

Part 4. Brief communications

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LUMPY SKIN DISEASE IN TURKEY

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Lumpy skin disease (LSD) is an economically important infection since the presence of the disease affects cattle health and export of cattle products. It is caused by *Capripoxvirus* and shows characteristic skin lesions in infected cattle. The disease was first reported in Zambia in 1929. It then spread to Africa, Middle East and recently to European countries like Bulgaria. The first Turkish outbreak of LSD was reported in 2013 in Kahramanmaraş. Until now, many cattle are affected and the disease spread to farms located in different parts of Turkey. After the first outbreak, rapid diagnostic methods have been used in order to identify disease outbreaks. Control and eradication programs have been applied by the Ministry of Food, Agriculture and Livestock of Republic of Turkey including contingency plan, killing and compulsory vaccination.

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INVESTIGATION OF ADAPTATION OF AVIAN INFLUENZA VIRUSES TO MAMMALIAN SPECIES

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Influenza A viruses are negative-sense, single stranded and segmented RNA viruses. They are zoonotic pathogens that continuously circulate in several animal hosts and undergo genetic drift and shift. These are responsible for causing human epidemics and sometimes pandemics.

Avian influenza H5N1, H7N7, H7N9, and H9N2 viruses have been hypothesized to cause the next pandemic, although there is no clear evidence that they have been successfully maintained in humans. To date, how avian influenza viruses adapt to mammalian species is still not completely understood. We try to answer the following questions:

- How fast do avian influenza viruses adapt to mammalian species?
- How do avian influenza viruses cross the species barrier to adapt to mammalian species?

To answer these questions, we performed three serial passages of a quail H9N2 virus in pigs and sequenced the broncho-alveolar lavage fluid (BALF) from pigs in all three experimental groups using universal and internal primers.

We concluded from virus titration and sequencing results, that the adaptation of an avian H9N2 virus to pigs seems to work. We saw a gradual increase of virus titers in the lung of animals after serial passages. Nucleotide mutations have been found in seven genes analyzed, many of them also leading to amino acid substitutions. The third passage H9N2 isolate induced obvious lesions in pig lungs.

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