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Study of the VP1 Epitopic Variation between Different Previous Isolates of FMDV type O

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The aim of the current study was to investigate the contribution of foot and mouth disease virus (FMDV), characterization and crossmatching of the circulating strains associated with the outbreaks. Epithelial tissue samples were collected and processed. After serotype conformation, isolation was done on LFBK αvβ6cell line and CPEs was observed after 16-48 hours. Total RNA was extracted by using the TRIzol method followed by the amplification of target gene by using Reverse Transcriptase Polymerase Chain Reaction (RT-PCR). Sequencing, Sequence alignment and 3-Dimensional protein analysis was performed of 5 representative samples. Conventional Reverse Transcriptase Polymerase Chain Reaction (RT-PCR) revealed 5 samples positive for the FMDV. Typing of highly viral loaded FMDV positive samples revealed that the tested samples belong to FMDV serotype O. Sequence alignment and 3D protein structure prediction was done and a number of substitutions were observed on the main immunogenic site of the FMDV VP1 structure protein. This epitopic crossmatching is important in the disease occurrence and evaluation of vaccine effectiveness and its failure.