Entire Genomic Sequence of Novel Canine Papillomavirus Type 13

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Papillomaviruses are associated with benign and malignant neoplasias of the skin and mucous membranes. The sequence of a novel canine papillomavirus was determined from DNA detected in the oral cavity of a dog. The sequence of the novel virus canine papillomavirus type 13 (CPV13) shares the highest levels of similarity with the Tau papillomaviruses CPV2 and CPV7.

Papillomaviruses are nonenveloped, icosahedral particles, approximately 50 nm in diameter, with a circular, double-stranded DNA genome of about 8,000 bp. Typically, they are host species-specific and tissue-restricted putative pathogens. Many of the known papillomaviruses are associated with benign and malignant neoplasias of the keratinizing and nonkeratinizing skin in humans and animals (3). More than 150 human papillomavirus types and also many animal papillomavirus types have been discovered, illustrating a broad genetic diversity (1, 3, 4). A dozen complete and a few partial canine papillomavirus (CPV) sequences have been published and linked to various neoplasias. Thus far, all CPVs were allocated to three different papillomavirus genera, i.e., Lambda, Tau, or Chi (1, 2, 5–14).

A cytobrush sample of a mixed-breed dog showing symptoms of oral papillomatosis was taken for diagnostic purposes. Total DNA was isolated from the sample, and a circular DNA was amplified by rolling circle amplification (RCA) and partially as well as entirely cloned into the BamHI, ClaI, or EagI site of a pBluescript II KS+ vector (Stratagene). The sequences of the RCA product and the genomic clones were determined independently using an ABI 377 (Applied Biosystems) sequencer, and primary sequences were assembled using ContigExpress software (Vector NTI Informax; Invitrogen), revealing a papillomavirus genome of 8,228 bp with a GC content of 47%. Pairwise sequence alignments were performed with the obtained sequence using the Needleman-Wunsch algorithm, and a phylogenetic tree was calculated based on the coding sequences for the E6, E7, E1, E2, L2, and L1 proteins (data not shown) (7).

The characteristic open reading frames E1, E2, E4, E6, E7, L1, and L2 and two noncoding regions between L1 and E6 (478 bp) and between E2 and L2 (914 bp) were identified on the nucleotide sequence of the novel isolate. Dyad symmetry repeats (TTGTTG and between E2 and L2 (914 bp) were identified on the nucleotide sequence data of CPV13 were deposited in GenBank under accession number JX141478.

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REFERENCES


