LETTER TO THE EDITOR

THE POSSIBLE ORIGIN OF RECENT HUMAN SARS CORONAVIRUS ISOLATE FROM CHINA

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Summary. – Phylogenetic analysis of Chinese SARS coronavirus (SARS-CoV) isolates based on a fragment of the spike gene indicated that a recent human SARS-CoV isolate from December 2003 was closer to some human SARS-CoV isolates from an earlier epidemic phase (November 2002–February 2003) than to the SARS-CoV-like viruses isolated from wild animals during previous epidemic phase (May 2003).

Key words: common palm civet; humans; phylogenetic analysis; SARS coronavirus

Emergence of SARS and identification of its etiological agent, SARS-CoV, started out studies on its phylogeny (Ruan, 2003; Tsui, 2003; Zhao, 2004). These have led to identification of C and T (Yexin and Xiaohong, respectively) genotypes of SARS-CoV (Wang, 2004). It has been hypothesized that SARS-CoV is currently transmitted from wild animals to humans. This idea was supported by identification of so-called SARS-CoV-like viruses in common palm civet (*Paradoxurus* hermaphroditus) and raccoon (*Procyon lotori)*, wild animals frequently occurring in southern China; the relatedness of these viruses was based on their sequence identity over 99% with SARS-CoV (Guan, 2003). However, contradictory data have been reported by Stadler *et al.* (2003); they have found the SARS-CoV-like viruses to be distinct from SARS-CoV. According to these authors, the possibility that animals acquire the virus also from other species should be admitted. Although it appears unlikely, humans could infect animals, as documented by a SARS-CoV transmission from man to pig (Chen 2005).

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Abbreviations: SARS-CoV = SARS coronavirus

To shed light on the controversial issue of circulation of SARS-CoV in the nature we analyzed evolutionary relationships among human SARS-CoV isolates from cases or epidemics occurring at different time (Zhao, 2004) and SARS-CoV-like viruses from wild animals on the basis of their spike protein gene and protein sequences (Table 1). Phylogenetic trees were constructed using the MEGA 3.0 program (Kumar, 2004) and Feline infectious peritonitis virus (FIPV) as outgroup. SARS-CoV and FIPV are known to be highly identical throughout the spike gene sequence (Stavrinides, 2004).

Phylogenetic analysis of human SARS-CoV isolates from different cases or epidemics and SARS-CoV-like viruses isolated from wild animals (Fig. 1) indicated that the recent human isolate of SARS-CoV from December 2003 (GD03T0013) was closer to some human SARS-CoV isolates from previous (November 2002–February 2003) epidemic phase (GZ02, CUHK-W1 etc.) than to SARS-CoV-like viruses (SZ1, SZ3, SZ13, and SZ16) isolated from wild animals during previous (May 2003) epidemic phase. The p-distances of GD03T0013 to GZ02 and CUHK-W1 were smaller than those to SZ3 (Table 2 and Fig. 1). This conclusion markedly differs from that of other author who claimed that, based on phylogenetic analysis, of this spike

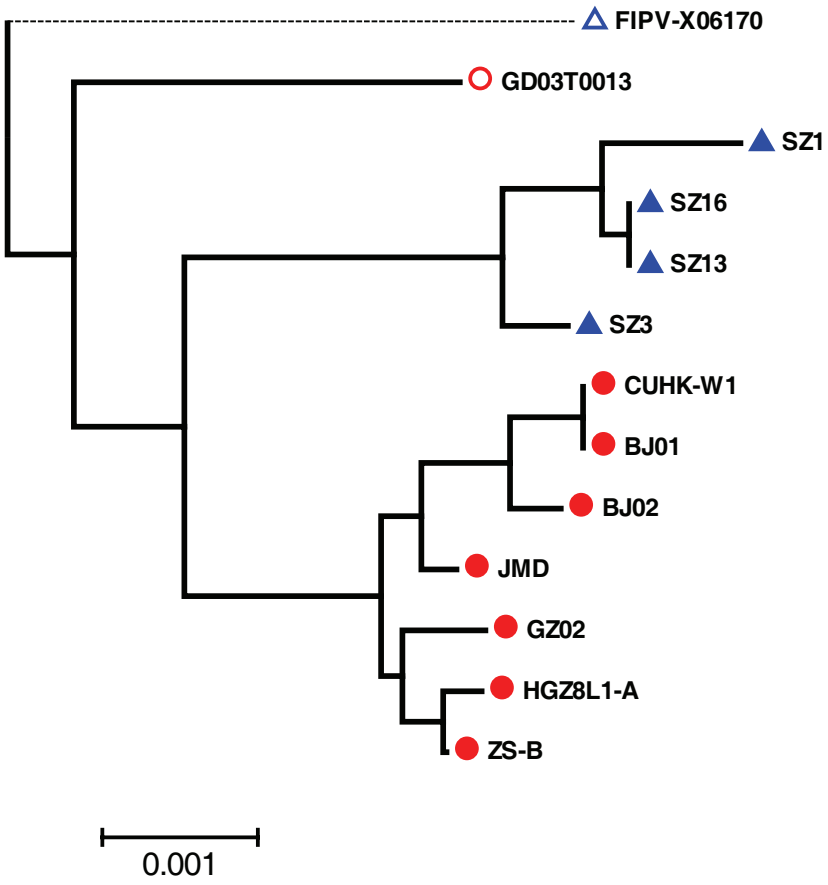

Fig. 1

Phylogenetic tree of SARS-CoV isolates and SARS-CoV-like viruses

The tree is constructed using p-distances of nucleotide differences. The bootstrap value was 5000. The length indicates the number of nucleotide differences per site of the spike gene. Full circles indicate genotype C isolates from humans from an earlier epidemic (November 2002–February 2003). Full triangles indicate animal isolates from previous (May 2003) epidemic. Empty circle indicates recent human isolate. Empty triangle indicates the outgroup.

Table 1. SARS-CoV isolates and SARS-CoV-like viruses compared in this study

Isolate/virus	Acc. No.	Source	Year
GD03T0013	AY525636	Human	December 2003
SZ1	AY304489	Common palm civet	May 2003
SZ3	AY304486		May 2003
SZ13	AY304487	Raccoon	May 2003
SZ16	AY304488	Common palm civet	May 2003
GZ02	AY390556	Human	February 2003
ZS-B	AY394996		November 2002–February 2003
HGZ8L1-A	AY394981		November 2002–February 2003
JMD	AY394988		November 2002–February 2003
BJ01	AY278488		February 2003
BJ02	AY278487		February 2003
CUHK-W1	AY278554		February 2003

Table 2. p-Distances of spike gene sequences of SARS-CoV isolates and SARS-CoV-like viruses

	ZS-B	JMD	HGZ8L1-A	GZ02	BJ02	CUHK-W1	SZ3	SZ16	SZ1
GD03T0013	0.504	0.504	0.531	0.478	0.557	0.531	0.584	0.637	0.743

gene, recent human SARS-CoV isolate (GD03T0013) was much closer to animal SARS-CoV-like viruses (SZ3 and SZ16) than to any human SARS-CoV isolate (Zhao, 2004; Huai *et al.*, 2005).

Summing up, we are of the opinion that our data on phylogenetic relationships and genetic distances of various SARS-CoV isolates and SARS-CoV-like viruses should be cautiously interpreted. In this context, it is likely that recent human SARS-CoV isolate is closer to an unknown SARS-CoV predecessor than to human SARS-CoV isolates or animal SARS-CoV-like viruses, all obtained from previous epidemic phase (November 2002–May 2003).

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