

SARS, MERS and the sunspot cycle

Jiangwen Qu and Chandra Wickramasinghe

The severe acute respiratory syndrome (SARS) and Middle-East respiratory syndrome (MERS) outbreaks pose a serious public health threat because of the high fatality risk. Research on the environmental factors underlying SARS and MERS epidemiology may provide useful insights into the occurrence of such outbreaks. This study suggests that double peaks in the sunspot cycle in 2002 and 2012 were associated with the emergence of SARS and MERS outbreaks. Potential mechanisms by which sunspot activity may influence such outbreaks in humans are discussed. Current and future surveillance efforts should be supported to construct a comprehensive early warning system involving sunspot activity for detecting future SARS and MERS outbreaks as early as possible.

In a letter to *Lancet*¹ published in 2003, it was suggested that the first outbreak of severe acute respiratory syndrome (SARS)-CoV in China may have involved a space-borne trigger. The speculation was that this might have taken the form of an RNA segment or cosmic rays that served to alter the genome of an already endemic corona virus.

Corona viruses define a large genus, which contains the largest known genomes for any RNA virus. Although a benign form of the human corona virus is known to be present in patients with common cold and could be regarded as an endemic virus, the puzzle relates to the sudden emergence of its more lethal variants. The first known case of SARS was recorded in Foshan, China in 2002. The outbreak began in the Guangdong Province and spread to humans supposedly from a reservoir of the virus that had already been established in civet cats and raccoon dogs; it eventually spread to 37 countries around the world². The total number of confirmed cases was 8096 and the average fatality rate close to 10%.

A decade later, in 2012, an outbreak of Middle-East respiratory syndrome (MERS)-CoV occurred in the Middle East with cases of illness spreading sporadically to other countries. Since September 2012, about 1791 cases were confirmed with an average fatality of 30%. The source of MERS-CoV is not fully understood, but genomic studies suggest an original reservoir in bats that was possibly later extended to include camels².

In relation to the sudden emergence of both SARS and MERS, we may pose the following questions: Why did the outbreaks emerge at the time they did? What factor/factors precipitated their emergence? What are the spillover mecha-

nisms from already established reservoirs of virus? How can we seek to predict or perhaps prevent the next outbreak in advance? This study seeks to address these questions.

The unsolved mystery relates to the cause of the sudden genomic change that evidently occurred in an endemic Corona virus, first in 2002 leading to SARS-CoV, and later in 2012 leading to MERS-CoV. One might consider several possible causes:

- (a) Spontaneously occurring mutations.
- (b) Mutations induced by ionizing radiation – cosmic rays or solar X-rays.
- (c) Hybridization involving recombination with a virus/virion component of external origin.

We consider (a) to be an unlikely option. In the case of (b) and (c), a connection with the sunspot cycle could be anticipated, since dramatic changes in solar activity could both cause changes in the flux of ionizing radiation that reaches the earth while also creating gateways for the rapid descent of nanometre-sized virions of possible cometary origin from a stratospheric reservoir. Hope-Simpson³ and Qu⁴ have already demonstrated that a connection exists between influenza pandemics and extrema (maxima or minima) in sunspot numbers. Furthermore, sunspot activity in extrema years was identified as an important risk factor in influenza pandemics⁴.

Figure 1 shows the smoothed-out sunspot numbers from 1950 to 2015 with points representing the dates of onset of SARS-CoV and MERS-CoV. We note that both these events coincide with double peaks in the sunspot cycle, the first in 2002 and the second in 2012. Sunspot numbers are strongly correlated with so-

lar activity, such as X-ray flares and total irradiance of the sun. Increased numbers of solar flares and coronal mass ejections produce numerous high-energy solar particles during the solar maximum period.

Point mutations, gene recombination and gene reassortment are thought to be the three basic mechanisms of viral emergence. Solar radiations are physical mutagens leading to natural point mutation and can lead to the emergence of new viruses. Recombination and reassortment of viral genes occur at highly variable frequencies in viruses with RNA as their genetic material. Multiplicity reactivation and cross-reactivation have also been proven to be general mechanisms of genetic recombination. Such reactivation has been observed in influenza viruses irradiated by various types of radiations such as ultraviolet light and gamma rays, in laboratories during the 1950s–60s. Most significantly, in our particular case, genetic data reveal that SARS-CoV and MERS-CoV are recombinants^{5,6}, and therefore recombination events were probably responsible for the outbreaks of SARS and MERS. The recombination involved a gene component that was either introduced from an external source or activated by events linked to the sunspot cycle as seen in Figure 1.

Sunspot activity in the maximum or minimum phase can significantly impact the earth's climate, thereby causing extreme climate events, such as high temperature, drought and severe cold^{7–10}. Strong scientific evidence points to bats as the natural reservoirs for SARS-CoV and MERS-CoV. The bats are highly mobile, sample large volumes of air, and are seasonally nomadic in response to local food availability. They also probably shift habitats or expand their scope of activities prompted by changes in food

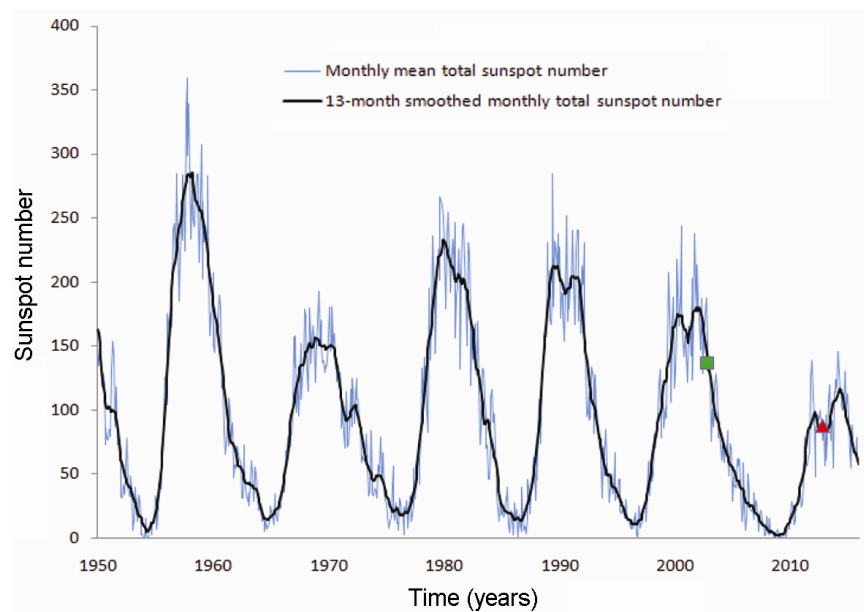


Figure 1. Mean sunspot numbers from 1950 to 2015. The square near 2002 on the curve marks the onset of SARS; triangle near 2012 marks the onset of MERS.

availability or habitat suitability that are in turn influenced by extreme climate events. The bats may migrate from the forests or caves and live closer to other animal populations such as civet cats. Civet cats and camels are considered as intermediate hosts of SARS-CoV and MERS-CoV. The migrating bats can shed large quantities of corona virus to their common living environment in their pursuit of food. In this process, the enhanced frequency of interspecies contacts can facilitate genetic recombination of any circulating corona virus components.

Solar radiation can inactivate corona viruses, but the resulting seemingly non-infectious inactivated viruses are in fact semi-infectious. Recombination is the process by which interspecies mixing of corona viruses can exchange genetic material. For recombination to occur, coinfection with two or more corona virus

strains is necessary. Semi-infectious particles deliver an incomplete set of viral genes to the cell that can, however, support a full cycle of replication.

Finally, we note that some ‘new’ corona viruses appear to have successfully acquired the ability to spread from animal hosts to humans through various human activities, such as the breeding or slaughter of civet cats and camels. In the longer term changes in solar activity and the intensity and frequency of sunspots could impact global warming and climate change¹¹. Global warming can directly affect the ability of individual bats to detect prey and indirectly their interspecies interactions with competitors and prey¹².

In conclusion, we suggest that an approach to a double peak in the sunspot cycle may serve as a potential forewarning of future pandemics. Together with other epidemiological data, this could be

a useful factor for strategic disease control planning.

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Jiangwen Qu is in the Department of Infectious Disease Control, Tianjin Centers for Disease Control and Prevention (Tianjin CDC), China CDC; Chandra Wickramasinghe is in Buckingham Centre for Astrobiology, Buckingham University, Buckingham, UK and Centre for Astrobiology, University of Ruhuna, Sri Lanka.*

**e-mail: ncwick@gmail.com*