Genetic Parameters for Hoof Disorders in Dairy Cattle

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Why care about lameness?

Heritability, what's all that about?

Genotype

Environment

Phenotype

σ^2 additive genetic variance

σ^2 non-additive genetic variance

σ^2 permanent environmental variance

σ^2 temporary environmental variance

σ^2 phenotypic variance

$$\text{Heritability } (h^2) = \frac{\sigma^2 \text{ additive genetic variance}}{\sigma^2 \text{ phenotypic variance}}$$

Objectives

- Quantify the contribution of additive genetics to variation in the presence and severity of hoof disorders

- Quantify their genetic correlation with mobility score

Materials & Methods

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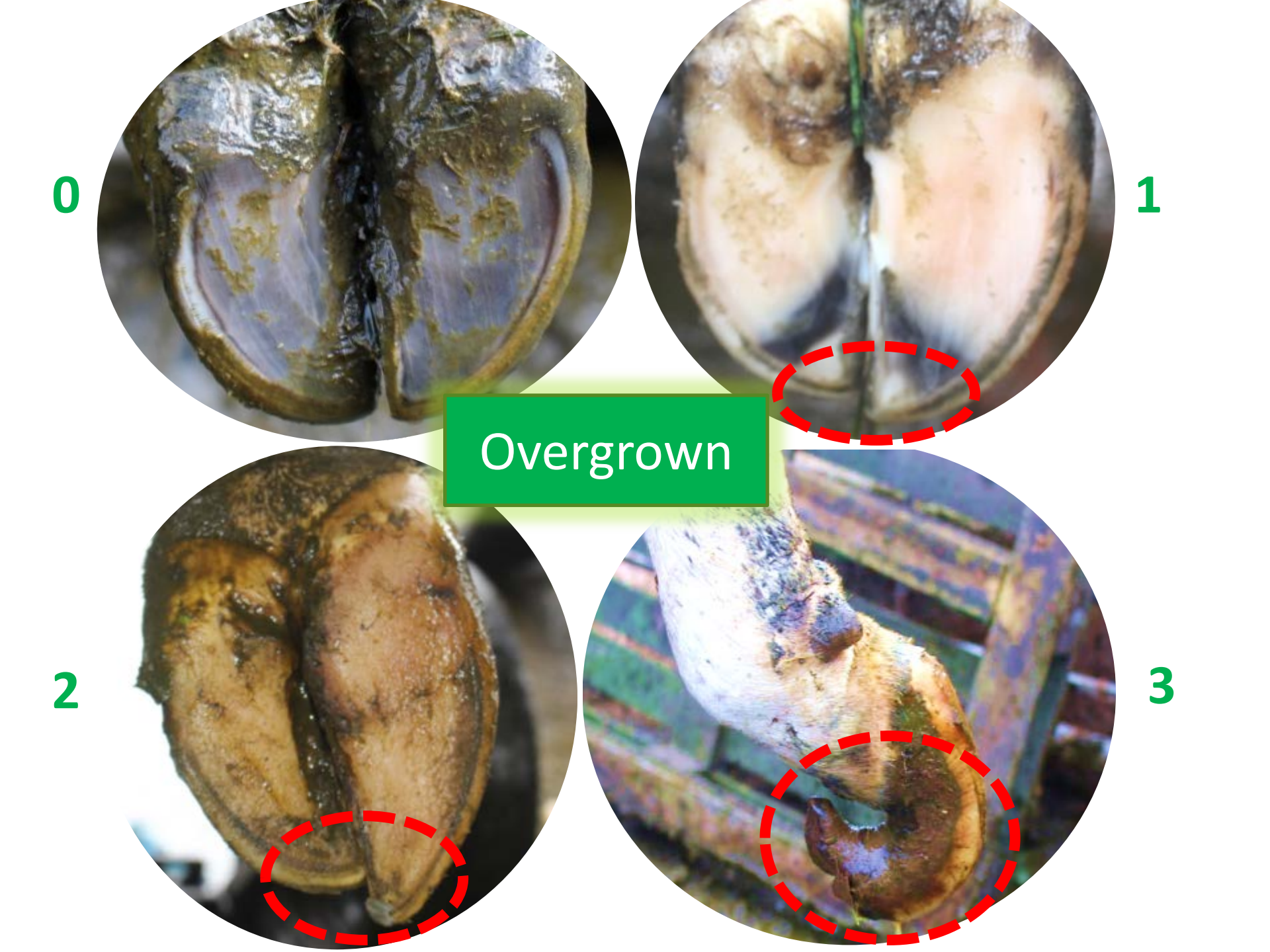
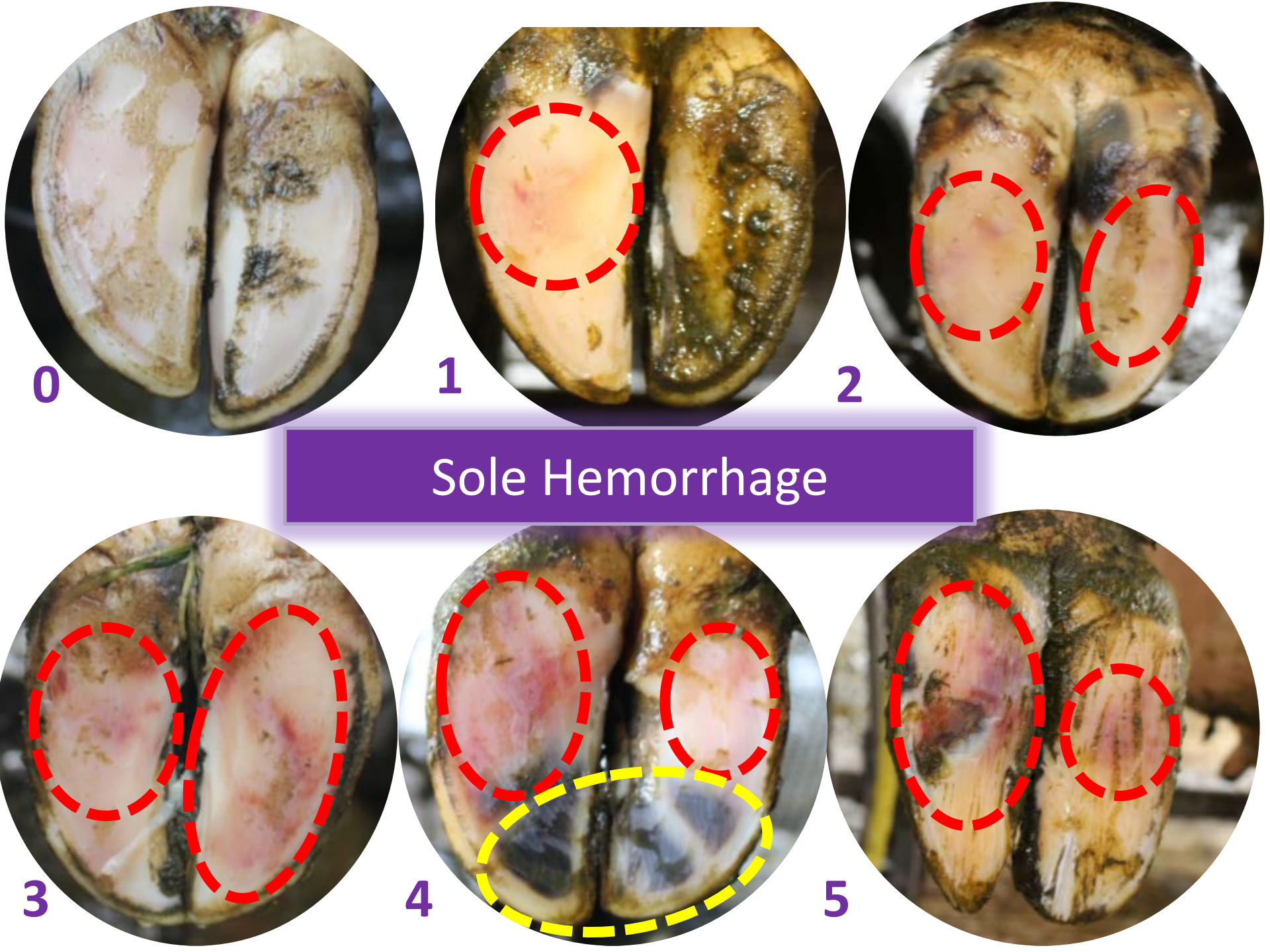
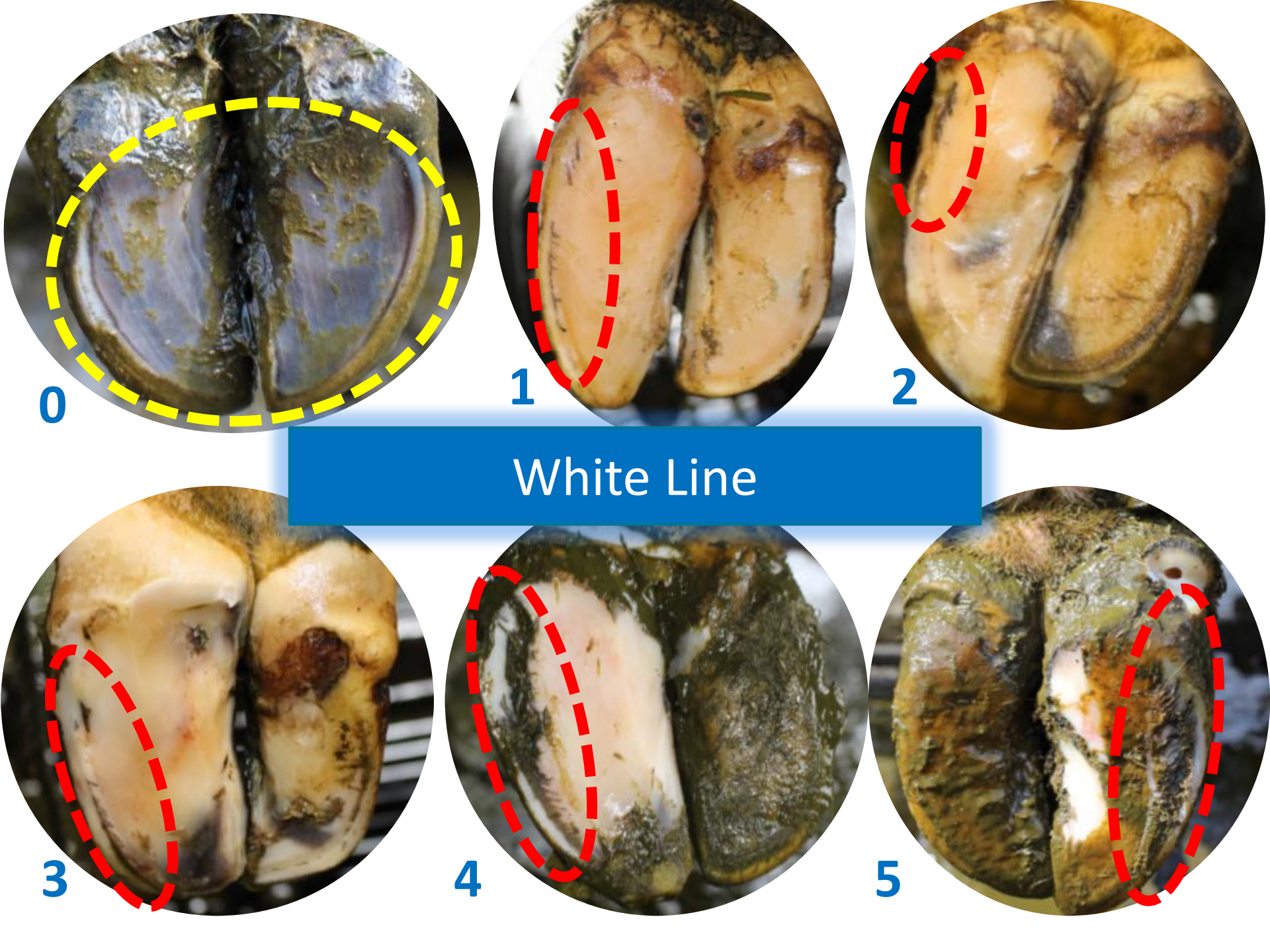
Hoof Trimming


0
1
Overgrown
2
3


0
1
2
Sole Hemorrhage
3
4
5


0
1
2
White Line
3
4
5

0

1

4,700 cows mobility scored

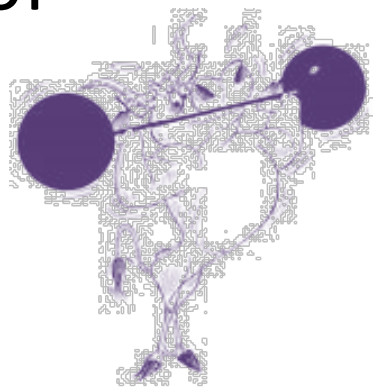
2

3

Poster 36.11 N.Byrne *et al.*

Data Edits

- Purchases after 01/01/2015
- Calving event > 365 days prior to hoof trimming
- Unknown sires
- Contemporary groups (HYS) < 5



6,966 animals in 222 HYS remain

Model

- Hoof disorder severity or presence — ***Dependent Variable***
- Parity (1, 2, 3, 4, 5, >5) — ***Fixed Effects***
- Age at calving relative to parity median (months)
- Stage of lactation (months)
- Interaction between hoof disorder scorer and trimming date
- Heterosis and recombination loss coefficients
- Herd-Year-Season of calving
- Direct additive genetic — ***Random Effects***
- Residual

Binary Trait Results

Overgrown

Prevalence = 52%
h^2 = 0.08 (0.02)
σ_g = 0.13

Sole Hemorrhage

Prevalence = 53%
h^2 = 0.24 (0.03)
σ_g = 0.22

White Line

Prevalence = 49%
h^2 = 0.12 (0.02)
σ_g = 0.15

Severity Trait Results

Overgrown

$h^2 = 0.16\ (0.03)$
$\sigma_g = 0.30$

Sole Hemorrhage

$h^2 = 0.26\ (0.03)$
$\sigma_g = 0.66$

White Line

$h^2 = 0.21\ (0.03)$
$\sigma_g = 0.57$

Genetic Correlations

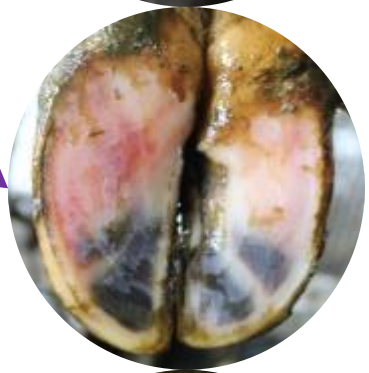
Mobility score

$h^2 = 0.08\ (0.03)$

$\sigma_g = 0.16$

Overgrown

0.37 (0.19)



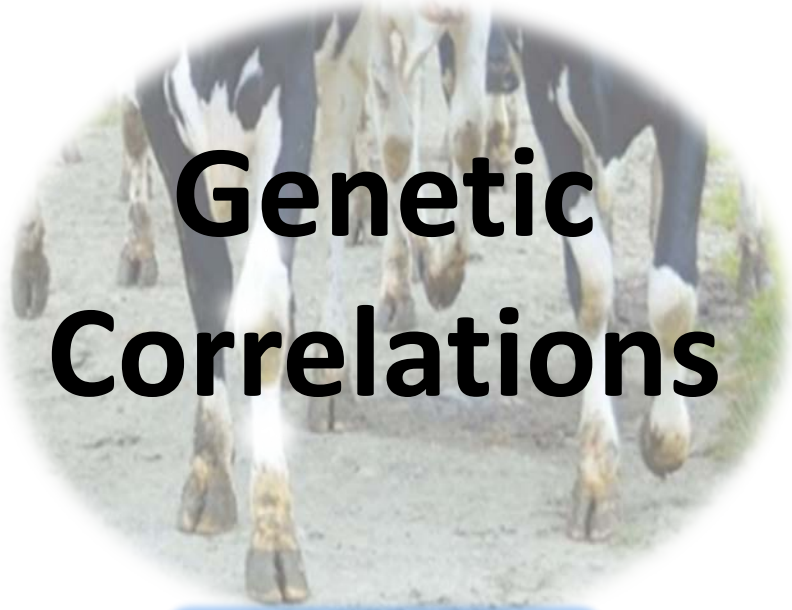
Sole Hemorrhage

0.13 (0.17)

White Line

0.18 (0.18)

Genetic Correlations



Overgrown

Sole Hemorrhage

White Line

0.19 (0.13)

0.53 (0.18)

0.36 (0.11)

Conclusions

- High phenotypic prevalence
- Ample genetic variation exists
- Moderate to highly heritability traits
- Positive genetic correlations between traits

Department of
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Talmhaíochta,
Bia agus Mara

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