

Molecular detection and phylogenetic analysis of Peste des petits ruminant's virus in QOM Province 2016 and 2018

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Abstract

Peste des Petits Ruminants (PPR) is a severe, highly infectious and fatal viral disease of small ruminants. Four lineages of the PPR virus have been identified globally based on sequence analysis nucleoprotein (N) and fusion (F) gene. The aim of this study was molecular detection and phylogenetic analysis recently circulating PPR virus in small ruminants in QOM Province in Iran. A total of 10 anti-mortem samples (mesenteric lymph node) were collected from clinically suspicious animals and examined for the presence of PPRV by a one-step RT-PCR assay. Samples positive with RT-PCR were subjected to subsequently genetically characterized by sequencing of the nucleoprotein (N) gene and phylogenetic analysis of PPR virus (PPRV) strains. Of the 10 clinical samples examined, 40.0% were positive with RT PCR for viral nucleic acid. The nucleotide sequence and phylogenetic analysis indicated that these isolates were clustered genetically with Lineage IV isolates of the PPRV. phylogenetic analysis and molecular findings of this study confirmed active lineage IV PPRV infections among goat populations in QOM Province. This study and latter studies revealed that the Iranian PPRV isolates belong to lineage IV and are closely related to the Pakistan, Tajikistan and India isolates of PPRV We recommended that more studies should be done from other parts of the country, especially the border areas, to more accurately illustrate the status and circulation of the active lineage of the PPR virus in Iran.

Key words: Peste des Petits Ruminants (PPR), Paramyxovirus, Molecular detection, Lineage

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