Combining test day SCS with clinical mastitis and udder type traits: RR model for joint genetic evaluation of udder health in Denmark, Finland and Sweden

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Nordic Cattle Genetic Evaluation

37th ICAR Session and Interbull Open Meeting, 31st May – 4th June, 2010, Riga, Latvia

Introduction

- **Udder health**
  - Economic efficiency of dairy production
  - Important trait in the Nordic dairy genetic evaluation

- **In 2006 - Denmark, Finland and Sweden**
  - Implemented a joint genetic evaluation (Johansson et al. 2006)
  - Nordic Cattle Genetic Evaluation (NCGE)
    - Runs the joint genetic evaluation

Introduction

- **Currently used model**
  - Multi-trait sire model based on lactation records:
    - Available TDSCS information is only utilized through SCS lactation averages
    - Only proofs for sires can be calculated

- **A multi-trait random regression model – needed**
    - Combines TDSCS with CM & udder type traits
    - Harmonizes models used across countries
      - **Needs estimation of genetic and phenotypic associations**

Objectives

- Estimate genetic & phenotypic associations between longitudinal TDSCS and CM and udder health traits, in first three lactations and

- Develop a random regression animal model for joint genetic evaluation of udder health in Denmark, Finland and Sweden

I

Variance components

Estimation of variance components

- Traits

TDSCS1	($\log_e$SCC) from monthly TD in 1000cells/ml 1st Lact.
TDSCS2	($\log_e$SCC) from monthly TD in 1000cells/ml 2nd Lact.
TDSCS3	($\log_e$SCC) from monthly TD in 1000cells/ml 3rd Lact.
CM11	Observation on mastitis 15 d before to 50 d after 1st calving
CM12	Observation on mastitis from 51 d to 300 d after 1st calving
CM2	Observation on mastitis 15 d before to 150 d after 2nd calving
CM3	Observation on mastitis 15 d before to 150 d after 3rd calving
UA	Fore udder attachment
UD	Udder depth

Estimation of variance components

- Data

No. animals	**25,562**
Cows with observations	**17,525**
Herds, no.	**50**
Mean test-day SCS, ($\log_e$ 1000cells/ml)	**4.41, 4.80, 5.03**[†]
Freq. of mastitis (%)	**13.0; 12.0; 21.0; 26.0%**[†]
Mean of udder type traits	**5.8; 6.3**
Records, no. - TDSCS	**158,711; 105,257; 56,021**[†]
- CM traits	**16,129; 16,093; 10,548; 8,732**[†]
- UA & UD	**10,305; 10,293**
Records, no. (Total)	**352,989**

[†] **In 1st, 2nd and 3rd lactations, respectively.**

Estimation of variance components

Model

$$\mathbf{y} = \mathbf{Xb} + \mathbf{H}_h\mathbf{h} + \mathbf{K}_k\mathbf{k} + \mathbf{Z}_\mathrm{a}\mathbf{a} + \mathbf{Z}_\mathrm{p}\mathbf{p} + \mathbf{e}$$

Where :

- **y** is a vector with observations on the nine different traits
- Vectors **b, h, k** contain the environmental effects
- vectors **a** and **p** contain additive genetic and non-genetic animal regression coefficients, respectively.
- Both additive genetic and non-genetic animal effects were modeled by a second order Legendre polynomial for TDSCS and intercept for the other traits leading to a 15×15 (co)variance matrix for each effect to be estimated.

$$\phi_\alpha(d) = [\mathrm{c}_0 \;\; \mathrm{c}_1 \; \mathrm{c}_2\,]^\mathrm{T},$$

- Lactation curve for TDSCS $\phi_\pi(d) = [\mathrm{c}_0 \;\; \mathrm{c}_1 \; \mathrm{c}_2 \;\; \mathrm{c}_3 \; \exp(wd)]^\mathrm{T},$

- Vector **e** contains residuals of the 9 traits.

Estimated heritabilities (diagonal), genetic (below diagonal) and phenotypic correlations (above diagonal) for CM, udder type traits and for selected days in milk of test-day SCS by mt-RRM for Danish Holstein

	TDSCS1					**TDSCS2**					**TDSCS3**										
DIM	30	60	160	210	310	30	60	160	210	310	30	60	160	210	310	**CM11**	**CM12**	**CM2**	**CM3**	**UA**	**UD**
30	**0.08**	0.51	0.37	0.32	0.23	0.18	0.18	0.17	0.16	0.13	0.13	0.15	0.14	0.14	0.12	0.14	0.11	0.05	0.04	-0.05	-0.08
60	0.97	**0.10**	0.46	0.42	0.26	0.20	0.22	0.21	0.20	0.16	0.14	0.17	0.17	0.17	0.14	0.11	0.14	0.06	0.05	-0.05	-0.09
160	0.80	0.92	**0.14**	0.58	0.33	0.23	0.27	0.27	0.26	0.21	0.15	0.20	0.22	0.22	0.18	0.05	0.16	0.08	0.05	-0.06	-0.09
210	0.75	0.89	1.00	**0.15**	0.39	0.24	0.28	0.29	0.28	0.23	0.15	0.20	0.23	0.23	0.20	0.04	0.16	0.08	0.05	-0.06	-0.10
310	0.70	0.78	0.86	0.88	**0.10**	0.22	0.26	0.28	0.29	0.26	0.14	0.18	0.21	0.21	0.21	0.10	0.06	0.07	0.05	-0.06	-0.10
30	0.90	0.94	0.88	0.85	0.77	**0.13**	0.61	0.44	0.38	0.28	0.23	0.25	0.23	0.22	0.18	0.05	0.09	0.21	0.09	-0.05	-0.09
60	0.83	0.91	0.94	0.93	0.84	0.97	**0.15**	0.57	0.52	0.34	0.25	0.29	0.29	0.28	0.24	0.06	0.10	0.20	0.10	-0.06	-0.10
160	0.68	0.81	0.94	0.95	0.87	0.86	0.96	**0.16**	0.61	0.42	0.24	0.30	0.33	0.33	0.30	0.07	0.10	0.15	0.10	-0.05	-0.11
210	0.64	0.77	0.91	0.93	0.87	0.81	0.93	0.99	**0.16**	0.46	0.23	0.30	0.34	0.34	0.32	0.07	0.10	0.13	0.10	-0.05	-0.11
310	0.59	0.68	0.77	0.79	0.85	0.72	0.81	0.90	0.93	**0.13**	0.20	0.25	0.29	0.30	0.32	0.06	0.10	0.09	0.08	-0.05	-0.11
30	0.87	0.90	0.83	0.80	0.68	0.97	0.92	0.81	0.77	0.71	**0.11**	0.64	0.38	0.29	0.23	0.05	0.06	0.12	0.21	-0.05	-0.08
60	0.85	0.90	0.88	0.86	0.74	0.97	0.96	0.88	0.84	0.73	0.98	**0.15**	0.55	0.48	0.36	0.06	0.07	0.13	0.20	-0.05	-0.10
160	0.76	0.86	0.91	0.90	0.81	0.92	0.97	0.94	0.91	0.78	0.91	0.97	**0.15**	0.64	0.48	0.08	0.08	0.12	0.14	-0.05	-0.11
210	0.72	0.83	0.91	0.91	0.84	0.90	0.96	0.97	0.95	0.83	0.87	0.94	0.99	**0.14**	0.51	0.07	0.08	0.11	0.12	-0.05	-0.11
310	0.56	0.68	0.80	0.83	0.86	0.74	0.85	0.94	0.97	0.98	0.72	0.77	0.84	0.89	**0.13**	0.06	0.09	0.11	0.08	-0.05	-0.11
CM11	0.57	0.56	0.49	0.47	0.46	0.56	0.53	0.47	0.46	0.46	0.55	0.53	0.50	0.49	0.45	**0.05**	0.03	0.05	0.05	-0.05	-0.10
CM12	0.62	0.65	0.62	0.61	0.55	0.68	0.68	0.62	0.60	0.55	0.67	0.68	0.66	0.65	0.56	0.66	**0.03**	0.07	0.04	-0.03	-0.06
CM2	0.63	0.66	0.63	0.61	0.55	0.70	0.69	0.63	0.61	0.56	0.69	0.70	0.67	0.66	0.57	0.67	0.97	**0.06**	0.11	-0.03	-0.06
CM3	0.62	0.64	0.59	0.57	0.51	0.68	0.66	0.60	0.58	0.54	0.67	0.67	0.64	0.63	0.54	0.68	0.81	0.93	**0.07**	-0.01	-0.04
UA	-0.22	-0.23	-0.21	-0.21	-0.22	-0.20	-0.20	-0.20	-0.21	-0.24	-0.18	-0.17	-0.17	-0.18	-0.22	-0.37	-0.22	-0.15	-0.13	**0.27**	0.32
UD	-0.39	-0.40	-0.37	-0.36	-0.37	-0.36	-0.37	-0.36	-0.36	-0.40	-0.35	-0.33	-0.32	-0.33	-0.37	-0.56	-0.38	-0.28	-0.25	0.80	**0.41**

II

Genetic Evaluation

Genetic Evaluation - **MODEL**

$$\begin{bmatrix} y_{tdscs1} \\ y_{tdscs2} \\ y_{tdscs3} \\ y_{cm11} \\ y_{cm12} \\ y_{cm2} \\ y_{cm3} \\ y_{UA} \\ y_{UD} \end{bmatrix} = [age] + [ym] + [hy5] + [ht] + [rc] + \begin{bmatrix} & & & & & & & \\ & & & & & & & \\ & & & & & & & \\ & & & & & & & \\ & & & & & & & \\ & & & & & & & \\ & & & & & & & \\ \tau_1 & \tau_2 & \tau_3 & \tau_4 & \tau_5 & \tau_6 & \tau_7 & \tau_8 \\ \tau_1 & \tau_2 & \tau_3 & \tau_4 & \tau_5 & \tau_6 & \tau_7 & \tau_8 \end{bmatrix} + \begin{bmatrix} \Sigma_{r=0}^{4} \phi_\pi(d)_r \beta_{S1} \\ \Sigma_{r=0}^{4} \phi_\pi(d)_r \beta_{S2} \\ \Sigma_{r=0}^{4} \phi_\pi(d)_r \beta_{S3} \\ \\ \\ \\ \\ \\ \\ \end{bmatrix} +$$

$$\begin{bmatrix} \\ \\ \\ hy_{cm\,11} \\ hy_{cm\,12} \\ hy_{cm\,2} \\ hy_{cm\,3} \\ hy_{ua} \\ hy_{ud} \end{bmatrix} + \begin{bmatrix} htd_{s1} \\ htd_{s2} \\ htd_{s3} \\ \\ \\ \\ \\ \\ \\ \end{bmatrix} + \begin{bmatrix} \Sigma_{r=0}^{2} \phi_\alpha(d)_r p_{S1} \\ \Sigma_{r=0}^{2} \phi_\alpha(d)_r p_{S2} \\ \Sigma_{r=0}^{2} \phi_\alpha(d)_r p_{S3} \\ p_{CM11} \\ p_{CM12} \\ p_{CM2} \\ p_{CM3} \\ p_{UA} \\ p_{UD} \end{bmatrix} + \begin{bmatrix} \Sigma_{r=0}^{2} \phi_\alpha(d)_r a_{S1} \\ \Sigma_{r=0}^{2} \phi_\alpha(d)_r a_{S2} \\ \Sigma_{r=0}^{2} \phi_\alpha(d)_r a_{S3} \\ a_{CM11} \\ a_{CM12} \\ a_{CM2} \\ a_{CM3} \\ a_{UA} \\ a_{UD} \end{bmatrix} + \begin{bmatrix} e_{s1} \\ e_{s2} \\ e_{s3} \\ e_{cm11} \\ e_{cm12} \\ e_{cm2} \\ e_{cm3} \\ e_{ua} \\ e_{ud} \end{bmatrix}$$

The covariables for coefficients $\beta_{..r}$ (r=0,…,4) were:

$$\phi_\pi(d) = [c_0 \;\; c_1 \; c_2 \;\; c_3 \;\; \exp(wd)]^T,$$

Genetic Evaluation - **PARAMETERS**

- Separate evaluations for **HOL**, **RDC** and **JER**
- Breed specific parameters (heritabilities) for the CM & udder type i.e. (6x6) part
- Genetic variance covariance matrix is of size 15x15
  - 3x 3 regression coeff. for SCS
  - 4 CM traits
  - 2 udder conformation traits

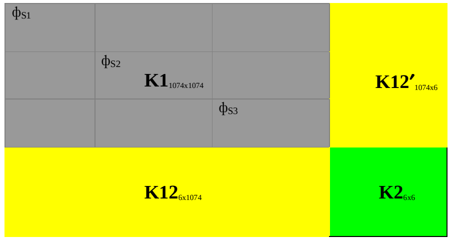
$$\mathbf{G}_{15x15} = \begin{bmatrix} \boldsymbol{\Phi}_{s1} & & & & & & & & \\ & \boldsymbol{\Phi}_{s2} & & & & \mathit{Symm} & & & \\ & & \boldsymbol{\Phi}_{s3} & & & & & & \\ & & & \mathbf{CM11} & & & & & \\ & & & & \mathbf{CM12} & & & & \\ & & & & & \mathbf{CM2} & & & \\ & & & & & & \mathbf{CM3} & & \\ & & & \mathit{Symm} & & & & \mathbf{UA} & \\ & & & & & & & & \mathbf{UD} \end{bmatrix}$$

Genetic Evaluation – **RANK REDUCTION**

Three different approaches were tested

1. **Rank reduction the variance matrix**
   - **Rank can only be reduced on the G matrix**
2. **Within trait rank reduction**
   - **Resulted in stronger reduction on TDSCS**
   - **Low correlation between FULL vs. Rank reduced model**

$\boldsymbol{G}_{1080\times1080}=$



3. **Rank reduction on the expanded correlation matrix**
   - Rank can be reduced both on the **Pe** and **G**

Genetic Evaluation – **RANK REDUCTION**

- Rank reduced - only on the **G matrix – from 15 to 12**
  - Corr between EBVs **Full vs Rank reduced model**
    - **~0.999 for bulls & cows**
    - **0.999 for TDSCS & 0.998 for CM traits**

- **Rank reduction resulted:**
  - Marked reduction in computational time & better convergence characteristics
  - Animal equations reduced
    - HOL from 124 to 100 million
    - RDC from 77 to 61 million
    - JER from 11 to 9 million

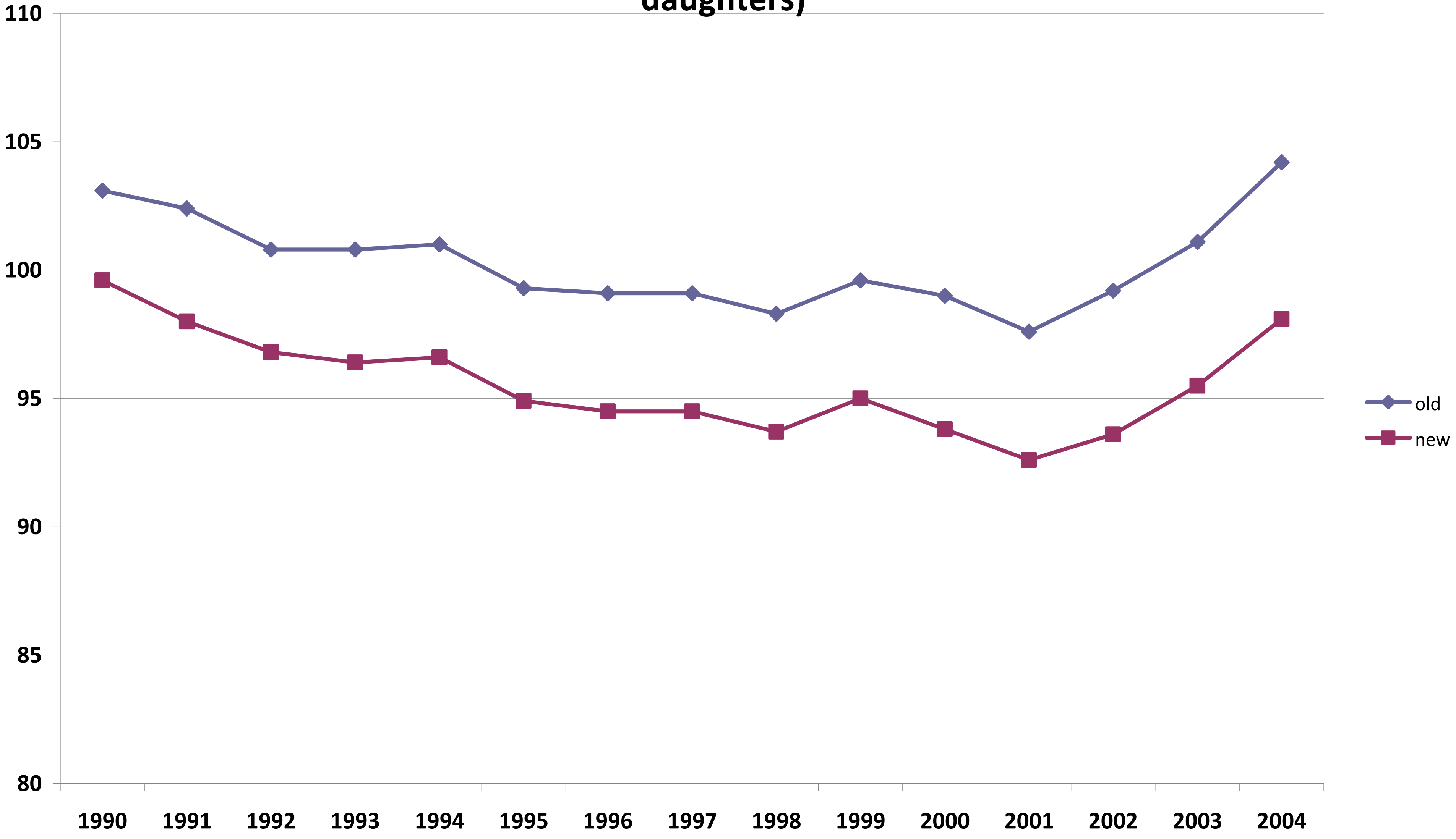
Genetic Evaluation - **SIZE**

Size of the genetic evaluation (in millions) for the different breeds

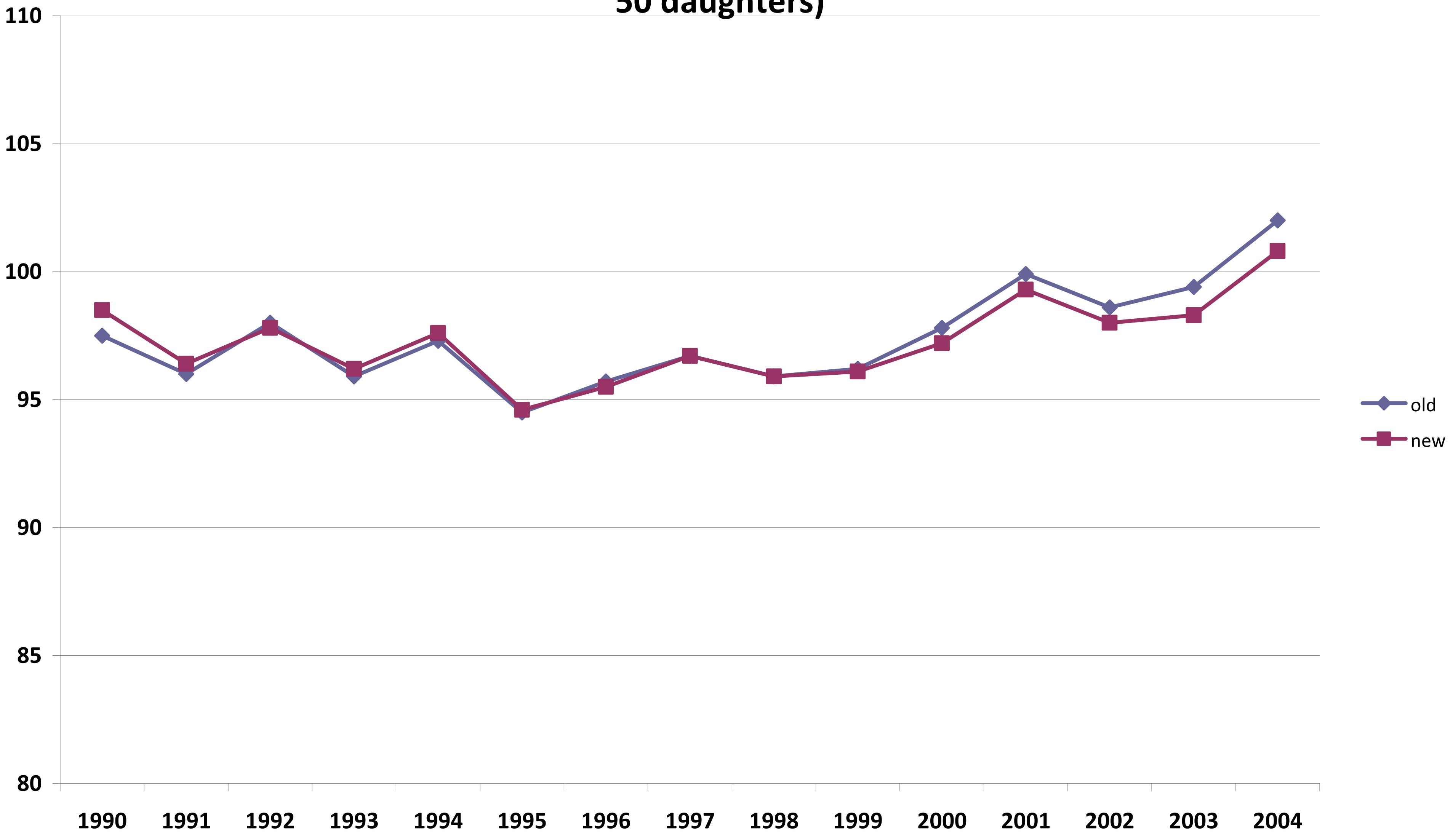
	HOL	**RDC**	**JER**
Cows with Obs. (No.)	6.5	4.1	0.6
Total observations	97.1	70.5	9.6
No. animal equations	100.0	61.3	9.3
No. total equations	217.1	137.1	18.1

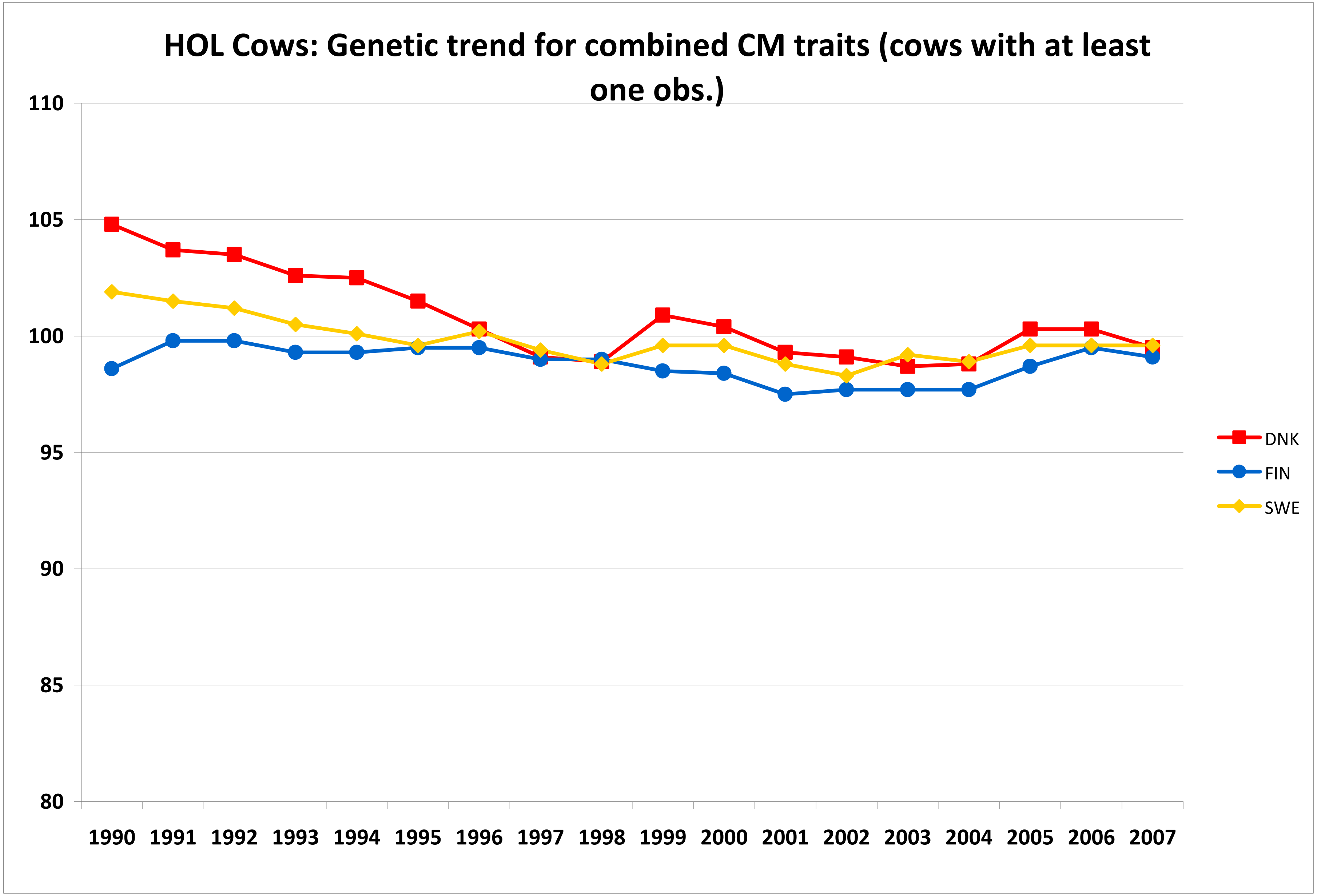
RESULTS

Genetic trends for **HOL bulls** for the combined CM traits (with at least 50 daughters)

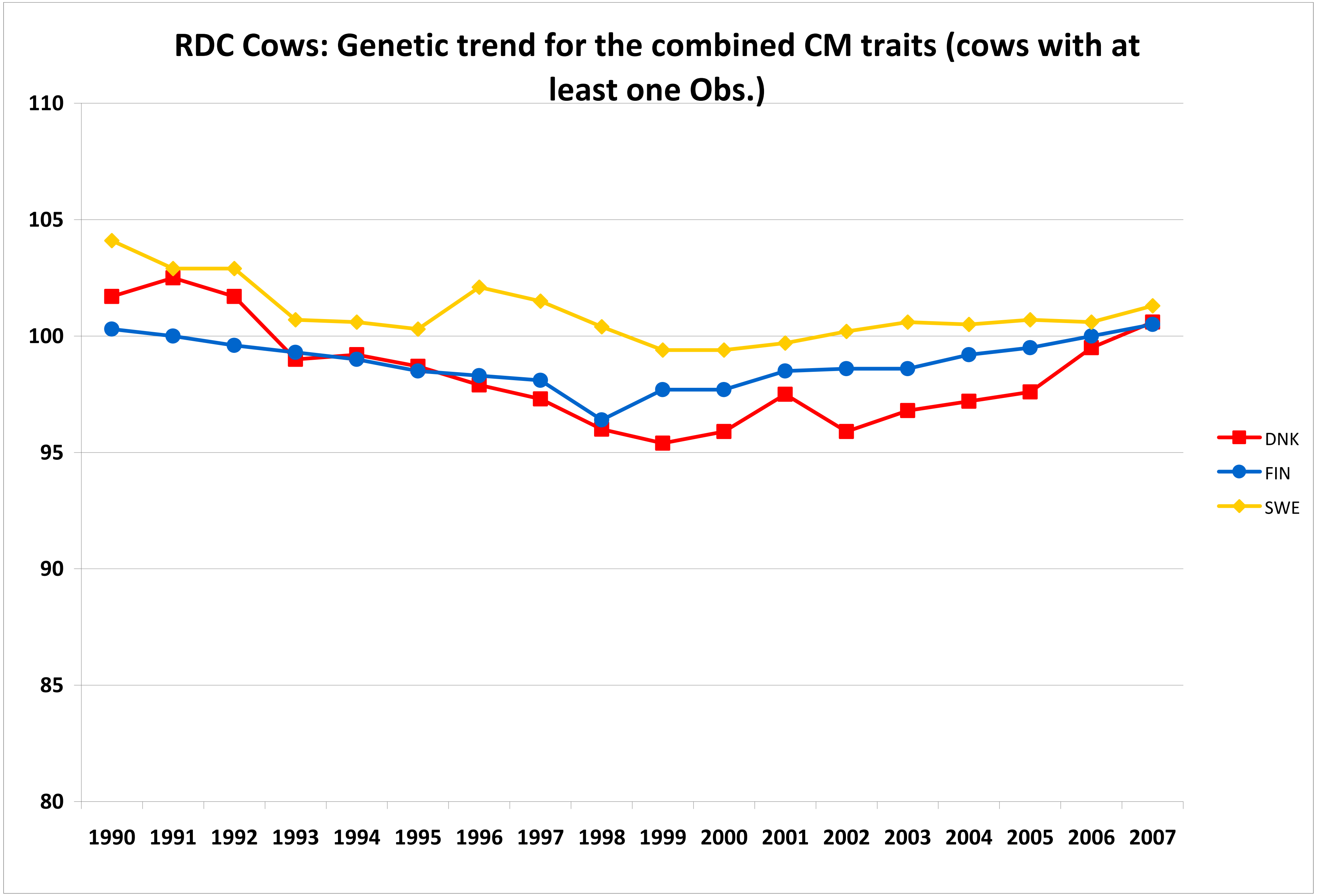


Genetic trends for RDC bulls for the combined CM traits (bulls with at least 50 daughters)



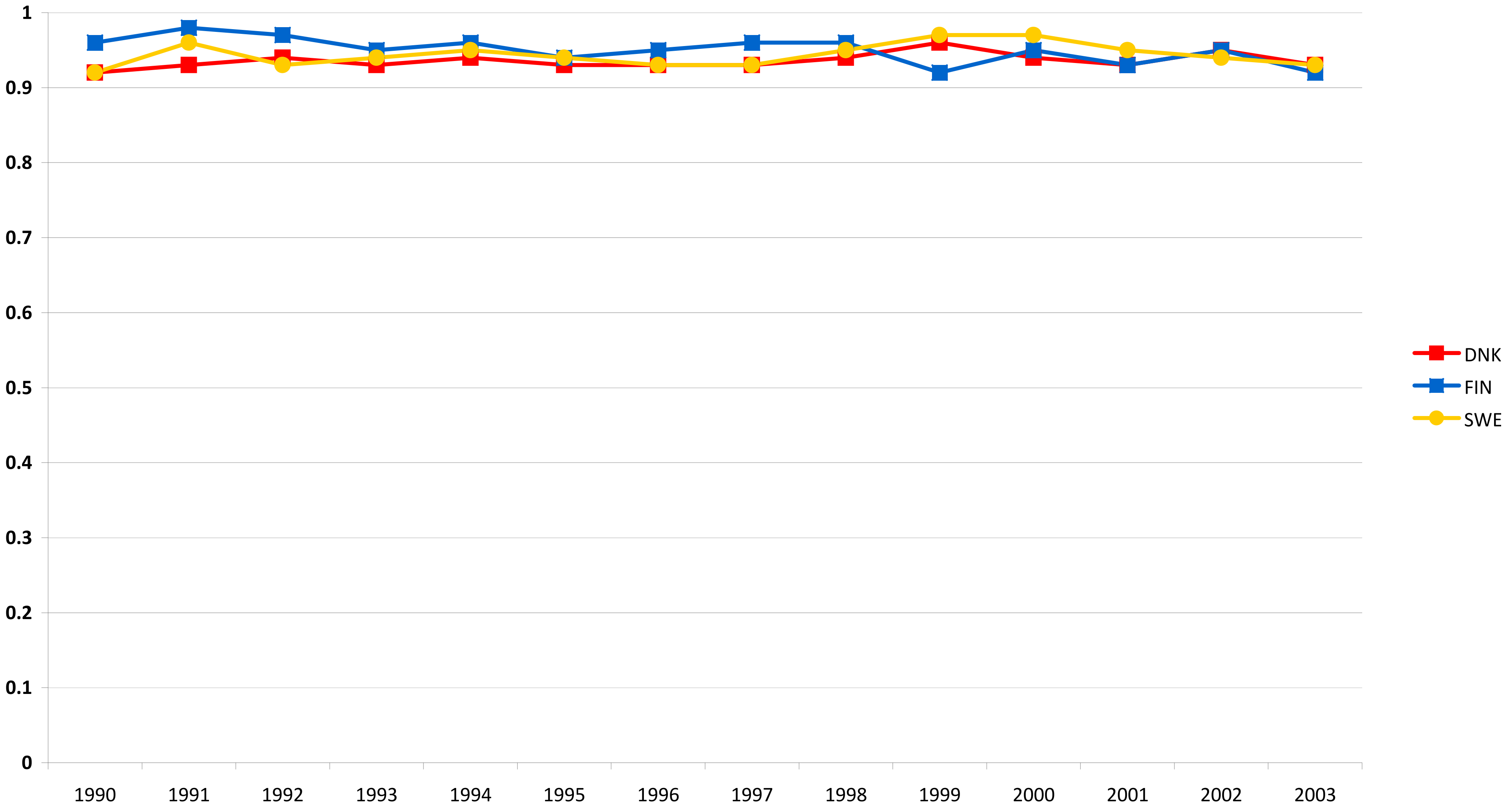


HOL Cows: Genetic trend for combined CM traits (cows with at least one obs.)

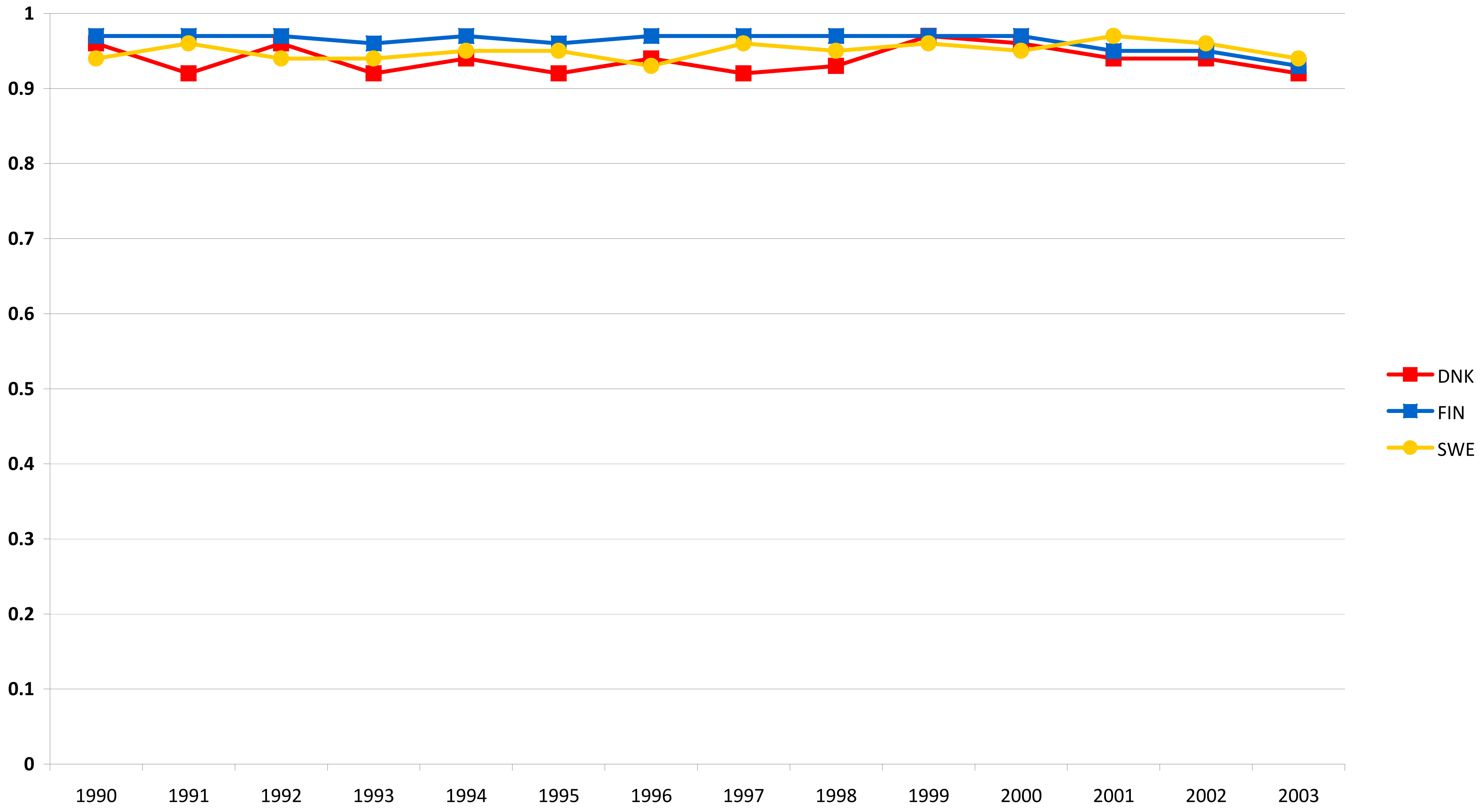


RDC Cows: Genetic trend for the combined CM traits (cows with at least one Obs.)

HOL correlations between old and new model bulls with at least 50 daughters



RDC correlations between old and new model for bulls with at least 50 daughters



Standard deviations (SD) of EBVs for combined CM traits (CMcomb) † from mt-RRM and mt-LAM for different groups of Holsteins: old bulls (born 1993-95, with ≥100 daughters), young bulls (born 2000-2002, with ≥ 20 daughters), and old and young Holstein cows with at least one observation (born in 1998 and 2004).

		Bulls/cows No.	MODEL	
		No. Bulls/Cows	mt-RRM	mt-LAM
Groups				
Bulls				
Old	**CM$_{comb}$**	**118**	**0.054**	**0.052**
Young	**CM$_{comb}$**	**957**	**0.052**	**0.046**
Cows				
Old	**CM$_{comb}$**	**195284**	**0.028**	**0.026**
Young	**CM$_{comb}$**	**108097**	**0.027**	**0.024**

† Values for CMcomb are based on combining EBVs for CM11, CM12, CM2 and CM3 with their respective weights

Conclusions

1. **Combining TDSCS with CM and udder type traits** in a mt-RRM lead to the development of a new joint genetic evaluation model for Denmark, Finland and Sweden

2. **The new model**
   - Makes efficient use of TDSCS information
   - Offers breeding values for both bulls and dams
   - Harmonizes udder health evaluation across the countries and
   - Provides herd-test-day solutions which can be used in herd management tools for herd monitoring purposes.

Acknowledgement

Nordisk Avlsværdivurdering
Nordic Cattle Genetic Evaluation

Thank you !