

# Cutaneous Papillomaviruses in Cervids: Unveiling a Silent Threat to Wildlife Health

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## Introduction

Papillomaviruses (PV) are small, non-enveloped DNA viruses known to produce lesions on the skin and mucous membranes (fibropapillomas and papillomas) of various species, including Humans [1–3]. The Cervidae PVs are represented by PV members of Xi, Phipa, Epsilon, Delta, and Dyokappa genus, and the Bovidae PVs include the genus Dyoxipapillomavirus.

Skin warts are the most common sign of infection with PV. They are usually benign tumours in the skin, but some can be malignant when they develop in the genital tract. PV replicates exclusively in keratinocytes [3,5]. The most common macroscopic manifestation of PV infections is the development of warts or papilloma's that are raised, rough, and well-demarcated growths on the skin or mucous membranes. The exact natural transmission routes for cervid PVs remain unclear, figure 1 represents some of the routes proposed.

The aim of this work is to examine the ecology of cutaneous PVs in cervids, their potential crossover with cattle, and the population-level importance of these infections

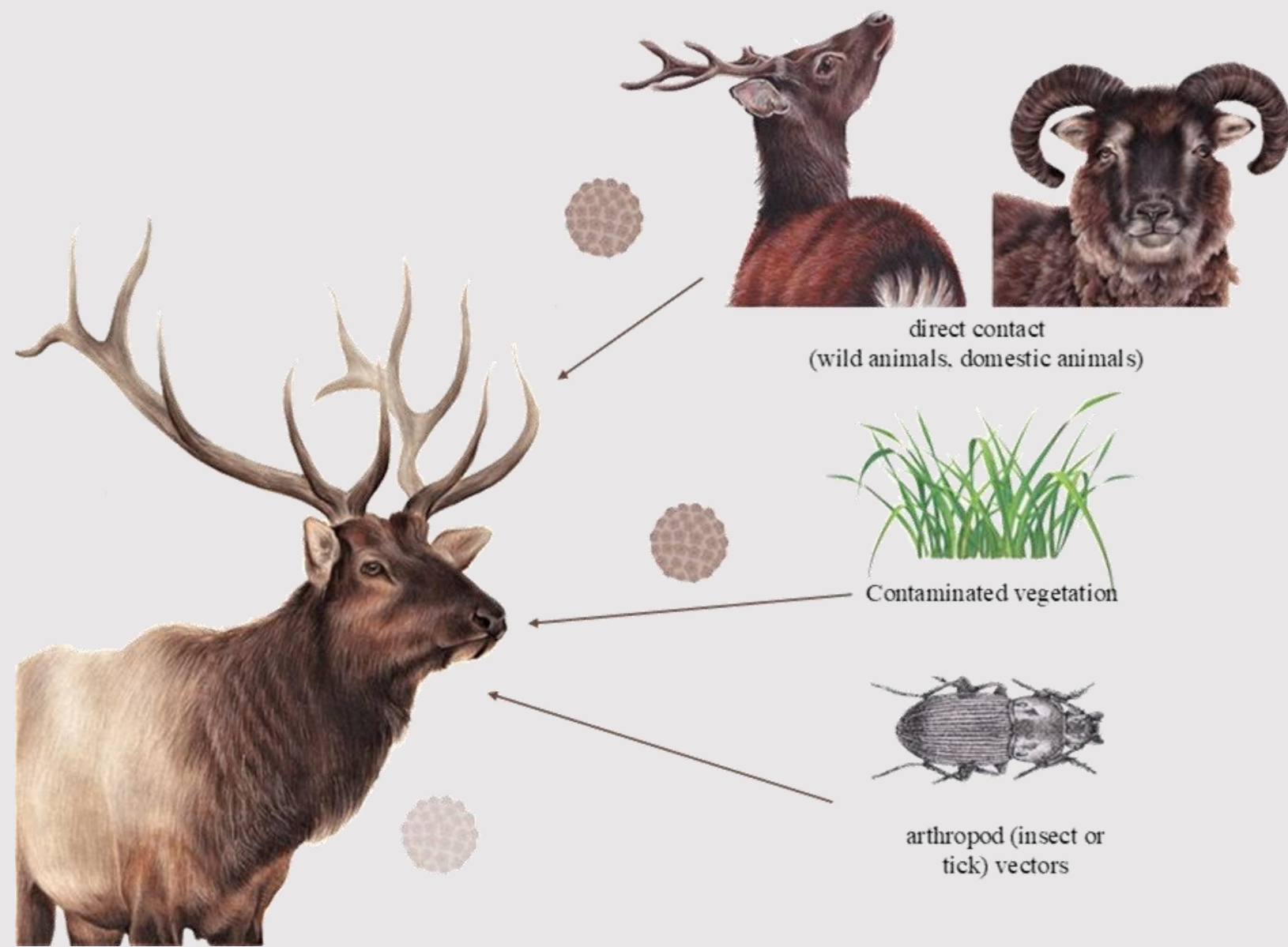


Figure 1: Transmission routes of cutaneous papillomavirus in cervids (Author: Andreia Garcês)

## Material and Methods

We searched the following : PubMed/MEDLINE, Scopus, Web of Science, CAB Abstracts, and Google Scholar. Gray literature included government and extension factsheets and conference proceedings. Searches were limited to English and languages accessible to the review team (Portuguese, Spanish, and French). Eligibility criteria were primary studies reporting clinical, histological, electron microscopy, serological, PCR, or genomic detection of papillomavirus in cervid species; case reports/series; cross-sectional surveys describing prevalence or frequency of cutaneous lesions attributed to PVs.

## Results

A total of 21 reports of PV infections in cervid species were identified between 1952 and 2024, spanning Europe, North America, and Oceania (Figure 2).



Figure 2: Map with the distribution of cases reported of cutaneous papillomavirus in cervids (Author: Andreia Garcês).

Table 1: Distinct PV types and association with different lesions in cervid species

PV type	Biological sample	Genera	Species
APV1	Cutaneous papillomas, pulmonary fibromatosis	Delta	Delta 1
CcaPV1	Pulmonary fibromatosis	Delta	Delta 5
CePV1	Pulmonary fibromatosis	Epsilon	UNC
CePV2	Cutaneous papillomas	Xi	UNC
OvPV1	Pulmonary fibromatosis	Delta	Delta 2
PpuPV1	Hair follicles	UNC	UNC
RalPV1	Cutaneous papillomas	Delta	UNC
RrPV1	Nasolabial neoplasia	Dyokappa	Dyokappa 2
RtPV1	No information	Delta	Delta 1
RtPV2	Eye swab	Xi	Xi3
Rt1PV1	Hair follicles	UNC	UNC

Six cervid genera were represented, being the dominant species *Cervus elaphus* (6 reports) (1985–2019) and *Capreolus capreolus* (7 reports). Species-specific papillomaviruses predominated, such as CePV, CcPV, and CcaPV (Table 2). Only three reports (15%) mentioned possible or suspected contact with livestock [3,4]. Most records lacked information on grazing overlap or fencing, limiting epidemiological interpretation. The few available cases hint at occasional exposure between wild cervids and cattle.

Reporting frequency increased markedly from the 2000s onward, paralleling advances in PCR and sequencing-based diagnostics. Earlier records (1950s–1980s) were primarily descriptive, whereas more recent studies identified specific PV genotypes and partial genomic sequences.

## Conclusion

Cervids are susceptible to species-specific papillomaviruses, often resulting in cutaneous or mucocutaneous papillomas and, in some cases, fibropapillomatosis. Current evidence indicates that these viruses are largely host-specific, with only limited and circumstantial indications of cross-species exposure, particularly at the wildlife–livestock interface. Cervid papillomavirus diversity remains understudied, with significant gaps in molecular characterization, epidemiology, and ecological context. The authors highlight the need for expanded surveillance, molecular sequencing, and ecological studies to better understand infection prevalence, virus evolution, and the potential role of cervids in PV ecology and cross-species transmission.

### References

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