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Title:	Structural & Functional Analysis of mutated s2m mobile genetic element present in human and bat/pangolin coronaviruses
Authors:	Pratap, Akhil .
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Abstract:	<p>The current COVID-19 pandemic highlighted the role of gaining a better understanding of the coronavirus life cycle. SARS-CoV-2, the disease's causative agent, is being extensively studied structurally in order to gain insight into key molecular mechanisms needed for its survival. Various conserved stem-loop elements are found in the untranslated regions (UTR) of the SARS-CoV-2 genome and are thought to be involved in RNA replication, viral protein translation, and discontinuous transcription. There is a lack of information about SARS-CoV-2 mutations and the effect of these polymorphisms on viral transmission load. The genomic sequence of SARS-CoV-2 was analysed to find variants in the 3'UTR region of its cis-regulatory RNA elements in this analysis. There was discovered a 43-nucleotide genetic element with a highly conserved stem-loop II-like motif (S2M). As compared to the S2M structures of bat/pangolin models, these polymorphisms tend to make the S2M secondary and tertiary structures in human SARS-CoV-2 models less stable. This gives RNA structures more mobility, which may be one of its defensive mechanisms against host defences or make it easier for it to enter host proteins and enzymes. While this S2M sequence may not be found in all human SARS-CoV-2 models, when it does, it is always highly conserved. It may be used as a target for vaccines and therapeutic agents in the future for mutated strains.</p>
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