

Molecular epidemiology of rabies virus in Bhutan

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The objective of this study was to understand the rabies virus strains circulating in domestic dog population in southern Bhutan. Twenty-three rabies virus isolates originating from dogs and other domestic animals were characterized by sequencing the partial nucleoprotein (N) gene (395 bp). Phylogenetic analysis was conducted and the Bhutanese isolates were compared with rabies viruses originating from other parts of the world. Bhutanese rabies virus isolates were found to be highly similar and did not form any distinct sub-groups, suggesting this viral group originated from a common ancestor. Phylogenetic study indicate that Bhutanese rabies strains were closely related to Indian strains and the Arctic-like-1 lineage circulating in South Asia and could be grouped together as a large cluster of South Asian Arctic-like-1 lineage. The translocation or trans-border movement of dogs along the border may have facilitated the spread of this rabies virus variant between the two countries.