Abstract:

This study aimed at determining the prevalence and characterizing the CaPV, determining the CaPV-PPRV coinfection prevalence and providing data about phylogenetic relationship between the fusion protein of PPRV and *P32* gene of CaPV. A total of 150 samples including animal swabs, tissues and blood were collected from unvaccinated goats in a PPR and/or Capripox outbreaks in South Kivu, Eastern of Democratic Republic of the Congo. Conventional PCR and reverse transcriptase (RT-) PCR were used respectively to amplify *P32, RPO30, GPCR* genes of Capripox virus and Fusion (F) protein of PPRV. Positive samples were sequenced for phylogenetic analysis.

Results: Out of 150 tested animals, 64.7% (n=97/150) were PPRV positive, 52.7% (n=79/150) were Capripox positive and 38.7% (n=58/150) were positive for both PPRV and CaPV. The pairwise comparison of *P32* gene of CaPV and *F* gene of PPRV showed 99.75% of identity percentage among goatpox virus sequences, 96.95% among PPRV sequences and 47.91% between CaPV and PPRV sequences.

Conclusion: The study has demonstrated high prevalence of CaP V-PPRV mixed infection in South Kivu. Lumpy skin virus disease (LSVD) is a lineage circulating which has a genetic relationship between its *P32* gene and the *F* gene of PPRV giving the challenge to differentiate the two diseases at the clinical farm level.