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MS02-1-6 A highly specific N7-guanine RNA cap methyltransferase in an unusual locus of large RNA virus genome
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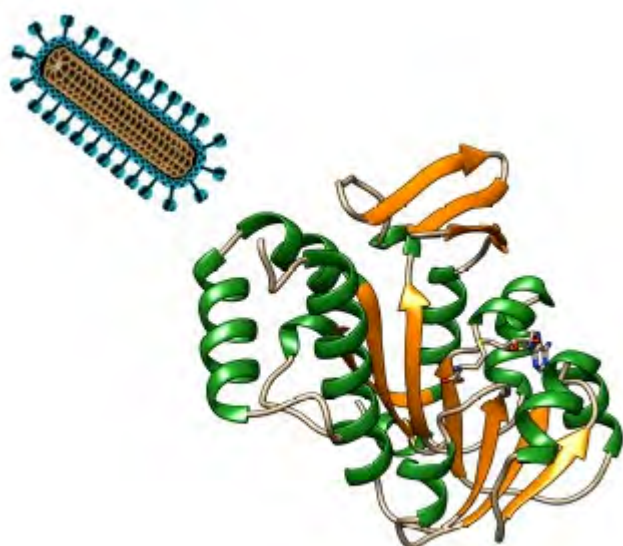
Abstract

The order Nidovirales is a diverse group of (+)RNA viruses, with a common genome organization and conserved set of replicative and editing enzymes (1). In particular, RNA methyltransferases plays a central role in mRNA stability and are considered beneficial to genome expansion (2). In Coronaviridae ; the best Nidovirales characterized family ; two separate methyltransferases, nsp14 (3,4) and nsp16 (5-7), perform the RNA-cap N7-guanine and 2'-OH methylation respectively, for generation of the m7GpppNm type I cap structure (8). Both enzymes are located in the ORF1b genomic region. The other Nidovirales families are however far less well characterized, and are sequentially distant making the identification of RNA / N7-guanine methyltransferase signature sequence difficult, obscuring our understanding about how RNA-caps are N7-methylated for these families. White Bream virus a Tobaniviridae, was lacking a N7-MTase signature at the expected genomic location. Recently it was proposed its presence in ORF1a, an odd genomic location for such an enzyme (9). Here, we demonstrate that the enzyme activity is N7-specific, and present the structure of a new N7-Mtase. This discovery helps to define better the N7-MTase family in its whole and we discuss the evolutionary advantages of such an appearance in this location of the genome

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Tobaniviridae N7-MTase



Key enzymes driving RNA virus evolution

