

# Genome-wide association study of insect bite hypersensitivity in Dutch Shetland pony mares

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## Introduction

- Insect bite hypersensitivity (IBH) is a common allergic skin disease in horses found throughout the world.
- IBH is caused by bites of *Culicoides* spp.
- The allergy causes a severe itch, which results in discomfort and disfiguration.
- IBH is a multifactorial disorder with partial genetic control.
- Knowledge on associated genes will enable more efficient selection and might contribute to prevention, diagnosis and therapy.



## Objective

Identify and quantify genomic associations with insect bite hypersensitivity in the Dutch Shetland pony population.

## Material and Methods

- Matched case-control design: 97 cases and 91 controls (36 paternal half-sib pairs).
- IBH phenotypes were recorded by studbook inspectors on whole broodmare population. Owners of mares that scored positive (= case) were asked for participation.
- Controls were at least 4 years-of-age and were located on the same farm as a case.
- Phenotypes were scored and blood was collected by a veterinarian.
- Single SNP logistic regression of 40,021 SNP.
- Odds ratios obtained from transformation of SNP effects.

## Results

- Matching successful, therefore no significant fixed effects.
- 24 SNP associated with IBH ( $-\log_{10}(P\text{value}) > 2.5$ ).
- Associations on multiple chromosomes. Most significant SNP on chromosome 27.
- Odds ratios of SNP effects varied between 0.17 and 5.43.

## Conclusions

- Analysis of matched case-control data identified genomic associations with insect bite hypersensitivity on multiple chromosomes.
- SNP effects were of practical value.

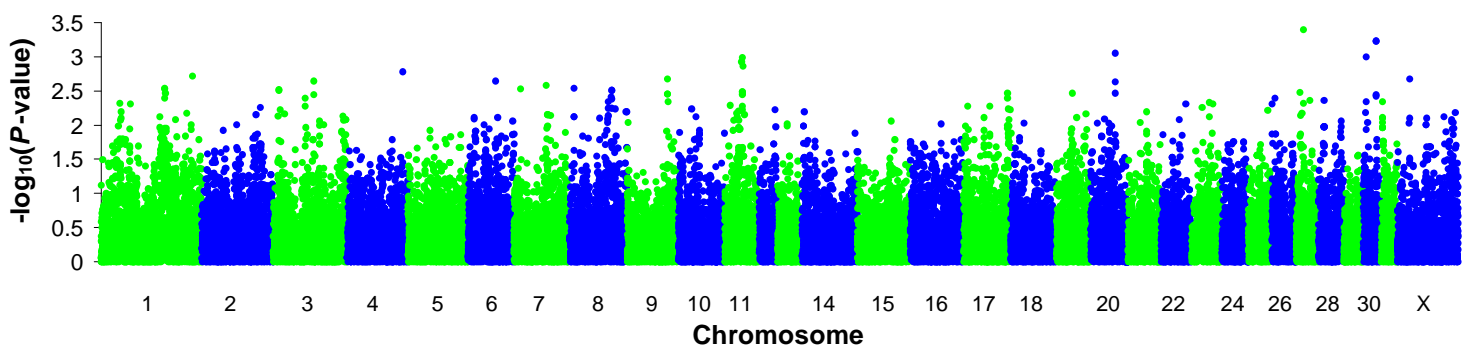


Figure 1. Genome-wide associations with insect bite hypersensitivity in Dutch Shetland pony mares.