

Improving Genomic Prediction for Claw-health Using Multi-trait Model

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Selection for claw-health

- Claw lesion is a major cause of lameness in dairy cattle.
- Increase costs of
 - veterinary treatments
 - involuntary culling
 - discarded milk (treatment with antibiotics)
- The third most costly disease in dairy farming
- The trait is included in the Nordic total selection index in 2011

Multi-trait genomic prediction

- Accuracy of EBV/GEBV can be improved by using information of correlated traits.
- More benefit for the traits with low h^2 and having small number of observations.
- Claw health: new trait, relatively small number of observations.
- Expected to get benefit using multi-trait genomic prediction.

Objective

- Investigate the genetic correlations between claw health and the other traits
- Compare genomic predictions for claw-health using single-trait and multi-trait models

Data

5,643 Nordic Holstein bulls genotyped with 54K chip.

Deregressed proof (DRP) of clawth health and the 15 other traits

Divided into training and test data by cut-off date (birth data) of 2006-01-01

Traininng: about 4300 for most of traits
 (1485 for claw health)

Test: about 800

Definition of claw health

Traits	Disorders (coding)	Mean
Digital Dermatitis (DE)	Interdigital (1), Digital (2)	0.16
Heel Horn Erosion (HH)	Mild (1), severe (2)	0.20
Skin Proliferation (SP)	interdigital hyperplasia or wart (1)	0.03
Sole Haemorrhage (SH)	Mild(1), severe (2)	0.21
Sole Ulcer (SU)	Mild (1), severe(2)	0.07
Cork screw claws (CSC)	Cork screw claws (1)	0.02
White line separation (WLS)	White Line Separation or Double sole (1)	0.06

Statistical model

- BLUP model with genomic relationship matrix (GBLUP)
- Single-trait and multi-trait models

Procedures of multi-trait model analysis

- Calculate genetic correlations (based on training data)
- Select 3 traits having highest correlations with claw health.
- Genomic prediction using single-trait, two-trait, three-trait, and four-trait models

Genomic prediction is carried out using DMU package

Reliability of genomic estimated breeding value (GBV) is measured as $r^2_{gbv} = \text{Cor}^2(\text{GBV}, \text{DRP}) / r^2_{\text{DRP}}$ for animals in the test data.

Unbiasedness is measured as regression of DRP on GBV

Results

The three traits having highest genetic correlation with claw health

Traits	Cor with claw
Longevity	0.32
Other health	0.19
Feet&legs	0.17

Reliability (r^2_{gbv}) and unbiasedness (Reg) of genomic predictions for claw health using single and two-trait models

Model	Cor between traits	r^2_{gbv} (%) for Claw	$Reg_{drp gbv}$ for Claw
Claw		24.4	1.01
Claw-Longevity	0.319	25.4	1.01
Claw-Other health	0.193	24.9	1.01
Claw-Feet&legs	0.173	25.1	1.02

➤ 1% increase of r^2_{gbv} by including longevity

Reliability (r^2_{gbv}) and unbiasedness (Reg) of GBV for claw health using three- trait and four-trait models

Model	r^2_{gbv} (%) for Claw	$Reg_{drp gbv}$ for Claw
Claw-Longevity-Feet&legs	25.8	1.01
Claw-Longevity-Other health	25.6	1.01
Claw-Feet&legs-Other health	25.5	1.02
Claw-three other traits	26.0	1.01

- 1.4% increase of r^2_{gbv} by including longevity and feet&legs
- Further improvement by including all three traits is negligible.

Conclusions

- Claw-health in general has a low correlation with other traits
- Even though, genomic prediction for this trait can be slightly improved using a multi-trait model
- A two-trait model including longevity or three-trait model including longevity and feet&legs could be a good alternative.
- More records are needed to get satisfied accuracy.

**Thank you
for your attention**