

Class: N-protein

Attributes:

SARS-CoV specific

Accession #: NP_828858

Synonyms: Orf 9a, nucleocapsid protein

Molecular weight: 50 kDa (relative molecular weight: 45,929 Da)

Number of amino acids: 422

Structure:

- contains lysine-rich sequence (KTFPPTPEPKDKKKKTDEAQ) aa 362-381 near C term not found in any other known coronaviruses(1)
- putative nuclear localization signal (KKDKKK, aa 370-376) (2)

Processing:

- the first aa, methionine is depleted and the second serine is acetylated showing phosphorylation doesn't happen in the predicted phosphorylation sites (3)
- found no phosphorylation in the whole molecule (3)

Location:

- positive signals distributed in cytoplasm and not predominantly localized in the nucleolus, unlike other coronavirus' that have distribution in nucleolus (2)

Functions:

- role for the nucleocapsid in the primary humoral immune response against SARS infection (2)
- recombinant N protein can be cleaved by caspase-3 so caspase-3 may cleave the N protein in vivo during the late phase of virus infection (3)
- expression of N protein causes increase in binding of c-Fos, ATF2, CREB-1, and FosB binding to promoter sequences (4)
- N protein does not activate NF-kB pathway (4)

Other coronaviruses

Synonyms: nucleocapsid protein

Molecular weight: N/A

Number of amino acids: N/A

Structure:

1)Homology:

- BCV N sequence is almost identical to human coronavirus OC43 and turkey coronavirus (5)

2)Domain Information:

- three highly conserved domains separated by **spacers A and B** (6)
- spacer B is largely dispensable for N protein function (7)
- domain I** (aa 1-139), basic (6)
- domain II** (aa 168-380), basic (6)
 - domain II is the RNA binding domain (8, 9)
 - RNA-binding activity encompasses amino acids 136 to 397 (9)
 - Further refined to amino acids 169-308 (8)
- domain III** (aa 406-455), acidic (6)
- SR-rich region consist of an island of 34 residues (amino acids 194-227) containing 11 serines and 7 arginines (5)
 - core motif of SSRXXSRXXSRXX can be found within all coronavirus N proteins (5)
 - important in protein-protein interactions and present in many splicing regulatory proteins
- five aromatic residues WYFY may be essential in forming hydrophobic interface between N monomers, N and M proteins or between N and cellular membrane (10)
 - Residues fall within region that is the most highly conserved region among all coronavirus N proteins
 - W126C mutation is especially critical for temperature-sensitive phenotype (10)

Processing:

- proteolytic processing (11)

Functions:

- N protein not necessary for RNA packaging (12)
- N protein has a role in translation control (13)
- ongoing protein synthesis is necessary for replication and N protein plays an important role in MHV replication (14)

Location:

- nucleolus (2)

Abundance: N/A

Responsibilities:

Collaborators:

Trimerize may promote efficient release of N protein from N protein
Restricts M protein to late Golgi and may provide measure of stability and contribute to the site of virus particle assembly
N binding to mRNA may alter its conformation allowing it to bind to M protein. May affect translation of RNA polymerase, disrupt normal cell division
N protein binds hnRNP-A1 to bring the leader RNA to the intergenic sequence of the template for initiation of subgenomic mRNA transcription

N-protein
M_protein
mRNA
hnRNP-A1

Interaction may be one of the mechanisms by which MHV regulates its discontinuous transcription	
Sequester ribosomal subunits for preferential translation of virus subGenomic RNAs	rRNA
Association with membrane lipid may be important for nucleocapsid uncoating and assembly	membrane
Caspase-3 can cleave N protein <i>in vivo</i> ; may have role in apoptosis	caspase-3 (3)

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