Genetic associations between functional longevity and health traits in Austrian Fleckvieh cattle

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Background (I)

- Increase of functional traits in breeding programs
  - Important determinants of profitable and sustainable dairy production

- Health traits
  - Farm economy, animal welfare and customer demands

- Main culling reasons in Austria
  - Fertility disorders (22.9%)
  - Udder diseases (13.5%)

- Ø longevity 3.80 years
  - Potential to improve

Background (II)

- Health disorders lead to early culling
  - Longevity decreases

- Genetic relations between longevity and health traits are most likely, but …
  - are not known so far due to
    - limited access to direct health data
    - methodology constraints

Objectives

- Conduct an approximate multitrait 2-step approach applied to yield deviations and de-regressed breeding values

- Estimate genetic parameters
  - Heritabilities
  - Genetic and residual correlations
    - Functional longevity (LONG)
    - Clinical mastitis (CM)
    - Early fertility disorders (EFD)
    - Cystic ovaries (CO)
   - Milk fever (MF)

Materials & methods

- ## 70,000 Fleckvieh cows (dual purpose Simmental)
  - 2 Austrian regions
  - Maximum 12.5% non-Fleckvieh-gene proportion
  - All 5 traits recorded
  - Born between 2004 and 2009
  - At least 20 daughters/sire

- ## Pedigree 200,000

- ## Programs
  - Survival Kit v6: YDs - functional longevity
  - MiX99: de-regressed breeding values - direct health traits
  - ApaX: Reliabilities
  - ASReml: Estimation of genetic parameters

Approximate multitrait 2-step approach

Step 1

EBV	LONG

EBV	CM EFD CO MF
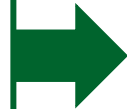
univariate evaluations
Statistical models of routine genetic evaluation

YD LONG

univariate de-regression

+ calculation weights (EOP)

Step 2

YD LONG

drEBV CM
drEBV EFD
drEBV CO
drEBV MF

+ weights

MT animal model

$$y^* = Xb + Za + e$$

Results & Discussion (I)

- Combination of different pseudo-phenotypes feasible

- Fast computing
  - Convergence of AI-REML algorithm 15 iterations / 40 hours

Results & Discussion (II)

	LONG	CM	EFD	CO	MF
LONG	0.15±0.01				
CM		0.06±0.01			
EFD			0.03±0.01		
CO				0.07±0.01	
MF					0.05±0.01

Results & Discussion (II)

	LONG	CM	EFD	CO	MF
LONG	**0.15±0.01**	0.63±0.05	0.29±0.08	0.20±0.07	0.20±0.08
CM		**0.06±0.01**			
EFD			**0.03±0.01**		
CO				**0.07±0.01**	
MF					**0.05±0.01**

Results & Discussion (II)

	LONG	CM	EFD	CO	MF
LONG	**0.15±0.01**	0.63±0.05	0.29±0.08	0.20±0.07	0.20±0.08
CM		**0.06±0.01**	0.14±0.09	0.16±0.07	0.37±0.08
EFD			**0.03±0.01**	0.42±0.08	0.34±0.09
CO				**0.07±0.01**	0.45±0.07
MF					**0.05±0.01**

Results & Discussion (II)

	LONG	CM	EFD	CO	MF
LONG	**0.15±0.01**	0.63±0.05	0.29±0.08	0.20±0.07	0.20±0.08
CM	0.09±0.006	**0.06±0.01**	0.14±0.09	0.16±0.07	0.37±0.08
EFD	0.02±0.006	0.02±0.006	**0.03±0.01**	0.42±0.08	0.34±0.09
CO	-0.02±0.006	-0.01±0.005	0.02±0.006	**0.07±0.01**	0.45±0.07
MF	0.02±0.006	0.00±0.005	0.02±0.006	-0.04±0.005	**0.05±0.01**

Conclusions

- Approach feasible

- **Moderate** to **high** genetic correlations **between functional longevity** and **direct health** traits

- **Low** to **moderate** genetic correlations **within direct health** traits

- Common genetic background exists

- Selection for healthy cows increases longevity (and vice versa)
  - Animal welfare
  - Farm economics

Thank you for your attention!

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2-step approach
First step – Calculation of pseudophenotypes

- Functional longevity - Survival analysis

$$h(t) = h_{0,ls}(\tau) * exp[\Sigma m(f_m(t) + hy_y(t) + s_i + 0.5mgs_j)]$$

→ Yield deviations

- Direct health traits – univariate animal model

$$y = Xb + Z_h h + Z_a a + Wp + e$$

→ univariate de-regression – de-regressed breeding values

- Effective own performance (EOP)

$$EOP_{i,m} = \frac{\alpha_i}{1-r^2_{im}} - \alpha_i$$

2-step approach
Second step – multitrait animal model

- Multivariate animal model

$$\mathbf{y}^* = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}$$