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 (-log₁₀(P-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.