

# **IDENTIFICATION OF THE EMERGENT PESTIVIRUS INFECTIONS OF SMALL RUMINANTS IN TAJIKISTAN**

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# INTRODUCTION

It is known that the spread of various infectious diseases among farm animals leads to tremendous economic damages. For livestock, particularly for sheep and goats farming, the greatest threat is caused by the peste des petits ruminants (PPR), which was determined as a transboundary and highly contagious disease of small ruminants by FAO and OIE. In almost all livestock farms in Tajikistan, diseases of the respiratory organs and the reproductive system of various etiologies are widely diagnosed. In Tajikistan, data on pestiviruses are quite fragmented, despite the spread of respiratory, intestinal and reproductive diseases. The identification and typing of viruses during mass outbreaks of diseases and the study of their etiology particularly in the sheep and goats' populations in Tajikistan is a relevant task of scientific research.

Identification and study of the pestiviruses that caused the respiratory and reproductive diseases in small ruminants in Tajikistan.



# MATERIALS AND METHODS

Samples of serum and parenchymal organs of slaughtered animals and aborted fetuses were sent to our laboratory. Totally 234 samples of serum and 32 post-mortem samples from thirteen districts of Tajikistan were examined.

## **Methods:**

- Virus isolation;
- Agar-Gel Immunodiffusion Test (AGID)
- RT-PCR and phylogenetic analysis



# RESULTS

## ○ **Agar-Gel Immunodiffusion Test (AGID)**

The results of the retrospective study in AGID had revealed 27% positive samples with BVDV antigen and 12% with PPRV antigen. A detailed analysis of the results determined that some samples were positive with both BVDV and PPRV antigens which composed 5% of the studied serum.

## ○ **Virus Isolation**

It has been determined that the virus is noncytopathogenic in cell cultures;

## ○ **RT-PCR and phylogenetic analysis**

- The BD virus was identified by RT-PCR. Phylogenetic analysis was determined that the border disease virus (Pestivirus D) supposedly belongs to the 3rd genetic group of BDV and in 90-91% was similar to the available isolates of GenBank..
- During an experimental study in AGID, when a PPR vaccine strain was used as a control positive antigen, its contamination was detected. The results were confirmed by RT-PCR and phylogenetic methods, which established that a series of a vaccine against PPRV was contaminated by the pestivirus H the so-called causative agent of Hobi-like pestivirus (BVDV-3).
- The sequences of the studied virus were submitted to GenBank (KX900607 and KX900608).



# CONCLUSION

- The emergent pestivirus D (BDV) for the first time was identified and isolated in small ruminants in Tajikistan.
- Based on phylogenetic analysis, it was shown that the virus can be assigned to the 3-genetic group of BDV..
- The contamination of a commercial vaccine against PPRV with a new, atypical Hobi-like pestivirus has been established.
- The dissemination of these pestivirus infections in the Central Asian region can significantly reduce the effectiveness of anti-epizootic measures against PPR.

