SYNOPSIS

Morbilliviruses belong to the family *Paramyxoviridae* of the *Mononegavirale* order of viruses. The *Mononegavirale* order contains viruses which contain negatively-polar, non-segmented and single stranded RNA genomes. This order contains some of most lethal pathogens known to the humankind. *Ebola virus* and *Marburg virus* are perhaps the most lethal human pathogens. *Rinderpest virus*, declared eradicated in 2011, was known to be the most significant cattle killer. Similarly the *Canine distemper virus* and *Rabies virus,* two topmost canine pathogens belong to this order.

The L protein in the viruses of *Morbillivirus* genus harbours the viral RNA-dependent RNA polymerase that replicates and transcribes the viral genome and also all the mRNA capping enzymes, *viz*. RNA 5' triphosphatase, guanylyltransferase, RNA (guanine-7-)methyltransferase and RNA 5' cap-dependent (2'-oxo-)methyltransferase. Moreover this protein can act as a protein kinase that can regulate the function of P protein which serves as a switch between transcription and replication.

mRNA capping is necessary for the virus for the purpose of exploiting host cellular machinery towards viral protein synthesis. The *Rinderpest virus* L protein serves as a model to study the capping enzymes of *Morbillivirus*. RNA triphosphatase (RTPase), the first enzyme of the capping cascade had earlier been located on the L protein. The RTPase minimal domain on the L protein was identified earlier by sequence homology studies done with RTPase proteins of *Baculovirus* and *Vaccinia virus* and cloned. The bacterially expressed recombinant domain was shown to possess RTPase activity. The enzymatic activity was characterized and the RTPase was found to be a metal-dependent enzyme which is highly specific to capping viral mRNA. Further characterization of the domain revealed that the domain also possesses nucleotide triphosphatase (NTPase), tripolyphosphatase and pyrophosphatase activities. Two site-directed mutants in motif-A of the domain: E1645A and E1647A were also tested and were found to be essential for the RTPase and NTPase activity. It was also recognized through these mutant studies that the active sites of RTPase and NTPase activities are partially overlapping.

Earlier work done with *Vesicular stomatitis virus* capping enzymes showed that the *Rhabdoviridae* family of viruses follow unconventional capping pathway utilizing an enzyme polyribonucleotidyltransferase (PRNTase) which transfers GDP to 5'-monophosphated RNA. Characterization of the RTPase activity which converts 5'-triphosphated RNA into 5'-diphosphated RNA is an evidence for the morbilliviruses utilizing the conventional eukaryotic capping cascade. The results show that *Paramyxoviridae* do not follow unconventional capping pathway for the mRNA capping as has been the paradigm in the past decade.

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