

## Single-step genetic evaluation for claw health traits in Switzerland

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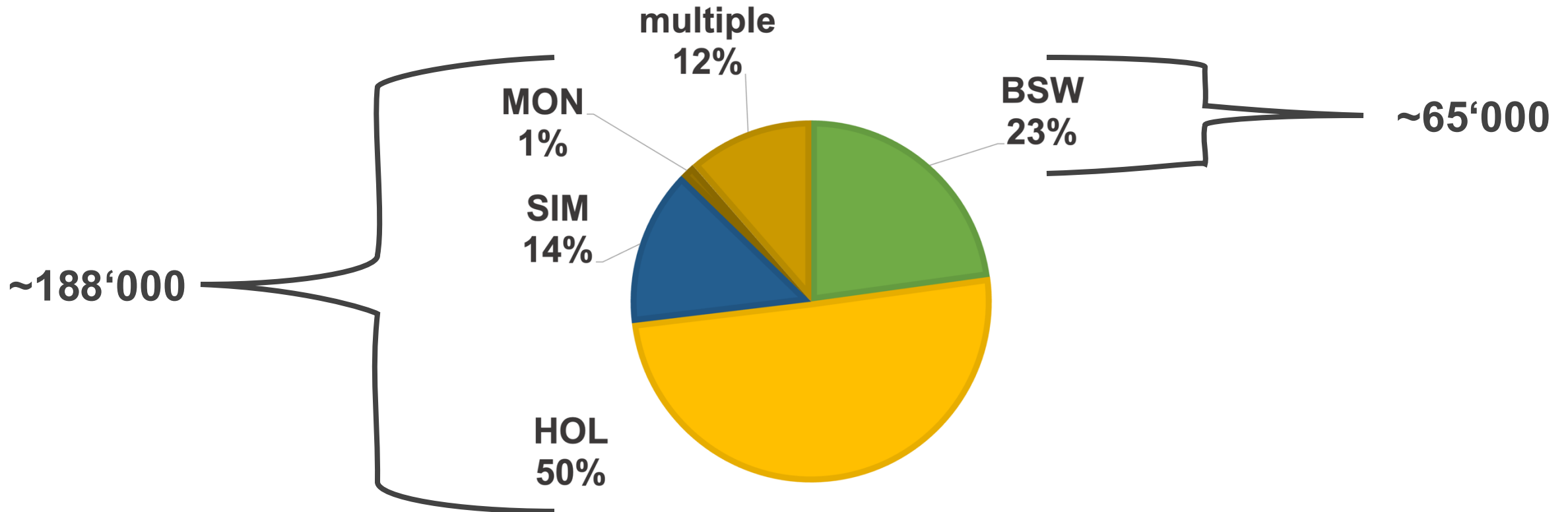
Interbull meeting, Louisville

# Claw health in Switzerland

- Third important culling reason
- Higher costs for farmers
- Resource project started in 2019
- Claw health data recorded by hoof trimmers during routine care
- Goal: Development of first breeding values for claw health
  - Single-step evaluation

# Raw data

## Data per breed



# Phenotypes and genotypes

## Phenotypes per animal and month:

- Brown Swiss:

33'464

- Holstein:

104'276

## Phenotype & genotype:

- Brown Swiss:

2'894

- Holstein:

5'284

## Genotyped animals:

- Brown Swiss:

146'609

- Holstein:

490'761

# Prevalences

<b>Trait</b>	<b>Brown Swiss (in %)</b>	<b>Holstein (in %)</b>
Dermatitis digitalis	7.8	20.9
White line disease	10.2	9.9
Other infectious diseases	37.6	45.8
Other non-infectious diseases	13.5	20.7

# Model: linear multi-trait animal model

- Fixed effects:
  - Parity
  - Trimmer x year
  - Stage of lactation
  - Year-month,
  - Recombination and heterosis  
(only for HOL & SIM)
- Random effects:
  - Herd-year-season
  - Permanent environmental effect
- Repeatability model
- Binary trait (0/1 coded)

# ssGTaBLUP

## Reducing computations by ssGTBLUP

Assume:  $\mathbf{G} = \mathbf{G}_0 + \mathbf{C}$

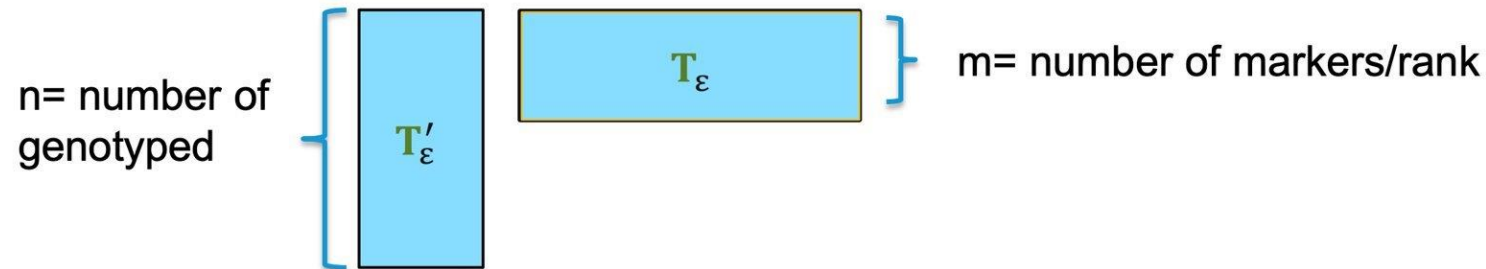
where  $\mathbf{G}_0 = \mathbf{Z}\mathbf{Z}'$  and  $\mathbf{G}_\varepsilon = \mathbf{G}_0 + \varepsilon\mathbf{I} \rightarrow \mathbf{G}_\varepsilon^{-1} = \frac{1}{\varepsilon}\mathbf{I} - \mathbf{T}_\varepsilon'\mathbf{T}_\varepsilon$

where  $\mathbf{T}_\varepsilon = \frac{1}{\varepsilon}\mathbf{L}_\varepsilon^{-1}\mathbf{Z}'$  and  $\mathbf{L}_\varepsilon\mathbf{L}_\varepsilon' = \frac{1}{\varepsilon}\mathbf{Z}'\mathbf{Z} + \mathbf{I}$

Woodbury matrix identity

$\mathbf{T}_\varepsilon$  has size  $n \times m$

→ Number of computations is  $2nm$  instead of  $n^2$

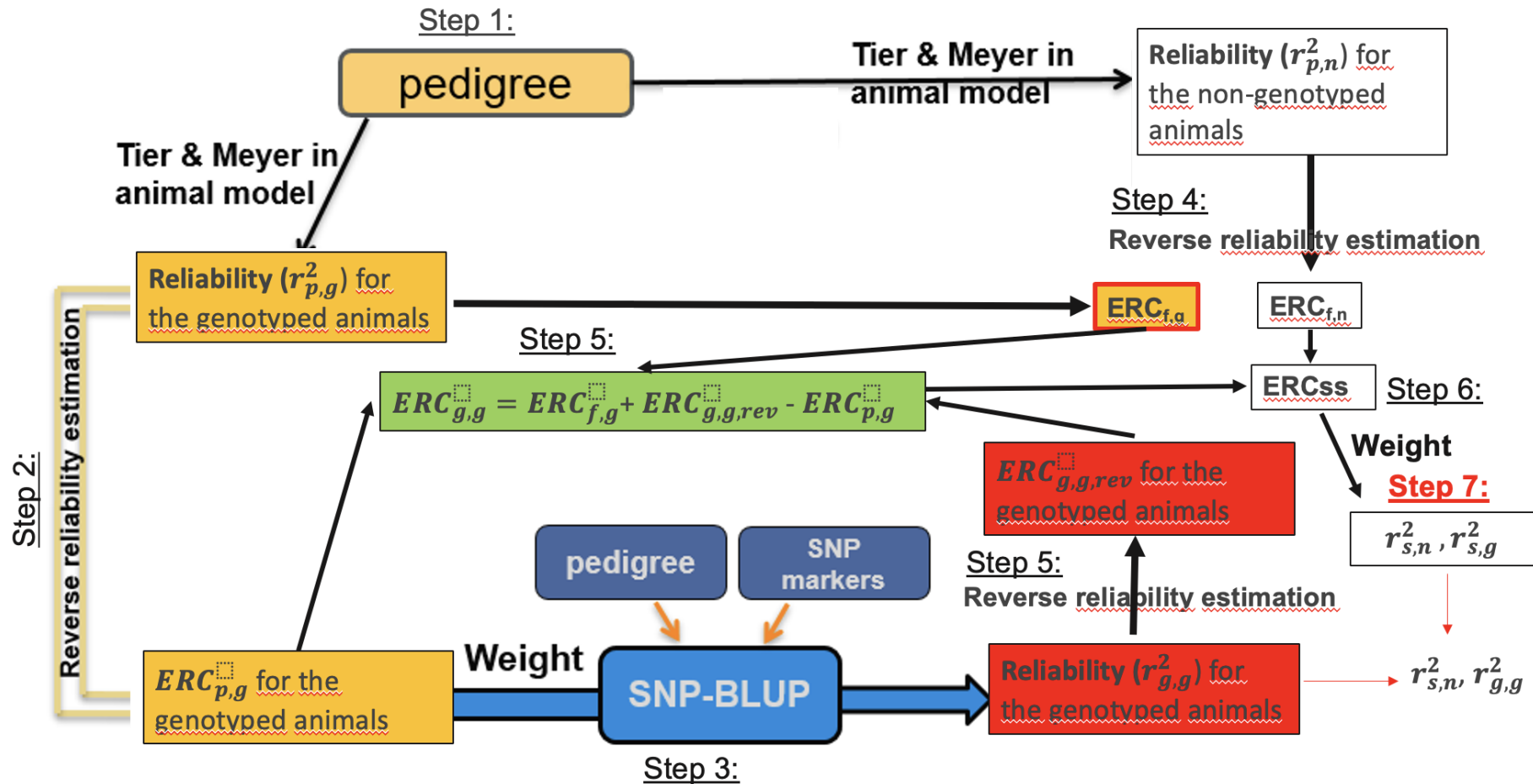


Size of  $\mathbf{T}_\varepsilon$  matrix is the same as the original marker matrix.

ssGTBLUP gives the same solutions as ssGBLUP with  $\mathbf{G}_\varepsilon^{-1}$  (e.g., Koivula et al. WCGALP 2018)

Slide by Ismo Strandén,  
WCGALP 2018

# Reliability estimation





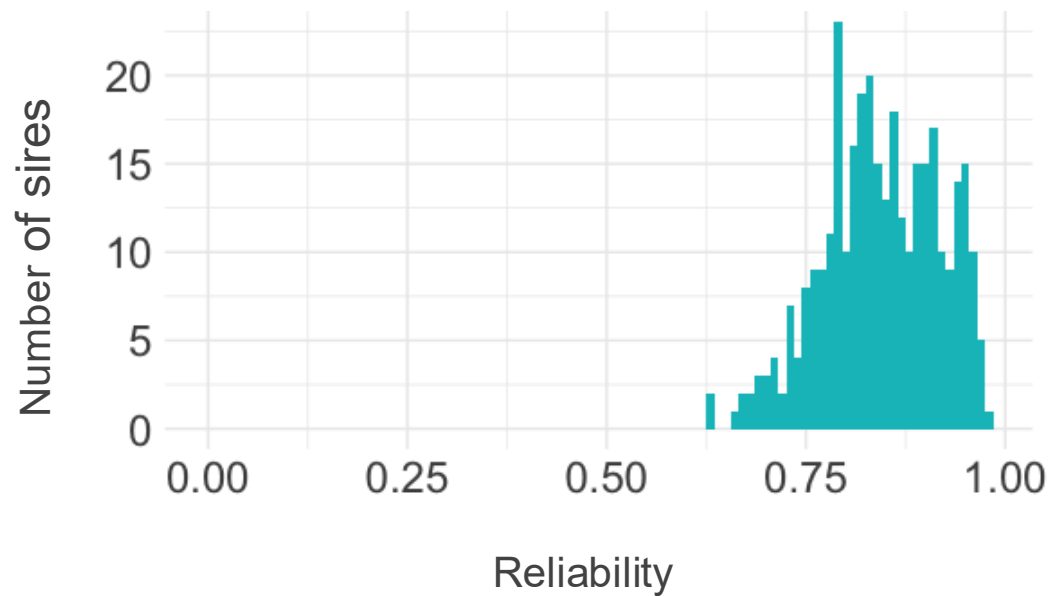
# Heritabilities

Trait	Brown Swiss	Holstein
Dermatitis digitalis	0.03 (0.006)	0.09 (0.003)
White line disease	0.07 (0.009)	0.05 (0.004)
Other infectious diseases	0.04 (0.004)	0.04 (0.002)
Other non-infectious diseases	0.04 (0.007)	0.06 (0.004)

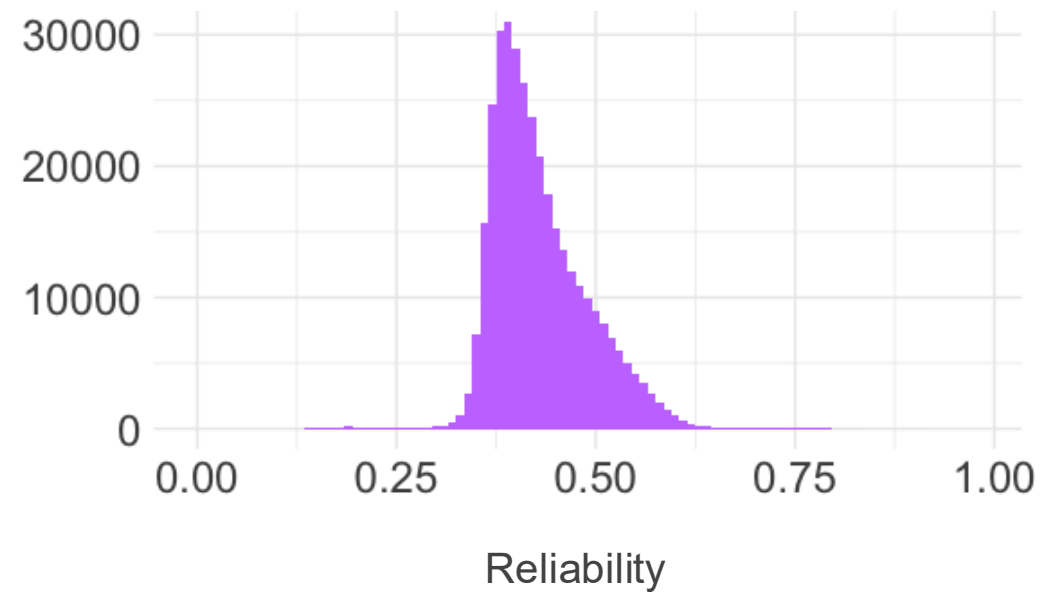
# Reliabilities

## Dermatitis digitalis - Holstein

Proven bulls

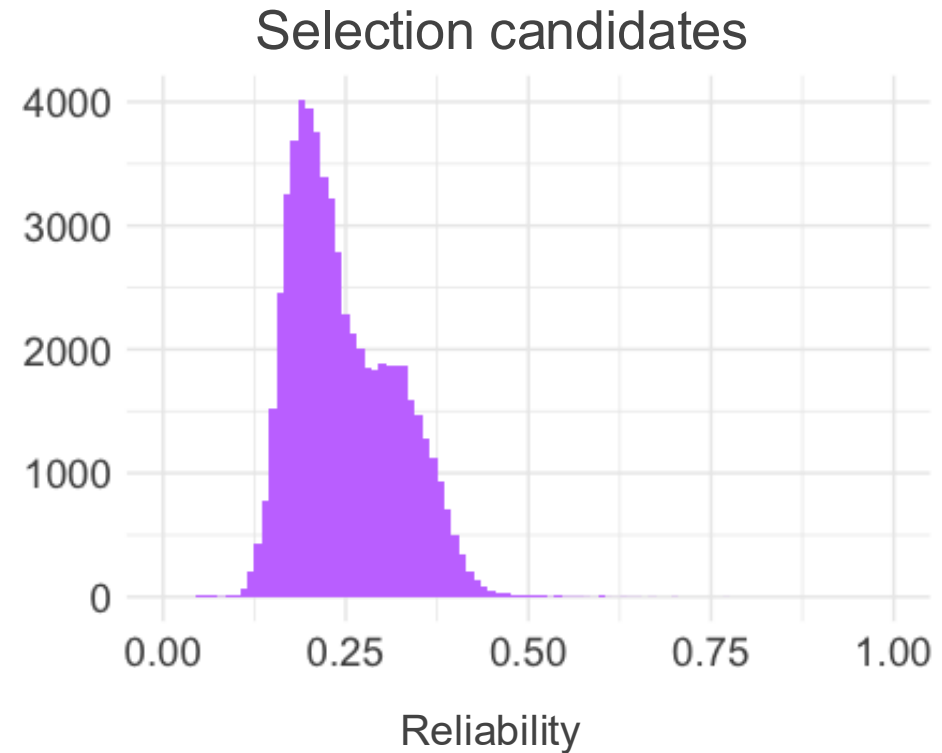
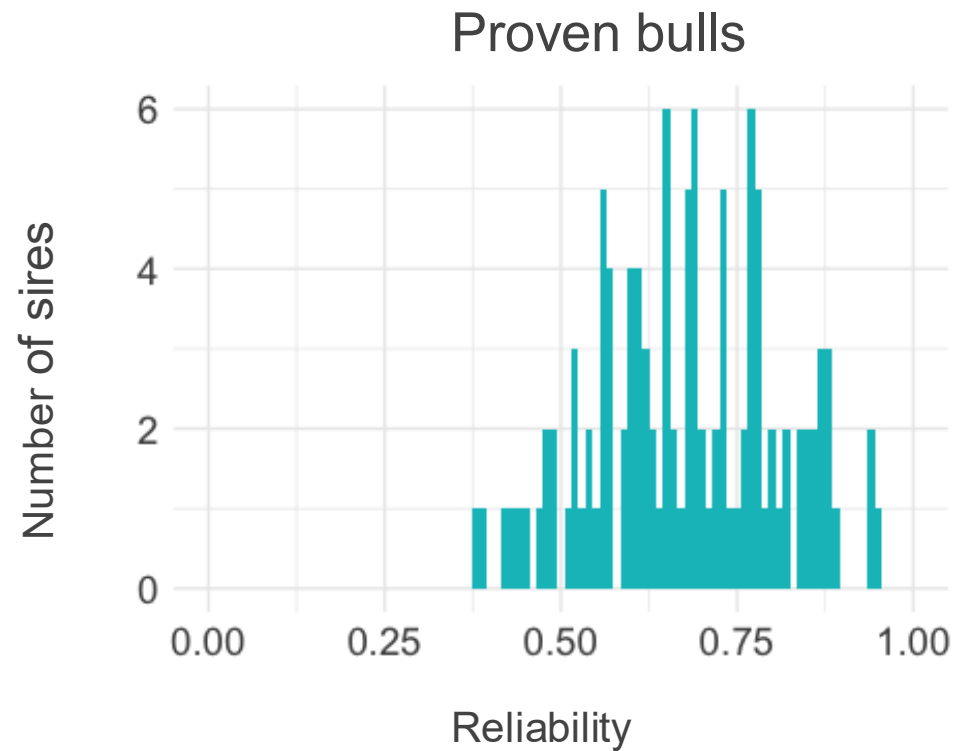


Selection candidates



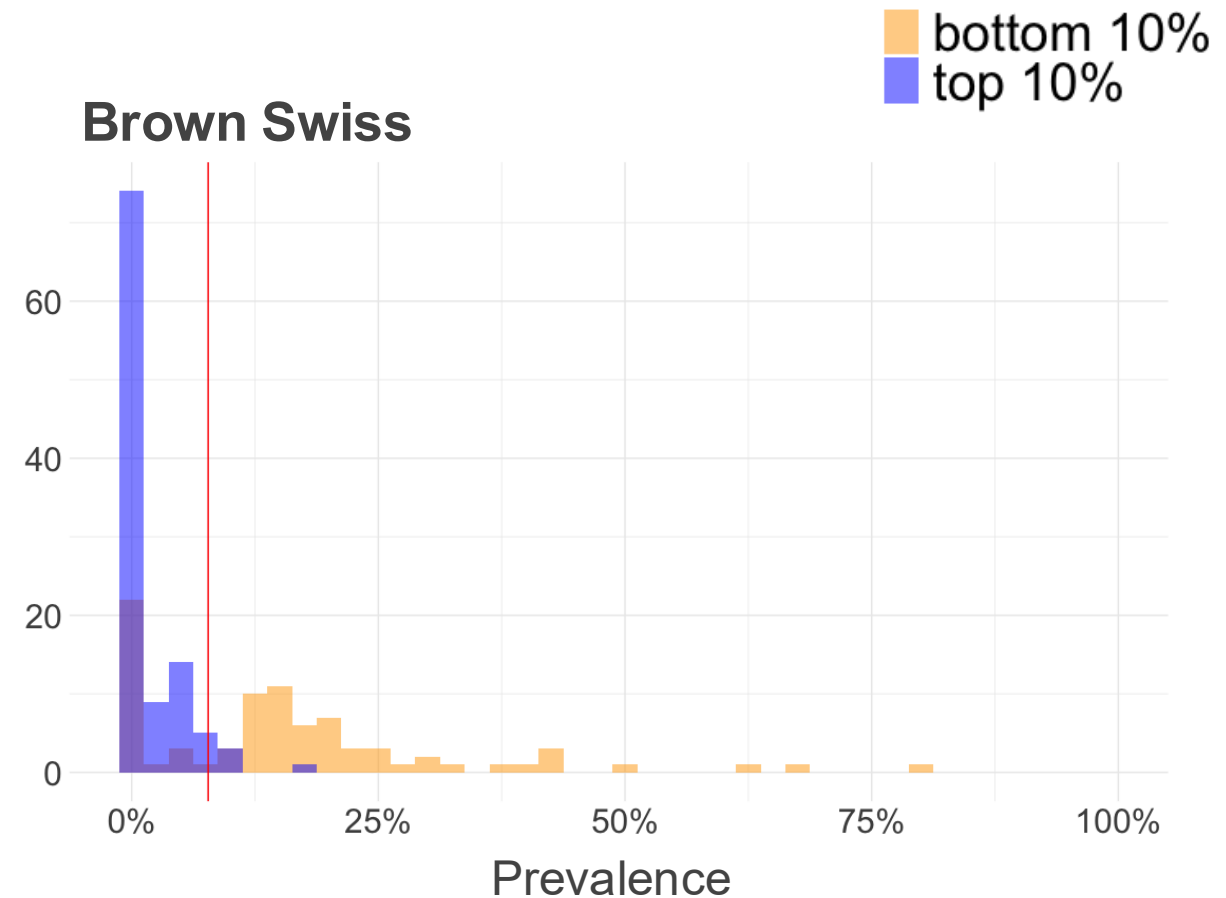
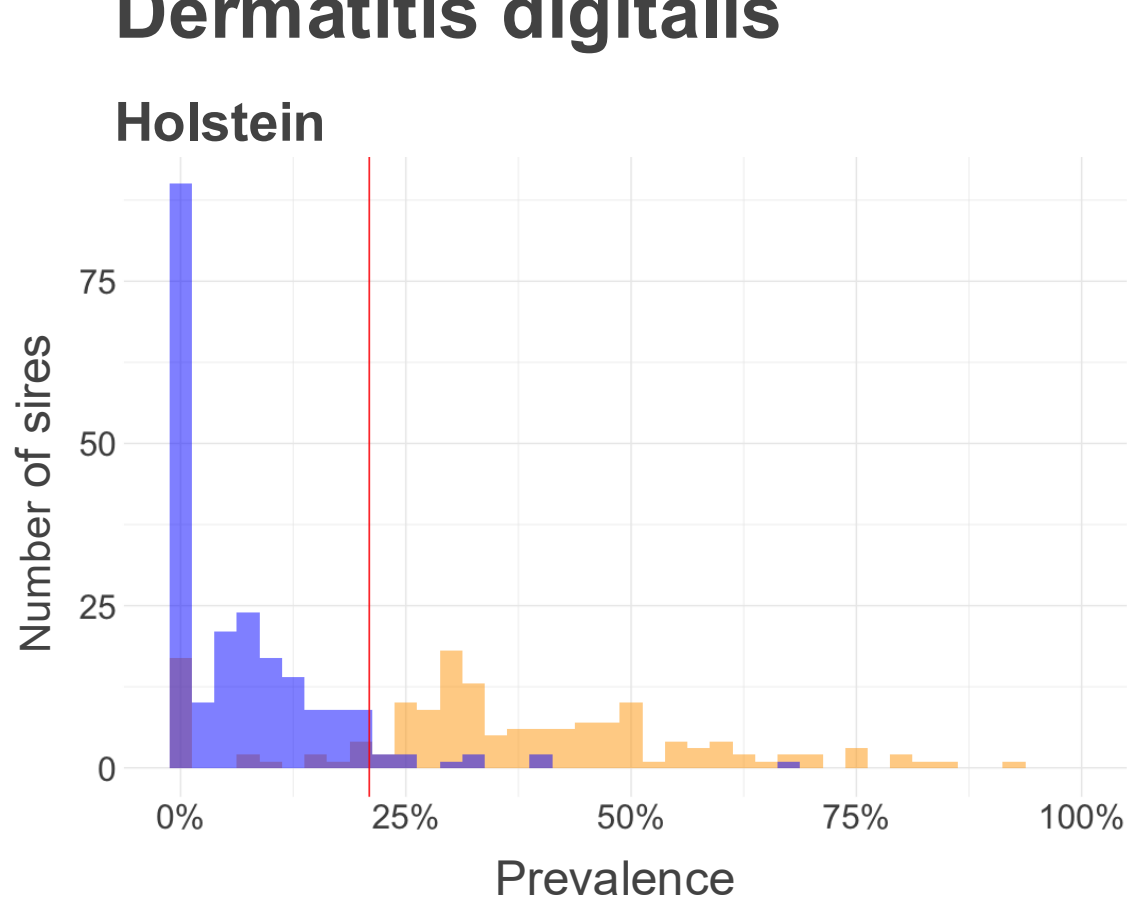
# Reliabilities

## Dermatitis digitalis – Brown Swiss



# Top-Bottom comparison

## Dermatitis digitalis



# Results

- Differences daughter prevalence top-bottom comparison: 14% - 35%
- Final result: claw health index
  - Evaluation specific weights
  - First publication in April 2025

# Challenges

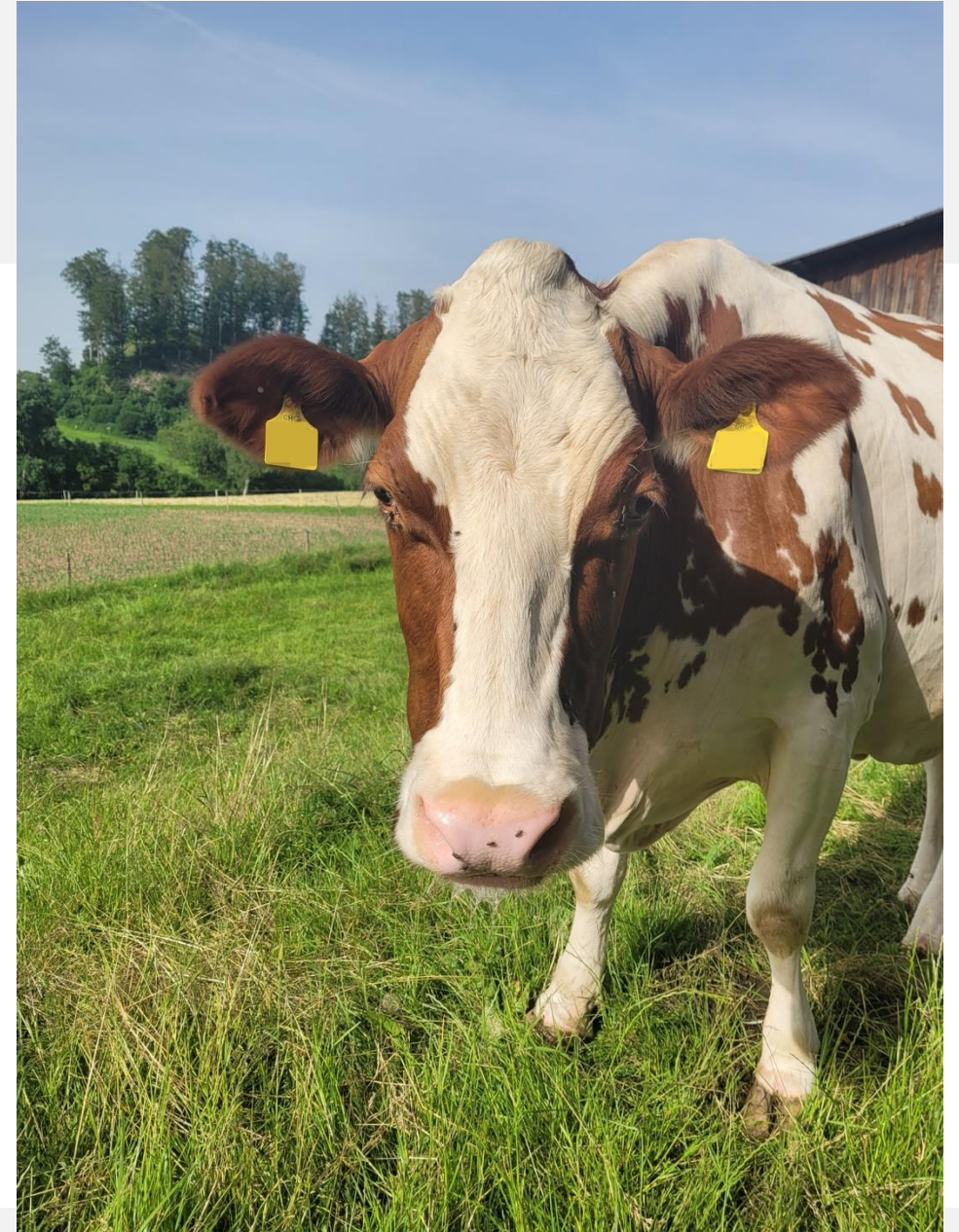
- Limited number of phenotypes
- Large number of genotyped animals with a weak genetic relationship with those providing phenotypic data
  - Definition of genetic groups
  - Avoid outliers

# Outlook


- Participation in the development of the new MACE EBV for claw health traits
  - Test run September 2025
- MACE integration

# Thank you for your attention!

Questions?



Thanks for funding!

 Schweizerische Eidgenossenschaft  
Confédération suisse  
Confederazione Svizzera  
Confederaziun svizra

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Office fédéral de l'agriculture OFAG  
Ufficio federale dell'agricoltura UFAG  
Uffizi federal d'agricultura UFAG

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