OPEN ACCESS

Journal of Virological Sciences

Research Article

Molecular Characterization of Recent Field Isolate of Lumpy Skin Disease Virus Compared to the Vaccinal Strains

Akram A. Salama[1], Moustafa A. Zaghloul[2*], Ahmed A. Zaghawa[1], Mohamed A. Nayel[1], Ahmed M. Elsafey[1], Mohamed F. Azooz[2], Hanem S. Harb[1] and Walid S. Mousa[1]

[1]Department of Animal Medicine and Infectious Diseases, Faculty of Veterinary Medicine, University of Sadat City, El-Menofia, Egypt; [2]Central Laboratory for Evaluation of Veterinary Biologics (CLEVB), Agricultural Research Center (ARC), Cairo, Egypt.

Abstract | The lumpy skin disease virus (LSDV), causes lumpy skin disease (LSD), is a transboundary viral disease of cattle that has a significant global economic impact. This study aims to identify the lumpy skin disease virus that circulated in El-Menofia Governorate between April 2020 and April 2022 by partially amplifying the EEV gene. Additionally, the amplified gene sequence was subjected to sequencing and phylogenetic analyses, and the acquired LSDV sequences were compared to those in GenBank. Using the standard polymerase chain reaction (PCR) and specific primers designed from the EEV gene, tissue samples from skin nodules (N = 40) and blood samples (N = 60) were collected from diseased animals. Sequencing and a phylogenetic tree construction were done on the amplified byproducts of samples from blood and nodules on cattle skin. By PCR technique, 55 samples out of 100 (55/100; 55%) were positive for LSDV. A representative sample was sequenced and had a very high identity percentage of > 99.7-100% with virulent LSDV isolated from Egypt (Sharkia Governorate) or different countries abroad (Kazakhstan, Turkey, Israel, and South Africa), while the identity with vaccinal strains of LSDV was 94.1%. The alignment analysis revealed a distinct 27-base deletion in the vaccine strains. Our results can be used to better understand the epidemiology of LSDV in Egypt and to build an effective disease control programme. Furthermore, our findings emphasize the importance of continuous surveillance and characterization of circulating LSDV strains, as well as the need to improve the DIVA strategy for distinguishing the vaccine strains from field viruses.

Received | December 31, 2022; **Accepted** | February 14, 2023; **Published** | Month 00, 0000
***Correspondence** | Moustafa A. Zaghloul, Central Laboratory for Evaluation of Veterinary Biologics (CLEVB), Agricultural Research Center (ARC), Cairo, Egypt; **Email:** moustafazaghlool@gmail.com
Citation | Salama, A.A., M.A. Zaghloul, A.A. Zaghawa, M.A. Nayel, A.M. Elsafey, M.F. Azooz, H.S. Harb and W.S. Mousa. 2023. Molecular characterization of recent field isolate of lumpy skin disease virus compared to the vaccinal strains. Journal of Virological Sciences, xx(x): xxx-xxx.
DOI | http://dx.doi.org/10.17582/journal.jvs/.....
Keywords | LSDV, EEV gene, PCR, Sequencing, Phylogeny, DIVA

Copyright: 2023 by the authors. Licensee ResearchersLinks Ltd, England, UK.
This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https://creativecommons.org/licenses/by/4.0/).