Resumen

Los virus del papiloma bovino son un grupo creciente de papilomavirus que infecta al ganado bovino, ocasionando la papilomatosis bovina. Este virus está relacionado con enfermedades de relevancia veterinaria y es considerado un modelo para el estudio del virus del papiloma humano, pues poseen características similares. Por lo anterior, se realizó la caracterización e identificación molecular del virus del papiloma bovino con el objetivo de determinar su diversidad genotípica en la zona. Para ello, se extrajeron verrugas de bovinos con papilomatosis encontrados en distintas fincas de Santo Domingo, Ecuador; luego, las verrugas obtenidas se sometieron a un proceso de extracción directa de ADN; posteriormente, se estandarizó una PCR para la amplificación parcial del gen L1 del BPV mediante un gradiente de temperatura en el proceso de anillamiento; los resultados se visualizaron por electroforesis en gel de agarosa y los productos de PCR fueron secuenciados mediante Sanger; finalmente, se elaboró un análisis filogenético con las secuencias obtenidas. Como resultados, se obtuvo una temperatura óptima de anillamiento de 48°C y luego de la secuenciación, se identificaron los tipos BPV1, BPV2, BPV4, BPV6, BPV8, BPV9, BPV10, BPV13, BPV14 y BPV43. Además, se identificó el nuevo tipo putativo BPV-CR2 proveniente de Costa Rica y el nuevo tipo viral BPV/BR-UEL08 reportado en Brasil. Adicionalmente, se reportó una nueva especie putativa del BPV, nombrada BPVEC2024_22.1, perteneciente al género *Xipapillomavirus*. Gracias a este estudio se logró determinar la diversidad genotípica del BPV en la zona, ayudando a identificar tipos virales asociados a múltiples enfermedades.

Palabras clave: BPV, papilomavirus, caracterización, PCR, secuenciación.

Abstract

Bovine papillomaviruses (BPVs) are a crescent group of papillomaviruses that infect cattle, causing bovine papillomatosis. These viruses are related to diseases with veterinary relevance and it are also considered as a model for the study of human papillomavirus, since its similar characteristics. Therefore, the aim of this study was to determinate the genotypic diversity of bovine papillomavirus in the area, by carrying out a characterization and molecular identification of this virus. To this purpose, a specific sampling protocol were followed to obtain warts from animals with papillomatosis located in farms near UFA-ESPE, then, a direct DNA extraction process was carried out to the warts obtained previously; subsequently, the partial L1 gene of BPV were amplified by a PCR process previously standardized by using a gradient of temperature in the annealing step. The DNA were visualized by agarose gel electrophoresis, PCR products were sequenced with Sanger and sequences were used for phylogenetic analysis. As results, an optimal annealing temperature of 48°C were obtained. After sequencing process, viral types BPV1, BPV2, BPV4, BPV6, BPV8, BPV9, BPV10, BPV13, BPV14 and BPV43 were identified. In addition, here we identified the putative novel viral type BPV-CR2 from Costa Rica and the novel viral type BPV/BR-UEL08 reported in Brazil. Furthermore, a putative novel specie of BPV was reported, named BPVEC2024_22.1, that is presumed to belong to the genus Xipapillomavirus. Thanks to this study, it was possible to determine the genotypic diversity of BPV in the area, helping to identify viral types associated with multiple diseases.

Key words: BPV, papillomavirus, characterization, PCR, sequencing.