

Clinical, Diagnostic and Therapeutic Implications of Coronavirus ORF8 Polyprotein Associated Nsp16 Protein-A Bioinformatics Approach

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Abstract

COVID-19 infections are rapidly spreading worldwide with more than 100000 death and thus understanding the molecular mechanism of tropism of human cells is an urgent need for drug design. We have described here a bioinformatics approach to predict the functional aspects of non-structural nsp16 protein of Corona virus. The COVID-19 7096 AA large polyprotein was degraded into sixteen proteins and last nsp16 protein was found an RlmE type rRNA Methyltransferase. Nsp16 has no similarity to bacterial RlmABCD but has 25 percent similarity to the bacterial RlmE MTase protein which methylates the U2551 2-hydroxy group of Ribose. The nsp16 proteins of different corona viruses like Covid-19, bat-coronavirus, SARS and MERS have strong homology. Mrm2 and Dim1 like yeast and mammalian rRNA methyltransferases have 26-33 percent homologies but not with 2'-O-capping MTase as reported previously. Rrp8 MTases also has no similarity to nsp16. We postulated that mitochondrial rRNA methylation of bronchial cells were mediated by the nsp16 protein causing inhibition of protein synthesis due to poor assembly of aminoacyl-tRNA or mRNA and peptidyl transferase at the PTC. This is one of the new molecular mechanism of corona virus cellular tropism and different than ACE-2 mediated blockage of cellular signalling to inhibit aldosterone biosynthesis with abnormal Na⁺ ions in cells. We also designed primers based on nsp16 cDNA sequence (nt 20659-21552, accession no MT121215) specific for Covid-19 diagnosis by RT-PCR. Antisense and ribozyme against Nsp16 may be another molecular approach to stop Coronavirus translation using nano-carrier drug delivery. Whereas phyto-chemicals from Indian medicinal plants may be studied to stop functions of Nsp16 RlmE Methyltransferase as another therapeutic approach against Coronavirus pathogenesis.

Keywords: Covid-19; rlmE MTase; New Drug Target; Corona Diagnosis; Corona Pandemic

Introduction

Coronaviruses (family Coronaviridae) are enveloped viruses with a largest positive sense, single-stranded RNA genome of 30kb [1,2]. On genetic and antigenic criteria, CoVs have been organised into three groups: α -CoVs, β -CoVs, and γ -CoVs [3-5]. Coronaviruses primarily infect birds, mammals and human, causing a variety of lethal respiratory diseases resembling the common cold, to lower respiratory tract infections such as bronchitis, pneumonia, and even severe acute respiratory syndrome (SARS). In recent years, coronaviral research must be augmented due to pandemic severe respiratory illnesses outbreaks claiming > 100000 deaths [6]. Covid-19 virus enter cells through ACE2 receptor-mediated endocytosis. The receptor ACE2, was abundant in lungs AT2 alveolar epithelial cell as well as cells in the kidney, heart and blood vessels [7]. One of the known regulators of endocytosis is the AP2-associated protein kinase-1 implicated novel target for therapeutic intervention. Figure 1 demonstrated the blockage of ACE-2 receptors prevents the aldosterone synthesis and thus deregulating Na⁺ absorption, blood pressure and normal renal function. We suggested a new role of cellular tropism by inhibiting cellular protein synthesis.

Discovery of new molecular target is urgent need for covid-19 and we target here rRNA methylase. There are more than 20 differ-

Figure 1: (A) Renin-Angiotensin System and problem associated with covid-19 binding to ACE-2 receptors preventing such signalling. (B) nsp16 methylates 21S rRNA in mitoribosome inhibiting protein synthesis. Hypothesis is due to loss of mitochondrial proteins oxidative phosphorylation may be prevented causing sudden death of Corona-infected patients.

ent classes of rRNA methyltransferases that modify 16S rRNA, 23S rRNA and tRNAs in bacteria but mammalian methyltransferases are more diverged [8]. Cfr and Erm methyltransferases are known for erythromycin and linezolid drug resistance in bacteria and others like Rmt, ArmA and Rlm methyltransferases are involved in ribosome biogenesis as well as modulator of drug resistance (Figure 2). Different isomers of Rlm (A-N) rRNA methyltransferases methylate at various positions of bacterial 23S rRNA conferring multi-resistant to macrolides and ketolides like erythromycin, telithromycin, and solithromycin. RlmA^{II} MTase has preference to N₁ of G748 of 23S rRNA [9]. RlmB MTase (protein id. BAI33654) modifies G2251 of 23S rRNA [10,11] while RlmC modifies m5U747

in 23S rRNA and RlmD is specific for m⁵U1939 [12]. RlmE (protein ids. RXP80948 and TJJ68081) and RlmF (protein ids. TZE44659; BAI32636) 23S rRNA 2'-O-U2552 methyltransferase also has detected in *E. coli* chromosome and plasmids. RlmE has similarity to RlmC but diverged in other isomers. RlmG (protein id. CRY88590) methylates at N₂ of G1835, while RlmH (protein id. QBF38433) methylates pseudo-uridine N₃ at position 1915 and RlmN (protein id. QBF37927) methylates C₂ at A2503. RlmH (UbeA) catalyzes the transfer of a methyl group from S-adenosyl-L-methionine (SAM) to the nucleotide at position m³ψ1915 of *E. coli* 23S rRNA. RlmI (protein id. QEP80348; MHW78000) also methylates *E. coli* 23S rRNA and RlmJ catalyzes the m⁶A2030 methylation of 23S rRNA during ribosome biogenesis in *Escherichia coli*. The active site of RlmJ with motif IV sequence 164DPPY167 is more similar to DNA m⁶A MTases than to RNA m⁶,2A MTases and the enzyme crystal structure was determined [13]. RlmM (YgdE; EC:2.1.1.186) enzyme catalyzes the SAM-dependent 2' O-ribose methylation of C2498 in 23S rRNA of *Escherichia coli*. RlmN installs a methyl group at the C2 position of A2503 of 23S rRNA, while it also methylates at tRNA at nucleotide A37 giving linezolid resistance in *S. aureus* [14]. RlmK/L (protein ids. MHY78137 and BAI29841) and both recombinant enzyme (YcbY) adds the m⁷G2069 and m²G2445 methylations in *Escherichia coli* 23S rRNA (Kimura, *et al.* 2012). TlyA from *Mycobacterium tuberculosis* has proven 2'-O-ribose MTase activity on C1409 of 16S rRNA and C1920 of 23S rRNA. The m⁸-A2503 modification by Cfr *in vivo* leads to a decreased level of modification of C2498 by RlmM indicating domain V in presence of the Cfr-catalyzed methylation prefers a conformation where the 2'-O of C2498 is no longer accessible for RlmM. In the mature ribosome, A2503 stacks between A2059 and G2061 at the opposite side of the peptidyl transferase loop, and possibly the methylation, apart from sterically hindering antibiotic binding, also increases the stability of the stacked structure [14]. However, ribose 2'-O-methylation similar to RlmB methylation of 2'-O of guanine, is the most abundant rRNA chemical modification to be essential for accurate and efficient protein synthesis in cells and has no role in drug resistance. Such enzymes are involved in capping of eukaryotic mRNA and modification of rRNAs and tRNAs. Human CMTr1/2 2'-O-linked methyltransferase has been purified and characterized [15]. Interestingly, Rlm MTases were rarely sequenced in plasmids of Enterobacteriaceae but in *Pseudorhodobacter sp* 1584kb unnamed plasmid indeed contained RlmF (EC:2.1.1.181) and RlmB methyltransferases and other RNA modifying enzymes (accession no. CP039965). The RlmD, RlmH and RlmN 23S rRNA Methyltransferases in large plasmid of *Acinetobacter baumannii* (accession no. CP035931, 1024kb) was reported. Surely, roles of Rlm family methyltransferases in multi-resistance remains controversial at this point. Although it has been reported that U1939 methylation is involved in reproducible resistance to fusidic acid and capreomycin. Mitochondrial rRNA of yeast contains three modified nucleotides: a pseudouridine at 2918, two 2'-O-methylated ribose at G2270 and U2791 located near the peptidyl center. Mrm2p is the orthologue of FtsJ/RsmJ which methylates U2791 of 21S rRNA of mitochondria in yeast and mammalian cells. Di-methyl Adenine modification in yeast was mediated by Dmt1 like m⁶ adenine of yeast and *Chlamydomonas* mitochondria (protein id. EDP08643). FtsJ2 and

Mrm2 methyltransferases are involved in 21S rRNA methylation in yeast as well as in human [16,17]. However, some 2'-O-MTases were also implicated in capping of mRNA at the 5'-end by methyl N⁷-methylguanosine linked *via* an inverted 5'-5' triphosphate bridge to the 5'-terminal nucleoside of the transcript [15]. Uncapped RNAs, such as nascent viral transcripts, may be detected as 'non-self' by the host cell, triggering an antiviral innate immune response through the production of interferons. Therefore, many viruses that replicate in the cytoplasm of eukaryotes have evolved 2'-O-methyltransferases (2'-O-MTases) to autonomously modify their mRNAs [18,19]. Virus-encoded 2'-O MTase enzymes involved in the synthesis of the RNA cap structure are different from those of host cells. As a consequence, these pathogenic cap-forming enzymes are potential targets for antimicrobial drugs [20]. Such human and rat capping MTases were distinct and no similarity to nsp16 or covid-19 RlmE MTase [21]. Thus, the report on capping 2'-O methylase activity of nsp16 (nsp13 in case of SARS) is interesting and likely a contamination of other methylase activities [22] but nsp16 has no similarity to mammalian 2'-capping methyltransferase [15].

Figure 2: Different types of rRNA Methyl Transferases characterized in bacteria. But nsp16 methyltransferase is unique for Coronavirus. We propose nsp16 is rlmE type 2'-O-Ribose 21S rRNA methyltransferase but not 2'-O capping mRNA methyltransferase as reported earlier.

Figure 3: Methylating positions in RNA by different rRNA Methyl Transferases. Nsp16 methylates Uridine 2'-O-Ribose (green).

Materials and Methods

The BLAST search was done using web portal www.ncbi.nlm.nih.gov/blast and retrieve of covid-19 and other corona viruses

cDNA sequences were done using web portal www.ncbi.nlm.nih.gov/nucleotide or protein. NCBI Primer Design Software was used for primer selection and Oligoanalyzer 3.2 software was used to analyze primer dimer and hairpin structure. Multalin Software and CLUSTAL Omega Software were used to multiple align of protein sequences and NCBI BLAST seq-2 analysis portal used to analyze homology between two sequences. NCBI pubmed portal (www.ncbi.nlm.nih.gov/pubmed) used to retrieve references and papers.

Result

We have analyzed the covid-19 genome and the proteins expressed by (+) sense 30kb rRNA genome (Figure 4). The polyprotein ORF1a is 7081 aa and last protein designated as nsp16 (Figure 4B) which has similarity to the *E. coli* RlmE methyltransferases which methylates Uridine²⁵⁵¹ 2'-O-Ribose of 23S rRNA (Figure 1C). Other non-structural proteins of large covid-19 polyprotein was shown in table 1. In table 2, we have demonstrated the plasmid-mediated (panel-1) localization of different Rlm methyltransferases as well as other rRNA methyl transferases (panel-3 involved in drug resistance through *mdr* genes and drug efflux genes (Table 2, panel-4). The *Treponema* sp RlmE also has some homology as demonstrated in figure 5. We searched different nsp16 proteins in variety of acute respiratory corona viruses and multi-align study (Figure 6A) demonstrated their homology and figure 6B demonstrated their phylogenic relation showing human covid-19 nsp16 was distinct than Avian or Feline or Canine Corona viruses. We have compared nsp16 protein with the many eukaryotic rRNA methyl transferases and found 30 - 33% homology at different regions showing some relations among Mrm2, Bud23 and Dim1 methyl transferases (Figure 7A) with best fit region also has predicted by multi-alignment (Figure 7B) but we also showed that 2'-O-Ribose Capping MTases were distinct and had no similarity to nsp16 (Figure 7C). Mitochondrial Mrm2 2'-O-ribose methyltransferase required for methylation of U2791 in 21S rRNA. Such search confirmed nsp16 is a distinct rRNA methyl transferase and may have specificity to mitoribosome.

Proteins	Function-1	Function -2
Nsp1	Transcription factor	Inhibits translation
Nsp2	Binds proinhibitin proteins	?
Nsp3	Transmembrane protease	ADRP activity
Nsp4, 5, 6	Transmembrane protease	proteases
Nsp7	Forms hexadecameric and DNA binding	RNA polymerase open complex
Nsp8	RNA primase	?
Nsp9, 10	RNA binding	Co-factor nsp14
Nsp12	RNA dependent RNA polymerase	
Nsp13	RNA helicase	5'-phosthatase
Nsp14	Exoendonuclease	?
Nsp15	Endoribinuclease	?
Nsp16	RNA biding	RlmE MTase

Table 1: Non-structural proteins of corona virus (protein id. QII57165).

Bacteria types	Plasmid: size and Accession number	MTases protein id (Cfr, Erm, Arm, Dcm, Dam)	Other <i>mdr</i> genes, toxin genes and metal resistant genes
<i>S. aureus</i>	pSA-01; 63.5 kb; KX274135	Cfr=ATB18028 ErmT=ATB18031 ErmB=AR044757	tetL=AR044726 aacA- aphD=AR044756 aadD=AR044732
<i>K. pneumoniae</i>	pK-109-R; 156.5 kb; KX029331	RmtG=APD70474 RsmH=APD70476; Dcm=APD70554	tetC; arr3; catB3; strB; StrA; QacE; sul1; blaCTX-M2; blaOXA1; aac6'-1b
<i>Cronobacter sakazakii</i>	pCsaCS931a; 4194kb; CP027108	RlmC=AXX00175 RlmK/ L=AXX00103 RlmI=AXX00086	mdtA, macA/B, MFS, RND
<i>Salmonella enterica</i>	P2, 728kb; LN868944	RsmE/ I=CRY88440/627 RlmG/ M=CRY88590/328 TrmB=CRY88455	Bla _{MBL} =CRY88289; AcrE, sptP
<i>Pseudorhodobacter</i> sp	P1, 1584kb; CP039965	RlmF=QC057550 RlmB=QC057183 RsmB=QC056847	Multidrug efflux = QC056662, QC057496; αβ Hydrolase = QC058033

Table 2: Rmt methyltransferases in bacterial plasmids causing alteration of ribosome structure and protein synthesis.

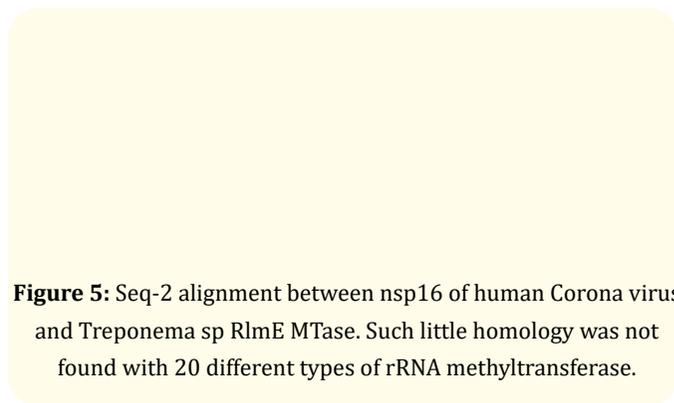
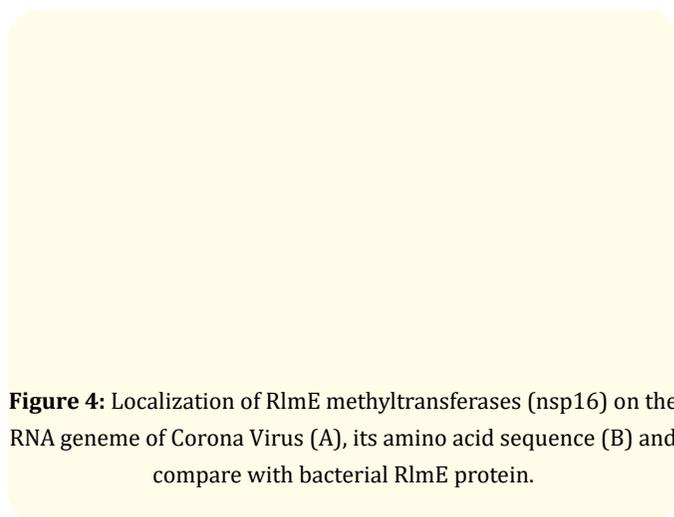


Figure 6a: Multi-alignment of nsp16 proteins of different corona viruses showing strong homologies.

Figure 6b: Phylogenetic analysis of RlmE MTases from different species. Human coronavirus rlmE methyltransferase appeared distinct.

Figure 7a: BLAST Seq2-alignment among eukaryotic rRNA Methyl Transferases and nsp16 protein of corona virus. (A) Rat RlmE-like protein (accession-NP_001100595), (B) Yeast Mrm2 MTase (accession-QHB08519) that methylates U2791 on 21S mitochondrial rRNA, (C) Yeast Bud23 MTase (accession-QHB07184) and (D) human Mrm2 MTase (accession- NP_037525) were compared with nsp16 of corona virus.

Figure 7b: Multialignment of different eukaryotic and corona virus rRNA methyl transferase showing best fit region but poor homology.

Figure 7c: No similarity of nsp16 RmtE protein with eukaryotic capping 2'-O-MTase.

Further, we designed the covid specific primers for the RT-PCR to detect the virus load during pathogenesis. The cDNA sequence nt. 20659-21552 (accession no. MT121215) was used to design four pairs of primers using NCBI Primer Design Software (Figure 8). Individual forward and reverse primer were BLAST searched and primer pair-4 appeared more specific for the diagnosis of covid-19 (Figure 9). The primers were further analyzed by OligoAnalyzer 3.2 Software to check the hairpin structure (Figure 10) and Dimmer formation (Figure 11). BLAST search indicated covid-19 specificity. Similarly, OligoAnalyzer analysis proved the melting point of hairpin structures varies between -12 to +23 degree centigrade well below of Tm 60 degree centigrade. Also dimmer formation with self or with reverse primer (pair-4) shown in figure 11 with delta-G -3 to-5 Kcal/mole reflecting a very good primer pair. GC content between 47 - 50% was also very good for RT-PCR as 1st strand synthesis with reverse transcriptase occurred at 48 degree centigrade. The BLAST search of forward oligo gave 100 covid genomic sequences with 100% specificity and no human sequence was detected in such extended search with 5000 genomic sequences (Figure 9). Other oligo pairs (primer pair-1) might be good to use but also hybridized to the SARS and MERS Coronaviruses [23]. We made restriction enzyme analysis (Figure 12A) showing single hexa-cutter enzymes and have chosen BglII, NheI and SspI enzymes (Figure 12B) for analysis of PCR product (564 bp) giving a unic pattern of agarose gel picture when restricted PCR products were compared with uncut RT-PCR product (Figure 12C). This help any

Figure 8: Selection of nsp16 specific primer pairs for RT-PCR. Primer pair 4 was Covid-19 specific and analyzed further

Figure 9: BLAST search result of nsp16F4 oligo sequence showing covid-19 specificity

Figure 10: Hairpin formation of nsp16F4 indicating low Tm of such self complex.

Figure 11: Dimmer formation of nsp16F4 and nsp16R4 primers showing low melting point of such dimmers. F means forward primer and R means Reverse primer. Nsp16 means coronavirus RlmE 2'-O-Ribose Uridine²⁵⁵¹ Methyl Transferase.

Figure 12: Analysis of the PCR product with nspF4/nspR4 primers. Restriction map of the PCR fragment (A); the 3 hexacutter single cut enzyme were chosen (B) and a 1% agarose gel in 1xTAE buffer for 2hrs at 50V stained with EtBr and under UV illumination (a prototype picture was made).

graduate student can see the data and can compare with own to sure that RNA is for COVID-19.

Discussion

We explained the possible role of RlmE methyltransferase (nsp16) in corona virus pathogenesis being a molecular target for drug design. The study is based on homology of nsp16 to bacterial RlmE methyltransferases and such enzyme was located in many coronaviruses like SARS and MERS. Viral capping MTase was shown as molecular target and thus nsp16 MTase could be an ideal target to block cellular tropism of covid-19. Three regions of ORF1ab polyprotein of covid-19 showed some homologies at the level of 20-25% (aa 1479-1569; aa3290-3360 and aa 4895-4935) with human capping MTase but not with nsp2 protein suggesting Covid-19 may code such enzyme [24,25]. From such analysis we concluded that nsp16 RlmE was not involved in mRNA capping [26,27]. But if human mitoribosome (21S and 12S rRNAs) be methylated by nsp16 protein is an interesting question but 23S rRNA prototype rRNA in human nucleus is 28S rRNA and some MTases (cfr and emrB) have 23S rRNA specificity rather than 16S rRNA (Figure 3).

We claim that our study is important for unknown microbe like covid-19 that is claiming > 90000 lives due to lack of drug. Non-structural viral proteins are ideal for drug discovery understanding molecular mechanism of pathogenicity. It was demonstrated that P7 protein of hepatitis C virus was the target of hexamethylene amiloride [28] whereas the rotavirus NSP4 viroporin domain was shown as calcium-conducting ion channel [29]. Coronavirus envelope protein or nucleocapsid protein have shown as molecular targets [30]. *Nigella sativa*, *Anthemis hyalina* and *Citrus sinensis* phytochemicals have some antiviral effect on Corona viruses replication [31]. Such anti-viral drug screening against covid-19 is an urgent need to control deadly pandemic nature of pathogenesis [32]. Various host factors have been postulated in the literature and need more elaborate study for drug design [33,34]. Targeting cellular autophagy may be one such application to control covid-19 mRNA genome release into cell cytoplasm [35]. Natural products have shown to regulate microbes and became good drugs controlling superbug bacteria, malaria and cancer [36-39]. The 7a protein of Coronavirus has shown to induce apoptosis by caspase-dependent pathways and thus antibody against 7a protein may be a drug against viral pathogenesis [40]. Interferon-alpha2b and ribavirin improve outcome in MERS-CoV-infected rhesus macaques giving a hope for the treatment of Covid-19 [41].

We have clearly demonstrated that nsp16 is a RlmE type methyl transferase that may methylates 21S rRNA of mitochondria but may be 28S rRNA of human bronchial cells also be methylated by nsp16 protein. Bronchial cells with ACE-2 receptors are target for Covid-19 and methylation of rRNAs in such target cells as well as kidney and heart cells may be possible causing abnormal protein synthesis. Such methylation may favours viral protein synthesis inhibiting cellular protein synthesis that have shown in many viral infections (Figure 4). In truth stopping Rennin-Angiotensin pathway (Figure 1) for aldosterone synthesis causes abnormal Na⁺ ions in cells lowering blood pressure and kidney function. Covid-19 RlmE type MTase has never be implicating in pathogenicity and thus we

have discussed a new direction of cellular tropism of Corona viruses. Nsp16 MTase has some similarity to the mmr2 and Dim1 rRNA methyl transferase of yeast and mammals (Figure 7). Yeast Rrp8 23S rRNA MTase has poor similarity to nsp16 but no similarity with human Rrp8 protein (data not shown). The primers designed (Figure 8) using Coronavirus *rlmE* gene sequence may be used for diagnosis and therapeutic discovery in the future. Heterogeneous phyto-antibiotics, gene therapy, anti-sense and ribozyme technology and nano-drug carriers may be future medicine against Covid-19 [36,42-45]. Astonishingly, nsp16 has homology to S1 ribosomal protein indicating its affinity to mitoribosome inhibiting ribosome turn over and protein synthesis.

Conclusion

We confirmed Nsp16 protein of Coronavirus as RlmE Methyl-Transferase which might be methylate Uridine 2'-Ribose of 21S rRNA of host mitochondria leading to alteration of mitoribosome structure and hence inhibition of protein synthesis. We hypothesized that sudden inhibition of mitochondrial oxidative phosphorylation in human bronchial and heart cells due to over expression of viral 2'-O ribose Uridine 2551/2791 Methyltransferase was one of the main reason of Coronavirus tropism.

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Conflict of Interest

No conflict of interest.

Ethical Issues

No patient was selected in this bioinformatics research.

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