Dear Editor in Chief,

We would like to submit our paper entitled "**Detection and phylogenetic analysis of *Peste des Petits Ruminants Virus* isolated from outbreaks in Punjab, Pakistan''** by Muhammad Munir, Siamak Zohari, Ali Saeed, Qaiser Mahmood Khan, Muhammad Abubakar, Neil LeBlanc, Mikael Berg.

As you know Peste des Petits Ruminants (PPR) is a highly contagious and often fatal morbilli-viral infection of both wild and domestic small ruminants. It causes serious economic losses in Asia, the Middle East and Sub-Saharan Africa. Recently, a number of studies have been conducted to ascertain the magnitude of the PPR problem in Pakistan to characterize the virus population and to define the trends and causes of its occurrence in Pakistan. However, almost always these studies have been based on either laboratory confirmation by detecting antibodies/antigen using ELISA or based on clinico-epidemiological observations.

Given the increase in circulation of PPR virus among susceptible populations and for future eradication concern of the FAO and OIE, it is of paramount importance to delve into the molecular and genetic characterization of the field PPR viruses. The objective of this communication was to detect PPRV in suspected outbreaks in the region by employing conventional and real-time PCR and then to use sequencing to provide phylogenetic analysis of nucleoprotein and fusion protein gene segments to get an insight genetic picture of PPRV.

This is the first report presenting the phylogenetic tree based on N gene from Pakistan and performing a parallel comparison of the trees of F and N gene together from Pakistani isolates, despite the fact that PPRV is one of the most devastating diseases for small ruminants in the country. The results of this study shed light on the PPR virus population in Pakistan and emphasize the importance of using molecular methods to understand the epidemiology.

This characterization would be valuable to analyze the genetic nature of PPRV not only in Pakistan but also in other neighboring countries. Findings in this study significantly advance the currently available sequence data on PPRV and will be first step to establish a domestic reference virus for future studies.

Finally, we would like to emphasize that there have been several outbreaks of PPRV reported in both sheep and goats in Pakistan and many other countries. Therefore, it was of supreme worth to characterize the genome of first PPRV isolate in Pakistan to properly understand the possible spread of PPRV and variability between PPRV isolates in the region. Thus, we believe that this article will be of substantial interest to the readers of Transboundary and Emerging Diseases. We have enclosed the article, comprising of four figures and one table.

All authors agree that Muhammad Munir will act as corresponding author concerning all matters of this manuscript. The authors also declare that they have no competing interests.

Sincerely,

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