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Short Communication

Genetic parameters and estimated breeding values of insect bite hypersensitivity in Belgian warmblood horses

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Abstract

Genetic factors involved in susceptibility to insect bite hypersensitivity (IBH) in Belgian warmblood horses (BWP) were investigated. Data relating to 3409 horses were collected using a questionnaire during sport competitions, BWP breeding days, breeder visits and phone calls. Horses were classified as IBH-affected or unaffected, based on two 'disease classifiers': a lifetime record, based on owner information (life_status) and another based on whether or not the horse was showing clinical signs at the time of questioning (clin_status). IBH prevalence, based on life_status, was 10% and 6.2% based on clin_status. The heritabilities estimated using threshold animal models varied from 0.65 to 0.78 on the underlying scale (0.18 to 0.26 on the observed scale). These research findings indicate that susceptibility to IBH is a heritable trait in BWP.

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Insect bite hypersensitivity (IBH) represents a hypersensitivity reaction to salivary antigens from numerous *Culicoides* spp. and possibly other biting insects (Fadok and Greiner, 1990). There are indications that genetic factors are associated with susceptibility to IBH (Marti et al., 1992). Published heritability estimates of IBH susceptibility in Icelandic horses, Dutch Shetland ponies and Friesian horses vary from 0 to 0.36 on the observed scale (Lange et al., 2004; Eriksson et al., 2008; Schurink et al., 2009, 2011). However, there are no reports of heritability coefficients of IBH susceptibility in warmblood horses.

Warmblood horses are of great economic importance, as they are commonly used in sport competitions and for recreation. IBH is a recognised problem in Belgian warmblood horses (BWP), with an estimated prevalence of 10% (Peeters et al., 2014). Estimated breeding values (EBVs) might allow selection against IBH, thereby reducing economic losses and improving animal welfare. The aim of the present study was to collect information about IBH in BWP stabled in Belgium by means of a questionnaire. Classification of Warmblood horses as IBH affected was based on the information provided by owners, including clinical signs during previous summers and taking into account the preventive measures undertaken by the owners.

Data were collected using the questionnaire during the summers of 2009 and 2011 as described by Peeters et al. (2014). A total of 3409 IBH records from 3143 horses with pedigree information was obtained. Horses were classified as IBH affected or unaffected based on two different definitions: ‘life_status’ and ‘clin_status’. The trait definition ‘life_status’ is a lifetime record and based on owner information. If the horse owner ever observed clinical signs of IBH, the horse was classified as life_status = 1. If the owner had

never observed any clinical signs, life_status = 0. The classification 'clin_status' was based on whether or not the horse was showing clinical signs of IBH at the time the owner completed the questionnaire. If the horse was showing clinical signs of IBH (according to the owner) at the time of questioning, clin_status = 1 and clin_status = 0 when the owner reported that the horse had no clinical signs of skin disease at the time of questioning. The IBH prevalence based on the 'life_status' was 10.03%, whereas IBH prevalence based on 'clin_status' was 6.2%.

A threshold model was applied using the Markov Chain Monte Carlo (MCMC) method. A Gibbs sampling algorithm implemented in MTGSAM was used to obtain marginal posterior distributions of model parameters (Van Tassel and Van Vleck, 1996). Single trait animal threshold models, assuming an underlying non-observable continuous random variable, called liability (λ), were applied for life_status and clin_status. The effects 'period of questioning', 'surrounding vegetation', 'age of horse' and 'stud size' were included as fixed factors in the model as defined by Peeters et al. (2014). The genetic variance prior was set to 0.1, relative to a residual variance σ_e^2 fixed at 1 to avoid identification problems. Uninformative priors were assumed for the other effects in the model. Markov chains of 37,500,000 cycles were generated and every 7500th sample was saved for analysis, resulting in 5000 records in total for each run. The MCMC output was analysed with the package 'coda' in the statistics package R. [1] Animal estimates were transformed into estimated breeding values (EBV) as recommended by Interstallion.[2]

[1] See: www.cran.r-project.org
[2] See: www.interstallion.org

Heritabilities on the underlying scale (h^2_{und}) were 0.78 with HPDR [3] of 0.61 to 0.91 for the classifier life status and 0.65 (HPDR 0.43–0.83) for the classifier clin_status. Differences between posterior means were not significantly different from 0. The heritability on the observed scale h^2_{obs} was 0.18 (HPDR 0.11–0.21) for clin_status and 0.26 (HPDR 0.21–0.31) for life_status when transformed from posterior means of heritabilities. The relationship between the proportion of IBH-affected offspring and the estimated breeding value (EBV) of stallions with at least 10 offspring is shown in Fig. 1. The correlation between EBVs estimated using life_status and EBVs based on clin_status was 0.78. Although this correlation is rather high, a graphical representation (Fig. 2) showed that 186 horses had higher EBV when using life_status compared with clin_status. One hundred and twenty four of these 186 horses had their own IBH records in dataset_all and 94% of these (116 out of 124 horses) were classified as IBH affected based on life_status (life_status = 1), but had no clinical signs at sampling (clin_status = 0). This is different for horses where EBV estimates based on life_status or clin_status were similar (differences smaller than 15 units). Indeed, only 0.07% of horses with similar EBVs had different phenotypes for the two classifiers (life_status vs. clin_status).

With an average prevalence of 10%, IBH can be considered a significant clinical problem in the BWP population. IBH susceptibility in horses has been shown to be heritable in other horse breeds (Schurink et al., 2009, 2011), but, heritability estimates for IBH susceptibility have not been previously calculated in a warmblood horse population. The results of the present study show that IBH susceptibility is a heritable trait with high heritability in the Belgian Warmblood horse population. For comparison, heritability for

[3] HPDR: 97.5% Highest Posterior Density Region

104 osteochondrosis in Warmblood horses has been estimated at 0.1–0.4 in animal threshold
105 models (Distl et al., 2013).
106
107 In the present study, data were collected using a questionnaire with face-to-face
108 contact between the investigator and the horse owner. This method is similar to that applied
109 in comparable studies involving Icelandic horses, where heritabilities of IBH susceptibility
110 were between 0 and 0.24, in a study of 984 German born Icelandic horses, using different
111 models and methods (Unkel et al. 1987). More recently, a heritability of IBH susceptibility of
112 0.08 was reported on the observed scale in Icelandic horses (Eriksson et al. 2008). That
113 particular study recruited 1250 Swedish born Icelandic horses sired by 33 stallions and used a
114 threshold sire model. However, the standard deviations reported were large, so heritabilities
115 on the observed scale were not significantly different from the heritabilities found in our
116 study.
117
118 Differences in the method of data collection might explain why the heritability of IBH
119 susceptibility in BWP on the observed scale is higher (0.26) than in Dutch Shetland ponies
120 and Friesian horses (0.08 and 0.07, respectively; Schurink et al., 2009; 2011). In the Dutch
121 studies, foal inspectors examined broodmares for the presence of clinical signs, so the IBH
122 history was not captured. Our method of having horse owners classify their animals as IBH
123 affected, based on whether previous episodes of clinical disease had occurred, might result in
124 higher heritabilities. The owner usually has knowledge of the horse's health over a longer
125 period of time and should be able to provide more complete and accurate information
126 (Eriksson et al., 2008), although this is dependent upon the accuracy of the clinical diagnosis.
127 Horse owners are usually aware of whether their horses are susceptible to IBH, because this
128 condition is relatively easy to identify and requires intervention to reduce clinical signs.

Awareness of the animal's history of IBH might be even more important when studying warmblood horses. Indeed, 70% of IBH-affected BWP are treated with preventive measures to reduce clinical signs during summer (Peeters et al., 2014). Therefore, the prevalence of clinical IBH was reduced from 10%, based on owner reporting compared with 6%, based on the presence of clinical signs at the time of questioning.

The estimate of heritability of IBH susceptibility, based on life-time status (scored by the owner) was 0.26 compared with 0.18, when based on status of the horse at the time of questioning. However, differences between posterior means are not significant, so it remains unclear whether the method of classification is the most likely explanation for differences in heritabilities of IBH susceptibility between warmblood horses and Dutch Friesian and Shetland horses. The sampling of the horses and owners might have induced some degree of bias into the heritability estimates, although attempts were made to avoid this, by including all horses of each respondent. Future data collection should be more generalised to better sample the population as a whole.

A strategy of allowing horse owners to classify their horses as IBH affected not only resulted in higher heritabilities but also in different EBVs for some susceptible horses that were not showing clinical signs at the time of the survey. This suggests that, in some cases, clinical phenotyping for the purpose of calculating EBVs could include information gathered from the owner, although this is dependent upon the accuracy of the clinical diagnosis.

Conflict of interest statement

None of the authors has any financial or personal relationships that could inappropriately influence or bias the content of the paper.

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199

200 **Figure legends**

201

202 Fig. 1. Relationship between the prevalence of IBH in offspring and the estimated breeding
203 value (EBV) of the sire. EBVs were calculated with a threshold animal model, using
204 life_status as classifier. Only stallions with at least 10 offspring are represented.

205

206 Fig 2: Plot of estimated breeding values (EBVs), estimated with threshold animal models
207 (TAM), using life_status (y-axis) or clin_status (x-axis) as the classifier. Horses are grouped:
208 life_status = 1 and clin_status = 1 (star), life_status = 1 and clin_status = 0 (plus sign) and
209 life_status = 0 and clin_status = 0 (open circle). Black dots represent EBVs of horses with
210 unknown life_status and clin_status. Correlation coefficient = 0.78.

211

Figure 1

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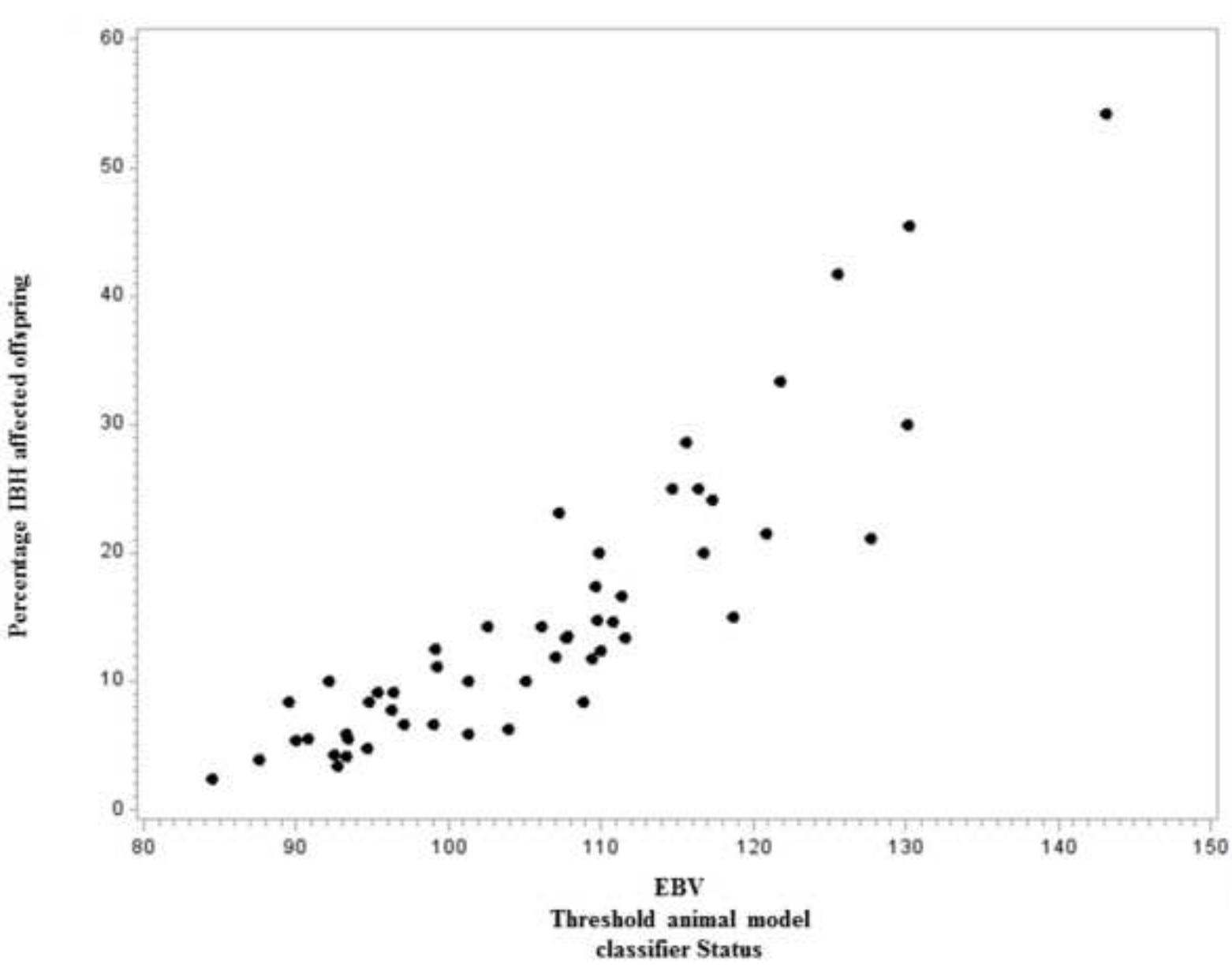

Figure 2

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