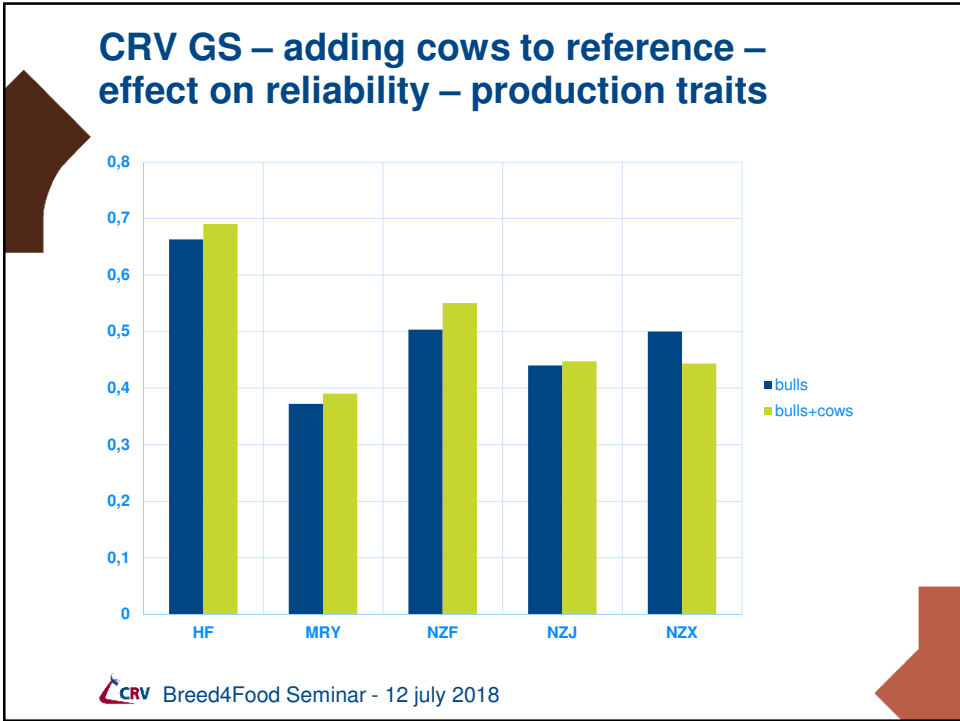
- Add cows
 - Phenotypes of cows have lower reliability compared to bulls
 - n cows contribute same information as 1 bull
 - n depends on trait, country, etc.
 - → Need many cows to significantly increase reliability
- Multi-breed genomic prediction
 - Combine reference populations of multiple breeds

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CRV GS – Add cows to reference pop.

Breed	Country	# ref. bulls	# ref cows
Holstein Friesian	NLD/FLA	37,923	110,535
MRY	NLD	444	2,041
NZ Friesian	NZL	8,599	10,496
NZ Jersey	NZL	1,851	3,056
NZ Crossbred	NZL	10,982	18,034
Fleckvieh	DEU/CZE	7,000	
Nelore	BRA		
Girolando	BRA		

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- ### How to increase reliability?
- Add cows
 - Phenotypes of cows have lower reliability
 - n cows contribute same information as 1 bull
 - n depends on trait, country, etc.
 - Multi-breed genomic prediction
 - Combine reference populations of multiple breeds / multiple countries
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Multi-breed GS – results CRV – DFCRC research project

- Research project 2012 – 2016
- Aimed at GS in Australia / New Zealand
- Partners: CRV and “Melbourne” group (Ben Hayes, Iona McLeod)
- Various combinations of reference populations

Val: NZF Training:	n_ref	Val: NZJ Training:	n_ref
NZF	2,257	NZJ	1,177
NZF+NZJ	3,440	NZJ+NZF	3,440
NZF+NZJ+NLAUF	10,785	NZJ+NZF+N LAUF	10,785

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CRV GS – combining breeds – effect on reliability – production traits



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CRV – DFCRC - conclusions

- Combining breeds can be beneficial but:
 - Benefit of adding breeds needs to be larger than negative effect of increasing effective population size
 - Model/method needs to handle across-breed effects and breed-specific effects in a proper way

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CRV GS – current situation

Breed	Cows in ref. pop.	Multi-breed
Holstein Friesian	April 2018	no
MRY	April 2018	no
NZ Friesian	Autumn 2018	no
NZ Jersey	Autumn 2018	no
NZ Crossbred	Autumn 2018	yes

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CRV – multi-breed GS research

- DairyBio – prolonged collaboration with “Melbourne” group
 - Further work on
 - Multi-breed models
 - Multi-breed / multi-country cow reference populations
- REDiverse
 - Horizon2020 funding
 - Biodiversity (and GS) in European Red Dairy breeds – MRY and many other breeds
- Breed4Food/STW: TOPBREED, GenoMIX