Equine herpesvirus 2 and 5 in actively racing Standardbred trotters: studies on viral load and genetic variation of gamma herpesvirus in nasal secretion

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Conclusion

Both EHV-2 and EHV-5 are frequently shed by healthy Standardbred trotters.

No association between viral load and clinical respiratory disease or poor performance.

Eleven unique nucleotide sequences and five unique amino acid sequences of the EHV-5 partial glycoprotein (gB) gene were detected. These strains could be classified within four gB genotypes (I-IV), where two of the identified genotypes did not match with any previously described strains.

Horses were in some cases identified with up to three different gB genotypes of EHV-5 at the same time.

Objectives

The objective for the first part of this study was to monitor the viral excretion of EHV-2 and EHV-5 from the upper respiratory tract in elite racing Standardbred trotters followed over one year, to identify if the viral load varied within individual horses and/or over season, and if it was associated with poor performance or clinical respiratory disease. The objective for the second part was to determine the genetic variation of gamma herpesvirus in nasal secretion within individual horses and over time.

Materials and Methods

Nasal swabs from 66 elite racing Standardbred trotters at four Swedish training yards (TY) were collected monthly during one year. Health status and performance was registered at each sampling occasion. Viral DNA was extracted from the nasal swabs and quantified using two newly developed and validated qPCR assays targeting the DNA polymerase gene of EHV-2 and EHV-5 respectively.

Samples from eight of the horses from one TY were analyzed with PCR targeting partial glycoprotein B gene of EHV-5 and paired-end amplicon sequencing with the Illumina MiSeq system.

The sequence reads were quality trimmed and connected requiring a minimum of 50 bp overlap. To remove sequencing and PCR artifacts, sequence variants which made up <5% of the final data were filtered away.

Results

A total of 663 samples were analyzed and 197 (30%) were positive for EHV-2 and 492 (74%) were positive for EHV-5. In 97% of the horses EHV-5 was detected at least once.

The NGS analysis of the partial gB gene resulted in 27 nucleotide sequences, 11 unique sequence types and 5 unique amino acid sequences. These sequences could be classified within four genotypes (I-IV) of the EHV-5 gB gene based on the degree of similarity of the nucleotide and amino acid sequences (Fig.1).

Three different dynamic patterns of EHV-5 infections in individual horses over one year were identified. (Fig. A-C)

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