


Development of integrated livestock breeding and management strategies to improve animal health, product quality and performance in European organic and 'low input' milk, meat and egg production

Subproject 1: Dairy cattle


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Wageningen, 16 March 2011


 

WP 1.1: Genomic selection for low-input & organic dairy farms



- GEBVs for conventional traits under rural farming conditions
- GEBVs for novel traits of interest in low input/organic dairy farms
- Tailor-made tools for selection schemes in low input/organic dairy farms (e.g. wheat for organic bread):
 - ✓ no need of "mainstream" genetics
 - ✓ shorter generation interval
 - ✓ < data collection
 - ✓ selection for "difficult" traits





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Material



- ~ 1200 Swiss Brown cows in Switzerland are currently being genotyped and phenotyped
- HD SNP chips (~800,000 SNPs) for some of the cows
- routine and unconventional phenotypes



In the meanwhile ...



- 1142 Swiss Brown bulls from national breeding programme in Switzerland
- 54K chip SNP
- EBVs for milk yield (high h^2 , 0.33) and non-return rate (low h^2 , 0.09)

A number of approaches and methods for genomic selection are being tested

Methods



1. **GBLUP**: assumes constant variance for SNP effects

- **Genomic relationship matrix**: Astle & Balding (2009), never applied to animal genetics
- SNP regression for the estimation of SNP effects

2. **Bayes C**: allows variance to vary from marker to marker, many SNPs with no effect few with large effect (this proportion estimated from data)



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Objectives



- GBLUB (Astle & Balding) vs BayesC
- EBVs vs DRPs (Rozzi & Schaffer, 1996)
- High vs low h^2
- With vs without sex chromosomes

All comparisons with cross-validation



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Preliminary results: G-matrix



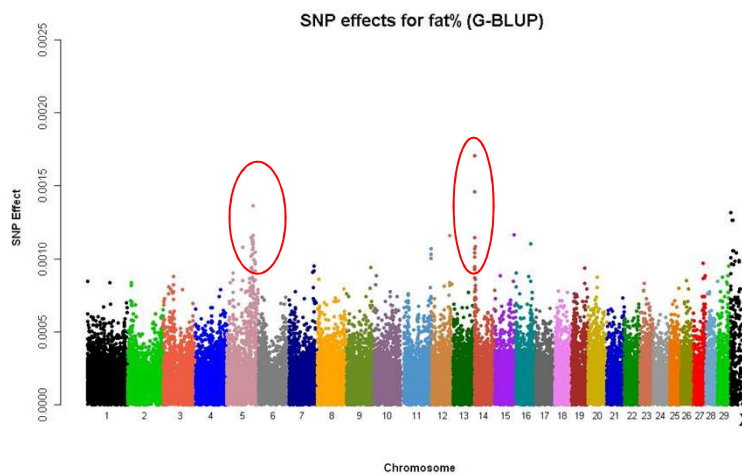
	Milk yield			NRR		
	Var(EBV)	Var(e)	logL	Var(EBV)	Var(e)	logL
Astle & Balding	171409	10997	-7218.55	57.58	3.58	-2706.86
Van Raden (1)	172279	13022	-7227.02	59.44	3.38	-2710.88
Eding & Meuwissen	195782	13018	-7227.92	60.21	3.50	-2709.76

Astle & Balding higher likelihood than other methods



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Preliminary results: SNP effects



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Preliminary results: accuracy of GEBVs



		GBLUP		BayesC		without X
Milk	<i>EBVs</i>	0.743	0.028	0.754	0.027	0.740
	<i>DRPRFs</i>	0.727	0.030	0.730	0.023	0.724
NRR	<i>EBVs</i>	0.726	0.031			0.726
	<i>DRPRFs</i>	0.650	0.038			0.657

- BayesC a bit better than GBLUP
- EBVs better than DRPs
- High h^2 better than low h^2
- No appreciable effect of markers on the sex chromosomes

Next steps



The results of the work on genomic selection in bulls will later be applied to the cows genotyped and phenotyped under the LIB project

- HD SNP chips
- New phenotypes: health traits, fertility traits etc ...
- Is genomic selection in low-input conditions different than in intensive farming?
- Is genomic selection a useful tool for low-input and organic farming?

WP 1.3: Breeding programme for low input & organic dairy cattle



Brown Swiss cattle (~1200 cows, ~36000 records)

low input farms in Switzerland (1.7 million hectares are grass: 1 million alpine pastures 0.7 million meadows and pastures)

Variance and covariance components

Heritabilities of production and reproduction traits

Genetic correlations between milk yields and other production traits

Genetic correlations between conception rates and corresponding test-day milk yields

Parameters needed to design breeding programmes for low input herds



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Available data




<i>Trait complex</i>	<i>Trait</i>	<i>No. records</i>	<i>Mean</i>	<i>SD</i>	<i>Min</i>	<i>Max</i>
Full Name	Abbreviation					
Production	Milk yield	MY (in kg)	33,799	22.25	6.59	1.6 53.2
	Fat%	Fat%	33,705	4.03	0.61	1.5 9.65
	Protein%	Pro%	33,713	3.43	0.35	2.23 5.82
	Lactose%	Lac%	33,713	4.83	0.2	2.11 5.55
	Somatic cell score	SCS	33,799	2.6	1.56	-3.64 9.64
	Milk urea nitrogen	MUN (in mg/dl)	33,710	24.68	8.55	5 90
Reproduction	Age at first calving	AFC (in d)	1388	939.49	100.68	700 1351
	Calving to 1 st service	CTFS (in d)	4486	69.95	28.30	6 320
	Days open	DO (in d)	4486	98.58	59.71	12 500
	Gestation length	GL (in d)	3466	290.30	5.93	242 300
	Calving interval	CI (in d)	3496	388.62	58.55	296 791
	No. insemination	NI	4484	1.68	1.09	1 11
	Calving ease	CE (scale 1-4)	4443	1.31	0.54	1 4
	Still-birth	SB (0 or 1)	4828	0.05	0.22	0 1
Correlation	Conception rates	CR (0 or 1)	3389	1.56	0.50	1 2
	Milk yield (cor)	MYc (in kg)	3389	23.0	4.75	6.0 41.8

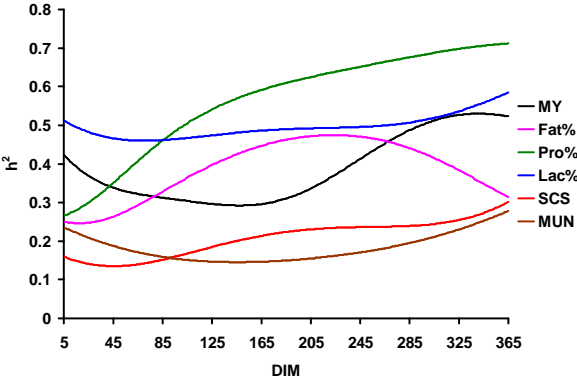


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Methods

- Random regression model
- Legendre polynomials
- E.g. h^2 production traits
- Something alike also for reproduction traits and genetic correlations





The graph plots heritability (h^2) on the y-axis (0 to 0.8) against DIM on the x-axis (5 to 365). The traits shown are MY (black), Fat% (magenta), Pro% (green), Lac% (blue), SCS (red), and MUN (brown). Pro% shows the highest heritability, increasing from ~0.25 to ~0.7. MY and Lac% show moderate heritability, peaking around 0.5. Fat% and SCS show lower heritability, around 0.3-0.4. MUN has the lowest heritability, around 0.1-0.2.


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Results


Apart from MUN, production traits have moderate to high heritabilities

	MY	Fat%	Pro%	Lac%	SCS	MUN
h^2 over DIM	0.39	0.39	0.56	0.50	0.21	0.18

Almost all fertility traits have low heritabilities

	CTFS	DO	CI	GL	NI	CE	SB
h^2 over Parity	0.05	0.03	0.02	0.21	0.04	0.07	0.14




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Discussion



- heritabilities in expected range (h^2 of production traits are higher than for reproduction traits)
- positive genetic correlation between MY and Fat% in earliest stage of lactation the mobilization of body fat reserves at the beginning of lactation
- negative genetic correlation between MY and SCS was found after DIM118 (also Jamrozik et al., 2010; Samore et al., 2008)
- positive genetic correlation between MY and MUN (more energy for milk and less to protein production \rightarrow $<$ protein \rightarrow $>$ MUN)
- negative genetic correlation (~ -0.7) between CR and MY (genetic selection for MY would probably lead to a decrease in CR)

Simulate daily observations of cows

Set up suitable breeding programs



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Hopefully ...



Low input breed project \neq low output project ☺



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The authors gratefully acknowledge co-funding from the European Commission, under the Seventh Framework Programme for Research and Technological Development, for the Collaborative Project LowInputBreeds (Grant agreement No 222623)

