



INCLUDING GENOTYPES IMPROVED THE GENETIC PREDICTIONS OF CLAW DISORDERS IN NORWEGIAN RED

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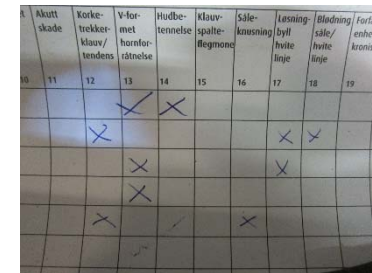
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CLAW HEALTH IN NORWEGIAN RED

- 2004 – Recording started
 - Claw health status at claw trimming
- 2014 – Claw health index
 - 4% of total merit index

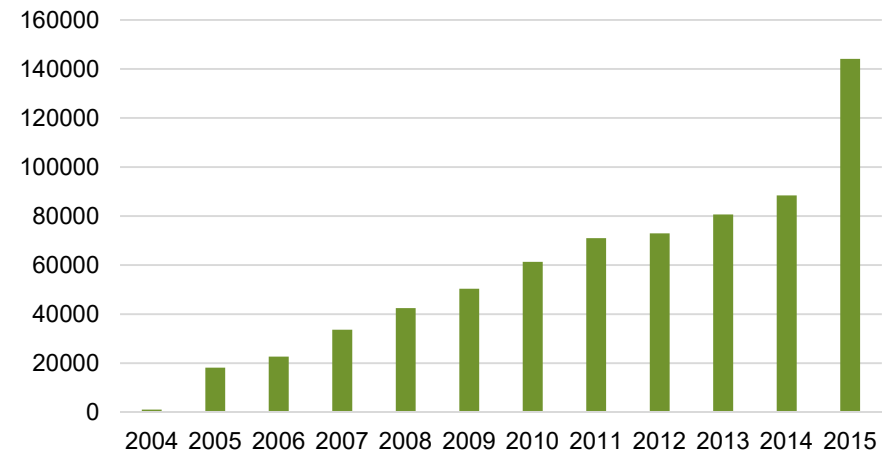


- 2014 – Electronic recording

Trait	Relative weight
Corkscrew claw	50
Infectious disorder	
Laminitis claw dis	






Total number of claw health records



AIM

Validate the effect of including genotypes of sires and cows in prediction of breeding values using single-step GBLUP

Claw disorders:

<p>Infectious claw disorders</p> <p>Digital dermatitis, interdigital dermatitis, heel horn erosion and interdigital phlegmon</p>	<p>Laminitis-related claw disorders</p> <p>Sole ulcer, toe ulcer, sole bleeding, white line fissure and white line abscess</p>	<p>Corkscrew claw</p>  <p>Photo: Katrine Halgaard</p>	<p>Heel horn erosion</p> 	<p>Sole ulcer</p> 
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DATA



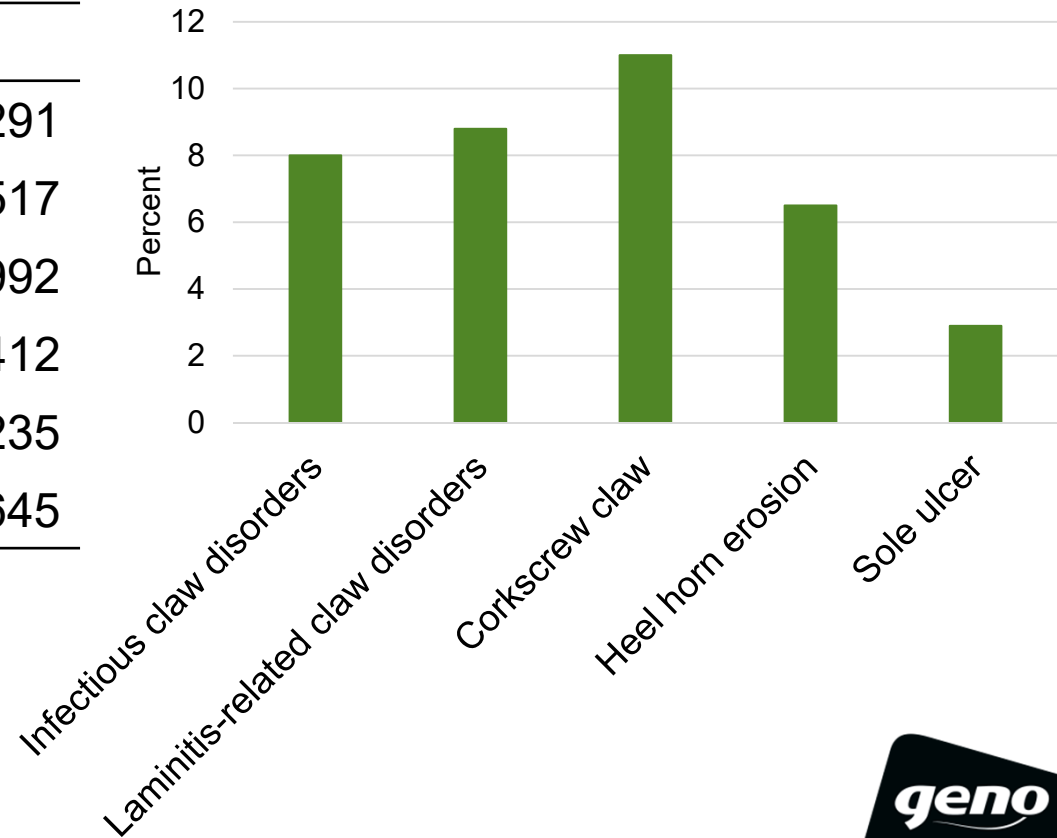
- Claw health records from Norwegian Dairy Herd Recording System
 - From 2004 to 2016
 - Lactating daughters of Norwegian Red AI sires
 - At least one record per parity
 - Herds with more than 10% or 10 normal claws reported
- In each parity a cow was defined as unaffected (0) or affected (1) for the 5 traits



DESCRIPTIVE STATISTICS

Data	
Records	410,291
Cows	263,517
Herds	6,992
Sires	2,412
Genotyped sires	2,235
Genotyped cows	2,645

Frequency of claw disorders
(% of all claw trimming records)



GENETIC PARAMETERS

Trait	Heritability
Corkscrew claw (CSC)	0.07
Infectious claw disorders (INF)	0.04
Laminitis-related claw disorders (LAM)	0.03
Heel horn erosion (HH)	0.04
Sole ulcer (SU)	0.03

Genetic correlations			
	LAM	CSC	SU
CSC	0.36		
INF	0.31	0.10	
HH			0.48



LINEAR ANIMAL MODEL

- Univariate model
 - Corkscrew claw
- Bivariate models
 - Infectious- and laminitis-related claw disorders
 - Heel horn erosion and sole ulcer
- Analyzed in DMU using BLUP and ssGBLUP

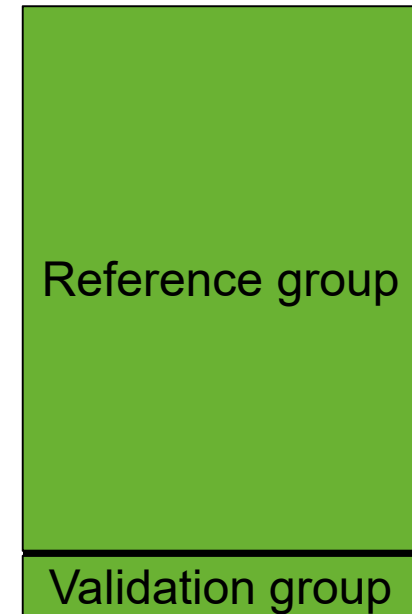
$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_{pe}\mathbf{pe} + \mathbf{Z}_h\mathbf{h} + \mathbf{Z}_a\mathbf{a} + \mathbf{e}$$

- Systematic effects:
 - parity, housing system, calving year and month, time of claw trimming and claw trimmer
- Random effects:
 - permanent environment, herd, animal, residual



10-FOLD CROSS VALIDATION

- 1,396 sires
with ≥ 30 daughters with claw health records
- Relationship matrices
 1. A-matrix
 2. H-matrix – sire genotypes
 3. H-matrix – sire and cow genotypes



INTERPRETATION

Correlation between

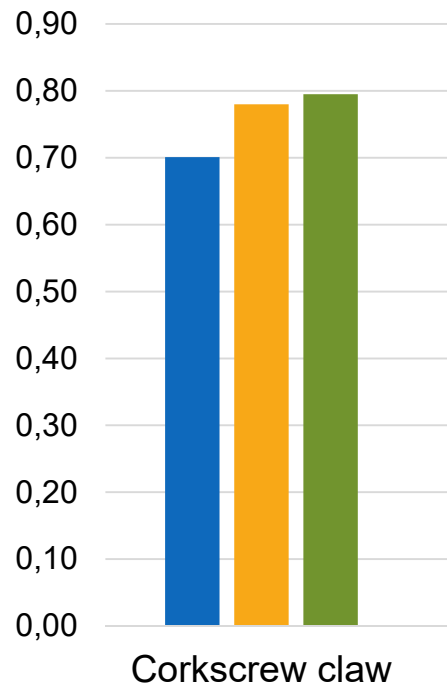
(G)EBV from validation sets* and GEBV from full dataset**

* **(G)EBV from BLUP or ssGBLUP**, dataset where phenotypes of daughters of validation sires are left out

** **GEBV from full dataset using ssGBLUP**, H-matrix including pedigree and genotypes of sires and cows



MEAN CORRELATION FROM CROSS VALIDATION



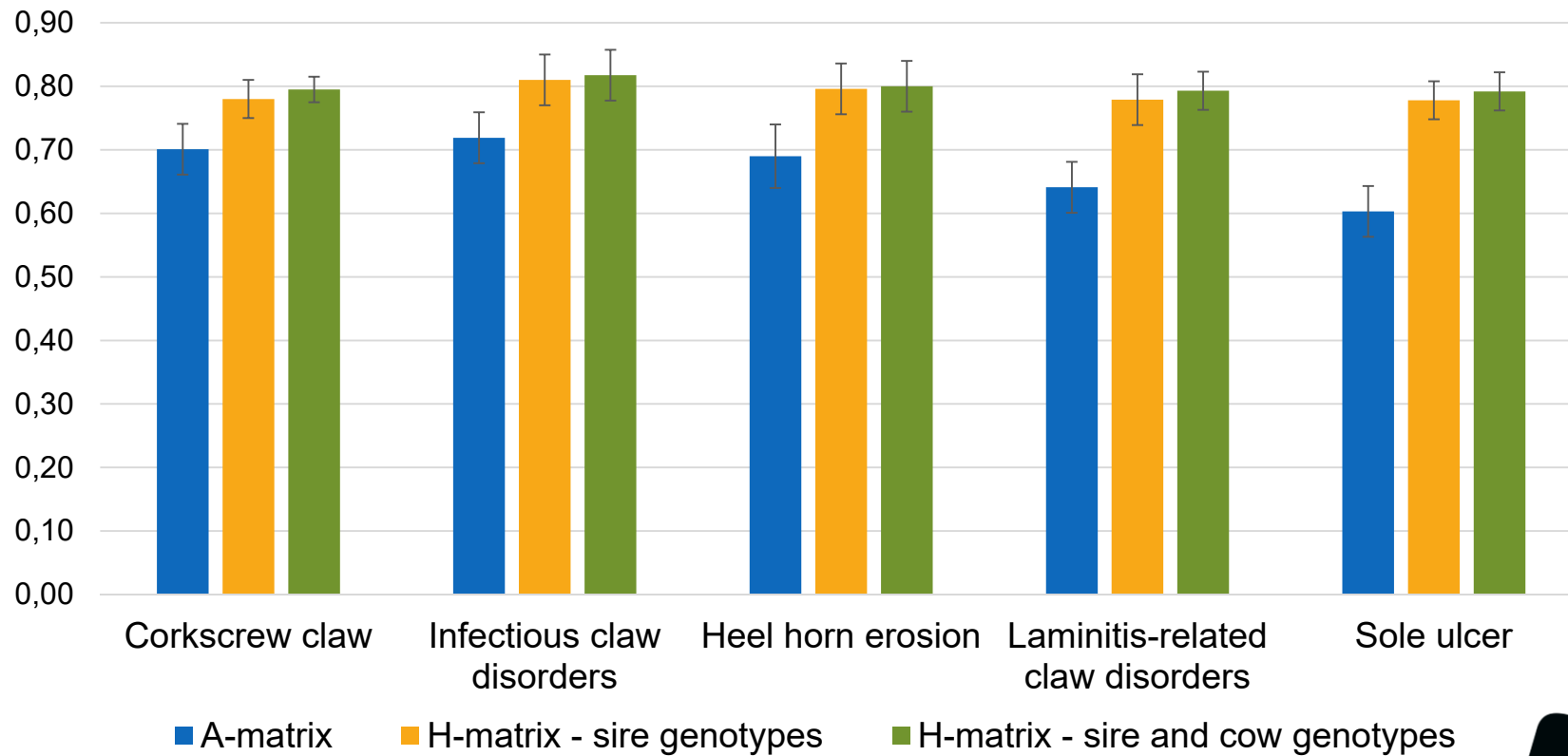
■ A-matrix

■ H-matrix - sire genotypes

■ H-matrix - sire and cow genotypes



STANDARD DEVIATION – CROSS VALIDATION



EFFECT OF COW GENOTYPES

- Inclusion of genotypes of cows resulted in marginal change
- Increase the number of cow genotypes
 - Select which cows to be genotyped
 - Randomly selected



SUMMARY

- Large effect of including sire genotypes
- Marginal improvement by including cow genotypes
- Increase number of phenotypes and genotypes

THANK YOU FOR THE ATTENTION

