

SYNOPSIS

02/11/2020

Review of "Genomic variance of the 2019-nCoV coronavirus"

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One-Minute Summary

- **Genomic and proteomic analyses** of 56 2019-nCoV genomes (54 full genome sequences and two partial sequences).
- **2019-nCoV** sequences were highly similar (>99% sequence identity), clustered together and were closely related to a bat-CoV (96.2% sequence identity), supporting the hypothesis of a bat animal reservoir of 2019-nCoV.
- 2019-nCoV was more **distantly related to SARS-CoV** (~80% sequence identity), whereas MERS-CoV was the most genetically distinct.
- Two hotspots of hypervariability were identified at nucleotide position 8789 (in ORF1ab), which is unlikely to introduce phenotypical changes and position 28151 (in ORF8), which may cause structural disorder of the protein; however, the significance of these is not known.
- Protein sequence analysis also showed close homology between 2019-nCoV and a bat-CoV (>80%) and more distant homology to SARS-CoV.

Additional Information

- Genomic comparisons were done using sequence alignments, phylogenetic analysis and categorical Principle Component Analysis.
- Among the 2019-nCoV sequences, a sequence from Germany and one from Shenzen showed the most variability.
- Variation in ORF8 generates two isoforms, ORF8-L (Leucine) and ORF8-S (Serine). ORF8-S (potential novel phosphorylation target) is predicted to be more disordered than ORF8-L (potential structural disorder in the C-terminal of protein).
- Key amino acid differences were identified between 2019-nCoV and SARS-CoV. These could inform which existing SARS treatments may or may not work.

PHO Reviewer's Comments

None.

Citation

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