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

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I. Croue[1,2,3], F. Fikse[4], K. Johansson[4], E. Carlén[4], G. Thomas[5],
H. Leclerc[1] and V. Ducrocq[2]

[1] Institut de l'Élevage, UMR1313, [2] GABI, INRA, AgroParisTech, Université Paris Saclay, 78350 Jouy-en-Josas, France
[3] AgroParisTech, 16 rue Claude Bernard, 75005 Paris, France
[4] Växa Sverige, Institutionen för Husdjursgenetik, SLU, Ulls väg 26, 756 51 Uppsala, Sweden
[5] Institut de l'Élevage, Chambre régionale d'agriculture de Picardie, 19 bis rue Alexandre Dumas, 80096 Amiens Cedex 3, France

Acknowledgments

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Introduction

- **Claw health: major issue in dairy cattle**
  - Welfare
  - Economic losses
  - Frequency

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  - Develop a genetic evaluation model
  - Deal with preselection

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

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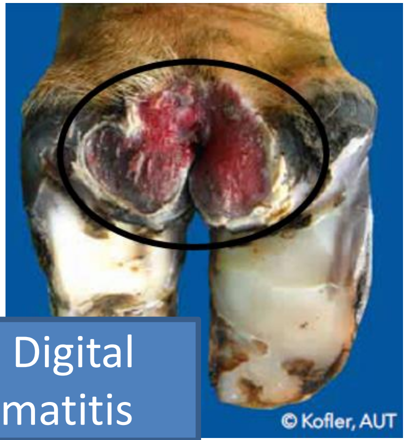
DD: Digital Dermatitis

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HHE: Heel horn erosion

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IH: Interdigital hyperplasia

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SHC: sole hemorrhage circumscribed

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SHD: sole hemorrhage diffused

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SU: sole ulcer

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WLF: white line fissure

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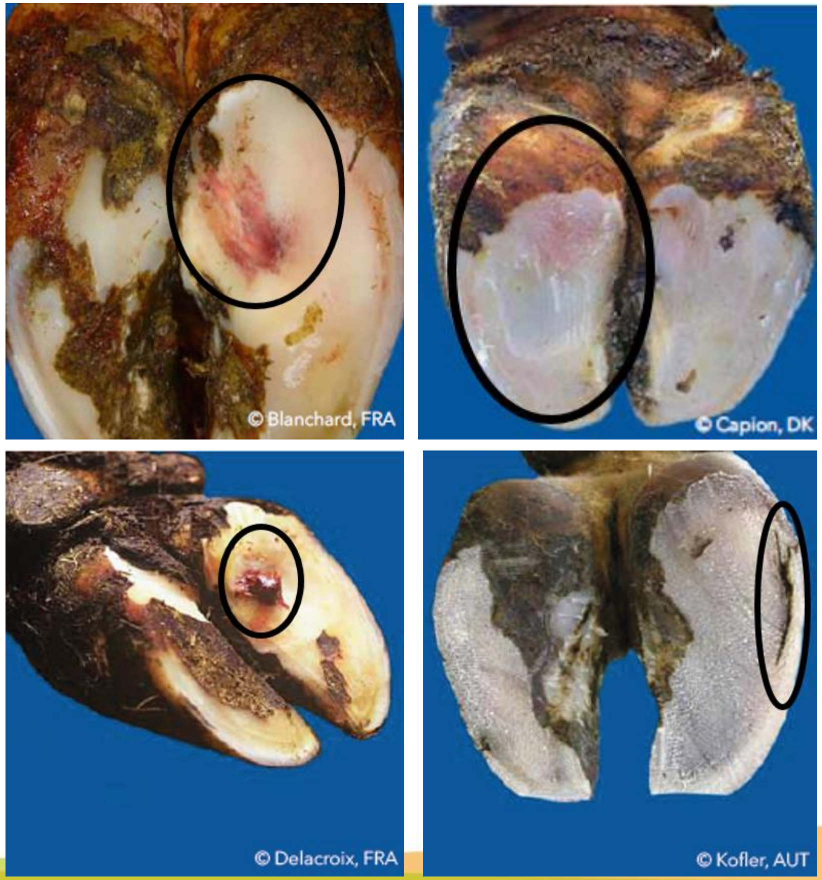
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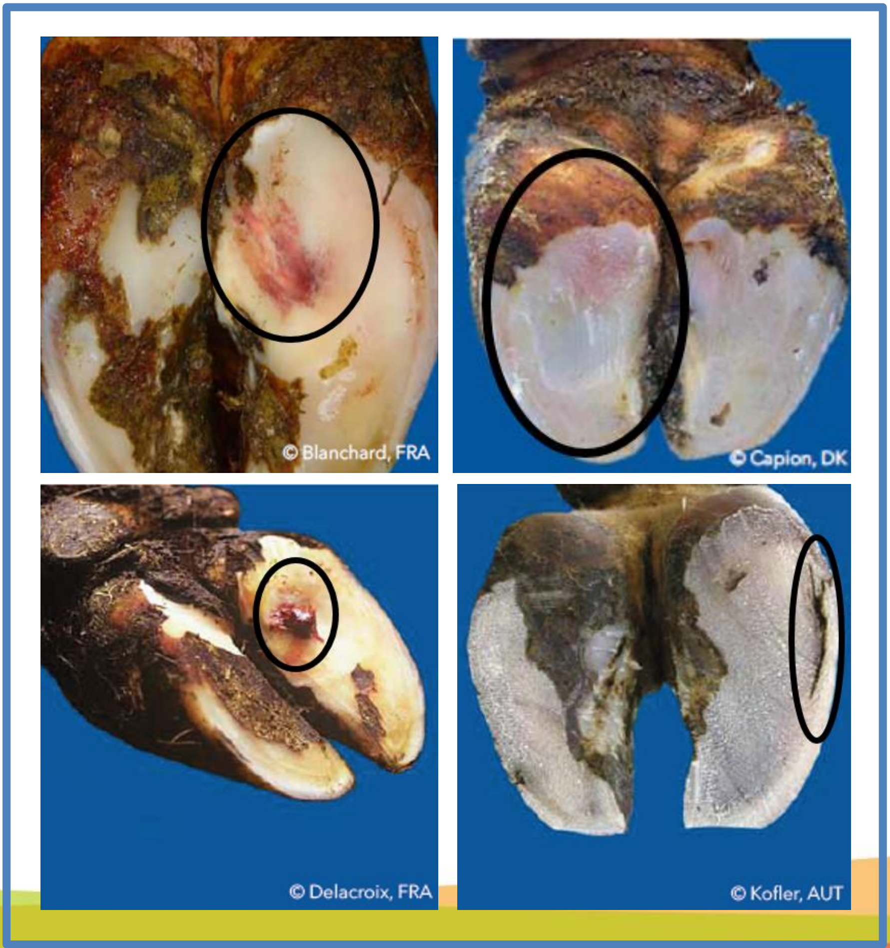
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Data

- **Phenotypes recorded by trained trimmers**
- **Data collection: April 2014 – August 2016**
- **Breed: Prim'Holstein**
- **Data selection**
  - Lactation: 1 – 3
  - 1 <= DIM <= 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 effet 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:**
  - trimmed cows only
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- **Scenario 2:**
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  - Non-trimmed cows « healthy » (0 for all lesion)
  - 7-trait model
- **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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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 fissue	-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 fissue	-0.07 (0.13)	0.15 (0.11)	-0.05 (0.12)

Preselection effect – conclusions

- **Low effect of preselection on heritabilities**

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- **Scenario 2: bias in genetic correlations: “Non-trimmed cows = healthy” hypothesis probably false**

Preselection effect – conclusions

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- **Scenario 3: exhaustive information**

Genetic parameters

- **Genetic parameters in scenario 3**

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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)
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- Moderate to high genetic correlations with trimming status

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- Want to know more?

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