

Phylogenetic analysis of lumpy skin disease virus (LSDV) from outbreak cases in Perak

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ABSTRACT

Introduction: Lumpy skin disease virus (LSDV) is a poxviral pathogen that is currently spreading across Asian countries, posing a significant threat to cattle populations. However, the origin of LSDV in Malaysia are not well documented. **Objective:** This study presents an outbreak investigation involving 910 samples from cattle exhibiting LSD-like clinical signs in Perak, Malaysia. **Materials and Method:** A total of 197 scabs, 166 nasal swabs, 373 blood samples, 159 pooled organs (PO) and 15 meats from species cattle presenting LSD-like clinical signs in Perak were subjected to molecular characterization for LSDV. Molecular detection was carried out using Polymerase Chain Reaction (PCR) based on targeting the p32 attachment protein gene of LSDV. **Results:** Out of 910 samples, 40.4% (n=368) samples were tested positive for LSDV; scabs (n=152), nasal swabs (n=72), plasma (n=126), PO (n=13), and meat (n=5). Two samples namely 6904/2021 and 7108/2021 from scabs were successfully amplified with a 472 bp amplicon of the specific region of fusion (F) gene and were further sent for sequencing to confirm virus. The phylogenetic analysis was performed by comparing nucleotide sequences of sheep and goat pox viruses as well as the vaccine and field strain of LSDV retrieved from GenBank. **Conclusion:** The phylogenetic analysis showed a 99.7 % homology with LSDV strains from neighboring Asian countries (Thailand and Vietnam), indicating the transboundary spread of the virus. These findings are crucial for LSDV molecular epidemiology and for devising effective control strategies. It is also important by implying continuous monitoring and strain characterization for differentiating vaccine strains from field strains in Malaysia.