TITLE: Isolation, Adaptation, Characterization and Molecular Analysis of Lumpy Skin Disease Virus (LSDV) Isolated from Cattle in Bangladesh Wetland area.

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BIOGRAPHY

I would like to introduce myself to you as I believe I have the skills, qualifications and experience necessary to make a significant contribution to this conference. I am Moslema jahan mou. I am from Bangladesh. I was born on 6 july 1998 in Bangladesh. I have 3 sisters. I completed Secondary and Higher secondary at my town, and got CGPA 5.00 in both board exams. I completed my B.sc at the age of 23 years from Rajshahi University department of Genetic Engineering and Biotechnology. And my CGPA is 3.79. Now I doing masters in Bangladesh agricultural university department of Microbiology and Hygiene. And I worked on several viruses and bacteria. I have over 20 publications that have been cited over 90 and my publication h-index is 6. I worked as a Research Assistant at the Virology lab in Bangladesh Agricultural University. I am self –motivated, energetic, enthusiastic and ever ready to learn new things. I am confident to ensure the highest level of professionalism and commitment to my any kind of work.

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ABSTRACT

The major cattle disease known as lumpy skin disease (LSD), which is common throughout Africa, is caused by the lumpy skin disease virus (LSDV). Since 2012, LSDV has become known as a prominent epizootic pathogen due to its quick spread outside of Africa into areas like the Middle East, Eastern Europe, and Asia. An LSD outbreak surfaced in Bangladesh in the middle of 2019, mostly in the division of Mymensingh. The objectives of this study were to isolate LSDV from infected cattle in Kishoreganj, Bangladesh, adapt it for cell culture, and carry out molecular identification. Twenty-two skin nodules from afflicted cattle were aseptically removed between July and September of 2023. The diagnosis of LSDV infection in cattles were confirmed through histopathological examinations, polymerase chain reaction (PCR), and sequence analysis, isolation and adaptation in cell line. Most LSD-infected animals showed fever, salivation, discharge, reduced milk yield, lymph node enlargement, and skin nodules. Ten (45.45%) out of 22 samples had positive LSDV PCR results. Histopathological analysis revealed reduced melanin, loss of stratum corneum, edematous dermis, structural derangement, skin thinning, and evidence of secondary infection. Based on phylogenetic analysis, strains from Neethling (Hervivac, Vaccine, Lumpyvac), India, and Bang-Chi(2019) were found to have more similarity, on the other hand, Greece, Serbia, Kenya, and Russia strains distantly related from our samples. Mutational analysis indicated several mutations throughout the RPO30, EEV glycoproteinand ITR of the identified strains. Protein structure analysis showed minor changes in the hydrophobic region of the RPO30, EEVGLy, ITR protein of the identified strains. Using the Vero cell line and the chorioallantoic membrane (CAM) route, LSDV was successfully isolated from these nodules through blind passages and subsequently propagated in embryonated specific pathogen-free (SPF) chicken eggs. The initially discovered LSDV isolates in Bangladesh were molecularly characterized and used as a vaccine seed. This study contributes to the development of practical preventive measures against LSD outbreaks by shedding light on the genetic composition of the LSDV that is circulating in Bangladesh.