Genetic trends for fertility in Swedish Red cattle using different models

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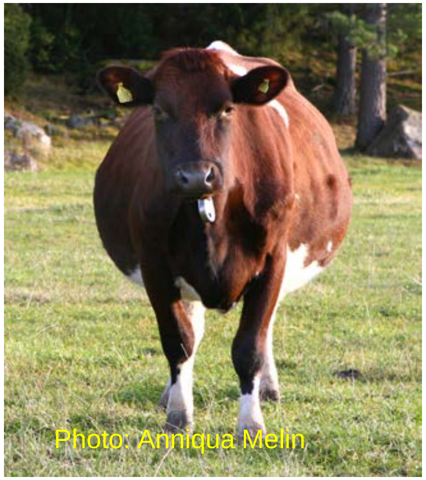
Background

- Functional traits since long included in the breeding goal of Scandinavian Red breeds.
- Female fertility still one of the most common reasons for culling in Sweden.
- A recent simulation study (Hansen Axelsson et al, 2011) suggested that with current Nordic (NAV) economic weights fertility traits would deteriorate.
- In current NAV genetic evalation, trait groups are evaluated separately and combined using an index, - a full MT-model was used in the simulation.


Photo: Sven Rosborn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Aim

To compare genetic trends for female fertility traits, udder health traits, and milk protein yield, for Swedish Red dairy cattle, using full and trait-wise MT models.

Material

Field data on Swedish Red from 1989-2007:

Fertility traits:

- No of ins. per service period in maiden heifers (NINS0), and cows (NINS1, NINS2).
- Interval calving – first ins. (CFI1, CFI2).

Udder health and conformation:

- Clinical mastitis (CM1, CM2).
- Lact. average somatic cell score (SCS1, SCS2).
- Fore udder attachement (UA1), and udder depth (UD1).

Production:

- 305-d protein yield (PY1, PY2).

Methods

- Pre-correction for heterogeneous variances due to year (herd-year for PY).
- Variance components estimated prior to estimation of genetic trends (DMU-AI software), animal and sire models, 3 lactations.

Methods – estimation of EBVs

Estimation of breeding values using animal models (DMU5 software).

Full multi-trait models :

- with and without heifer records on NINS.

Trait-wise multi trait models:

- fertility traits,
- fertility traits excluding heifers,
- udder health and conformation traits
- protein yield.

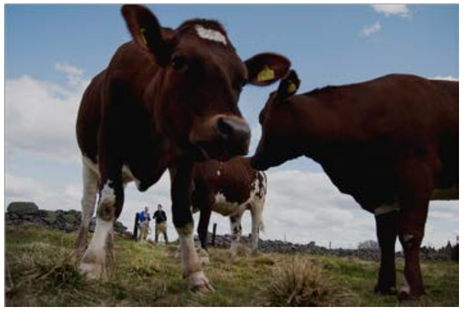
Methods – regression coefficients

Regression coefficients for estimated breeding values on birth year were estimated (SAS Proc GLM)

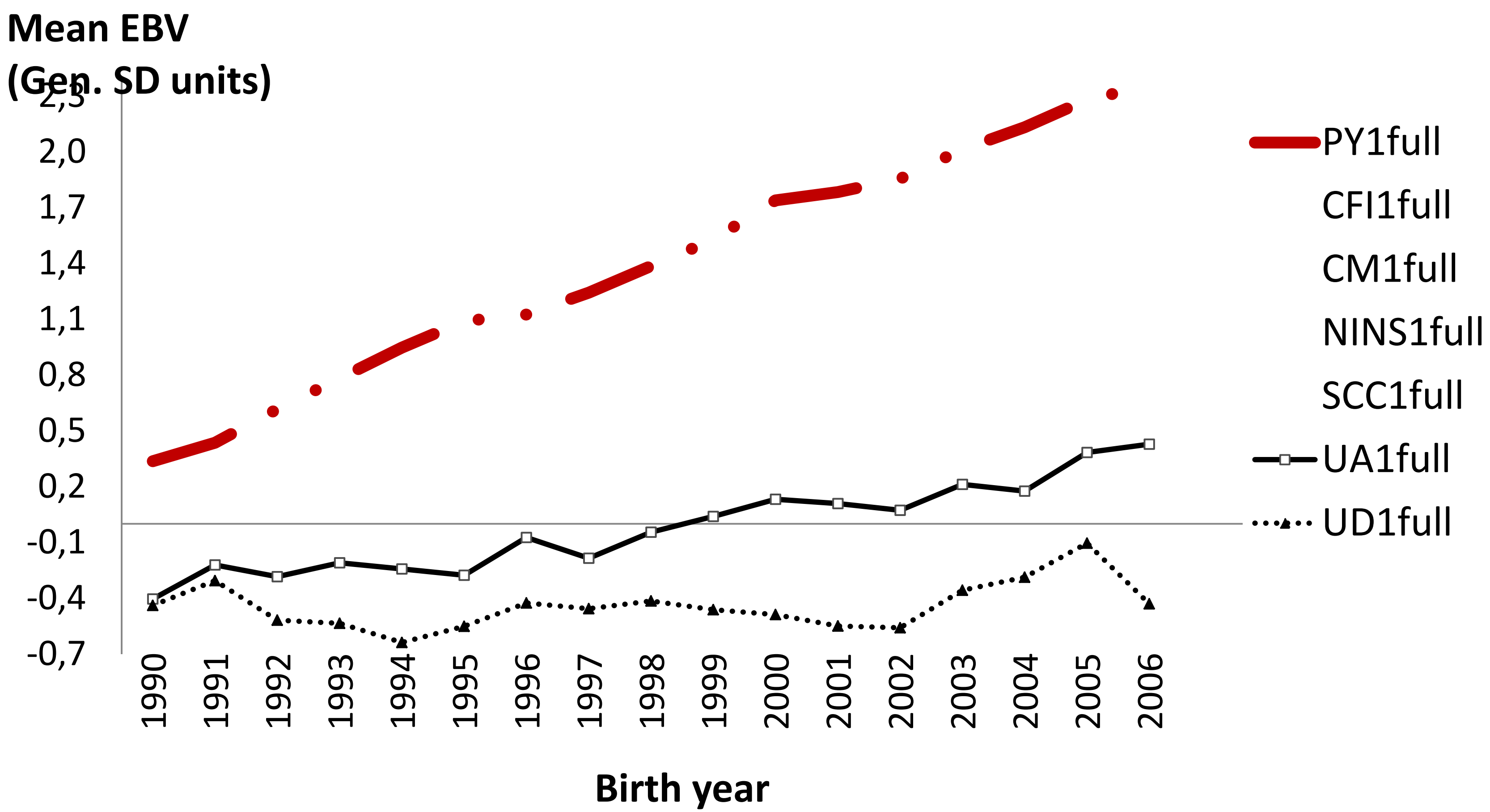
- for Swedish AI bulls born from 1990,
- for maiden heifers and cows born from 1990, with own records, after Swedish AI sires.

Methods – Rank correlations

- EBVs for NINS, CFI, CM and PY were weighted into a TMI using NAV economic weights.
- Spearman rank correlations estimated between
  - indices from evaluations with full MT-model (TMIfull) and trait-wise MT-models (TMItw).
  - EBVs for single traits from full and trait-wise MT model.



Results – estimated genetic (cow) trends 1st lactation



Clearly favorable trends estimated for protein yield and fore udder attachement.

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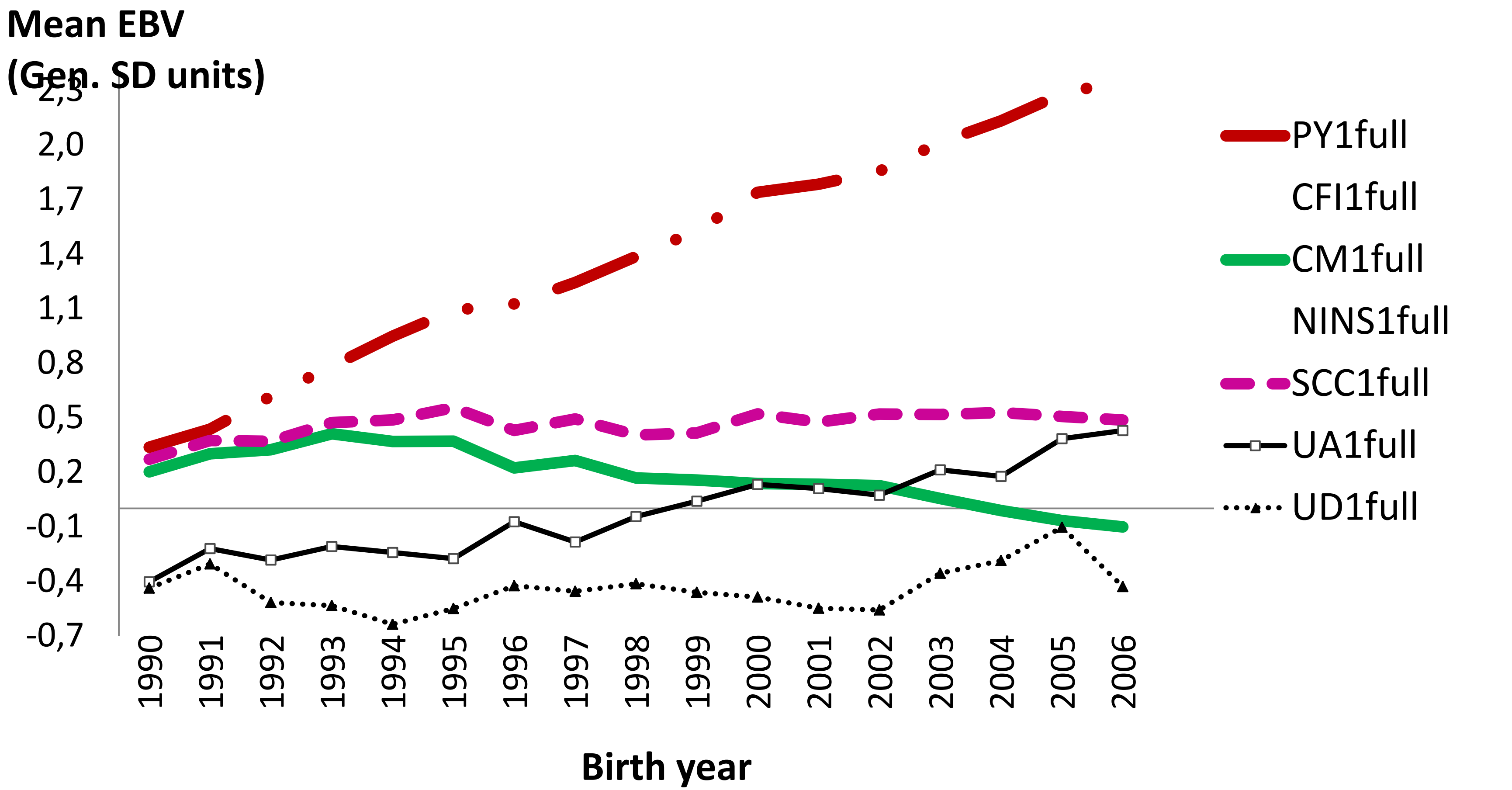
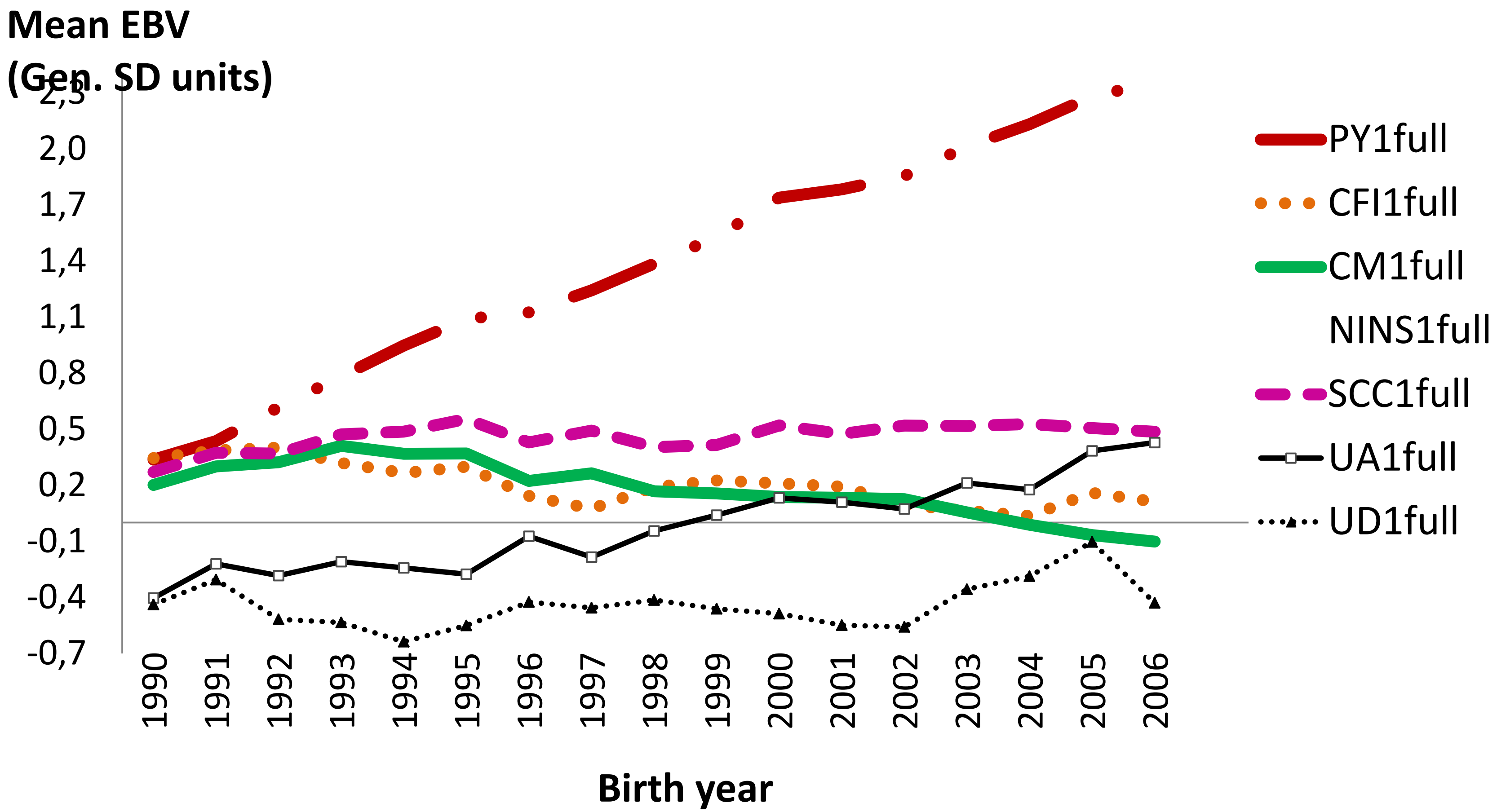


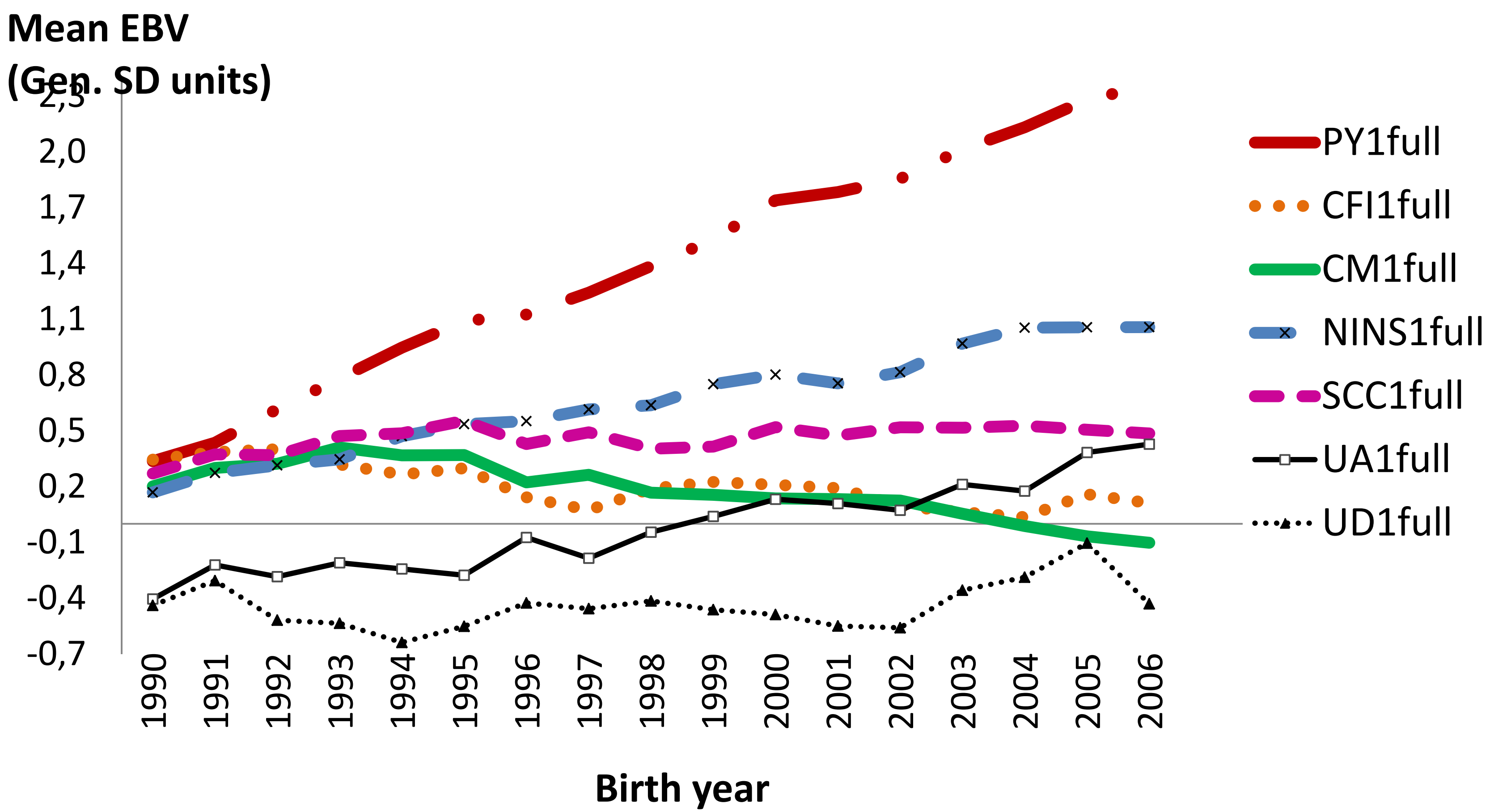
Neutral to favorable trends for CM and SCS. Slightly unfavorable cow trends for CM and SCS in 2nd lactation, but neutral during the last years.

Results – estimated genetic (cow) trends 1st lactation



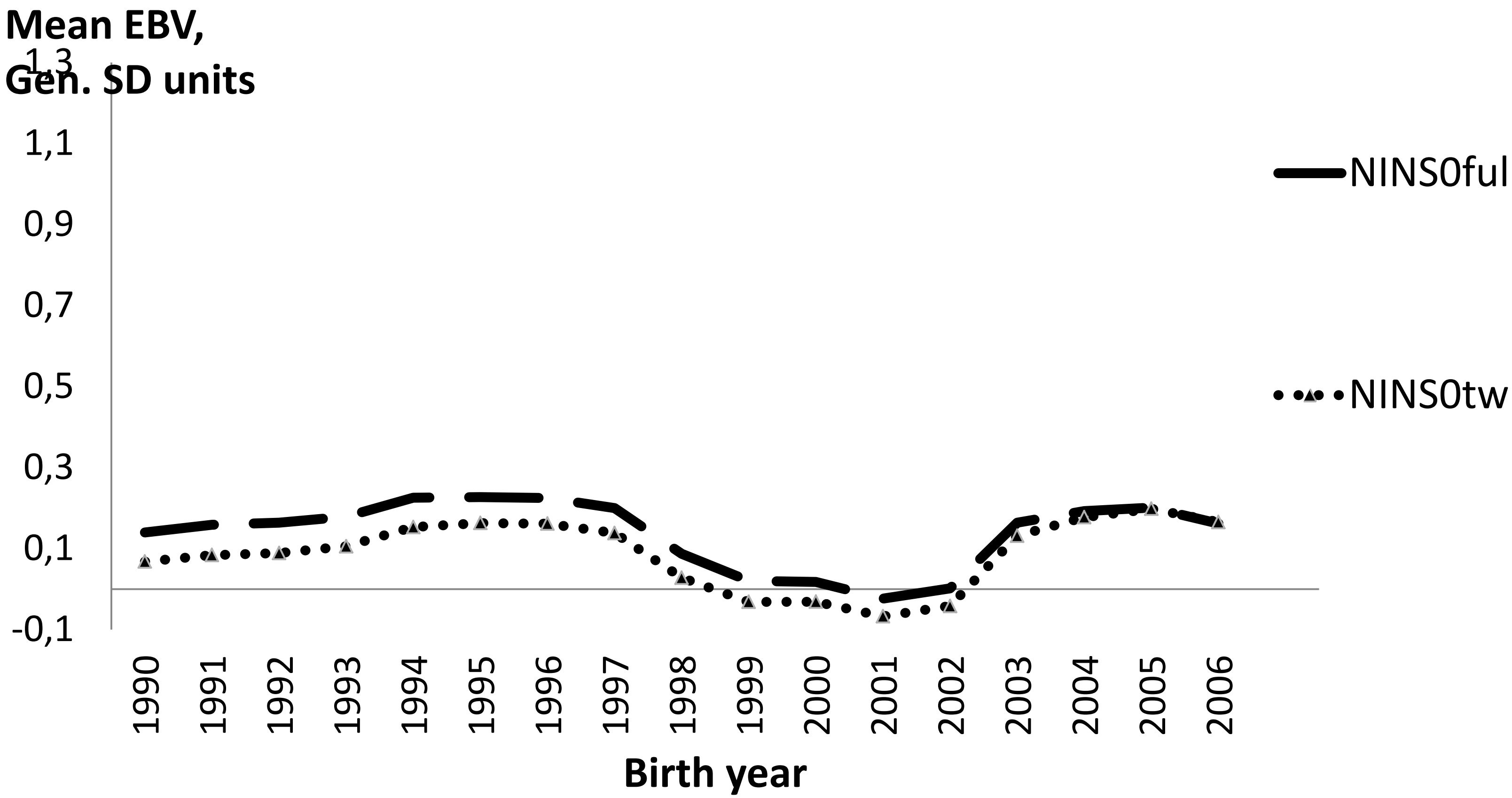
Favorable trends estimated for CFI.

Results – estimated genetic (cow) trends 1st lactation



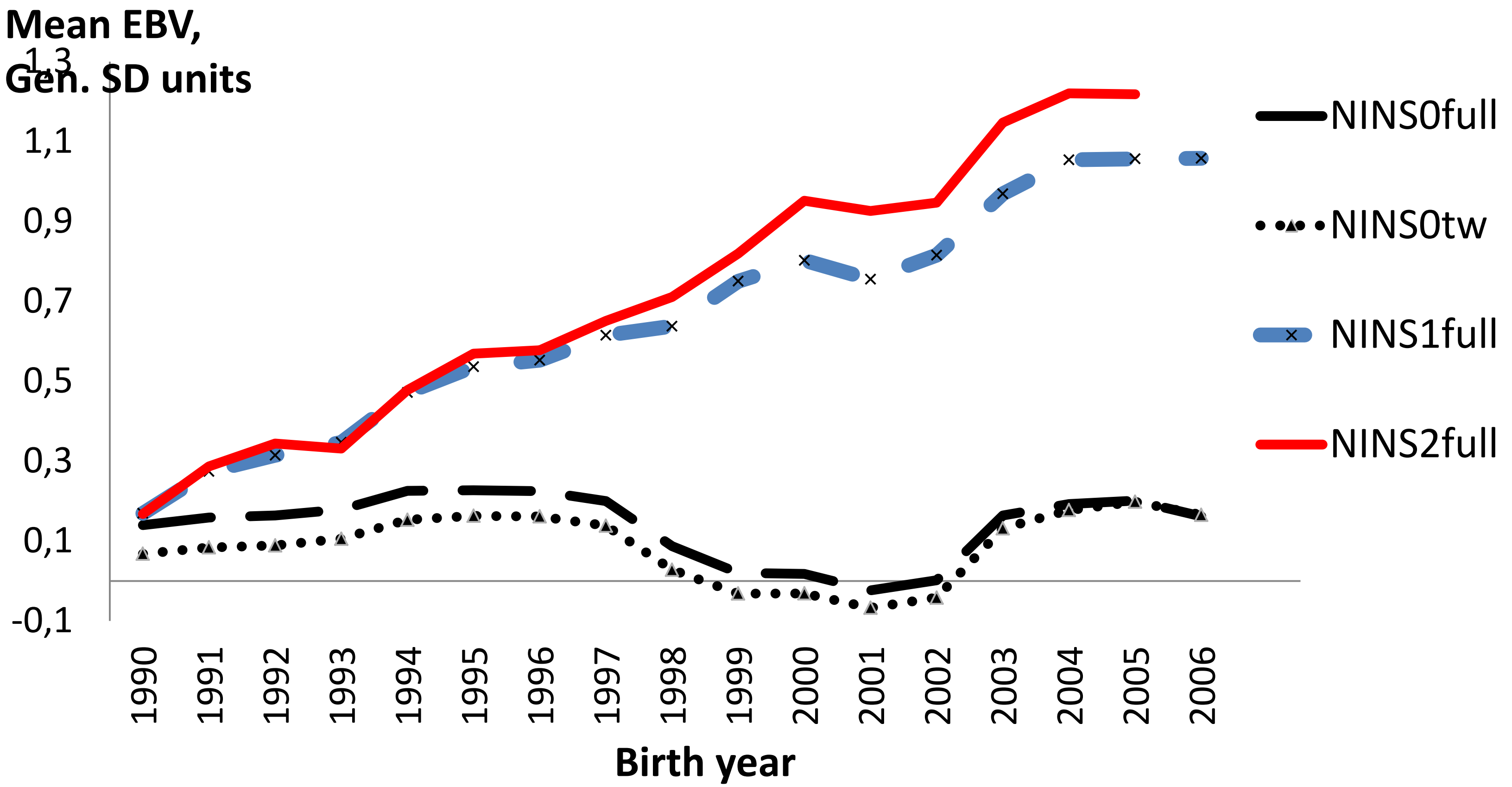
Slightly unfavorable for NINS in lactating cows.

Results – estimated genetic (cow) trends NINS full and trait-wise MT model



Neutral trends for NINS in maiden heifers.

Results – estimated genetic (cow) trends NINS full and trait-wise MT model



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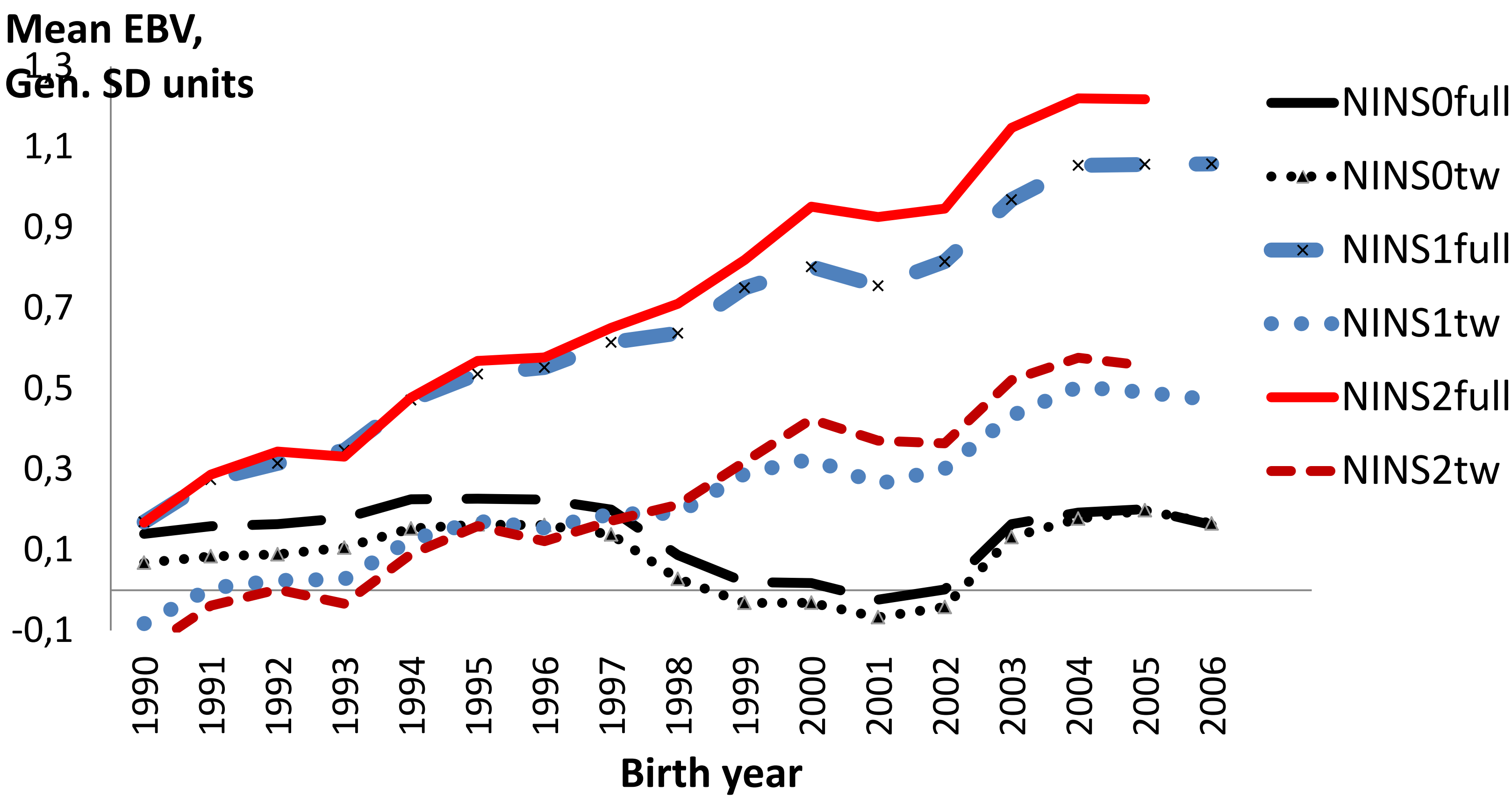

NINS seemed less unfavorable with trait-wise MT-model than with full MT-model.

Results – estimated genetic trends

- Regression coefficients about twice as high for NINS in lactating cows with full MT-model compared with trait-wise MT-model.
- Smaller than expected effect of excluding heifer information.

Results – Rank correlations

Spearman rank correlations between indices and EBVs estimated with full MT and trait-wise MT models.

Correlated indices or EBVs[1]	Cows born 2000-2005 N = 91,461	AI bulls 1990-2003 N = 1,322	AI bulls 1990-1991 N = 204	AI bulls 2002-2003 N = 146
TMIfull-TMItw	0.983	0.999	0.998	0.996
NINS1full– NINS1tw	0.916	0.956	0.975	0.962
NINS2full-NINS2tw	0.897	0.933	0.958	0.931
CFI1full-CFI1tw	0.966	0.975	0.985	0.967
CFI2full-CFI2tw	0.921	0.939	0.966	0.852

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Results – % co-selected

% co-selected bulls using full MT model and trait-wise MT model among the 100 top-ranked bulls.

Correlated indices or EBVs[1]	AI bulls born 1990-2003
TMIfull – TMItw	94%
NINS0full – NINS0tw	91%
NINS1full – NINS1tw	71%
NINS2full – NINS2tw	69%
CFI1full – CFI1tw	85%
CFI2full – CFI2tw	82%
CM1full – CM1tw	91%
CM2full – CM2tw	88%
PY1full – PY1tw	98%
PY2full – PY2tw	93%

To sum up..

- Neutral or favorable genetic trends estimated for most functional traits in the study. Slightly unfavorable trends for NINS in lactating cows.
- Risk of overlooking unfavorable trends in functional traits unless especially production is included in the MT-model.
- With current Nordic economic weights, this would only slightly change the choice of bulls, however.
- With selection across generations the proportion of young vs. proven bulls may be suboptimal if genetic trends are under/over estimated.

Thank you for your attention!

Photo:Anniqua Melin

We gratefully acknowledge the Swedish Dairy Association (Växa Sverige) for providing data.