Equine recurrent airway obstruction (RAO) is likely dependent on a complex interaction of genetic and environmental factors and shares many characteristic features with human asthma. A hypersensitivity reaction to fungal spores and other allergens is proposed as the etiology of recurrent airway obstruction (RAO), but it is still unclear whether and which allergens elicit IgE-mediated reactions in RAO.

The goals of the present study were to investigate if there are differences between the families of two RAO-affected sires and between RAO-affected and control horses within these families for total IgE levels and allergen specific IgE and IgG subclass levels and whether quantitative trait loci (QTL) could be identified for these parameters.

The offspring (n=121) of two RAO-affected stallions (S1 and S2) were grouped by stallion and their lung health status (HOARSI 1–4, Horse Owner Assessed Respiratory Index) and total IgE ab levels and specific IgE, IgGa, IgGb and IgG(T) levels against recombinant *Aspergillus fumigatus* 7 (rAsp f 7) measured by ELISA in their sera.

There was no significant effect of HOARSI or sire on total IgE levels, but a significant effect of gender and age. Mares had higher total IgE levels than geldings and total IgE levels decreased with increasing age of the horse (Spearmann Rank correlation coefficient \( r_{sp} = -0.28; p<0.01 \)). rAsp f 7 specific IgGa levels, but not the other IgG subclasses or IgE abs, were significantly higher in RAO-affected than in healthy or mildly affected horses. The comparison of the two sires revealed significantly higher rAsp f 7 specific IgGa and IgE levels in the offspring of S1 than in those of S2. rAsp f 7 specific IgGa levels were positively correlated with rAsp f 7 specific IgE levels \( r_{sp} = 0.78, p<0.0001 \). These results provide evidence for effects of disease status and genetics on IgGa and allergen-specific IgE, but not on total IgE levels, which were higher in younger animals, possibly due to an increased parasite burden. A panel of 257 microsatellite markers covering the 31 equine autosomes, which were chosen as a well-spaced, polymorphic selection, were used to genotype the stallions and their offspring. A correlation of genotype with ab levels was examined for each of the IgG and IgE subclasses described. Ten QTLs affecting total IgE or rAsp f 7 specific IgE, IgGa, IgGb or IgG(T) were identified on eight chromosomes.
Keywords: horse, recurrent airway obstruction, immunoglobulin levels, genetics
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