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Subject PRO/AH/EDR> SARS - worldwide (138): etiology

SARS - WORLDWIDE (138): ETIOLOGY

A ProMED-mail post

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Date: Sat 7 Jun 2003

From: Henry L Niman, PhD <henry_niman@hms.harvard.edu>

Comment: Sequence Analysis Update

[There are now complete genome sequences in GenBank for 18 isolates of human SARS coronavirus and 2 partial genome sequences. 17 of the 18 complete sequences of isolates of the human SARS coronavirus exhibit the same 29-nucleotide deletion relative to the genome sequences of at least 2 civet cats -- and one of the 18 human isolates (the GZ01 sequence). The additional 29 nucleotides in the GZ01 and the civet cat sequences bring open reading frame (ORF) 10 in frame with ORF 11 and may generate a protein with 122 amino acids and a transmembrane domain. This protein (if real) would be missing in 17 out of 18 SARS coronavirus infections. Dr. Niman has sent the following additional comments. - Mod.CP]

The updated sequences of GZ01 (including the sequence of the 122-amino-acid protein created by the 29-nucleotide insert), BJ02, BJ03, BJ04 have just been made available at GenBank.

The completed genomes of BJ02, BJ03, BJ04, and GZ01 allow for a full data set for the 5 Metropole Hotel Mutations. Not surprisingly, none are found in GZ01, BJ02, or BJ03. However, 2 are found in BJ04 (C9404T and A21721G).

BJ04 is the first reported isolate that has only some of the 5 Metropole Hotel Mutations. All 5 mutations are found in Tor2, Urbani, HKU39849, SIN2500, SIN2677, SIN2679, SIN2740, SIN2774, CUHK-Su10, TW1, and ZJ01. None of the 5 mutations are found in GZ01, BJ01, BJ02, BJ03, or CUHK-W1.

Details on the BJ04 patient are not widely known, but since the BJ04 isolate was the most recent submission to GenBank by the Beijing Genomics Institute and since, at the time of initial submission it was the least completed sequence, it seems possible that the isolate was from a patient who developed SARS later than patients from whom GZ01, BJ01, BJ02, and BJ03 were isolated by the Beijing Genomics Institute.

Therefore, it seems that evolution of the viruses isolated from visitors to the Metropole Hotel may have gone through the following sequence of mutations.

- (1) A 29-nucleotide deletion -- found in all human isolates except GZ01 (and 2 civet cats);
- (2) 2 Metropole Hotel Mutations (C9404T, A21721G) -- found in BJ04;
- (3) 3 additional Metropole Hotel Mutations (G17564T, C22222T, C27827T) -- all 5 Metropole Hotel mutations found in the 11 isolates listed above.

Further examination of the revised sequences suggest that there are 7 Metropole Hotel specific mutations, in addition to the 29-nucleotide deletion. 2 of the mutations which were initially just found in Beijing isolates have now also been found in GZ01. Thus, it seems that the sequence of mutations is as follows:

- (1) The 29 nucleotide deletion (found in all isolates except GZ01);
- (2) Two mutations (A19838G and C27243T) in CUHK-W1;
- (3) Two mutations (C9404T and A21721G) in BJ04.

Combining the 4 mutations above with G17565T, C22222T, and C27827T produces the 11 isolates with all 7 mutations plus the 29-nucleotide deletion.

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[PromED-mail is not an appropriate forum for further discussion of fine sequence analysis of this type. Interested subscribers wishing to pursue this analysis should contact Dr. Niman directly. -Mod.CP]

[see also:

SARS - worldwide (74): etiology [20030427.1039](#)
SARS - worldwide (68): etiology [20030425.1010](#)
SARS - worldwide (64): etiology [20030423.0996](#)
SARS - worldwide (63): etiology [20030423.0994](#)
SARS - worldwide (53): etiology [20030417.0935](#)
SARS - worldwide (51): etiology [20030416.0925](#)
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Severe acute respiratory syndrome - worldwide (17) [20030322.0713](#)
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Undiagnosed illness - Vietnam (Hanoi): RFI [20030311.0595](#)
Pneumonia - China (Guangdong) (07) [20030221.0452](#)
Pneumonia - China (Guangdong): RFI [20030210.0357](#)
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