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Molecular Characterization and Cytopathogenecity of Lumpy Skin Disease Virus in Egypt

A Thesis Submitted by

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Abstract

Lumpy skin disease virus (LSDV) still has a constant threat and causing a serious economic burden to cattle and buffaloes in Egypt. Recently, LSD has been aggressively distributed in different governorates of Egypt causing severe losses in animal wealth. The progressive shift of the outbreak in Egypt during 2018 raised concerns that the disease continue to spread despite excessive vaccination campaigns. This study was carried out to molecularly characterize LSDV strains circulating in Egypt during 2016 to 2019 outbreaks based on PCR assay targeting the GPCR and P32 genes. Also, study the growth kinetic of recent LSDV isolate to determine the culture properties of recent LSDV isolate that could be useful to develop more effective LSDV vaccine and diagnostic purposes. One hundred eighty one tested samples were positive for LSDV with different Ct values and a total of 159 samples were positive using gel-based PCR assay specific for LSDV. Phylogenetic analysis showed that the GPCR and P32 genes of recent LSDV circulating in Egypt fall within the cluster of field LSDV found worldwide with an overall 98.9-100% nucleotide identity and did not reveal significant genetic variations when compared with LSDV previously characterized in Egypt, indicating that all circulating strains in Egypt in this period more genetically closest to local reference strain, LSDV Egypt/89 Ismailia and LSDV isolate Evros/GR/15 than to vaccine SPPV Romanian strain. In addition, a comparative study of LSDV growth kinetic on MDBK and Vero cell line revealed that Vero cells were the best susceptible cells for the propagation of LSDV with best harvesting time 72hrs P.I. This is the first study to characterize the LSDV field isolates in Egypt based on two genes; the P32 and GPCR nucleotide sequences of LSDV that could be of a great importance in providing up to date analysis regarding the genotypic nature of circulating LSDV strains in different governorates of Egypt. Furthermore, multigene analysis and whole genome sequencing will greatly improve the accuracy of the molecular characterization and differentiation between Capri poxviruses in Egypt.

Key words: LSDV, virus isolation, MDBK, Vero, Growth kinetic, Real time PCR, Phylogenetic analysis, GPCR, P32, Egypt.

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