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Developing Innovative and Sustainable Approaches to Prevent the Spread of Goat Plague Disease in Democratic Republic of Congo

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Abstract

Peste des petits ruminants (PPR) or "goat plague" is an acute viral disease of small ruminants caused by PPR virus (PPRV). The disease causes high morbidities of up to 100 % and mortality rates ranging between 50 and 90 % in goats and sheep leading to high economic losses. The disease was first reported by FAO and OIE in the Democratic Republic of Congo (DRC) in 2008. The aim of the current study was to confirm and characterise PPRV using reverse transcriptase polymerase chain reaction (RT-PCR) and to establish their phylogenetic relationship by sequencing the nucleoprotein (N), fusion (F) and hemagglutinin (H) genes but also evaluate the prevalence of PPRV specific antibody by competitive enzyme-linked immunosorbent assay (cELISA) and determine specific in-country risk factors associated with the disease patterns. Samples including oculonasal swabs, tissues and whole blood were obtained from live goats and/or sheep with clinical presentation suggestive of PPR for virus characterisation and serum for antibody-PPRV detection. The clinical signs observed in sampled goats and/or sheep suspected with PPR included proliferative and self-resolving lesions around the muzzle and lips of involved animals, serous mucopurulent nasal and ocular discharge, fever, diarrhea, lacrimation, matting of eye lids, cutaneous nodules, erosions on the soft palate and gums and labored breathing. The screening of 150 samples by RT-PCR indicated an overall prevalence of 64.7 %. Phylogenetic analysis based on the sequencing of N, F and H genes indicated that PPRV obtained from Eastern DRC clustered genetically with PPRV strains of Lineage III, together with PPRV from East Africa. Therefore the control of this disease is important in order to avoid the spread of the virus in the entire country and across. An overall PPRV seroprevalence of 45.3 % (n=320) was determined. A multilevel nominal logistic model using JMP-Pro software and Stata 11 indicated that the likelihood of goats and sheep being infected with PPRV increased significantly when animals shared water sources, herd size increased, animal age increased, exotic breed, communal grazing systems and farm-to-farm animal exchange. PPRV is circulating in South Kivu and several risk factors are associated with its sero-status including spacial and farm management.

Keywords: Democratic Republic of Congo, molecular characterisation, peste-des-petits ruminants, risk factors, seroprevalence

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