

Random Heterosis and Recombination Loss Effects in a Multibreed Evaluation for Nordic Red Dairy Cattle

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Introduction

- ◆ **Nordic red breed evaluation for yield traits**
 - multibreed evaluation across Denmark, Finland and Sweden
 - each country's population is considered as different breed
 - **countries are linked by crossbred animals**
 - multiple trait random regression meta-model
 - each country is considered as a different trait
 - genetic correlation across countries is set to 1.0

- ◆ **Reliable estimates for heterosis and recombination loss are important**
 - otherwise: → **bias in EBVs and genetic levels of the countries**

Aim

**Modelling of heterosis and recombination loss
when crossbreeding information is weak
for some important crosses**

◆ **Heterosis**

favourable gene effect in a crossbred offspring due to dominance

◆ **Recombination loss**

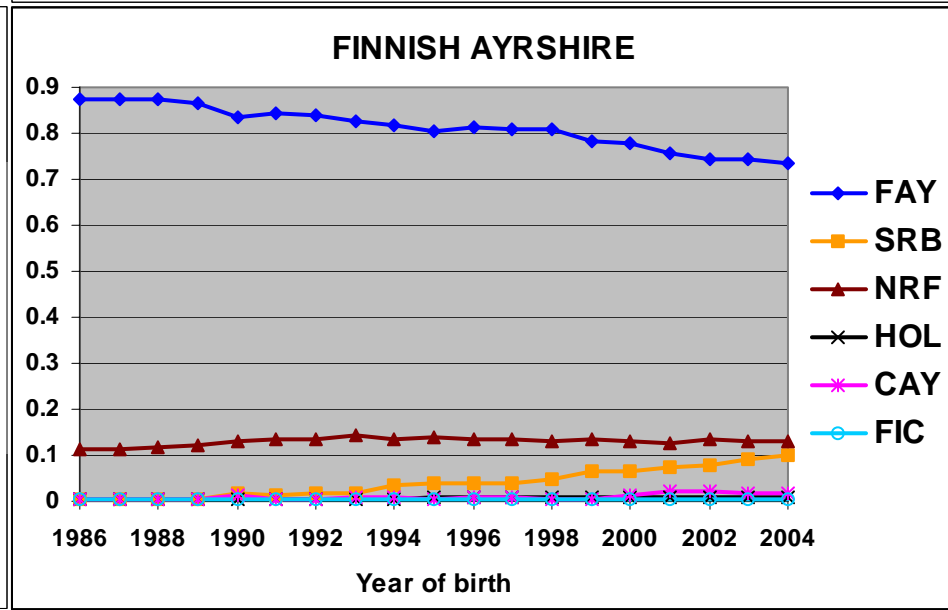
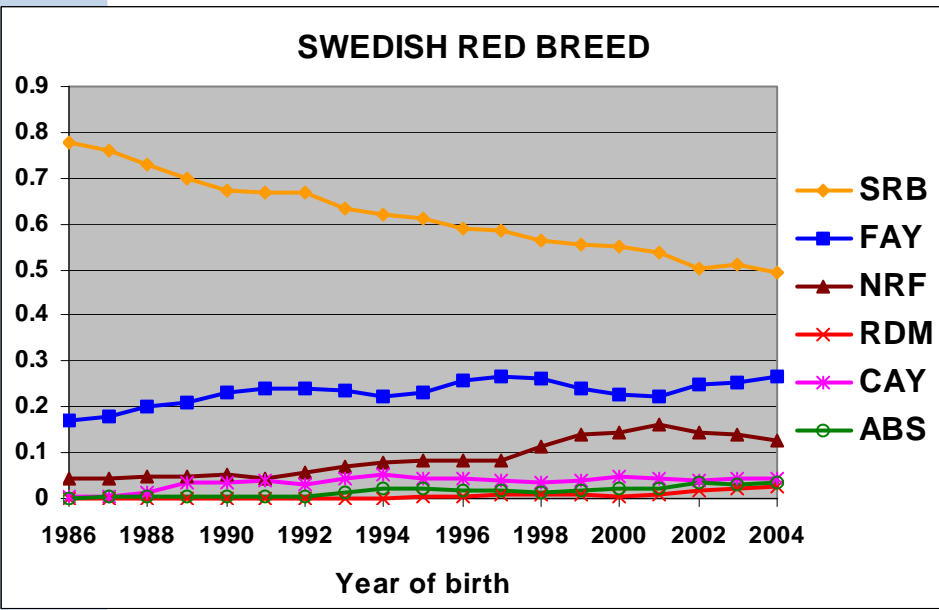
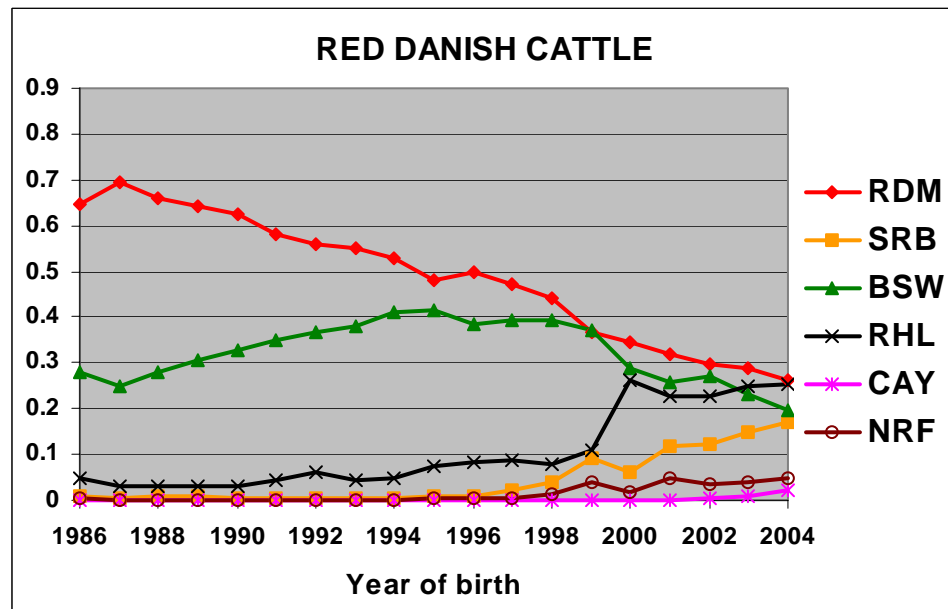
unfavourable gene effect in crossbreds due to the breakdown of parental epistatic gene complex

Breeds

Number of animals by breed of sire given for the three main breeds

Breed of sire	Red Danish Cattle		Finnish Ayrshire		Swedish Red Breed	
	Bulls	Cows	Bulls	Cows	Bulls	Cows
Red Danish Cattle	3,435	444,355	0	2	119	4,732
Finnish Ayrshire	23	406	8,982	1,502,803	445	19,703
Swedish Red Breeds	251	17,851	532	17,396	6,544	1,134,556
Norwegian Red Cattle	54	360	199	857	444	8,048
Canadian Ayrshire	0	198	47	1,393	70	5,031
(Red) Holstein	233	3,836	13	1,472	3	128
Brown Swiss	1,009	14,804	0	0	0	0

Change in breed shares over time



◆ Heterosis

favourable gene effect in crossbred offspring

$$h_{AB}^k = p_A^s p_B^d + p_B^s p_A^d$$

◆ Recombination loss

unfavourable gene effect due to the breakdown of parental epistatic gene complex

$$r_{AB}^k = (p_A^s + p_A^d)(p_B^s + p_B^d) - h_{AB}^k$$

Cross	h^k	r^k
1.0 A x 1.0 B (F1)	1.0	0.0
0.5 A, 0.5 B x 0.5 A 0.5 B (F2)	0.5	0.5
0.25 A, 0.25 B, 0.5 C x 0.5 D	1.0	0.3

Breed combinations

Breeds with significant gene contributions by country

	Denmark	Finland	Sweden
Main breed	RDM	FAY	SRB
Other breeds	SRB, FAY, BSW, NRF, RHL, JER, BBR	SRB, NRF, CAY, FBW, FIC	FAY, RDM, NRF, CAY, RHL, BSW
Breed combinations	28	15	21

◆ Challenge

- for some crosses crossbreeding information is too little
- co-linearity between genetic groups and heterozygosity in cows
- differences in the magnitude of the different crossbreeding effects
- **unreliable estimates would cause biased EBVs**

Modelling of heterosis

- ◆ **A mean heterosis effect**
 - fixed regression on total heterozygosity
 - modelled across countries
 - covariables are scaled by 1/100 of the phenotypic mean
- ◆ **Country-specific random heterosis effects**
 - random regression on specific heterozygosity
 - for each of the 5 most important crosses within each country
 - variance: 1.0 → SD of estimates \cong 1% of phenotypic mean
- ◆ **Correlations between same heterosis effects across countries**
 - $r=0.95$

Heterosis effects in the Nordic model

Finnish traits:

$$y_{tf} = \dots + c_{TOTf} h_t + c_{FAY \times SRBt} h_{1tf} + c_{FAY \times NRFt} h_{2tf} + c_{SRB \times NRFt} h_{3tf} + c_{FAY \times CAYt} h_{4tf} + c_{FAY \times FBWt} h_{5tf} + \dots$$

Swedish traits:

$$y_{ts} = \dots + c_{TOTs} h_t + c_{SRB \times FAYt} h_{1ts} + c_{FAY \times NRFt} h_{2ts} + c_{SRB \times NRFt} h_{3ts} + c_{SRB \times CAYt} h_{4ts} + c_{SRB \times RDMt} h_{5ts} + \dots$$

Danish traits:

$$y_{td} = \dots + c_{TOTd} h_t + c_{RDM \times SRBt} h_{1td} + c_{BSW \times SRBt} h_{2td} + c_{RDM \times BSWt} h_{3td} + c_{RDM \times RHLt} h_{4td} + c_{BSW \times RHLt} h_{5td} + \dots$$

covariables are scaled by 1/100 of the phenotypic mean of the trait

$$\text{var}(h) = 1.0$$

$$r_{(h1tf, h1ts)} = r_{(h2tf, h2ts)} = r_{(h3tf, h3ts)} = r_{(h1td, h5ts)} = r_{(h2td, h5ts)} = 0.95$$

Recombination loss is modelled the same way as heterosis

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Applications

- ◆ **Joint Nordic test-day model for red breeds**
 - 27 traits (milk, protein, fat x 3 lactation x 3 countries)
 - 3.9 million animals
 - 46 million records (TD and 305d yields)

- ◆ **Control run (USUAL WAY)**
 - all heterosis and recombination loss effects were fixed
 - no crossbreeding effect was modelled across traits

Results

Sample of estimates for difficult estimable crossbreeding effects
(in % of phenotypic mean)

Effect	Cross	Trait	Model	
			RANDOM	USUAL WAY
Heterosis	BSWxRHL	3 rd lact. milk, DNK	6.2	11.9
Heterosis	NRFxFAY	1 st lact. fat, SWE	1.3	6.9
Recomb. loss	SRBxNRF	2 nd lact. milk, FIN	-4.7	-16.7
Recomb. loss	FAYxSRB	3 rd lact. fat, FIN	-3.3	-8.5

RANDOM: fixed crossbreeding effect across countries; random crossbreeding effects within countries
USUAL WAY: all crossbreeding effects fixed

Results

Heterosis estimates for crosses in Denmark, Sweden and Finland for 1st lactation protein yield (in % of phenotypic mean)

Crosses	RANDOM			USUAL WAY		
	Danish cows	Swedish cows	Finnish cows	Danish cows	Swedish cows	Finnish cows
RDMxSRB	6.2	6.7		6.1	7.4	
BSWxSRB	6.4	6.7		8.9	7.4	
FAYxSRB		2.3	2.4		2.6	3.3
FAYxNRF		0.7	0.8		8.0	-1.0
SRBxNRF		2.8	2.7		6.0	5.3

RANDOM: fixed crossbreeding effect across countries; random crossbreeding effects within countries

USUAL WAY: all crossbreeding effects fixed

Results

Recombination loss estimates for crosses in Denmark, Sweden and Finland for 1st lactation protein yield (in % of phenotypic mean)

Crosses	RANDOM			USUAL WAY		
	Danish cows	Swedish cows	Finnish cows	Danish cows	Swedish cows	Finnish cows
RDMxSRB	-2.3	-2.4		-1.8	-1.9	
BSWxSRB	-2.5	-2.4		-2.8	-1.9	
FAYxSRB		-2.6	-1.9		-1.5	-3.4
FAYxNRF		-4.3	-4.5		-7.5	-2.9
SRBxNRF		-3.1	-3.2		-8.5	-12.7

RANDOM: fixed crossbreeding effect across countries; random crossbreeding effects within countries

USUAL WAY: all crossbreeding effects fixed

Effect on estimated breeding values

(modelling crossbreeding effects as random)

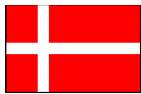
- ◆ **genetic level of Red Danish Cattle increased**
- ◆ **genetic level of Finnish Ayrshire decreased**
- ◆ **significant re-ranking in top bulls and cows**
 - share of Danish top bulls increased from 17% up to 22%
 - share of Finnish top bulls decreased from 59% down to 54%
 - share of Swedish top bulls remained the same

Conclusion

Modelling crossbreeding effects as random

- ◆ regressed unreliable estimates towards mean estimates
- ◆ allowed differences in the magnitude of crossbreeding estimates for different crosses
- ◆ ensured that crossbreeding effects did not harm genetic levels of the countries

Acknowledgement



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NAV

Nordic Cattle Genetic Evaluation