

Genetic parameters for female fertility in Nordic dairy cattle

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Background



Nordic Cattle Genetic Evaluation

- Sweden, Finland and Denmark

The fertility model implemented in 2003 is under updating

- first update May 2015: from sire model to multi-lactation multi-trait animal model
- second update in 2016: revision of model effects and variance components

Updated VCE with correlations needed

Sampled data



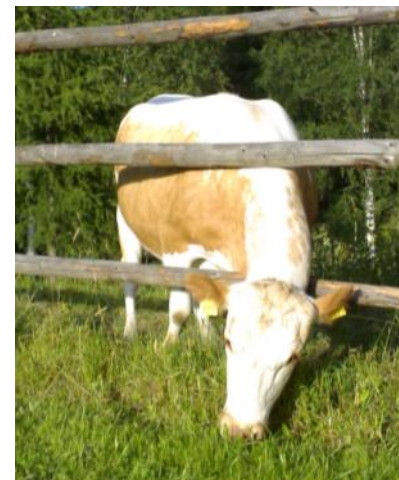
Holstein and **Nordic Red Dairy Cattle (RDC)**

400 herds in Sweden with minimum 12 (**8**) first-calvers / year

Years 1995 – 2011

	HOL	RDC
Females with records	144 392	103 653
Sires with daughters	14 111	10 397

Sampled data, traits



- 1. non-return rate in 56 days [0 or 100]**
NRR0, NRR1, NRR2, NRR3
(*heifers, 1st, 2nd and 3rd parity*)
- 2. interval from the first to the last service [days]**
IFL0, IFL1, IFL2, IFL3 (*per parity*)
- 3. interval from calving to the first service [days]**
ICF1, ICF2, ICF3 (*per parity*)

Models

Multivariate, multilactation sire model

- 11 traits; heifers + cows (1. – 3. parities)

Fixed effects:

- 1) herd*birth year (heifers) or herd*actual calving year (cows)
- 2) insemination year-month (for NRR and IFL) or actual calving year-month (for ICF)
- 3) heifers' first insemination age

EM-REML, MiX99

(MiX99 Development Team, 2015, Luke, <http://www.luke.fi/mix99>;
Matilainen, Mäntysaari, Lidauer, Strandén & Thompson, 2012)

Results (1): heritabilities



Holstein: h²

	NRR0	IFL0	NRR1	ICF1	IFL1	NRR2	ICF2	IFL2	NRR3	ICF3	IFL3
NRR0	0.007	-0.75	0.74	0.10	-0.30	0.68	0.10	-0.21	0.44	0.14	-0.27
IFL0	-0.44	0.011	-0.57	0.15	0.47	-0.4	NRR: 0.01				
NRR1	0.02	-0.01	0.012	0.29	-0.52	0.8	IFL: 0.01 - 0.04				
ICF1	0.01	0.01	0.03	0.056	0.50	0.3	ICF: 0.06 - 0.07				
IFL1	-0.02	0.03	-0.30	0.00	0.038	-0.39	0.64	0.97	-0.29	0.65	0.93
NRR2	0.01	-0.01	0.03	0.02	-0.01	0.012	0.29	-0.40	0.87	0.31	-0.39
ICF2	0.01	0.01	0.01	0.13	0.09	0.04	0.058	0.61	0.40	0.96	0.61
IFL2	-0.01	0.03	-0.04	0.04	0.09	-0.29	-0.01	0.041	-0.30	0.64	0.91
NRR3	0.01	0.00	0.03	0.03	-0.02	0.03	0.02	-0.01	0.013	0.42	-0.35
ICF3	0.00	0.02	0.00	0.09	0.06	0.02	0.15	0.09	0.05	0.068	0.63
IFL3	-0.02	0.03	-0.03	0.04	0.08	-0.03	0.05	0.10	-0.29	-0.02	0.044

RDC: h^2

	NRR0	IFL0	NRR1	ICF1	IFL1	NRR2	ICF2	IFL2	NRR3	ICF3	IFL3
NRR0	0.008	-0.90	0.52	0.18	-0.29	0.23	0.02	-0.06	0.51	0.14	-0.42
IFL0	-0.50	0.014	-0.48	0.06	0.51	-0.01	0.02	0.02	0.51	0.14	-0.42
NRR1	0.02	-0.01	0.010	0.15	-0.58	0.7	0.02	0.02	0.51	0.14	-0.42
ICF1	0.02	-0.01	0.03	0.049	0.55	0.1	0.02	0.02	0.51	0.14	-0.42
IFL1	-0.02	0.03	-0.35	-0.01	0.022	-0.55	0.62	0.88	-0.67	0.66	0.91
NRR2	0.01	-0.02	0.02	0.02	-0.02	0.007	-0.05	-0.56	0.57	-0.14	-0.45
ICF2	0.01	0.00	0.01	0.10	0.05	0.05	0.026	0.66	-0.17	0.86	0.54
IFL2	-0.01	0.02	-0.03	0.03	0.06	-0.35	-0.03	0.032	-0.46	0.81	0.86
NRR3	0.01	-0.01	0.02	0.00	-0.02	0.03	0.02	-0.03	0.008	-0.13	-0.66
ICF3	0.00	0.02	0.00	0.09	0.06	0.02	0.15	0.09	0.05	0.034	0.63
IFL3	-0.01	0.02	-0.03	0.04	0.06	-0.04	0.04	0.10	-0.34	-0.03	0.042

NRR: 0.01

IFL: 0.01 - 0.04

ICF: 0.03 - 0.05

Results (2): Genetic correlations within traits

Within traits genetic correlations ranged from moderate to high across the different parities



Holstein: h^2 diagonal, r_g upper triangle, r_p lower triangle

	NRR0	IFL0	NRR1	ICF1	IFL1	NRR2	ICF2	IFL2	NRR3	ICF3	IFL3
NRR0	0.01	-0.75	0.74	0.10	-0.30	0.68	0.10	-0.21	0.44	0.14	-0.27
IFL0	-0.44	0.01	-0.57	0.15	0.47	-0.54	0.05	0.40	-0.36	0.04	0.43
NRR1	0.02	-0.01	0.01	0.29	-0.52	0.88	0.19	-0.48	0.78	0.19	-0.48
ICF1	0.01	0.01	0.03	0.06	0.50	0.38	0.91	0.44	0.48	0.87	0.45
IFL1	-0.02	0.03	-0.30	0.00	0.04	-0.39	0.64	0.97	-0.29	0.65	0.93
NRR2	0.01	-0.01	0.03	0.02	-0.01	0.01	0.29	-0.40	0.87	0.31	-0.39
ICF2	0.01	0.01	0.01	0.13	0.09	0.04	0.06	0.61	0.40	0.96	0.61
IFL2	-0.01	0.03	-0.04	0.04	0.09	-0.29	-0.01	0.04	-0.30	0.64	0.91
NRR3	0.01	0.00	0.03	0.03	-0.02	0.03	0.02	-0.01	0.01	0.42	-0.35
ICF3	0.00	0.02	0.00	0.09	0.06	0.02	0.15	0.09	0.05	0.07	0.63
IFL3	-0.02	0.03	-0.03	0.04	0.08	-0.03	0.05	0.10	-0.29	-0.02	0.04

Non-return rate, genetic correlations across parities in Holstein

	NRR1	NRR2	NRR3
NRR0	0.74	0.68	0.44
NRR1		0.88	0.78
NRR2			0.87

In **RDC** the correlations ranged between 0.23 – 0.76

Interval from first to last service, genetic correlations across parities in Holstein

	IFL1	IFL2	IFL3
IFL0	0.47	0.40	0.43
IFL1		0.97	0.93
IFL2			0.91

In **RDC** the correlations ranged between 0.33 – 0.91

Interval from calving to the first service, genetic correlations across parities in Holstein

	ICF2	ICF3
ICF1	0.91	0.87
ICF2		0.96

In **RDC** the correlations ranged between 0.86 – 0.88

Results (3): Genetic correlations between the traits

Between traits correlations ranged widely;
the highest values were estimated within lactations



Genetic correlations between traits in Holstein

	IFLO	NRR1	IFL1	ICF1
NRR0	-0.75	0.74	-0.30	0.10
IFLO		-0.57	0.47	0.15
NRR1			-0.52	0.29
IFL1				0.50

NRR and IFL in heifers had a stronger correlation than NRR0 and IFL in later parities

Genetic correlations between traits in Holstein

	IFLO	NRR1	IFL1	ICF1
NRR0	-0.75	0.74	-0.30	0.10
IFLO		-0.57	0.47	0.15
NRR1			-0.52	0.29
IFL1				0.50

Unfavorable correlation between NRR and ICF

Genetic correlations between traits in Holstein

	IFLO	NRR1	IFL1	ICF1
NRR0	-0.75	0.74	-0.30	0.10
IFLO		-0.57	0.47	0.15
NRR1			-0.52	0.29
IFL1				0.50

Positive correlations between interval traits

Genetic correlations between traits in Holstein

	IFLO	NRR1	IFL1	ICF1
NRR0	-0.75	0.74	-0.30	0.10
IFLO		-0.57	0.47	0.15
NRR1			-0.52	0.29
IFL1				0.50

In **RDC** the differences compared to HOL spanned from 3 to 20 % in NRR and in IFL ; and in ICF1 from 10 to 80 %

Results (4): Phenotypic correlations

Estimated phenotypic correlations were low as expected

exception: NRR and IFL had a moderate negative correlation within parities



Holstein: phenotypic correlations (h^2 on diagonal)

	NRR0	IFL0	NRR1	ICF1	IFL1	NRR2	ICF2	IFL2	NRR3	ICF3	IFL3
NRR0	0.01	-0.75	0.74	0.10	-0.30	0.68	0.10	-0.21	0.44	0.14	-0.27
IFL0	-0.44	0.01	-0.57	0.15	0.47	-0.54	0.05	0.40	-0.36	0.04	0.43
NRR1	0.02	-0.01	0.01	0.29	-0.52	0.88	0.19	-0.48	0.78	0.19	-0.48
ICF1	0.01	0.01	0.03	0.06	0.50	0.38	0.91	0.44	0.48	0.87	0.45
IFL1	-0.02	0.03	-0.30	0.00	0.04	-0.39	0.64	0.97	-0.29	0.65	0.93
NRR2	0.01	-0.01	0.03	0.02	-0.01	0.01	0.29	-0.40	0.87	0.31	-0.39
ICF2	0.01	0.01	0.01	0.13	0.09	0.04	0.06	0.61	0.40	0.96	0.61
IFL2	-0.01	0.03	-0.04	0.04	0.09	-0.29	-0.01	0.04	-0.30	0.64	0.91
NRR3	0.01	0.00	0.03	0.03	-0.02	0.03	0.02	-0.01	0.01	0.42	-0.35
ICF3	0.00	0.02	0.00	0.09	0.06	0.02	0.15	0.09	0.05	0.07	0.63
IFL3	-0.02	0.03	-0.03	0.04	0.08	-0.03	0.05	0.10	-0.29	-0.02	0.04

Conclusions



Heritability estimates were low

- lowest for NRR (~ 0.01)
- highest for ICF in HOL (0.06 – 0.07)
- between breed largest difference in heritability was found for ICF

Genetic correlation estimates ranged from moderate to high within traits (across parities)

-> parities should be modelled as different traits

Between different traits the genetic correlations were moderate

Correlation structure similar between HOL and RDC

The VC can be used for the fertility traits

21 in the updated model

Thank you for your time!



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