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# Molecular Epidemiological Analysis of Rabies Virus in Mumbai Region of India

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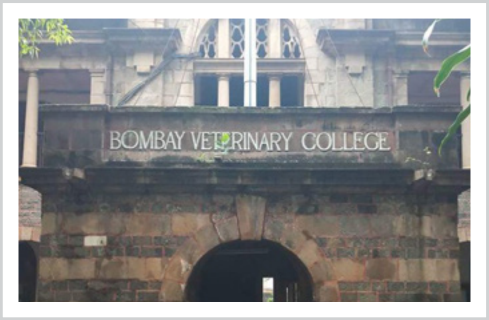
## Abstract

Rabies is one of the negligible fatal acute viral disease of the central nervous system, which is a serious public health problem and is responsible for over 30, 000 deaths in Asia and Africa alone.Rabies caused by a neurotropic virus belonging to the Lyssavirusgenus of family Rhabdoviridae. Rabies virus Nucleoprotein (N) gene highly conserved gene mainly used for genetic analysis whereas Glycoprotein (G) plays a critical role in the pathogenesis of the disease. Despite the importance of rabies for animal and human health, little is known about the evolutionary dynamics of Rabies virus in dog populations and patterns of biodiversity. To address these questions on a small scale, a total of 50 dog brain samples suspected for rabies were screened by Seller's staining test (SST), Mouse Innoculation Test (MIT) and Direct Fluorescent Antibody Test (dFAT),G gene PCR and N gene PCR. Out of 50 samples,28 were positive by SST, 34 were positive by MIT, 38 by dFAT, 40 by both Nand G gene PCR. Randomly 6 samples were sequenced for N and G gene and the sequences were submitted to gene Bank. The phylogenetic analysis (PA) of N gene revealed that 6 isolates in Mumbai region (MR) belonged to a single Arctic lineage. Time scaled phylogeny of partial N gene revealed that the most recent common ancestor (TMRCA) for the sequences belonged to the cluster from 2006.68 with 95% HPD 2005-2008, which is assigned to Indian lineage I. PA of G gene revealed that the RVs circulating in MR are divided into 3 lineages. Time scaled phylogeny by Bayesian coalescent analysis method estimated that TMRCA for sequences under study was 1993 and Indian clusters was 1962. In conclusion, the phylogenetic analysis of N gene revealed that 6 isolates belonged to single Arctic lineages along with other Indian isolates and they were clustered into a single lineage and were closely aligned to the isolates from Afghanistan and Bangladesh indicating that these strains are circulating in Indian subcontinent. Based on the G gene sequences the isolates were divided in to single lineage, but divided in to 3 clades which reflected the antigenic diversity between the isolates, that is responsible for the pathogenicity of the isolates.

## Biography

Dr. Rajesh Raghunath Pharande has completed his PhD in year 2019 from Mumbai Veterinary College. He is working as Assistant Professor in Mumbai Veterinary College since last 10 years. He has 14 Publications, two best presentation awards in International Conference, Guided two Post Graduate students. Has been serving as an Research co-ordinatar, Nodal officer and Assistant Editor member in The Bombay Veterinary College Journal.



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