Summary

In the current study we have investigated the last sporadic outbreaks of lumpy skin disease in Three Egyptian Governorates (Al-Minia, Damietta and Beni-Suef).

A total of 1400 clinically suspected cattle from different ages and both sex were examined clinically. Clinical examination showed that diseased cattle had the following signs; increase in body temperature that ranged from 39.8ºC to 41.5ºC. The duration of fever was variable and extended up to 12 days in some cases. Feverish cattle showed increased nasal secretions, salivation, loss of appetite, reduced milk production, depression, and reluctance to move. Fever usually followed within two days, by the development of nodules on the skin and mucous membranes.

Cutaneous nodules varied from one to seven centimeters in diameter and the full skin thickness was included. The distribution of the skin nodules varied greatly among examined cattle. Some animals showed localized nodular eruption while the majority of diseased animals showed generalized distribution of the nodules covering the entire integument. Most of clinically diseased animals developed edema in the dewlap and limbs and/or enlargement of draining superficial lymph nodes like the pre-scapular and pre-femoral ones. Some diseased cattle recovered from the cutaneous nodules within several months but the recovery, in most cases, was incomplete leaving deep holes or scars on the skin.

Diseased animals showed several complications and pneumonia was pronounced in most of cases and it was a common sequel in animals having lesions in the mouth and respiratory tract.

Cutaneous nodule samples were collected from diseased animals for virus isolation and identification. Virus isolation was done on CAM of SPF-ECE. In the third passage of the samples on ECE, CAM showed characteristic pocks of

small sizes within five days post inoculation. Eight out of 25 LSD suspected samples gave the characteristic lesions on CAM of SPF-ECE.

Two PCR runs were applied on tissue homogenates obtained from CAM showing characteristic lesions. The first PCR run was applied using Capripoxvirus specific primer set whose expected product size is 192 bp. Six DNA extracts that showed positivity to Capripoxvirus specific PCR were confirmed to be LSDV through another PCR run based on LSDV specific primers with an expected product size 1237 bp.

Out of six positive 192 bp PCR products, four positive products were sequenced including isolates from the three Governorates. P32 gene partial sequencing was done using Capripox specific primer set. Sequence analysis of the obtained sequences (Egypt-BSU/Minia-1/2011, Egypt-BSU/Damietta/2012, Egypt-BSU/Beni-Suef-1/2012 and Egypt-BSU/Beni-Suef-2/2012) revealed high identities between all of the four isolates and so two PCR products (from Damietta and Beni-Suef Governorates) obtained by LSDV specific primer set (with 1237bp expected product size) were subjected to gene sequencing. This target part contains genes which encode for two hypothetical proteins; LSDV001 and LSDV002 (homologous to LSDV156 and LSDV155, respectively).

Complete sequence of ORF of LSDV001 gene of our selected Egyptian isolates from Damietta and Beni-Suef Governorates (Egypt-BSU/Damietta/2012 (Accession no KF588351), and Egypt-BSU/Beni-Suef-2/2012(Accession no KF588352) revealed that this gene contains 477 nucleotides and encodes for 159 amino acids. Sequence analysis revealed that both isolates are closely related to each other with 99% nucleotides and amino acids identities. Deduced amino acid sequence analysis of LSDV001 of different capripoxvirus isolates revealed high similarities among different isolates with greater relatedness of GTPV to LSDV isolates than do SPPV isolates.

Complete sequence of ORF of LSDV002 gene of our selected Egyptian isolates (Egypt-BSU/Damietta/2012 (Accession no KF588353) and Egypt-BSU/Beni-Suef-2/2012 (Accession no KF588354) revealed that this gene contains 393 nucleotides and encodes for 131 amino acids. Sequence analysis revealed that both isolates are closely related to each other with 98% nucleotides and 97% amino acids identities. LSDV002 gene of our isolates Egypt-BSU/Beni-Suef-2/2012 and Egypt-BSU/Damietta/2012 showed great nucleotide and amino acids similarities to LSDV-Egypt-Ismailiya/1989 with nucleotide identity 98% and 99% and amino acids identity 96% and 99% for Beni-Suef and Damietta isolate, respectively.

Hisopathological examination of the suspected skin lesions showed moderate vacuolation and acanthosis of the prickle cell layer in the epidermis. Some cells in the epidermis showed eosinophilic intracytoplsmic inclusion bodies (single, large bodies, occupying large area of the cytoplasm). Similar inclusions were detected within histiocytes of the dermis.

In the dermis, the papillary layer appeared highly congested and edematous. The dermis also showed vasculitis, thrombosis, necrosis and perivascular cellular infiltrates including macrophage, lymphocytes, eosinophils and neutrophils associated with a proliferation of the fibrous connective tissue (fibroma like).