

Title: Genetics of insect hypersensitivity in the Dutch Shetland Pony
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Introduction

Insect hypersensitivity is an allergic reaction of the horse to the bite of certain insects. It is the most common allergic skin disease in horses. The disease has different names in different parts of the world. These other names include 'sweet itch', 'summer eczema', 'Queensland itch', 'allergic dermatitis' and 'Sommerekzem'.

For many years the cause of this disease was unknown. In 1953 however, it was proved that insects were the cause of this eczema. The insects that cause this disease are from numerous *Culicoides* and *Simulium* species. The disease is caused by one of two types of hypersensitivity to antigens: type I (immediate and late phase) or type IV (delayed). Other causes of the disease (e.g. allergies to food) are not ruled out completely.

The disease is not present all year round, but depends on the presence of insects. In the warm seasons the disease will manifest itself in horses. In summertime affected horses suffer from itching dermatosis in different regions of the body. The skin of tail and manes is affected, but also back and belly can be affected. Itching in these regions can become so severe that the horse is not fitted for working or sport purposes anymore. In the wintertime, with the disappearance of insects, the symptoms disappear, to come back in the next year.

The incidence of the disease between and in breeds varies. The disease appears to affect more pony breeds than horse breeds. According to some authors factors like age, sex and color are also of influence. The pathogenesis of the disease is influenced by many factors, both genetic and environmental. Effective measures to treat the disease are not known.

About the genetics of this disease little is known. A genetic background is suspected, but not much research is done. A study on a German population of Icelandic horses ruled out a monogenic recessive mode of inheritance or a dominant mode of inheritance and a polygenic mode of inheritance is expected.

Problem

The Shetland herd book considers the disease as the most problematic disease at the moment. Preventive measurements such as covering or indoor housing are hardly realistic for keeping such a robust pony breed. There are indications that a genetic background plays a role in the hypersensitivity. The Shetland herd book considers reduction of the hypersensitivity through selection a more realistic way. The aim of this study is to investigate if a genetic component for the prevalence of insect hypersensitivity is present in the Dutch Shetland pony population.

Material and Method

In the summer of 2003 inspectors were instructed to score the dams of the foals at the foal inspections for the incidence and severity of insect hypersensitivity. Beside insect hypersensitivity the way of housing of the mares at home was scored. For insect hypersensitivity 1 denoted an animal that had no insect hypersensitivity, 2 an animal that showed a few signs and 3 an animal

that was clearly affected. For housing condition the classes were as follows: 1 for animals that were kept in a pasture, 2 for the mixture of indoor and pasture and 3 for animals that were kept indoor. Together with the score for insect hypersensitivity, the registration number of the horse and area where the horse came from (so-called: breeding region) was scored. This resulted in data from 3351 animals. These data were linked to the database of CR-Delta for pedigree information, racegroup, age and height of the mares. The screening of the data and the investigation of the influence of the risk factors was performed using SAS. The heritability of insect hypersensitivity was estimated using ASReml.

Results

The frequencies for the scores of insect hypersensitivity were as follows:

Score for insect hypersensitivity	1	2	3
Number of animals	3073	208	70
Percentage of animals	91,7%	6,2%	2,1%

No animal was kept in a housing system that consisted of only indoor housing, 97,9% was kept only in pastures and 2,1% was kept in a mixture of indoor and pasture. 15 different inspectors scored the animals in 25 different regions. An inspector often scored all the animals in one particular region. Therefore 2 models were calculated in SAS, one model including inspector, way of keeping, age, racegroup and height as factors and one model including region, way of keeping, age, racegroup and height as factors. The first model was the best fitting and therefore used in further calculations with ASReml. In this model inspector and way of housing were significant factors.

The heritability of insect hypersensitivity is calculated with ASREML. 9085 animals were included in the pedigree, resulting in (at least) 4 generations per animal provided the animal's parents (and their ancestors) are known. The model used was an animal model. Way of housing and inspector were included as primary fixed effects. The animal was included as random effect.

With these data a heritability has been estimated for insect hypersensitivity. The resulting solution was: $0,0560 \pm 0,0246$, with a σ^2_a of 0,0066 and a σ^2_e of 0,1122.

Conclusion and discussion

Considering the low heritability estimate in this study and the low frequency of insect hypersensitivity in the scored animals, at present a selection for insect hypersensitivity will give few results. The genetic component causing the disease is low and if used in the breeding program it will take several generations to reach a considerable decrease of insect hypersensitivity in the Dutch Shetland pony.

For this dataset all the mares with a foal in 2003 are in principle scored. This leads to a unique dataset, since no preselection has been made on the animals and all the animals are scored. There has never been a study to the inheritance of insect bite hypersensitivity on such a large scale.

This study is based on the first group of animals scored for this disease in the Netherlands. In 2004 again the mares were scored at foal inspections. Two fixed effects were considered in the calculations, while these were more in other studies. Regular scoring of the animals over several years, possibly with more factors than the ones scored in this study, will give a better view of the situation and will maybe lead to other heritability estimates.