Predicting lifespan of dairy cows
Phenotypic and genetic change during life

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Introduction - Longevity

- Longevity = productive lifespan = days between 1st calving and last test date
  - Available when cow is culled

- Current genetic evaluation in The Netherlands
  - Piecewise Weibull Model
  - Survival Kit software (Ducrocq & Sölkner)
  - Predictors included with selection index
Introduction - Longevity

Problem:
- Breeding values fluctuate too much
- Especially from 1\textsuperscript{st} to 2\textsuperscript{nd} crop information

Hypothesis:
- Model is too simplistic in modelling the genetic variation in longevity
- Assumes longevity is genetically same trait during life
Aim

Investigate the phenotypic and genetic (co-)variation of longevity

1. During total lifespan

2. Within and across lactations
Material and methods – Data

- National dataset available from CRV
  - Pedigree (20M), lactations (40M), movements (100M)

- Total dataset
  - Per cow one record for each month in productive life
  - Cows present in period 1988 - 2012
  - 370M records of 10M cows in total

- Dataset sized down
  - 27 herds
  - ~25K black & white cows (1-120 months in productive life)
  - ~600 sires
  - ~850K records
Material and methods – Genetic analysis

- Random regression model

\[ Y = X\beta + Za + Zp + e \]

\( Y \) = survival (1 – 120 months in productive life)

\( \beta \) = fixed effects
- Herd-year-season of calving
- Year-season of observation
- Parity-month in lactation
- Parity-year-season of calving
- Age at first calving (2\(^{nd}\) order Legendre polynomial)
- Month in life (4\(^{th}\) order Legendre polynomial)

\( a \) = additive genetic random effect

\( p \) = permanent environment random effect

- 2\(^{nd}\) order Legendre polynomials for \( a \) and \( p \)
Material and methods – Genetic analysis

- Time covariables for a and p in random regression (RR)
  1. During total lifespan
     - RR on months in life (MIL)
  2. Within and across lactations
     - RR per parity on months in milk (par x MIM)
     - Parity 1, 2, 3+ with a maximum of 18 months in milk

- Use of uncorrelated residual classes
  1. MIL: 40 classes of 3 months
  2. par x MIM: 3 parity groups x 18 MIM classes

- Analysis with ASREML (Gilmour et al., 2009)
Results – phenotypic means (MIL)
Results – phenotypic means (par x MIM)

![Graph showing parity x months in milk with number of records and monthly survival.]

- Number of records:
  - Parity x months in milk:
    - 6: 35,000
    - 12: 28,000
    - 18: 21,000
    - 6: 14,000
    - 12: 10,000
    - 18: 6,000

- Monthly survival (percentage):
  - Parity x months in milk:
    - 6: 98%
    - 12: 96%
    - 18: 94%
    - 6: 92%
    - 12: 90%
    - 18: 88%
## Results – Genetic parameters (MIL)

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<th>variance in %</th>
<th>phenotypic mean (%)</th>
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Results – Genetic correlations (MIL)

months in productive life

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Color bar:
- 1.00
- 0.75
- 0.50
- 0.25
- 0.00
- -0.25
- -0.50
- -0.75
- -1.00
Results – Genetic correlations (par x MIM)

parity x months in milk

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-0.25  -0.50  -0.75  -1.00
0.00   0.25   0.50   0.75  1.00
Conclusions

- Survival is a different trait across and within lactations
  - Differences in phenotypic means
  - Genetic correlations < 0.90

- Modelling in a more complex way to get:
  - Better understanding of survival
  - More stable breeding values
Thank you for your attention

Questions?

Project is part of

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