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Genetic evaluation of claw health traits accounting for potential preselection of cows to be trimmed

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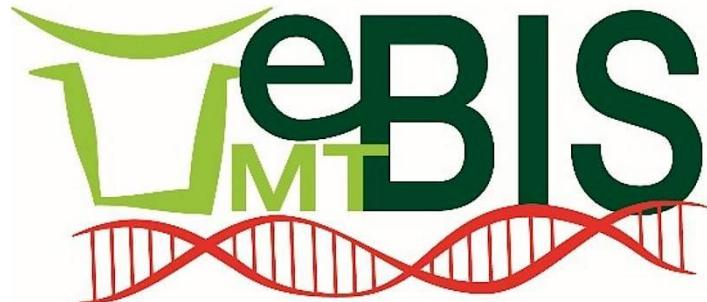
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Acknowledgments



APIS-GENE
Invest Innovate Exploit



Introduction

► Claw health: major issue in dairy cattle

- Welfare
- Economic losses
- Frequency



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► Objectives

- Develop a genetic evaluation model
- Deal with preselection

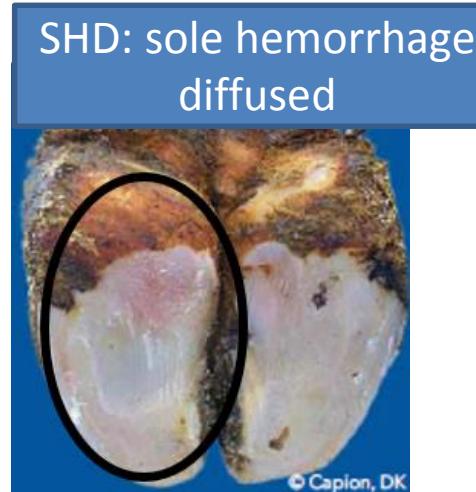
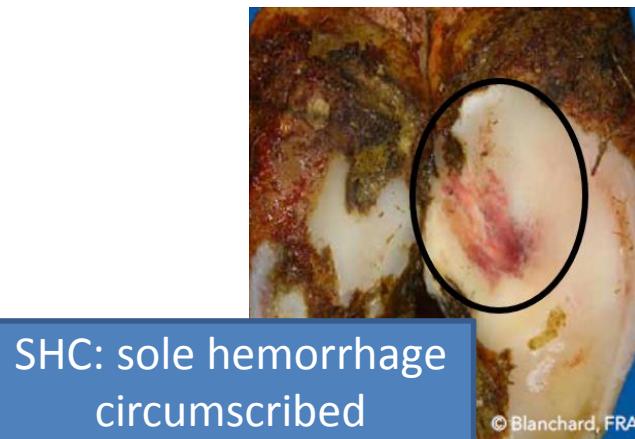
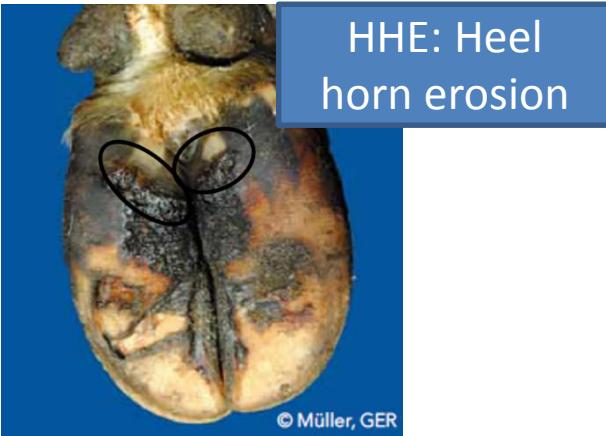
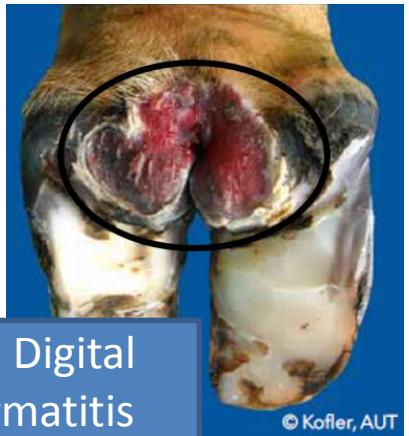


Traits

- ▶ Claw health traits considered: claw lesions (ICAR defined)
- ▶ Presence/absence of the lesion

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Infectious



Non-infectious



Data

- ▶ **Phenotypes recorded by trained trimmers**
- ▶ **Data collection: April 2014 – August 2016**
- ▶ **Breed: Prim'Holstein**
- ▶ **Data selection**
 - ▶ Lactation: 1 – 3
 - ▶ $1 \leqslant \text{DIM} \leqslant 550$
 - ▶ Official milk recording
 - ▶ Both hind claws trimmed
 - ▶ ≥ 5 cows per visit
 - ▶ 1st trimming information only
- ▶ **25 511 trimmed cows + 31 888 contemporary non-trimmed cows**

Prevalences

► Prevalences on trimmed cows

Digital Dermatitis	29%
Heel Horn Erosion	53%
Interdigital Hyperplasia	8%
Sole Hemorrhage Circumscribed	16%
Sole Hemorrhage Diffused	43%
Sole Ulcer	7%
White Line Fissure	14%
At least one lesion	82%

Statistical model

- Multi-trait linear animal model (Wombat, Meyer 2007)

- $y_{ijkl} = \mu + hv_i + p_j + s_k + a_l + \varepsilon_{ijkl}$

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- p_j : fixed effect of parity
- s_k : fixed effect of lactation stage
- a_l : animal genetic effect, ε_{ijkl} : residual error

Scenarios to account for preselection

► Scenario 1:

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- 7-trait model

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- Non-trimmed cows « healthy » (0 for all lesion)
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- Trimmed cows + contemporary non-trimmed cows
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► Scenario 3:

- Trimmed cows + contemporary non-trimmed cows
- No lesion phenotype for non-trimmed cows (missing value for all lesions)
- 8-trait model: 7 lesions + trimming status: 1 if trimmed, 0 if not

Preselection: are traits with/without non-trimmed cows the same traits?

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- ▶ **Genetic correlations between identical traits in scenario 1 (trimmed cows only) and scenario 2 (healthy non-trimmed cows)**

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- ▶ **Genetic correlations between identical traits in scenario 1 (trimmed cows only) and scenario 2 (healthy non-trimmed cows)**

Lesion	Genetic correlation
Digital dermatitis	0.93 (0.06)
Heel horn erosion	0.99 (0.11)
Interdigital hyperplasia	0.99 (0.10)
Sole hemorrhage circumscribed	0.98 (0.20)
Sole hemorrhage diffused	0.74 (0.32)
Sole ulcer	1.00 (0.11)
White line fissure	1.00 (0.10)

Preselection effect - heritabilities

- ▶ Heritabilities on the underlying scale, in the three scenarios

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Lesion	Scenario 1	Scenario 2	Scenario 3
Digital dermatitis	0,14 (0,02)	0,14 (0,02)	0,15 (0,02)
Heel horn erosion	0,06 (0,01)	0,06 (0,01)	0,07 (0,01)
Interdigital hyperplasia	0,27 (0,04)	0,27 (0,03)	0,29 (0,04)
Sole hemorrhage circumscribed	0,05 (0,01)	0,05 (0,01)	0,05 (0,01)
Sole hemorrhage diffused	0,03 (0,01)	0,02 (0,01)	0,03 (0,01)
Sole ulcer	0,16 (0,03)	0,17 (0,02)	0,18 (0,03)
White line fissure	0,14 (0,02)	0,11 (0,02)	0,14 (0,02)

Preselection effect – genetic correlations

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► Genetic correlations among infectious traits

Traits	Scenario 1	Scenario 2	Scenario 3
Digital dermatitis – heel horn erosion	0.66 (0.10)	0.75 (0.06)	0.69 (0.08)
Digital dermatitis – interdigital hyperplasia	0.74 (0.06)	0.79 (0.05)	0.76 (0.06)
Heel horn erosion – interdigital hyperplasia	0.60 (0.11)	0.67 (0.07)	0.64 (0.09)

Preselection effect – genetic correlations

► Genetic correlations between infectious and non-infectious traits

Traits	Scenario 1	Scenario 2	Scenario 3
Digital dermatitis – sole hemorrhage circumscribed	-0.37 (0.13)	0.10 (0.12)	-0.29 (0.13)
Digital dermatitis – sole hemorrhage diffused	-0.23 (0.15)	0.30 (0.12)	-0.11 (0.14)
Digital dermatitis – sole ulcer	0.06 (0.11)	0.33 (0.09)	0.12 (0.11)
Digital dermatitis – white line fissure	-0.14 (0.11)	0.04 (0.10)	-0.12 (0.11)
Heel horn erosion – sole hemorrhage circumscribed	-0.20 (0.17)	0.32 (0.12)	-0.09 (0.16)
Heel horn erosion – sole hemorrhage diffused	-0.19 (0.18)	0.55 (0.11)	0.03 (0.16)
Heel horn erosion – sole ulcer	0.20 (0.13)	0.46 (0.09)	0.28 (0.12)
Heel horn erosion – white line fissure	-0.07 (0.13)	0.15 (0.11)	-0.05 (0.12)

Preselection effect – conclusions

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- ▶ Scenario 2: bias in genetic correlations: “Non-trimmed cows = healthy” hypothesis probably false
- ▶ Scenario 3: exhaustive information

Genetic parameters

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	Infectious traits				Non-infectious traits				
	DD	HHE	IH	SHC	SHD	SU	WLF	Trim	
DD	0.09 (0.01)	0.69 (0.08)	0.76 (0.06)	-0.29 (0.13)	-0.11 (0.14)	0.12 (0.11)	-0.12 (0.11)	0.47 (0.09)	
HHE		0.05 (0.01)	0.64 (0.09)	-0.09 (0.16)	0.03 (0.16)	0.28 (0.12)	-0.05 (0.12)	0.77 (0.08)	
IH			0.09 (0.01)	-0.08 (0.14)	-0.12 (0.15)	0.05 (0.11)	-0.08 (0.11)	0.48 (0.09)	
SHC				0.02 (0.01)	0.55 (0.18)	0.81 (0.12)	0.44 (0.15)	0.23 (0.14)	
SHD					0.02 (0.01)	0.31 (0.16)	0.08 (0.16)	0.34 (0.14)	
SU						0.05 (0.01)	0.58 (0.10)	0.40 (0.10)	
WLF							0.06 (0.01)	0.03 (0.11)	
Trim								0.04 (0.01)	

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- ▶ Low heritabilities => genetic variability? => Coefficients of genetic variation
- ▶ Two genetically distinct lesion groups
- ▶ Moderate to high genetic correlations with trimming status

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- ▶ => implementation of genetic evaluation
- ▶ Want to know more?



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Thank you all for your attention!