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Molecular genotyping, histopathological and immunohistochemical studies of bovine papillomatosis

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Abstract

Background: Bovine papillomatosis (BP) is considered the most common health problem in large cattle farms.

Aim: This study attempts to confirm clinically suspected BP in cattle by polymerase chain reaction (PCR) assay, histopathology, immunohistochemistry (IHC), and genotyping analysis of local isolates.

Methods: According to morphological appearance and lesion features, a cross sectional study of 54 clinically diagnosed BP cattle was assigned to this current investigation from May to August (2021) in Al-Kut district (Wasit Province, Iraq) private veterinary clinics using purposive sampling technique based on set criteria. The cattle were diagnosed clinically, and the tissues were collected and some fixed in 10% neutral buffered formalin and other stored frozen and examined by histopathological technique, IHC, and PCR assays.

Results: Using PCR assay, all cattle were positive for the BPV *L1* gene. According to detect the *L1* gene, analysis of the phylogenetic tree showed that local BPV cattle isolates were closely related to the NCBI-BLAST BPV type-1 and type-2 of the Polish equine isolate (KF284133.1) and BPV Brazilian *Bostaurus* isolate (MH187961.1), respectively. Histological detection showed there were acanthosis, hyperkeratosis, epidermal thickening, severe infiltration of mononuclear cells, massive hemorrhage, dermal fibroplasias, multifocal spongiosis, moderate neovascularization, moderate to severe elongation of the retention ridge towards the dermis, parakeratosis, rings of calcification, and necrosis with nuclear pyknosis of some spinosum cells. Immunohistochemical findings of tumor necrosis factor-alpha, epidermal growth factor receptor and Fascin showed a significant variation in values of immunoreaction in the dermis and epidermis. These results ranged from negative (0) to mild positive (+1) to moderate positive (+2) reactions.

Conclusion: The study provided essential molecular and genotyping data to improve our knowledge by emphasizing the crucial of IHC as an elegant diagnostic method to detect cellular alterations.

Keywords: Cattle warts, Iraq, Papillomavirus, PCR, Sequence.

Introduction

Bovine papillomatosis (BP) is a common skin-specific disease of cattle that is promoted by a paraphyletic group of circular double-stranded DNA viruses, bovine papillomaviruses (BPV). The latter belongs to the Papillomaviridae family which represents the oldest and widest family of viruses (Abouelkhair and Kennedy, 2022). There are several distinct BPVs in cattle that are classified based on their site and type of lesion including BPV-1 (Mathewos *et al.*, 2021), BPV-2 (Mathewos *et al.*, 2021), BPV-3 (Pfister *et al.*, 1979), BPV-4 (Campo *et al.*, 1980), BPV-5 (Campo *et al.*, 1981), BPV6 (Jarrett *et al.*, 1984) and BPV-7 (Ogawa *et al.*, 2007).

The information of transmission method of BP between animals is limited due to unclear transmission mechanism (Pang *et al.*, 2019). However, the animal populations in restricted spaces are more vulnerable and

susceptible to infection due to the direct and indirect virus-spreading behavior (Ugochukwu *et al.*, 2019). The possible mechanisms of transmission are vertical spreading, arthropod vectors, and direct skin contact (Roperto *et al.*, 2019; Ata *et al.*, 2021). The method of BPV spreads through the blood is attracting attention to extensively study the possible methods of transmission which can occur via non-epithelium tissues (Savini *et al.*, 2019) and fluids (Meng *et al.*, 2021). In adults, BPVs are unable to penetrate the host skin; thus, minimum abrasions in the skin are required to initiate the infection. Exposure of skin lesions to BPV leads to the initiation of infection followed by transformation and proliferation of infected epithelium's basal cells, which develop into benign papilloma or fibropapilloma (Mathewos *et al.*, 2021). In the field, there are different types of papillomatosis. Cutaneous papilloma is the most prevalent type among cattle and displays distinct

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morphologies, such as the atypical filiform and typical pedunculate (cauliflower) forms that present the verrucous aspect (Constable *et al.*, 2017; Daudt *et al.*, 2018).

Although the clinical diagnosis of BP is usually performed when alterations are well characterized in the epidermis, histology and immunohistochemistry (IHC) for stained papilloma tissues can allow an identification of epidermal pathogenic alterations and reveal viral proteins, respectively (Russo *et al.*, 2020; Hassanien *et al.*, 2021). Molecular techniques, in particular polymerase chain reaction (PCR), are important and essential diagnostic tools that are usually applied to confirm infection through the detection of specific DNA of BPV (Emin *et al.*, 2022). Due to the validity and accuracy of PCR test, applying this method can lead to exploring valuable insights into the characteristics of genomic data (Kiselev *et al.*, 2020; Kubacki *et al.*, 2021).

Worldwide, the disease is undoubtedly one of the most widely studied due to its significant effects on the veterinary sector. In Iraq, available data remain limited and need to be elucidated because the prevalence of disease has still developed greatly in the last 10 years (Hamad *et al.*, 2017; Mansour *et al.*, 2019; Al-Salihi *et al.*, 2020). Therefore, the current study aimed to confirm clinically suspected BP cattle by using PCR assays, histology, and IHC, with genotyping of local isolates to be documented in the National Center for Biotechnology Information (NCBI).

Materials and Methods

Study animals, design, and topography

A gross sectional study was performed using 54 cattle arrived at the private veterinary clinics in Al-Kut district (Wasit province, Iraq) from May to August (2021). The topography of the current study is including all regions around Al-Kut district in addition to Al-Kut center. The animals were diagnosed clinically to be infected with papillomatosis based on morphological appearance and features of lesions. The set criteria that allowed only the cattle with obvious lesions and clinically diagnosed to employ in this study using purposive sampling technique.

Sample collection

After injection of lidocaine 5% (Cat No.# N01BB02, ADVANZ, UK) around each lesion, surgical removal of papillomas using a scalpel was performed under aseptic conditions. The collected samples of each animal were divided into two parts; one was kept into a plastic container containing 10% neutral buffered formalin for histology/IHC examination, while the second part was kept into a plastic tube and kept frozen for molecular examination.

Molecular genotyping

According to protocol (B) of G-spin™, DNAs were extracted from tissue samples using the total DNA Extraction Kit (Cat.No.#IBT-QMS-GT1704, Intron

Biotechnology, South Korea). The DNA purity and concentration were measured using a Nanodrop system (Thermo-Scientific, UK). Targeting the conserved region of BPV *L1* gene (nt 7250 to 3225) with GenBank access number (KF284133.1), one set of primers was designed to amplify the region [F (5'-CAGTGTCTATCGGGGCCAAA-3') and R (5'-AATTCAAGAGGAGGGCAAGGC-3')] with 53.8°C annealing temperature, manufactured by Scientific Researcher Co. (Iraq). The PCR Premix Kit (Cat No.# 162770, Bioneer, South Korea) was used to prepare the mastermix with forwards and reverse gene sat a 20 µl final volume. PCR reaction was performed in thermocycler (Bio-Rad, USA) under the following conditions of: 1 cycle predenaturation (95°C/5 minutes), 35 cycles of denaturation (95°C/30 seconds), annealing (58°C/30 seconds) and extension (72°C/1 minute), and 1 cycle final extension (72°C/5 minutes). The electrophoresis of agarose-gel (1.5%) stained with Ethidium bromide was applied for the resulting PCR products, and then examined under a UV-transilluminator (Wised, South Korea). The samples were considered positive at 409 bp.

For genotyping, six positive PCR products were sent to the MacroGen Company (Seoul, South Korea) to be sequenced by the modified Sanger method. Fasta data of DNA sequences were subjected to MEGA software and the UPGMA program for phylogenetic tree analysis and multiple sequence alignment analysis. Finally, all the analyzed local isolates were named and documented in NCBI GenBank to obtain specific access numbers.

Histology

Following formalin fixation, tissues were exposed to ascending grades of ethanol for dehydration, followed by xylene for clearing, and exposure to paraffin for infiltration, embedding, and blocking. The block was sectioned using the Ultra-Thin Semiautomatic Rotary microtome (MRS3500, Histo-line, Italy) at a thickness of 4–5 µm and mounted on a slide. All prepared slides were stained with the hematoxylin and eosin (Cat. No.# ab245880, Abcam, India), and examined by a trinocular light microscope (MEIJI, Japan) at X10 and X40.

IHC

Envision FLEX IHC kits (Cat. No.# 126522-001, Dako, Denmark) were used to detect tumor necrosis factor-alpha (TNF-α), epidermal growth factor receptor (EGFR), and Fascin. Following the manufacturers' instructions, paraffin-embedded tissues were mounted on positively charged glass, deparaffinized by xylene, rinsed with distilled water and TBS, incubated with antigen retrieval solution at 60°C and then incubated in a water bath at 97°C for 25 minutes. The tissues were flooded with peroxidase block solution for 10 minutes and then with the anti- (TNF-α, EGFR and FASCIN) primary and secondary antibodies, followed by incubation with freshly prepared chromogen for 10 minutes. Then, the tissues were exposed to a counter stain (Mayer's hematoxylin) for 3 minutes.

After dehydration with three ascending ethanol concentrations, the slides were immersed in xylene, mounted with DPX, covered with cover slips and examined under a light microscope at $\times 10$ and $\times 40$. The results of IHC were classified based on their reactions as negative (–), mild positive (+1), moderate positive (+2), and strong positive (+3).

Statistical analysis

The obtained data was documented and managed using excel sheet (Microsoft excel, 2016). One-way analysis of variance was applied to analyze the IHC data by using GraphPad Prism (version 6.0.1) Software (GraphPad Software Inc., USA). The differences at $p < 0.05$ were considered significant among their values.

Ethical approval

The current study was approved by the Scientific Committees of both Colleges of Veterinary Medicine and Dentistry at the University of Wasit (Wasit Province, Iraq) as the work is under their guidelines.

Results

PCR identification and phylogenetic tree recording

Molecular assessment by conventional PCR of all clinically suspected BP lesions (Fig. 1) revealed that

all the studied cattle ($n = 54$) were positive for the BPV *L1* gene (Fig. 2). Analysis of the phylogenetic tree according to derive the *L1* gene alignments identified that the local BPV cattle isolates; Deltapapillomavirus 4 isolate Cattle-No. 1, Deltapapillomavirus 4 isolate Cattle-No. 3 and Deltapapillomavirus 4 isolate Cattle-No. 4 were closely related with NCBI-BLAST BPV type-1 (KF284133.1). Local BPV cattle isolates *Bostaurus* papillomavirus 2 isolate Cattle-No. 2, *Bostaurus* papillomavirus 2 isolate Cattle-No. 5, and *Bostaurus* papillomavirus 2 isolate Cattle-No. 6 were closely related with NCBI-BLAST BPV type-2 (MH187961.1) (Illustrations 1–6). NCBI-BLAST homology sequence analysis recorded a highly identity of the local Deltapapillomavirus 4 isolate Cattle-No. 1, No. 3 and No. 4 with the GenBank-NCBI BPV Polish equine isolate (KF284133.1) with 99.22%, 100% and 99.47% identity, respectively. However, the local *Bostaurus* papillomavirus 2 isolate Cattle-No. 2, No. 5 and No. 6 were more identical to the GenBank-NCBI BPV Brazilian *Bostaurus* isolate (MH187961.1) with 100%, 99.55% and 99.66% identity, respectively (Table 1, Fig. 3).



Fig. 1. Left lateral view of studied cattle clinically diagnosed with BP.

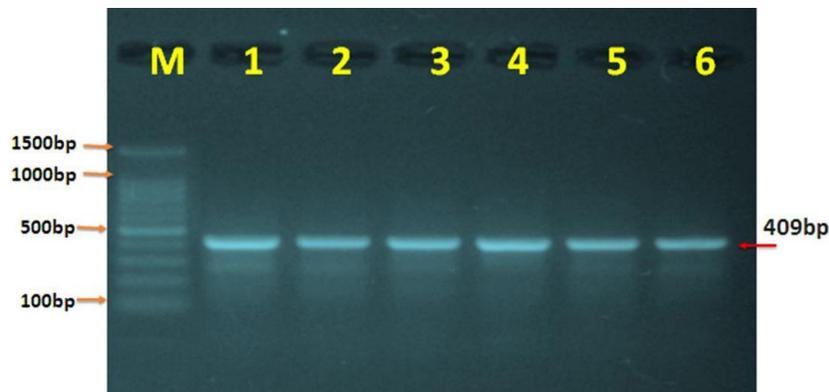
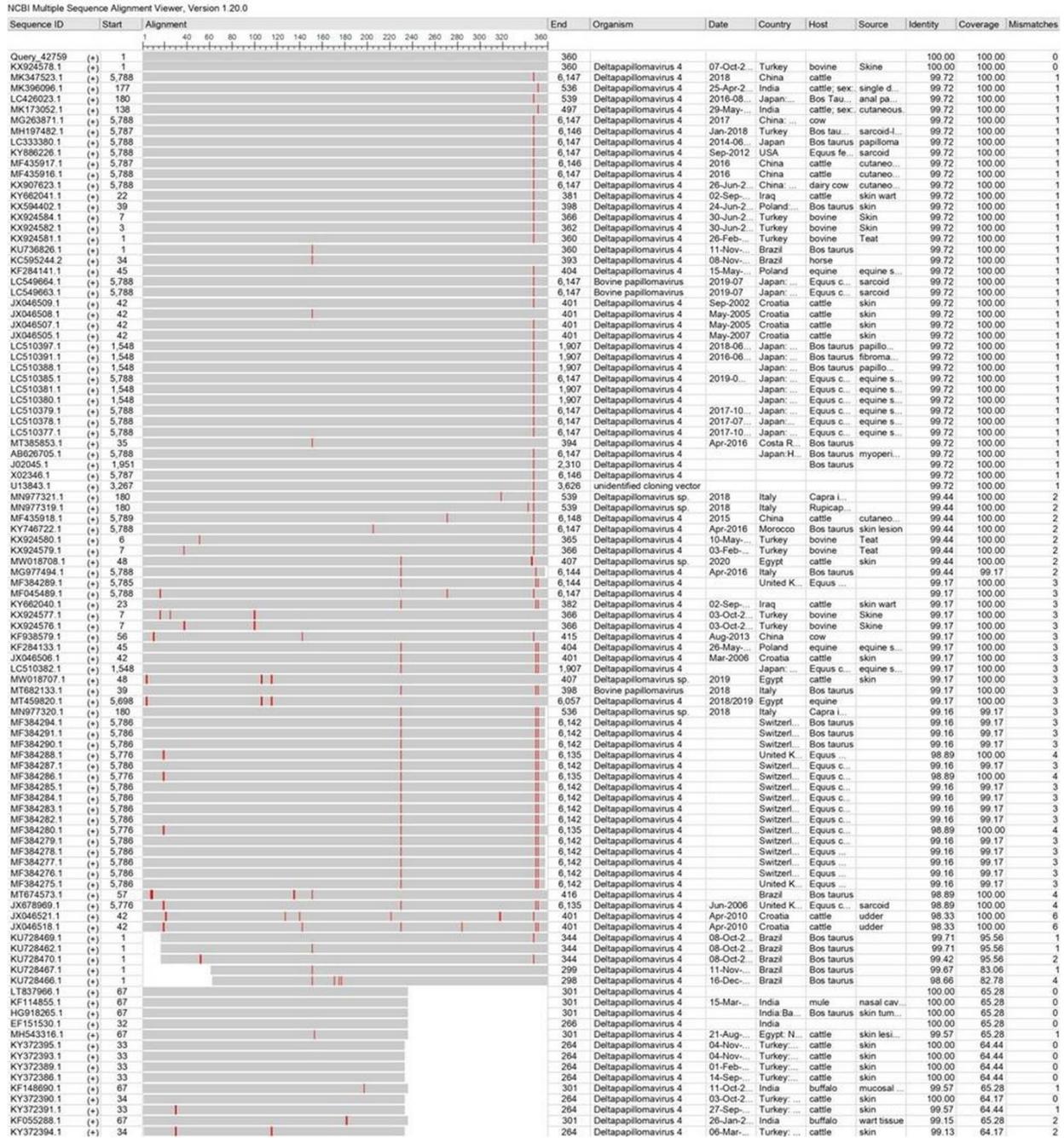


Fig. 2. PCR expression of the BPV *L1* gene in agarose gel electrophoresis. M: ladder marker (1,500–100 bp); lanes 1–6: representative positive PCR samples at 409 bp.



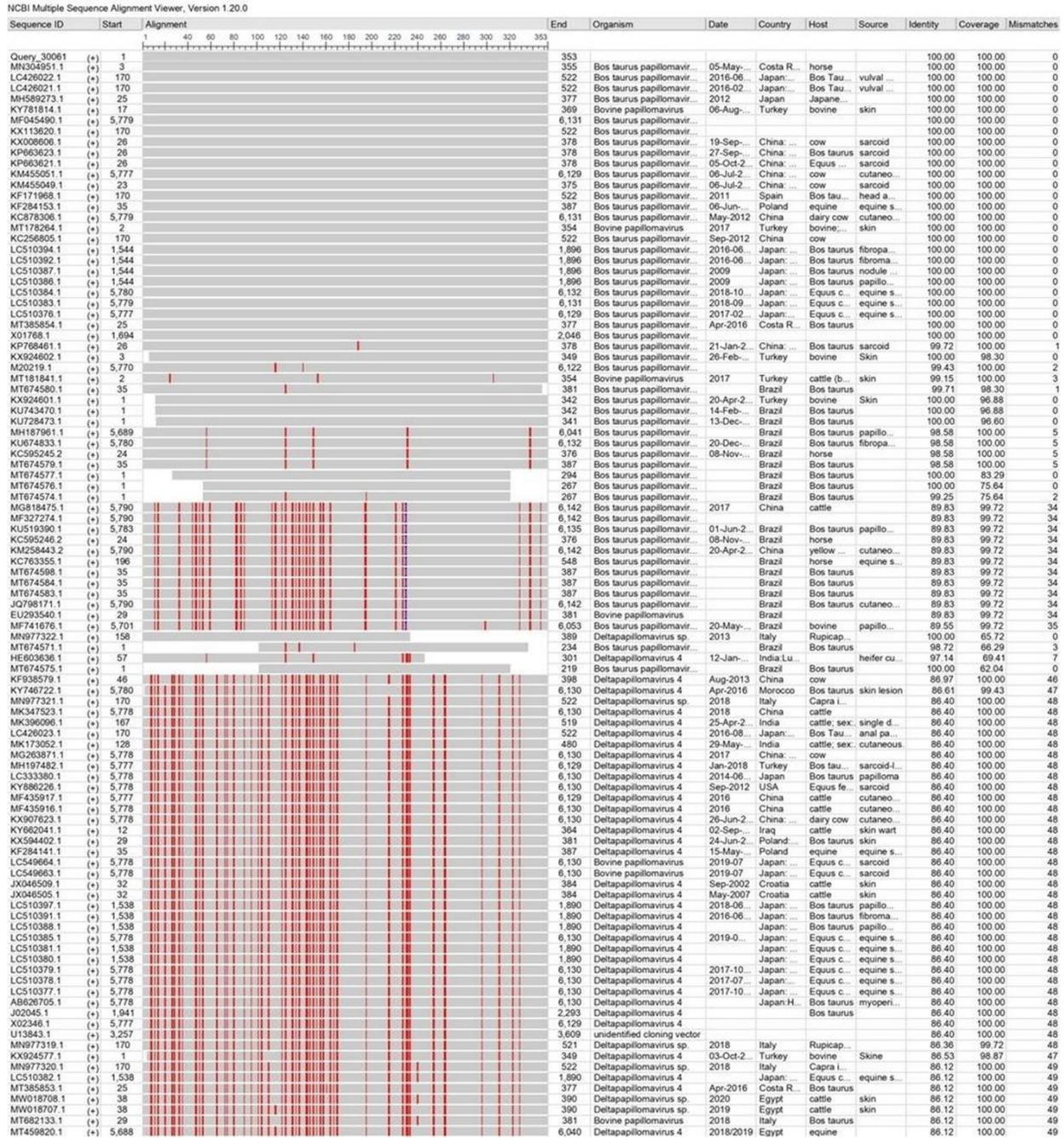
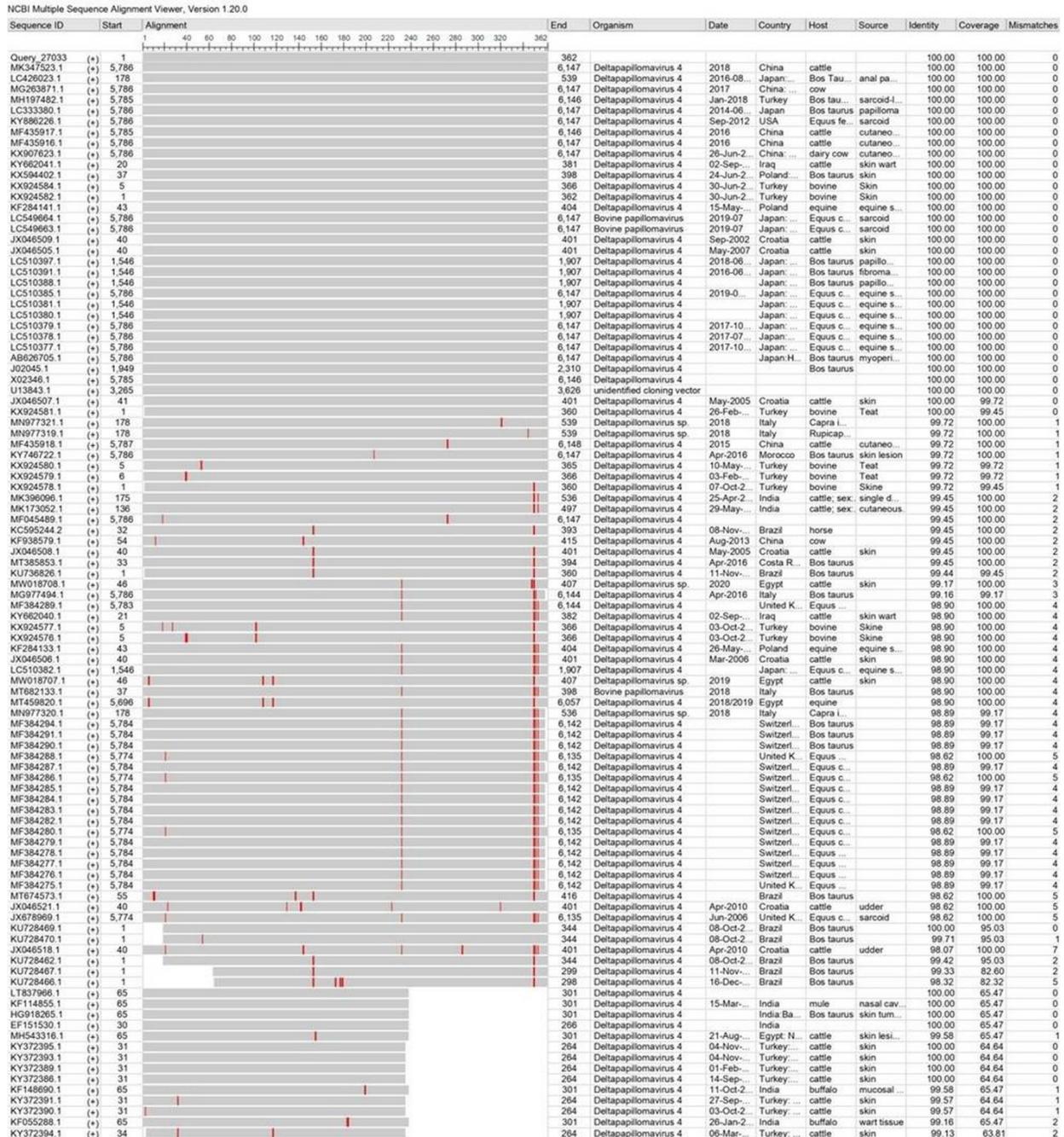


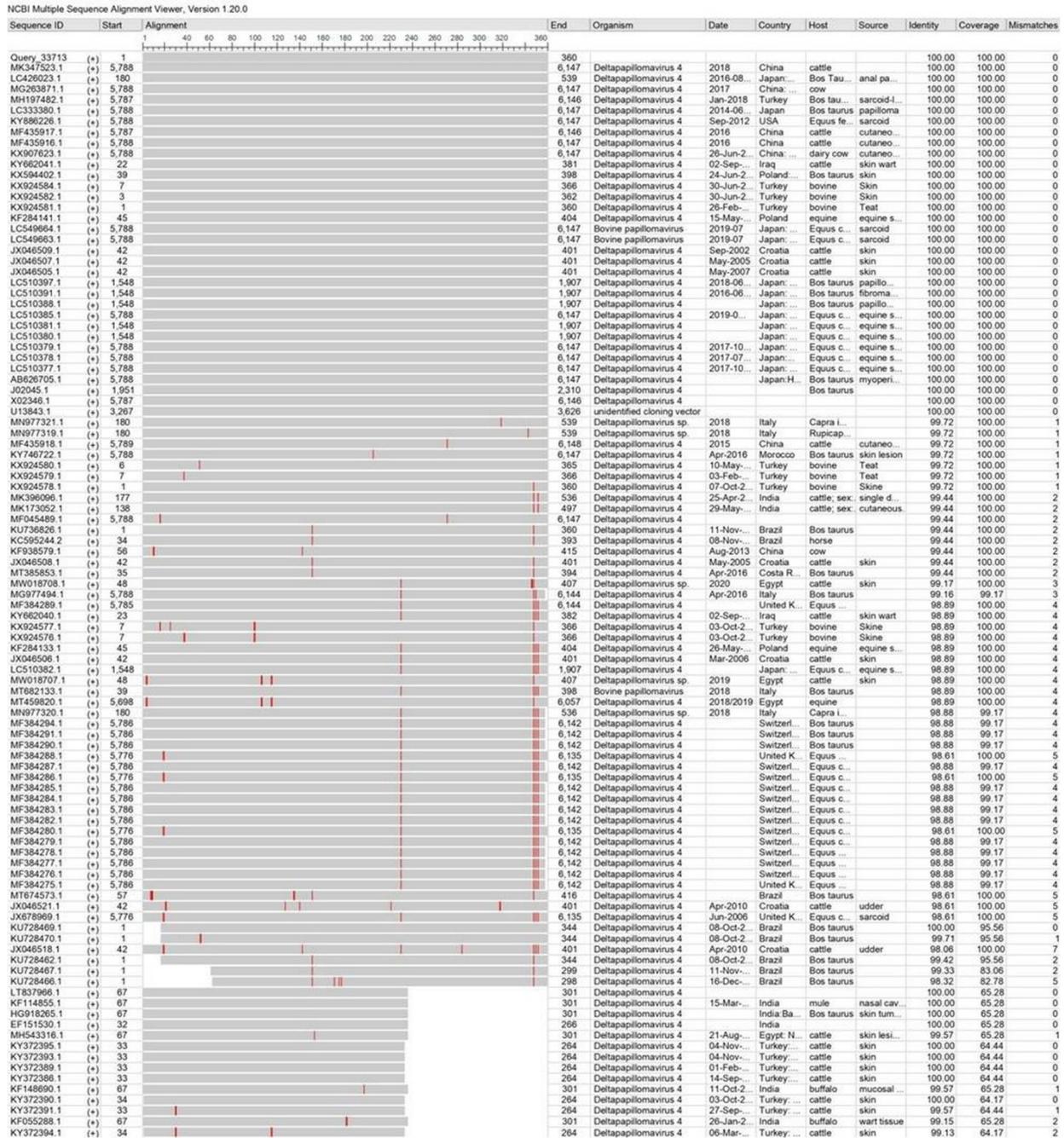
Illustration 2. NCBI multiple sequence alignment for local isolate 2 (MW658348.1).

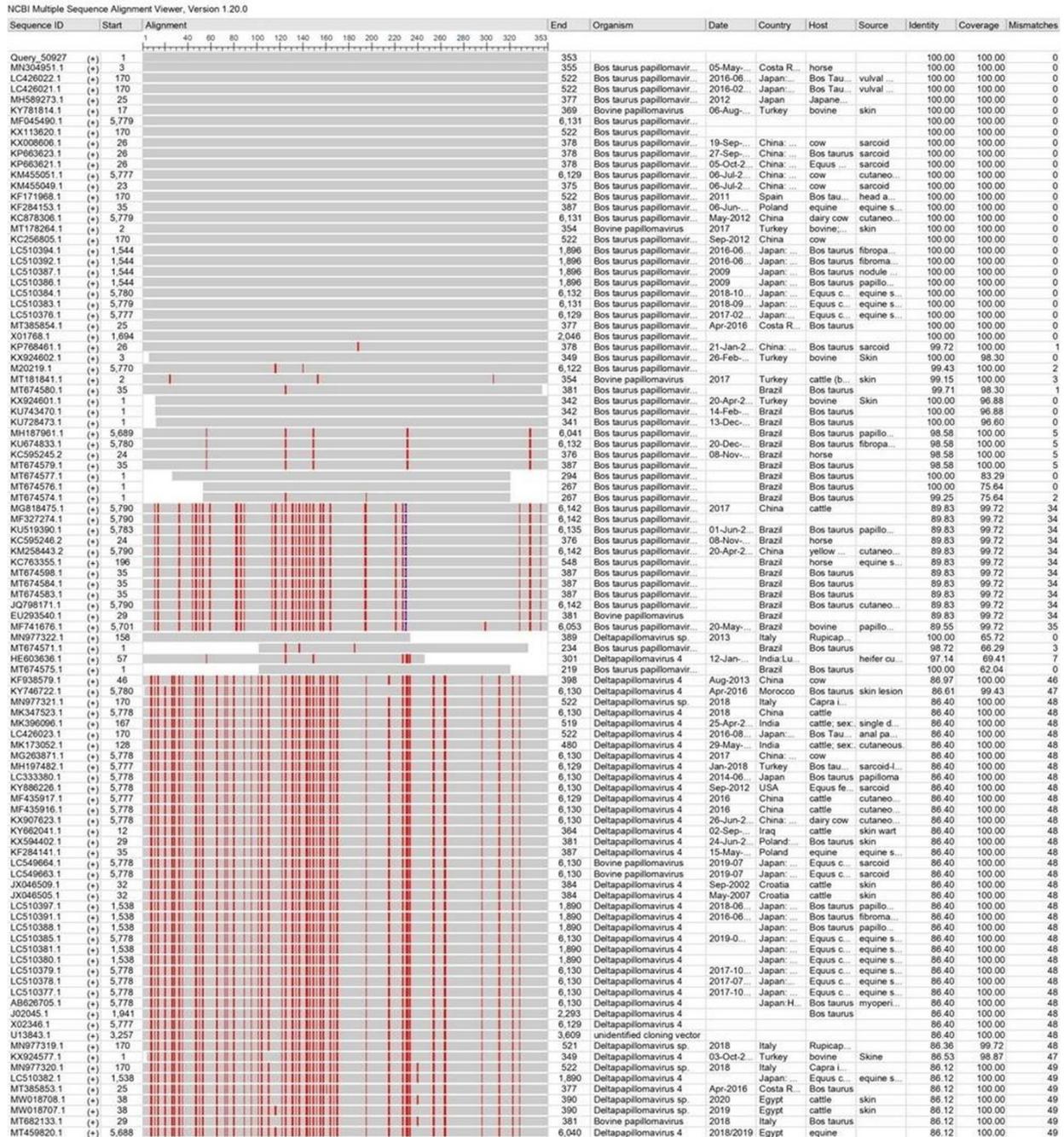
acanthosis with moderate elongation of the retention ridge towards the dermis that showed dense fibrous tissue with infiltration of inflammatory cells (Fig. 4F). Hyperkeratosis, parakeratosis, severe elongation of the retention ridge towards the dermis and signs of calcification observed on the epidermal surface (Fig. 4G). Finally, necrosis in the epidermal layer, mainly in basal cells with nuclear pyknosis of some spinosum cells, was observed (Fig. 4H).

Immunohistochemical detection

In the present study, the expression of TNF- α , EGFR and FASCIN markers was targeted using IHC. The results of the immunoreactions interestingly displayed significant variation among the examined skin layers (dermis and epidermis), which ranged from negative (0) to mild positive (+1) to moderate positive (+2) reactions (Figs. 5–7).







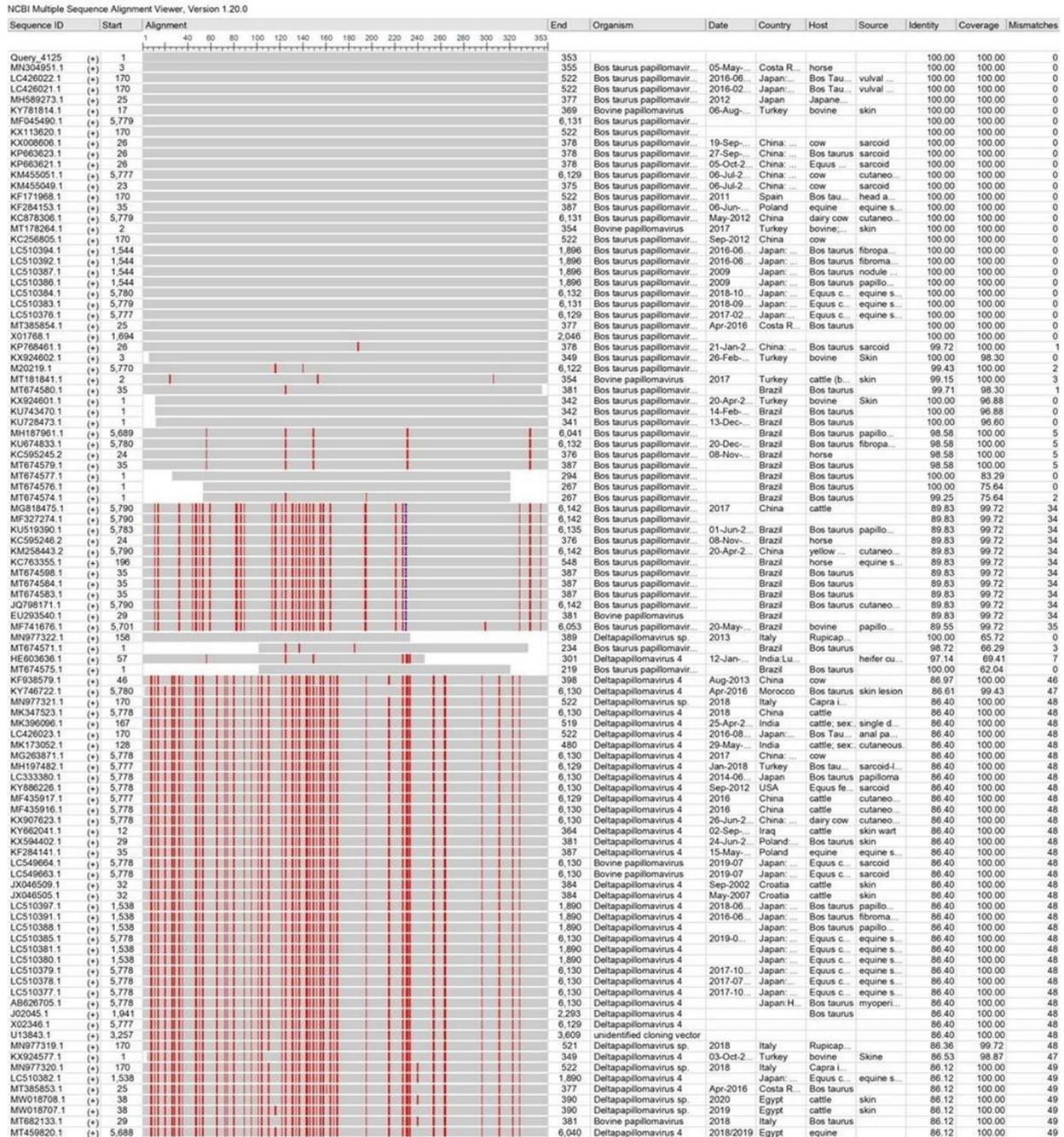


Table 1. Identity (%) sequencing between local BPV isolates and NCBI-BLAST BPV isolates based on NCBI-BLAST homology.

Local BPV isolate			BPV NCBI BLAST isolate		
Name	Access no.	Type	Access no.	Source-host, country	Identity (%)
Deltapapillomavirus 4 isolate Cattle-No. 1	MW658347.1	Type 1	KF284133.1	Sarcoid, Equine, Poland	99.22
<i>Bostaurus</i> papillomavirus 2 isolate Cattle-No.2	MW658348.1	Type 2	MH187961.1	Papilloma, <i>Bos taurus</i> , Brazil	100
Deltapapillomavirus 4 isolate Cattle-No. 3	MW658349.1	Type 1	KF284133.1	Sarcoid, Equine, Poland	100
Deltapapillomavirus 4 isolate Cattle-No. 4	MW658350.1	Type 1	KF284133.1	Sarcoid, Equine, Poland	99.47
<i>Bostaurus</i> papillomavirus 2 isolate Cattle-No. 5	MW658351.1	Type 2	MH187961.1	Papilloma, <i>Bos taurus</i> , Brazil	99.55
<i>Bostaurus</i> papillomavirus 2 isolate Cattle-No. 6	MW658352.1	Type 2	MH187961.1	Papilloma, <i>Bos taurus</i> , Brazil	99.66

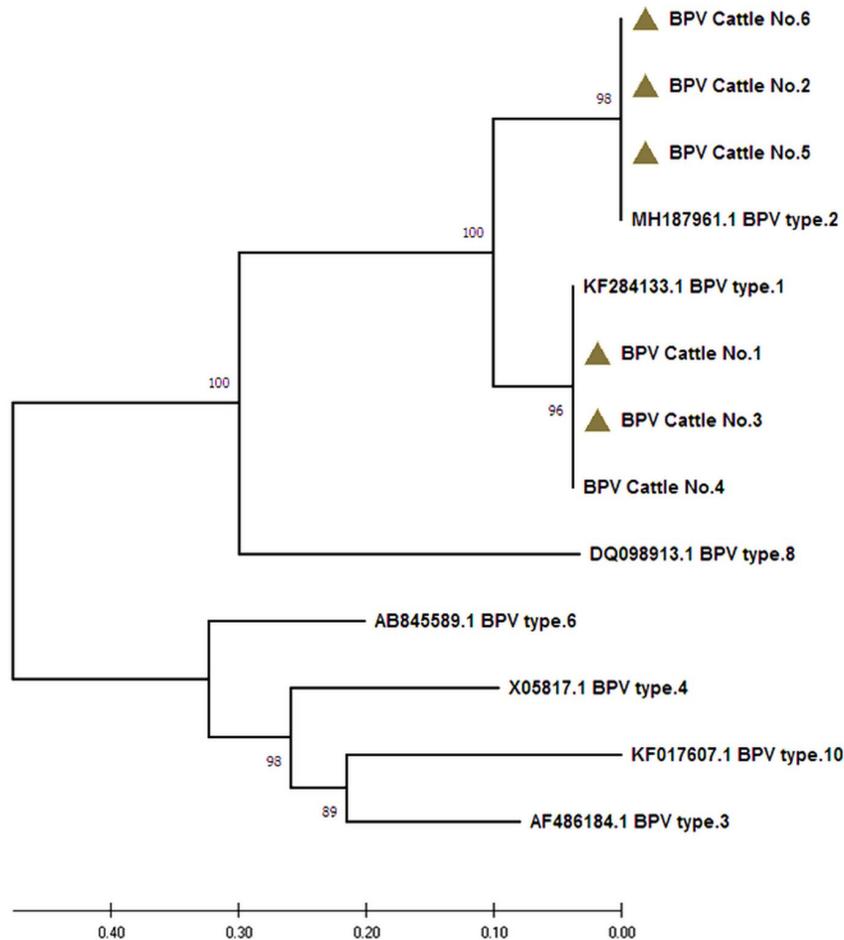


Fig. 3. Analysis of phylogenetic tree according to the L1 gene in local BPV isolates. A UPGMA tree in MEGA (version 6.0) was applied. The local BPV isolates exhibited a close relationship to NCBI-BLAST isolates in terms of total genetic changes (0.4%–0.10%).

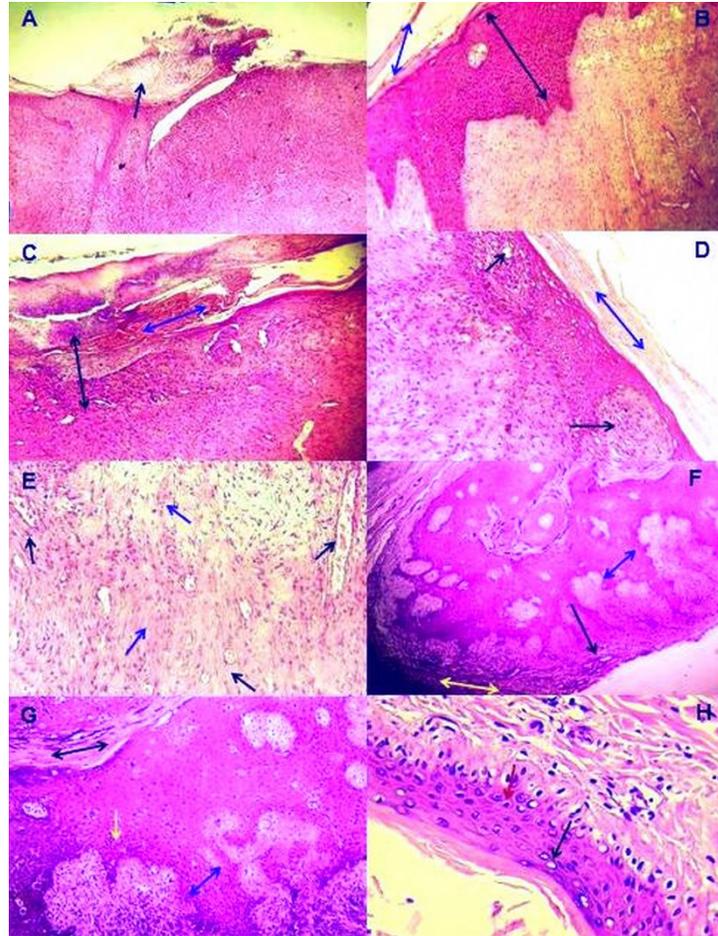


Fig. 4. Histopathological changes in skin lesions infected with BP. (A): Mature finger like projection papillae with rete pegs which grown in the stratum corneum in the epidermis of skin ($\times 400$); (B): Thickening of epidermis due to diffuse hyperplasia in the stratum spinosum layer (Black dual arrow) with hyperkeratosis (Blue dual arrow) ($\times 100$); (C): Severe infiltration of MNCs in epidermis and dermis of skin (Black dual arrow) with massive hemorrhage in epidermal layer (Blue dual arrow) in addition to dermal fibroplasia ($\times 100$); (D): Multifocal spongiosis (Black arrow) with hyperkeratosis (Blue dual arrow), ($\times 200$); (E): Dermis with moderate neovascularization (Black arrow) and fibroplasia due to fibrous connective proliferation (Blue arrow), ($\times 200$); (F): Marked acanthosis (Yellow dual arrow) with moderate elongation of retention ridge towards dermis (Blue dual arrow) and rings of calcification observed in epidermal surface (Black arrow), ($\times 100$); (G): Hyperkeratosis, parakeratosis, severe elongation of retention ridge towards dermis, acanthosis (Blue dual arrow) and infiltration of inflammatory cells (Yellow arrow), ($\times 200$); (H): Necrotic finding in epidermal layer mainly in basal cells (Black arrow) with nuclear pyknosis of some spinosum cells (Blue arrow), ($\times 400$). All sections were stained with H&E, and the images represent all study animals.

El-Mandrawy and Alam (2018) identified that infected cells were more susceptible to TNF stimulation by releasing various cytokines and inducing inflammation in various tissues at the viral stage of the disease. Başbuğ *et al.* (2016) suggested that high levels of TNF- α may be involved in the assessment of the clinical course of the disease. Goodman *et al.* (2011) determined that the combination of TNF and recombinant vaccine based on virus protein rapidly reduced infection; however, the overall picture obtained during anti-TNF treatment of infected animals is unclear and may reveal some differences. It has been suggested that the convenient support for TNF antiviral effects comes from the fact

that the family of viruses contains a variety of factors that regulate TNF-related activities. Many poxviruses encode soluble versions of TNF receptors and, more importantly, disrupt the viral TNFR gene in a virus, leading to a reduction in virus virulence (Kerr *et al.*, 2015; Alvarez-de Miranda *et al.*, 2021). Growth factors are crucial for the growth, development and homeostasis of almost all organisms and are required for tissue specialization, apoptosis, cell survival and viability, and fate determination (Mukai *et al.*, 2018; Koons and Mikos, 2019). Growth factor receptors transmit extracellular signals by activating intracellular messengers or by transporting the receptors

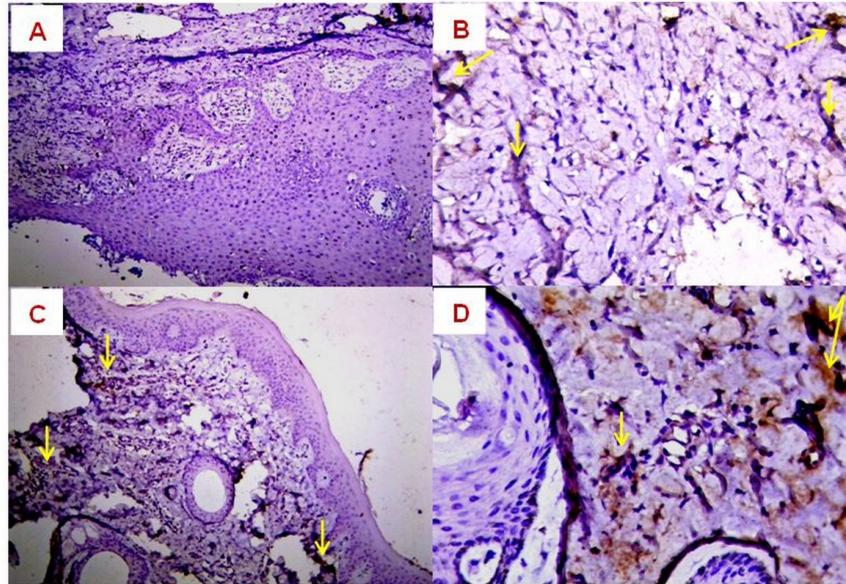


Fig. 5. Expression of TNF- α in BP skin lesions using IHC with Mayer's hematoxylin. (A): 0 ($\times 100$); (B): +1 ($\times 400$); (C): +2 ($\times 200$); (D): +2 ($\times 400$) reactions.

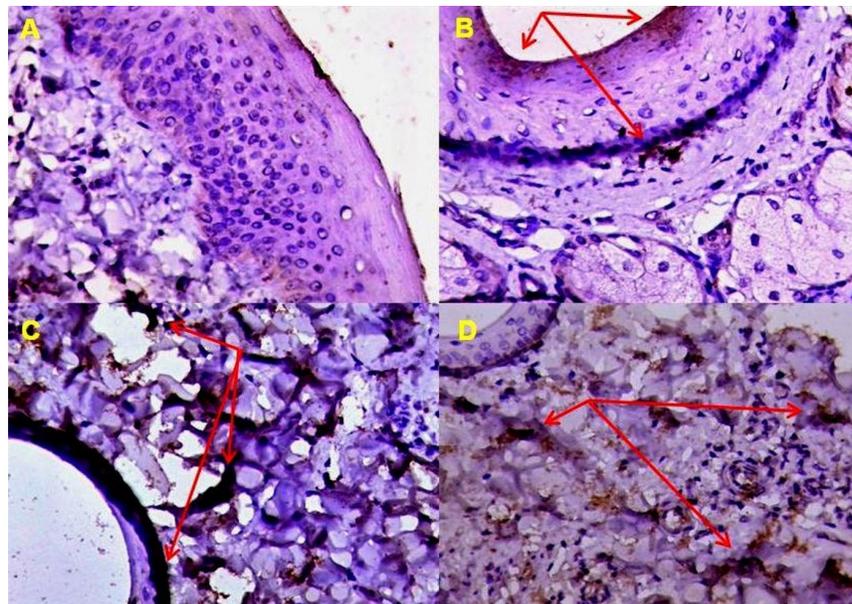


Fig. 6. Expression of EGFR in BP skin lesions using IHC with Mayer's hematoxylin. (A): 0 ($\times 100$); (B): +1 ($\times 200$); (C): +1 ($\times 400$); (D): +2 ($\times 200$) reactions.

directly to the nucleus (Liu *et al.*, 2020). EGFR is a specific factor receptor of transmembrane proteins that share structural and functional similarities (Nagano *et al.*, 2018). Although, EGFR is a key indicator involved in predicting the diseases and their prognostic value, however, the EGFR-IHC role is still unclear. Several studies have reported that reduced signals of EGFR and other tyrosine kinase receptors are associated with

disease, while increased activity is associated with the development of various tumors (Lian *et al.*, 2019; Xia *et al.*, 2020; Hong *et al.*, 2022). Suppression of binding sites of EGFR signaling at the level of extracellular receptor or tyrosine kinase intracellular activity may inhibit EGFR expression networks and thus improve patient outcomes (Kitamura *et al.*, 2020; Wingert *et al.*, 2021). Several authors have suggested that the increased

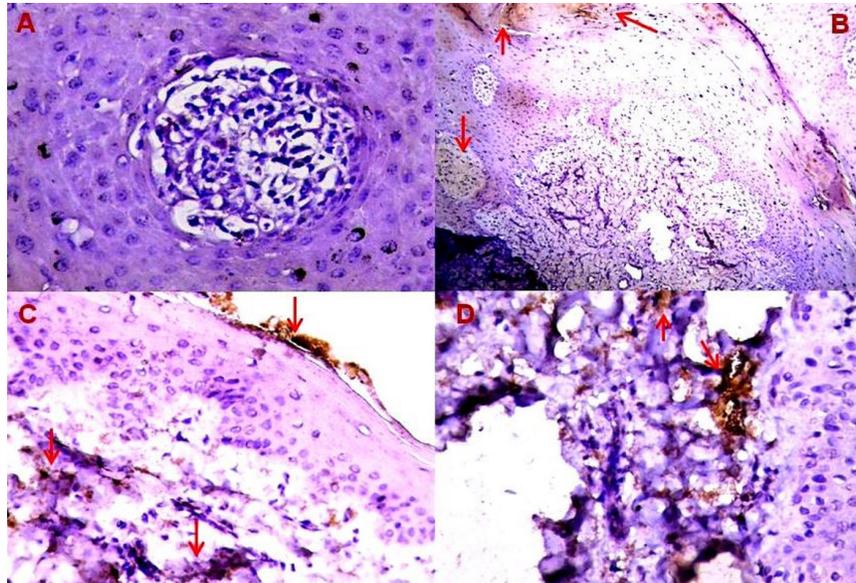


Fig. 7. Expression of Fascin in BP skin lesions using IHC with Mayer's hematoxylin. (A): 0 ($\times 400$); (B): +1 ($\times 100$); (C): +1 ($\times 400$); (D): +2 ($\times 400$) reactions.

expression of EGFR has negative impacts (Kwon *et al.*, 2018; Hashmi *et al.*, 2019; London and Gallo, 2020), while others maintain the opposite (Pidugu *et al.*, 2019; Feng *et al.*, 2020; Lamtha *et al.*, 2022). However, meta-analysis data summarizing the results of various studies show that exposure to EGFR is not an independent predictor of survival in various diseases (Yang *et al.*, 2019; Nastaly *et al.*, 2020; Atef *et al.*, 2021).

Fascin represents a family of active binding proteins that are localized in stress fibers and throughout the proliferation of various cells, such as myoblasts and glioma cells (Ogunlade *et al.*, 2020). This protein is unique to muscle and cell types, such as glial cells, neurons, antigen-presenting dendritic cells, and endothelial cells (Zhang *et al.*, 2022). This observation suggested that Fascin plays a role in cell movement or interaction with other cell types (Chung *et al.*, 2022).

Conclusion

Interestingly, the BPVs exhibited a cytopathic role that interacted with cellular structure and function and promoted cytological and histomorphological changes; however, the number of available studies remains low. Thus, the current study highlights the interesting essential data that provide insight into mechanisms to acknowledge the possible oncogenesis and pathogenesis of BPV. Furthermore, the study emphasized that IHC is a specific crucial diagnostic tool that provides precise detection of the cellular and intracellular distribution of viral and antigenic proteins using specific antibodies. Moreover, targeting other PV types in cattle and other animal species, disease prevalence, animal breeding biosafety evaluation and fundamental vaccine roles and production are of great interest.

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Authors' contribution

HJG: Clinical examination of study animals, collection of papilloma samples, molecular examination and documentation of local isolates in the NCBI. SJA: Histological and immunohistochemical processing of papilloma tissue samples, and created stained slides. TJH: Histopathological and immunohistochemical examination and reading of the slides by light microscopy. Data analysis was performed by both HJG and SJA. The authors have read and approved the final version of this manuscript as they participated in the writing of the manuscript.

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Conflict of interest

The authors declare that there is no conflict of interest.

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