Genetic evaluation of bovine papillomavirus types detected in equine sarcoids in Poland

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Abstract

Background: Equine sarcoids are the most common neoplasms in horses. Bovine papillomavirus type 1 (BPV-1) is the main viral type identified in equine sarcoids in Europe.

Objective: The aim of the present study was to genetically evaluate BPV types based on DNA analyses of the CDS of the L1 gene. The presence of BPV DNA was confirmed by Degenerate Oligonucleotide-Primed Polymerase Chain Reaction (DOP PCR) with FAP59/FAP64 consensus primers.

Results: The DNA was detected in 21/40 (52.5%) of clinically diagnosed sarcoids. More than half of 14 isolates (66.7%) shared 100% homology with BPV-1 Deltapapillomavirus 4 isolate 09 asi UK (Acc. No. MF384289) and 99% nucleotide identity with BPV-1 isolate EqSarc1 (Acc. No. JX678969). A comparison with BPV-1 isolate EqSarc1 revealed one silent mutation in C5827T which did not change the aminoacid codon. The remaining 6 isolates (28.6%) shared 100% nucleotide identity with the BPV-1 (Acc. No. X02346) “wild type” isolate, and 1 isolate (4.8%) demonstrated 99% nucleotide identity with BPV-2 (Acc. No. M20219).

Conclusions: Variants of BPV-1 isolate EqSarc1 (Acc. No. JX678969) constitute the most prevalent type of BPV-1 in Polish horses.

Key words: bovine papillomavirus, equine sarcoid, disease ecology, FAP59/FAP64

Introduction

Neoplastic diseases pose a growing problem in both humans and animals worldwide. Selected neoplasms have an infectious etiology. An example can be cervical cancer that evolves mainly as infection caused by human papillomavirus types 16 and 18 (HPV-16 and 18). Papillomaviruses (PVs) are generally small, non-enveloped, double-stranded DNA viruses with circular genomes which infect all species in the world and are usually species-specific. They belong to the Papillomaviridae family which comprises 29 genera, from Alphapapillomavirus to Dyoiotapapillomavirus, with several species, types, subtypes and variants (Bernard et al. 2010). Classification is based on genomic DNA homology, especially in the L1 highly conserved open reading frame.