

Heritability of insect bite hypersensitivity in Dutch Friesian breeding mares

Anouk Schurink

Bart Ducro
Johan van Arendonk

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Animal Breeding & Genomics Centre

Introduction - IBH

Insect bite hypersensitivity (IBH)

- Chronic, recurrent, seasonal dermatitis
- Allergic reaction: intense itch
 - Cause: bites certain *Culicoides* spp.
- Clinical symptoms
- Discomfort and disfiguration
- No effective treatment or prevention



Culicoides obsoletus



Affected pony



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Introduction - IBH

- Multifactorial cause
- Heritability estimates (0.08-0.36)
 - Icelandic horses
 - Shetland ponies
- Common maternal environment
 - Resemblance maternal half-sibs: genetics & environment
 - Common maternal environment 0.20 (Unkel et al., 1987)

Introduction - aim

1. Estimate **heritability** of insect bite hypersensitivity in Dutch Friesian breeding mares
2. Estimate the effect of **common maternal environment** on insect bite hypersensitivity



Materials and methods – data collection

- Dutch Friesian breeding mares
- During organized foal inspections
- 12 inspectors
- Year: 2004, 2008



Scored for IBH

Studbook entrance

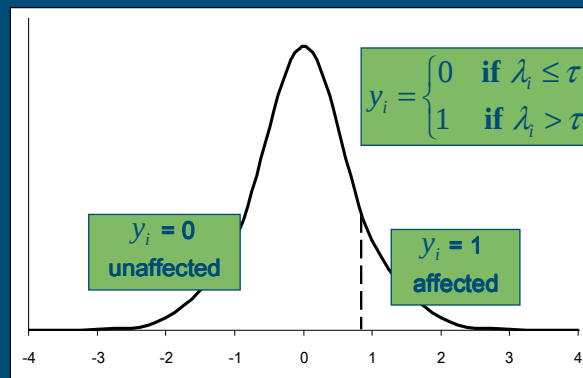
- Score clinical symptoms of IBH
 - 0 = absent, 1 = dubious/mild, 2 = clear
 - Binary

Materials and methods – data

- ~3,800 scores
 - 89% July, August, September
- ~3,500 mares
 - 9% (n = 310) scored in both years
 - 9 yr (SD = 4.2 yr)
- Mares descended from
 - ~150 sires
 - ~2,500 dams
 - 26% dams (n = 669): 2-6 progeny

Materials and methods – model

■ Threshold animal model



Materials and methods – model

■ Threshold animal model

$$y_i = \begin{cases} 0 & \text{if } \lambda_i \leq \tau \\ 1 & \text{if } \lambda_i > \tau \end{cases}$$

■ Inverse probit link function

$$\mu_i = \Phi(\eta_i)$$

■ $\eta = \mu + \text{age} + \text{region} + \text{yearmonth} + \text{inspector} + \text{dam} + \text{animal} + \text{pe}$

- dam: common maternal environment (without pedigree)
- animal: additive genetic effect of mare (with pedigree)
- pe: permanent environment of mare (repeated observations)

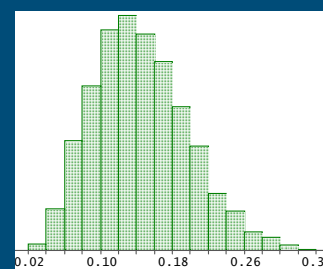
Materials and methods – Bayesian analysis

- Bayesian analysis
 - MCMC methodology
 - Gibbs sampling algorithm
 - iBay (Janss, 2008)
- Flat priors
 - 10 independent chains
 - 210,000 cycles/ chain
 - Burn-in period: 10,000 cycles
 - Store every 500th sample

[illegible]

Results and discussion

- Prevalence 18.2%
 - 2004: 18.5%
 - 2008: 17.2%
- Repeatability 0.39 (SD = 0.11)
- 95% HPDR 0.18 – 0.60
- Heritability 0.15 (SD = 0.05)
- 95% HPDR 0.06 – 0.26



Posterior distribution heritability

Results and discussion

■ Heritability on underlying scale

Research	h^2_{obs} (SE)	h^2_{und} (SE)
Our research	0.07	0.15 (0.05)
Schurink et al. (2009)	0.08 (0.02)	0.24 (0.06)
Eriksson et al. (2008)	0.08	0.27 (0.17)
Lange (2004)	0.36 (0.08)	0.65
Unkel et al. (1987)	0 - 0.24 (0.12)	

Results and discussion

- Common maternal environment 0.17 (SD = 0.06)
 - Common maternal environment 0.20 (Unkel et al., 1987)
- 95% HPDR 0.05 – 0.29
- Resemblance due to:
 - Uterus environment
 - Management breeder
 - Other environmental aspects e.g. habitat
- Previous genetic parameters overestimated?

Results and discussion

- Common maternal environment 0.17 (SD = 0.06)
 - Common maternal environment 0.20 (Unkel et al., 1987)
- 95% HPDR 0.05 – 0.29

	h^2 (SD)	r (SD)
With common maternal environment	0.15 (0.05)	0.39 (0.11)
Without common maternal environment	0.18 (0.06)	0.54 (0.10)

- Previous genetic parameters overestimated?

Conclusions and implications

- IBH is a heritable trait
- Take into account common maternal environment
 - Prevent overestimation genetic parameters
- Traditional breeding program not efficient
 - Progeny testing increases generation interval
 - Genomic information needed



Contact information

Anouk Schurink
Animal Breeding and Genomics Centre
Wageningen University
P.O. Box 338, 6700 AH Wageningen
The Netherlands
E-mail: Anouk3.Schurink@wur.nl
Tel.: +31 317 482207