

Mutation Rate Analysis of PPR Virus in Fourteen Different Countries

**Gulshan Wadhwa^{1*},
Usman Sayeed²,
Qazi Mohd Sajid
Jamal²**

¹ Department of Biotechnology, Ministry of Science & Technology, New Delhi

² Department of Biotechnology, Microbiology and Bioinformatics, Integral University, Lucknow

Address for correspondence:

E-mail: gulshan.dbt@nic.in

PPR is an acute, febrile viral disease of small ruminants which causes a severe disease in the sheep and goats. PPRV is highly contagious disease with high fatality rate of 68-70%. This study has been undertaken to identify the sites in the various strains of the virus 255bp across the world. The study was undertaken to characterize a 255bp *Pest des petits* gene from Ruminants from 14 different countries. The sequence was obtained

by sequencing nucleoprotein (N) gene segments and phylogenetic analysis was applied from sheep and goats. 255bp samples collected from 14 different countries by NCBI. The phylogenetic analysis based on the 255 bp nucleotide gene sequences of PPRV from 16 different locations clustered MEGA software them into lineage 4 along with classification of PPRV into lineages based on the N gene sequence.