Spanish Flu, SARS, MERS-CoV by CO₂ Emission and Maximal Sunspot Number

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ABSTRACT

The 1918 Spanish flu, 2002 severe acute respiratory syndrome (SARS), and 2012 Middle East respiratory syndrome coronavirus (MERS-CoV) were investigated to reveal their causes and routes of transmission. They have the common features such as 1) the induction by viruses (Spanish flu; avian influenza virus (AIV), SARS and MERS-CoV; coronavirus), 2) the outbreak during the maximal sunspot number, 3) the aeolian desert dust region (Spanish flu; Saharan, SARS; Asian, MERS-CoV; Arabian), and 4) similar incubation period (AIV; 5, SARS; 2 - 7, MERS-CoV; 5 days), 5) different transmission reservoir (Spanish flu; aquatic bird/swine, SARS; bat, MERS-CoV; bat/dromedary camel). When carbon dioxide (CO₂) combustion emissions were simultaneously high at the maximal sunspot number, UV radiation in the Poles was so extensive to mutate the aquatic virus through the food web to be the fundamental reason for these pandemic. Guangdong Province and Hong Kong in China are the source of 2002-2003 SARS. The stranded dead whales and dolphins along the coast of the Persian Gulf might be fed on by coastal animals in the Arabian Desert to transmit MERS-CoV. Mutations in the hot temperature in the Arabian Desert and Persian Gulf, and the maximal sunspot numbers were observed in Saudi Arabia. Saudi crude burn in power plants since 2009 with coincidental outbreaks of MERS-CoV in Saudi Arabia since 2012 peaking in 2014. The reduction of CO_2 emissions by nuclear power plants is a unique solution to decrease MERS-CoV outbreaks.

1. INTRODUCTION

Over the past 100 years there have been serious diseases with high mobidity and mortality. Three viruses known as avian influenza virus (AIV) [1], severe acute respiratory syndrome (SARS) coronavirus [2], and the Middle East respiratory syndrome coronavirus (MERS-CoV) [3], have been experimentally inac-

tivated by ultraviolet (UV) light-based UVC photochemical treatment. Spanish flu in 1918, SARS in China in 2002, and MERS-CoV in Saudi Arabia in 2012, have common features such as 1) the induction by viruses such as Spanish flu; AIV, SARS and MERS; coronavirus, 2) the outbreak during the maximal sunspot number, 3) the aeolian desert dust region (Spanish flu; Saharan, SARS; Asian, MERS-CoV; Arabian), 4) similar incubation period (AIV; 5, SARS; 2 - 7, MERS-CoV; 5 days), 5) different transmission reservoir (Spanish flu; aquatic birds/swine, SARS; bat [4], MERS-CoV; bat [5]/dromedary camel). UV radiation is too strong for the aquatic virus to survive during the maximal sunspot number. However, a limited number of mutant viruses in the Poles survived and were transmitted by migratory birds or humpback whales and then evolved as deadly viruses in the form of the 1918 Spanish flu, 2002 SARS, and 2012 MERS-CoV in Continents during the maximal sunspot number, as shown in Figure 1. To understand further, we can consider the following analogy. Steak can be served as welldone, medium, and rare. Similarly, the maximal sunspot number, equivalent to the case of "welldone", produces the strongest ultraviolet (UV) radiation to induce the least number of aquatic viruses in the Poles as deadly mutants for 2002 SARS in Hong Kong of China. UV radiation is mild enough for the aquatic virus to survive during the minimal sunspot number, so its mutant viruses are transmitted as AIV to the Continents [6]. Overall human activity has helped add carbon dioxide to the atmosphere at levels not seen for 800,000 years. Reducing greenhouse gas emissions is the best way to reduce climate impact [7].

The present study investigated the individual serious diseases of the 1918 the Spanish flu, 2002 SARS, and 2012 MERS-CoV revealing their causes and routes of transmission to prevent future human fatalities.

2. SPANISH FLU

The most lethal influenza pandemic in modern history was the H1N1 Spanish flu, which killed approximately 50 to 100 million people around the world between 1918 and 1919. The origin of the 1918 pandemic is now clear. The virus had features of an avian virus (H1N1) with an intermediate host of swine. Increased CO_2 emissions in Spain from 1918-1919 thinned the ozone layer causing the increases of UV radiation and temperature. Figure 2 describes carbon dioxide emissions from fossil fuel burning, 1850-1950.

Temperature increase enhanced the ice-melting in the Poles to decrease algae beneath the ice, so that penguins feeding on algae starved, making them vulnerable to AIV which was transmitted by migratory birds. Spain is located as a stop-over of three migratory birds flyways; The East Atlantic, Black Sea/Mediterranean, and East Africa/West Asia. Therefore, there could have been frequent chances of contact between AIV infected migratory birds and wild domestic birds, the latter transmitting highly pathogenic avian influenza (HPAI) to humans to cause an enormous number deaths of humans in 1918. Furthermore, there was Saharan aeolian input over western Europe [10] including the Iberian Peninsula of Spain from North Africa. Aeolian particles carried bacteria [11] and thus AIV could be hosted by such bacteria which transmitted AIV via the stream of Saharan aeolian input to Spain. It has been suggested that the 1918 Spanish flu was caused by the increases of CO_2 emissions during the Second Industrial Revolution (1870-1914) and the First World War (1914-1918), whereas the thin ozone layer was made by CO_2 increase to allow the extensive UV radiation in the Poles for mutant of low pathogenic avian influenza (LPAI) AIV. Migratory birds, in contact with penguins and guillemots, transmitted LPAI to Continents which mutated into HPAI H1N1 in the favorable Spanish environments (cold temperature, low humidity, basic pH, low salinity, enough food, low UV radiation) from October to December in 1918. The abrupt increase of global carbon dioxide emissions from fossil fuel combustion caused the thin ozone hole while the maximal sunspot number (Figure 1) allowed the maximal UV radiation in the Poles. Therefore, when carbon dioxide combustion emission was simultaneously high at the maximal sunspot number, the UV radiation on the surface of the Poles was so extensive, it mutated the aquatic virus through the food web. This eventually infected penguins in the Antarctic or guillemots in the Arctic as LPAI until transmitted by migratory birds to the Continents as LPAI/HPAI or finally HPAI to humans, which could be the fundamental cause of the 1918 Spanish flu.

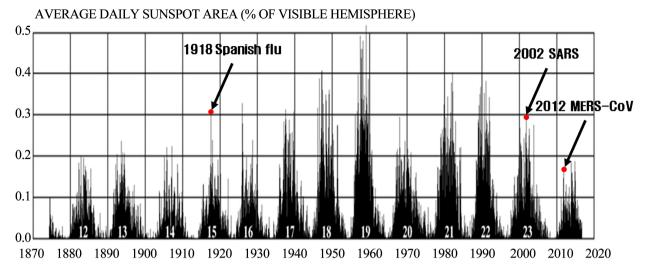


Figure 1. Maximal sunspot numbers as a function time [8] for outbreaks of 1918 Spanish flu, 2002 SARS, and 2012 MERS-CoV.

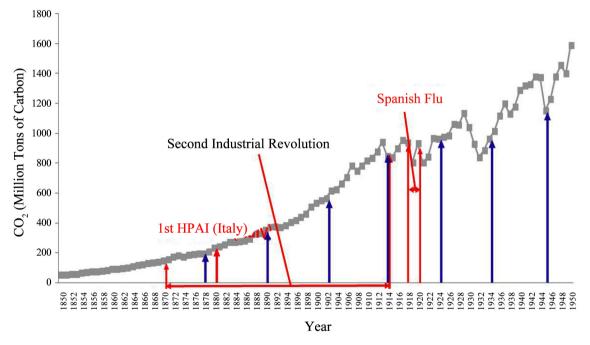
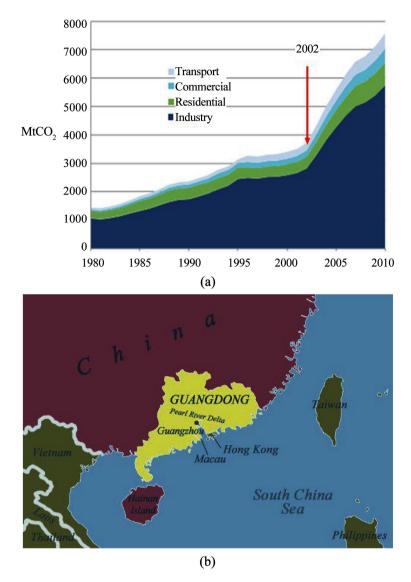
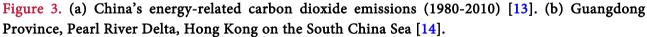


Figure 2. Carbon dioxide emissions from fossil fuel burning, 1850-1950, where blue line indicated the minimal sunspot number [9].

3. SARS

Marine mammals such as the Baiji dolphin in China's Yangtze River could be the reservoir of AIV although functionally it has been extinct since 2004 [12], presumably caused by climate change due to the abrupt increase of Chinese Industry with enormous CO_2 emissions at the beginning of 2002, as shown in **Figure 3(a)** [6]. The ozone layer becomes thin under the abrupt increase of CO_2 emissions creating the strong UV radiation for extensive mutation. The maximum sunspot numbers were significantly recorded in 2000-2003, as shown in **Figure 1**. Coincidentally, there were outbreaks of SARS in southern China between November 2002 and July 2003 resulting in 774 deaths.





Guangdong Province in China has favorable environments with enough food, waters, and low UV radiation for habitats of migratory birds and is an ideal stopover for migratory birds flying from the Antarctic via Australia. It is therefore expected that Guangdong Province and Hong Kong with industrial complex increasing the global carbon dioxide emissions were the source of 2002-2003 SARS, as shown in their maps surrounded by South China Sea and Hainan Island (Figure 3(b)) [15].

SARS is a viral respiratory disease of zoonotic origin caused by the SARS coronavirus (SARS-CoV). Between November 2002 and July 2003, an outbreak of SARS in Guangdong Province in China caused an eventual 8098 cases, resulting in 774 deaths reported in 37 countries [16] with the majority of cases in China [17] (9.6% fatality rate) according to the World Health Organization (WHO) [17]. No cases of SARS have been reported worldwide since 2004 [18]. In late 2017, Chinese scientists traced the virus to cave-dwelling Horseshoe of bats in Yunnan Province [4]. The Guangdong Province borders Guangxi Province, where 80% of Chinese oysters are produced. Oysters are the reservoir of aquatic algae, which can be infected by the Antarctic mutant virus through transmission from migratory birds. During the maximal sunspot number, there can be the strongest UV radiation to induce deadly mutant virus in the Continent for humans.

Along the coastal areas of the Shenzhen Bay, a mangrove forest is the habitat for about 100,000 migratory birds of 40 species, some of which are endangered [19]. Wetlands are critical habitats for birds. Conservation efforts in the Guangdong Haifeng Wetlands and other wetlands should focus not only on wintering migratory birds, but also on birds residing in Guangdong [20].

Since Guangdong Province and Hong Kong are located on the long coastline of the South China Sea with mild temperatures, high relative humidity and ideal habitats with small islands for migratory birds, such locations could be the source of 2002-2003 SARS. **Table 1** summarizes environments for the outbreak of SARS.

4. MERS-COV

There were the maximal sunspot numbers during the onset of MERS-CoV in 2012 and the peak outbreak of MERS-CoV in 2014 (Figure 4). MERS-CoV peaked in 2014 and continued until now (Figure 5) with 2248 outbreaks, 798 deaths, and 27 countries reported globally [21].

The evolutionary origins of MERS-CoV are unknown [23]. While camels are thought to be important for the transmission of MERS-CoV, bats sampled in Uganda [5] are widely considered to be the evolutionary source of the virus. The origins of the virus are not fully understood but, according to the analysis of different virus genomes, it is believed that it may have originated in bats and was transmitted to camels sometime in the distant past. Although dromedary camels are now known to be the immediate animal source of the 82 recent MERS epidemic, the evolutionary origin of MERS-CoV remains obscure [24]. Since the enzyme cofactors are minerals available from desert dust [11], MERS-CoV can be activated in the environment by aeolian dust *i.e.* the Arabian Desert, which is in contact with the Arabian Sea where hump-back whales remain year-round without movement to the Antarctic. There are chances of mating between humpback whales in Arabian Sea and the ones in Madacascara (15,000 out of 80,000 populations), the latter

Sequence	Environments for Outbreak of SARS	Cause Coal combustion, Figure 3(a)		
1	Increased CO ₂ emission			
2	Thin O ₃ hole	Increased CO ₂ emissions		
3	High UV radiation	Thin O ₃ hole and maximum sunspot number in 2000, 2001, 2002, 2003, Figure 4		
4	High aeolian desert dust	Gobi and Thar Deserts		
5	High rice/wheat	Frequent route of migratory birds flyways		
6	Ideal habitat	Guangdong Province wetlands and mangrove forest for migratory birds		
7	Mild water temperature	16°C - 27°C easy to express viral activity		
8	High relative humidity	70% - 80% easy to express viral activity		
9	Low salinity	The Pearl River Delta of the East River, North River, and West River filled with hundreds of small islands, easy to express viral activity		
10	Long coastline	4300 km facing the South China Sea as good habitat for migratory birds		

Table 1. Environments for outbreak of SARS in Guangdong Province of China between November2002 and July 2003 resulting in 774 deaths reported in 37 countries.

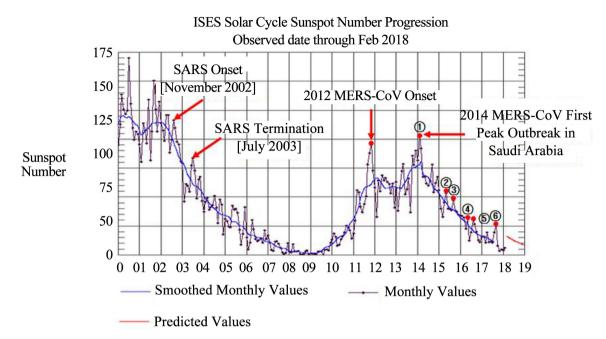


Figure 4. Sunspot number profile (2018/03) [22] with corresponding outbreaks of SARS and peaks of MERS-CoV in Figure 5.

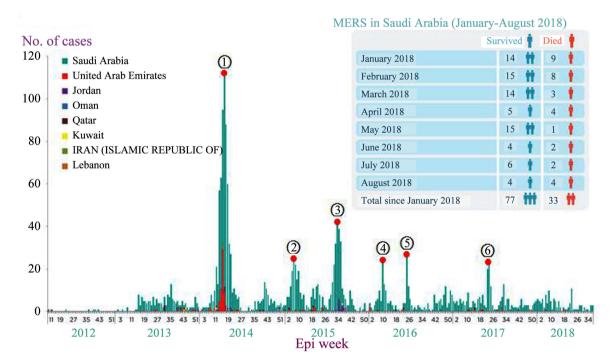


Figure 5. Laboratory-confirmed cases of MERS-CoV reported in Eastern Mediterrane Region, April 2012-August 2018 [21].

migrating to the Antarctic. It is possible for the non-migratory humpback whales in the Arabian Sea to be infected by the aquatic mutant virus in the Antarctic through the feeding process or mating with the migratory humpback whales from Madacascara. Such a transmitted aquatic mutant virus could have evolved in influenza virus evolution in the humpback whale reservoirs leading to mutation, reassortment, and recombination, as suggested by Yoon [25].

As shown in **Table 2**, Saudi Arabia has the largest outbreak of MERS-CoV with the longest coastlines in the Persian Gulf and the Red Sea, the widest coverage of the Arabian Desert, and the largest crude oil and gas production for the largest CO_2 emissions. The United Arab Emirates (UAE) has the second largest MERS-CoV and the second longest coastline of the Persian Gulf, wide coverage of the Arabian Desert, and the second largest crude oil and gas production for the second largest CO_2 emissions. It is therefore suggested that the outbreak of MERS-CoV is related with the length of coastlines of the Persian Gulf, the area of the Arabian Desert, the CO_2 emissions from crude oil and gas combustions.

Kim [6] found that regions of skin cancer outbreaks with strong UV radiation have the fewest AIV outbreaks. Bats usually stay in dark caverns and feed always during the night. Bats are not radiated by UV in their lifetime because they are only active at night and stay in dark caverns during the day. Therefore, bats are good reservoir hosts for all kinds of viruses like Spanish flu, SARS, and MERS-CoV, which are vulnerable to UV radiation.

The dromedary or Arabian camel, as pictorially illustrated in **Figure 6**, has transported people and materials in the Middle East and North Africa for thousands of years. After comparing DNA of wild and early-domesticated dromedaries as much as 7000 years old with the genetic samples of more than 1000 modern dromedaries, it was determined that the Southeast Arabian Peninsula was the birthplace of dromedary domestication. Camels are one of the most surprising members of the extended hippo family tree. DNA studies found that hippos are closely related to whales. The ecological differences might explain two divergent evolutions. The "sister group" to hippos includes, not only whales, but also dolphins and porpoises [26].

A 2013-14 study of dromedaries in Saudi Arabia concluded the unusual genetic stability of MERS-CoV coupled with its high seroprevalence in the dromedary makes this camel a highly probable host for the virus. The full genome sequence of MERS-CoV from dromedaries in this study showed a 99.9% match to the genomes of human clade B MERS-CoV. Another study in Saudi Arabia showed the

Country	Population (2018)	¹⁾ MERS-CoV Outbreak	²⁾ Coast	line	Arabian Desert	³⁾ Gas	⁴⁾ CO ₂
Country	(Millions)	(2012. 3-2015. 6)	Persian Gulf	Red Sea	Area	Reserves	Emissions
Saudi Arabia	33.6	1028	•	•	•	298	478
UAE	9.5	77	Ø	×	Ø	215	199
Qatar	2.7	13	Ø	×	Ø	858	65
Jordan	9.9	19	×	0	Ø	-	19
Oman	4.8	6	Ø	×	Ø	25	55
Bahrain	1.6	1	Ø	×	0	6	31
Kuwait	4.2	3	Ø	×	Ø	63	81
Egypt	95.7	1	×	•	×	-	197
Yemen	2.9	1	×	Ø	Ø	-	27
Lebanon	6.1	1	×	×	×	-	15
Iran	82.0	6	•	×	×	1183	560

Table 2. Factors inducing MERS-CoV outbreak.

Notes; ¹⁾ from Europe CDC Report (2015. 6. 11) ²⁾ \bigcirc : Long, \bigcirc : Medium, \bigcirc : Short, \times : Not Applicable. ³⁾ 2017 Estimated (tcf), ⁴⁾ 2010 CO₂ (Million Metric Tonnes).

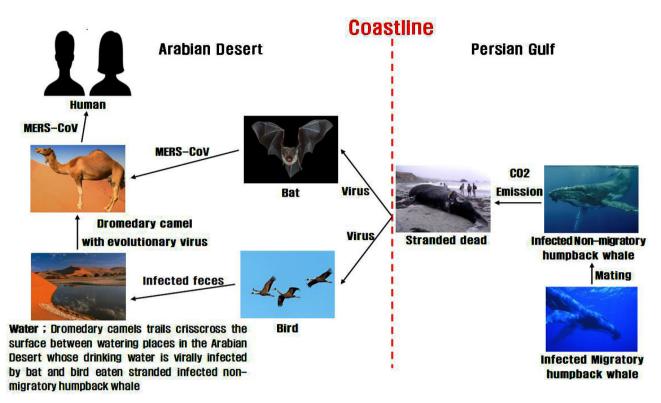


Figure 6. Pictorial presentation of MERS-CoV transmission from infected migratory humpback whale via infected non-migratory humpback whales in the Persian Gulf to humans via reservoir-host dromedary camels in the Arabian Desert.

presence of MERS-CoV in 90% of the evaluated dromedaries and suggested that camels could be the animal source of MERS-CoV [27].

The Saharan Desert in Egypt and Iran Desert in Iran have dromedary camels. The key regions and parameters for MERS-CoV outbreak appeared to be the Persian Gulf, the Arabian Desert, and CO_2 emissions for Saudi Arabia, UAE, Qatar, Jordan, Oman, and Iran. Therefore, the reduction of CO_2 emissions by using nuclear power plants is a unique solution to decrease MERS-CoV outbreaks, especially in Saudi Arabia, UAE, and Qatar (Table 2).

There was a close linearity ($R^2 = 0.8539$, p value = 0.0010) between MERS-CoV outbreak and the maximal sunspot number, as shown in Figure 7.

It is therefore expected that there can be a serious MERS-CoV outbreak during the maximal sunspot number (Figure 4), as occurred sharply in Figure 5 in 2014.

Genetically speaking, humans are more evolved than birds. During the maximal sunspot number there were deadly diseases contracted by humans such as Spanish flu, Asian flu, Hong Kong flu, SARS, and MERS-CoV. During the maximal sunspot number, there is the strongest UV radiation which induces the worst evolutionary mutants in the Poles, transmitted by both of migratory birds and humpback whales causing harm to humans. On the other hand, there were outbreaks of AIV during the years of the minimal sunspot number, as linearly correlated ($R^2 = 0.9967$) by Kim [6]. During the minimal sunspot number, there is a strong UV radiation which induces the bad mutants for causing serious damage mainly to poultries. During the minimal sunspot number HPAI H5N1 spread all over the world to killing mainly poultries [6]. However, there were serious diseases like the 1918 Spanish flu, 1957 Asian flu, 1968 Hong Kong flu, 2002 SARS, and 2012 MERS-CoV, which killed mainly humans during the CO₂ emissions increase and the maximal sunspot number. It can be summarized as; 1) The sunspot number is a good index for prediction of deadly diseases for either humans or poultries, 2) There have been serious diseases contracted by

humans during the CO_2 emissions increase and the maximal sunspot number, 3) There have been poultry diseases of AIV during the CO_2 emissions increase and the minimal sunspot number.

Weekly distribution of MERS-CoV and maximal sunspot number in the Persian Gulf countries are shown in **Table 3** with data in **Figure 5**.

It is necessary to prepare for diseases in poultries during the minimal sunspot number while doing the same for humans at the time of the maximal sunspot number. The sunspot number is a good index to predict the scope and the extent of deadly diseases not only for poultries but also for humans.

Non-migratory humpback whales stranded along the coastline of the Persian Gulf were infected by migratory humpback whales with the mutant virus in the Poles, transmitting MERS-CoV to humans via bat and dromedary camel in the Arabian Desert, as pictorially shown in **Figure 6**. It can be postulated that migratory humpback whales in Madagascara, that have a population of 15,000, may travel to the Arabian Sea or the other way for mating with non-migratory humpback whale, a population of less than 400. Non-migratory humpback whales residing year-round in the Arabian Sea may be infected by migratory humpback whales during the mating process. The infected non-migratory humpback whales may travel to the Arabian Sea, whose feces secondarily infects other whales and dolphins in the Persian Gulf surrounded by CO_2 emissions sources (**Table 2**). Such infected whales and dolphins could be stranded and die along the coastline of the Persian Gulf, as conceptually drawn in **Figure 6**. Coastal animals such as birds and bats, feed on the infected strained whales to transmit the infected virus inland, which can be evolutionarily

Sequence (Figure 5)	Date (Year/Week)	Maximal Sunspot Number (Figure 4)	MERS-CoV Outbreak (Figure 5)
1	2014/16	102	113
2	2015/06	55	24
3	2015/32	45	42
4	2016/10	32	24
5	2016/25	32	26
6	2017/22	22	24

Table 3. Weekly distribution of MERS-CoV and maximal sunspot number in the Persian Gulf countries.

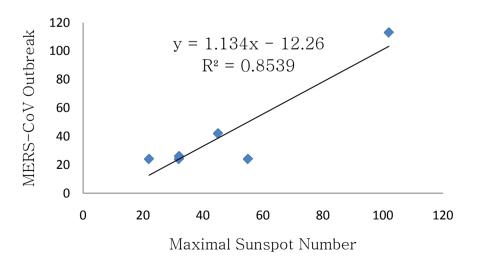


Figure 7. Relation of the MERS-CoV outbreak with the maximal sunspot number from 2014 to 2017.

changed to MERS-CoV via the reservoir of dromedary camel in the Arabian Desert in suitable conditions including high sulfur, low water, and high CO_2 emissions during maximal sunspot number. The conditions of the Arabia Desert such as sulfur composition and CO_2 emissions cannot be changed, but the sunspot number has an 11 year period with 14 months standard deviation. The maximal sunspot number can be predicted by data available in Brussels in Belgium and Ottawa/British Columbia of Canada. Furthermore, it is hard to prevent non-migratory humpback whales in the Arabian Sea and Persian Gulf from mating with migratory humpback whales in Madagascara. Simple floating barricade at the Strait of Hormuz (width 10 km, depth 80 m) (Figure 8(a)) may prevent of the movement of whales and dolphins into the Persian Gulf during the limited period of the maximal sunspot number to prevent a MERS-CoV outbreak in the Persian Gulf countries including Saudi Arabia, UAE, and Qatar.

Table 2 shows that the outbreak of MERS-CoV in each country is mainly related with parameters such as covering coastline lengths of the Persian Gulf surface area of the Arabian Desert, gas reserves removing the residual CO_2 during LNG production, and CO_2 emissions from combustions of crude oil and gas for electricity. The contribution of the Red Sea is minimal since there was only one outbreak of MERS-CoV in Egypt and Yemen, respectively. It is evident that the Persian Gulf and the Arabian Desert are the main sources of MERS-CoV along with CO_2 emissions from gas and crude oil combustions. The population of Egypt (95.7 millions) with a single outbreak of MERS-CoV is far greater than that of Saudi Arabia (33.6 millions). Therefore, the possibility of the Red Sea as the infection zone is excluded. Rather, the Persian Gulf is expected as the major infecting area due to the stay of non-migratory humpback whales with CO_2 emissions from crude oil and natural gas. Most of the outbreaks of MERS-CoV occurred in Saudi Arabia, most of which is covered by the Arabian Desert (**Figure 8(b)**).

It was revealed that the dromedary camel is the reservoir host of MERS-CoV, whose distribution is known to be at the Sahara Desert, Arabian Desert, Syrian Desert, Iran Desert, and part of the Australian Desert. Since MERS-CoV occurred mainly in the Arabian Desert with peak value in Saudi Arabia (Table 2 and Figure 5), there can be a breakthrough of MERS-CoV in the boundary between the Arabian Desert and the Persian Gulf. There are non-migratory humpback whales in the Arabian Sea (Figure 8(a)) and the Arabian Desert (Figure 8(b)) with the Strait of Hormuz between the Persian Gulf and the Gulf of Oman, as shown in Figure 8(a).

As compared with the population numbers, it is evident that Saudi Arabia, UAE, and Qatar have the highest outbreaks of MERS-CoV due to the factors (Table 2) such as the Arabian Desert area, coastline length of the Persian Gulf, and CO_2 emissions by combustions of crude oil and natural gas. It is suggested CO_2 free nuclear power plants are used to prevent MERS-CoV to halt the spread of serious diseases in the Middle East induced by increased CO₂ emissions, especially during the maximal sunspot number. Non-migratory humpback whale may evolute the infected virus in the Persian Gulf after mating with migratory humpback whales infected in the Antarctic either in Madagascara or in the Arabian Sea. The feces of non-migratory humpback whales infected by the worst virus in the Antarctic, evolutionarily mutated during the maximal sunspot number under strong UV radiation, to be released in the Persian Gulf and fed on by coastal animals such as birds, bats, dolphins, and whales. The stranded dead whales and dolphins on the seashore of the Persian Gulf, ultimately caused by a lack of immunity and infection by the worst virus from the Antarctic, are fed on coastal animals to the Arabian Desert, where bats and dromedary camels are present to transmit the evolutionary virus in the form of MERS-CoV under various environmental conditions such as high sulfur, high temperature, and low water in the Arabian Desert, high relative humidity and high CO₂ emissions in the Persian Gulf. To prevent the outbreak of MERS-CoV it is suggested that dead whales or dolphins are burned on the seashore of the Persian Gulf, and bats in the coastline of the Persian Gulf are eliminated. The movement the non-migratory humpback whales in the Arabian Sea should be watched so they do not pass the Strait of Hormuz and not to stay inside of the Persian Gulf enriched with CO₂ emissions, especially during the maximal sunspot number.

The reduction of CO_2 emissions by nuclear power plants is a unique solution to decrease MERS-CoV outbreaks, especially in Saudi Arabia, UAE, and Qatar.



(a)

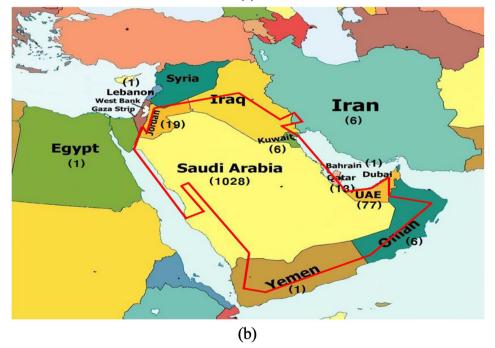


Figure 8. (a) Persian Gulf, Strait of Hormuz, Gulf of Oman, and Arabia Sea [28]. (b) Countries surrounded by the Arabian Desert [29]. Red line is the boundary of the Arabian Desert while numbers in parenthesis indicated MERS-CoV outbreaks in each country [30].

5. TRANSMISSION ROUTE OF MERS-COV

Some of the natural resources available in the Arabian Desert are oil, natural gas, phosphates, and sulfur. Enhanced CO_2 emissions by oil and natural gas induce the ozone hole deterioration with the increase of UV radiation, especially during the maximal sunspot number of 2012 to 2014 (Figure 4). Extensive UV radiation induces viral mutations in the Poles. Besides, the Arabian Desert has ample sulfur (SO₄)

5.67 - 46.04 meq·L⁻¹) [31] while two amino acids of cysteine and methionine have sulfur. The effects of cysteine mutations of human immunodeficiency virus [32] and methionine mutation in melanoma kindred [33] have been studied. It is postulated that there are viral mutations in the Arabian Desert due to high CO_2 emissions from the combustions of crude oil and natural gas in the Persian Gulf along with gaseous and soil sulfur during the maximal sunspot number (Figure 4), whose peak pattern was similar to the outbreaks of MERS-CoV in Saudi Arabia in 2014 (Figure 5) with strong linearity (R² = 0.8539) in Figure 7.

The transmission route of MERS-CoV is not clear so far. Strong UV radiation in the Poles during the maximal sunspot number might mutate the aquatic virus, bacteria, algae, krill, and humpback whales. Humpback whales usually migrate to Continents for breeding. However, humpback whales in the Arabian Sea have been known to be non-migratory for 70,000 years [34]. On the other hand, there are 15,000 migratory humpback whales in nearly Madagascar among global 80,000 ones.

Mutations in hot temperature in the Arabian Desert, high CO_2 emissions with refinery systems, non-migratory humpback whales (viral infection), enhanced salinity of 40 ppt by desalination plants in the Persian Gulf, maximum ultraviolet radiation during the period of maximal sunspot number in 2012, 2013, 2014 (Figure 4), are expected in Saudi Arabia with the widest Arabian Desert and the longest coastlines in the Persian Gulf.

Fe-replete dusts from the Arabian and Syrian deserts were blocked by high Omani mountains (~3000 m) during the late Southwest Monsoon (Aug.~Sep.) so that desert dusts could not reach the southern Omani coast, where many volcanoes are active (e.g. 13 volcanoes in Yemen), Saudi Arabia (24), Iran (7), Iraq (1), India (4), and Pakistan (7). Oxygen minimum zones in the Arabian Sea form due to the oxidation of volcanic sulfur compounds of S, SO₂, SO₃, and H₂SO₄ to sulfates (SO_4^{2-}) by consuming the dissolved oxygen (DO) in waters. Therefore, the contribution of volcanic S compounds to the southern Omani coast during the late Southwest Monsoon is much greater than those of Fe from deserts. Vertical profile of O₂ at the southern Omani coast showed severely O₂-depleted waters (DO < 0.2 mg·l⁻¹, ~9 μ M O₂) from 170 m to 1000 m depth due to extensive consumption of DO in waters by the volcanic S compounds, while minimum limit of DO content for living fish of about 5 mg·l⁻¹ DO (156 μ M O₂) was available from its oceanic surface to 80 m depth [35]. Thus, the volcanic S compounds deposited on the surface ocean appear to dissolve their S compounds extensively at the depth range of 170 m and 1000 m, where phytoplankton cannot live due to toxic volcanic chemicals (SO₂, H₂S, HCl, HF, H₂SO₄) [36] in waters. In contrast, the concentration of diatom *Pseudonitzschia* was maximal between 45 to 80 m (or upper 80 m) depth in HNLC region [37]. Since humpback whales prefers to stay at 50 m, the Arabian Sea can be a good habitat for humpback whales.

6. MUTATION BY UV RADIATION

Steak is usually served welldone, medium, or rare. Similarly, the maximum sunspot number, being equivalent to "welldone", produces the strongest UV radiation. This induced the worst aquatic viral mutation in the Poles, leading to 2002 SARS in Guangdong Province in China. Hong Kong is surrounded by Guangdong Province, whose west edge is in contact with Beibu Gulf and Hainan Island [38]. Due to lack of turbulence, the Beibu Gulf is a good fishery farm of oysters, supplying 80 % of oyster production in China. Oysters feed aquatic algae such as diatoms covering more than 40% algae in the ocean. Therefore, oysters are a good reservoir of infected aquatic virus, bacteria, and phytoplankton of diatoms, transmitted from Antarctica by migratory birds and humpback whales. Guangdong and Hong Kong are populated regions that consume many oysters and chickens and have low UV, enough rice, many migratory birds at mangrove forests, and wide coastal areas. This could be the reason why Guangdong province and Hong Kong have been known as the origins of 1996-1997 AIV and 2002-2003 SARS. Furthermore, there were humpback whales in Guangdong and Hong Kong [39], whose infected feces could have been released to coastal animals such as birds and bats [4] to infect to wild birds, poultry, and humans for transmission of AIV and SARS. 1996-1997 AIV during the period of minimum sunspot number, is equivalent to the analogy of steak cooked, of "rare" for the mild UV radiation to induce a bad aquatic viral mutant in the Poles

for AIV, transmitted by migratory birds and humpback whales in Guangdong Province and Hong Kong in China. Along the coastal areas of the Shenzhen Bay in Guangdong Province in China, a mangrove forest is the habitat for 100,000 migratory birds [19]. Furthermore, Guangdong Haifeng Wetlands are valuable for waterbirds and wintering migratory birds [20]. Therefore, Guangdong and Hong Kong are vulnerable to the diseases transmitted by migratory birds and humpback whales such as AIV and SARS.

UV radiation is too strong for the aquatic virus to survive under the period of the maximum sunspot number. However, limited number of mutant viruses in the Poles survived and were transmitted by migratory birds or humpback whales, evolving as deadly virus as in SARS or MERS in Continents during the maximal sunspot number. To prepare for a future pandemic like Spanish flu, SARS and MERS-CoV, it is important to predict each outbreak by both the maximal sunspot number (Figure 1) and the abrupt increase of CO₂ emissions (Figure 3(a)).

7. OUTBREAK ENVIRONMENTS FOR MERS-COV

Since September 2012, the WHO has been notified of 2,254 cases of infection including 800 deaths related us MERS-CoV. The majority of these cases were reported from Saudi Arabia (1871 cases, including 724 deaths with a case-fatality rate of 38.7%). 27 countries have reported cases of MERS-CoV [16]. Major reservoir hosts are known as African bat and dromedary camels (Figure 6). It is interesting to note that humpback whales in the Arabian Sea do not migrate but reside during the year-round. MERS was induced by camels and has been present in Saudi Arabia as well as Jordan, Oman, Qatar, United Arab Emirates, Yemen, Iran, and Kuwait since 2012. As Antarctica is the source of virus [6], MERS emerged from Antarctica and was transmitted by among humpback whales from Antarctica to the Arabian Sea. 15,000 migratory Madagascara humpback whales out of a total global population of 80,000, may mate with non-migratory Arabian Sea humpback whales, the latter being infected by the Antarctic aquatic virus without movement to the Antarctic. Aquatic virus infected humpback whales release feces in the Arabian Sea, whose nutrient subsidies are fed on by Arabian fish and aquatic microorganisms and are transmitted to coastal animals such as birds, bats, seals and whales. Camel in the Arabian Desert may evolute the virus which is mutated as MERS-CoV and transmitted to humans, as shown in Figure 6.

The evidence for humpback whale presence in the Persian Gulf was confirmed in the period of 1883-2017: Bassore Bay, Iraq; Doha, Qatar; Kuwait Inner harbour, Kuwait; Qeshm Island, Iran. Arabian Sea humpback whales may enter the Persian Gulf with some regularity. The non-migrating population of humpback whales *Megaptera novaeangliae* inhabit the northern Arabian Sea year-round [40]. Baleen whales, dugong, blue whales, minke whales, humpback whales, killer whales, pilot whales, sperm whales, fin whales, toothed whales, dolphins and porpoises are known to reside in waters off the Arabian Peninsula [41]. The Persian Gulf is part of the habitual range of the Arabian Sea humpback whale population, and has been since at least the mid-Holocene [42].

Figure 9 shows the sequential flow diagram of humpback whales infected by the aquatic virus for MERS-CoV.

Figure 8(b) shows that Jordan is mainly covered by the Arabian Desert while the Red Sea is also in contact with Jordan through the Port of Aquaba, which can be why Jordan is one of the largest MERS-CoV outbreaks after Saudi Arabia and UAE. Note that Bahrain had the first patient even located on an island in the Persian Gulf. Dromedary camels from a farm in Qatar proved to be positive for MERS-CoV [43]. It is evident that the number of MERS-CoV outbreaks are the highest in Saudi Arabia (1028) which has the longest coastline in the Persian Gulf and largest surface area of the Arabian Desert. The UAE has the second longest coastline of the Persian Gulf with the second largest number of MERS-CoV outbreaks (77). Jordan has the second largest surface area surrounded by the Arabian and Syrian deserts with the third largest outbreak (19), followed by Qatar (13), Oman (6), and Kuwait (6). It can be thus postulated that the humpback whales mainly on the coastline of the UAE may release their feces transmitting the infected evolutionary virus of MERS-CoV to dromedary camels by coast animals such as birds and bats.

Outbreaks of MERS were observed in countries surrounded by both the Arabian Desert (Figure 8(b)) and the Persian Gulf (Figure 8(a)).

Figure 10(a) shows the contour lines of the depth in the Arabian Gulf, whose 20 m contour indicated that all the countries in the Persian Gulf induced MERS-CoV. It can be postulated that migratory humpback whales near Madagascara may visit the Arabian Gulf coastline and release the infected feces, transferring the virus to coastal animals such as birds, bats, seals, non-migratory humpback whales for the reservoir of MERS-CoV. Productivity is highest in the northern region of the Arabian Sea. In **Figure 10(b)** red is the highest productivity and blue is the lowest. In the summer monsoon season winds drive waters away from the coast causing upwelling that brings cold nutrient rich waters to the surface. As a result there is high productivity in the summer. In the winter there is a deep mixed layer and convective mixing the injects nutrient rich waters from the subsurface to the surface promoting high productivity. There is high productivity in the summer and in the winter [45] in the Arabian Sea, compared with other humpback whale in habitats in the world. The Arabian Sea is the unique humpback whale habitat fewer than 100 -400 whales that reside there permanently, while nearby Madagascara has 15,000 humpback whales. Since the Arabian Sea has high productivity (**Figure 10(b**)), Madagascara humpback whales may visit the Persian Gulf for feeding and mating.

The Arabian Gulf is a shallow marginal semi-enclosed sea situated in the northern-eastern Arabian Sea, with mean depth at only 35 m and less than 100 m in depth over its entire extent (Figure 10(a)). Since 20 m depth lines in Figure 10(a) surround Oman, United Arab Emirates, Qatar, Bahrain, Saudi Arabia, Kuwait, Iraq, and Iran, corresponding to countries of MERS-CoV outbreaks, it is postulated that coastal

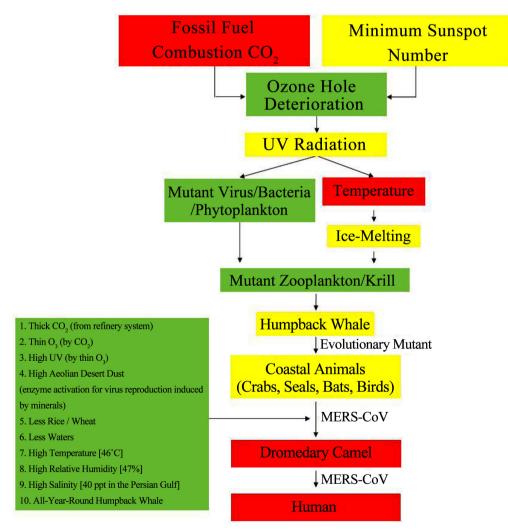


Figure 9. Sequential flow diagram of humpback whales infected by the aquatic virus for MERS-CoV.

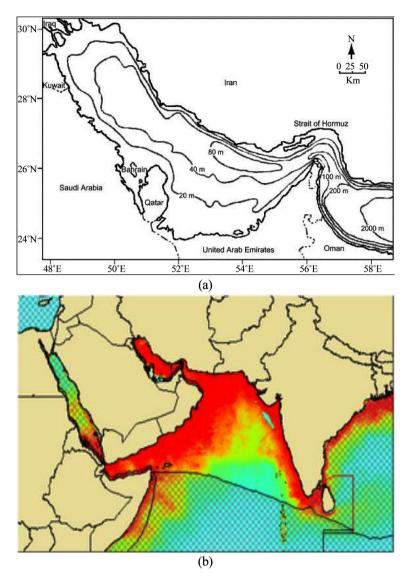


Figure 10. (a) Coastal countries with the Arabian Gulf in depth [44]. (b) Productivity in the Arabian Sea [43].

animals such as birds, bats, crabs, shrimps, and non-migratory humpback whales are reservoirs of MERS-CoV mutated from the aquatic virus to the MERS-CoV infected camel in the Arabian Desert. The main topographic features are a deep channel on its northeast side off the coast of Iran, and shallow areas on the west side off the coasts of Kuwait, Saudi Arabia, Qatar and the UAE. The Arabian Gulf is connected to the Gulf of Oman via the narrow Strait of Hormuz, which is constructed 56 km wide at its narrowest point by the Musandam Peninsula [44]. The Persian Gulf acts as an inverted estuary with salinity greater than the Arabian Sea e.g. salinity values exceeding 40 ppt (parts per thousand) around the island of Bahrain, and the coasts of Qatar and the UAE.

Dromedary camels are the reservoir host of MERS-CoV. Dromedary camels can be found in the Sahara Desert, Arabian Desert, Syrian Desert, Iranian Desert, and part of the Australian Desert. The cause of the main outbreak of MERS-CoV in Saudi Arabia can be the mutant transmitted by non-migratory humpback whales in the Persian Gulf. There were cases of MERS-CoV in East Asia in the following; Saudi Arabia (1028), UAE (77), Jordan (19), Qatar (13), Oman (6), Kuwait (6), Iran (6). As shown in Figure 8(b), Saudi Arabia has the longest coastlines of the Persian Gulf and the Red Sea along with the widest area of

Sequence	Environments for	Cause Crude oil and combustion, production of LNG with removal of CO ₂		
1	Increased CO ₂ emission			
2	Thin O ₃ hole	Increased CO ₂ emissions		
3	High UV radiation	Thin O ₃ hole and maximum sunspot number in 2012 2013, 2014) in Figure 4 in the Poles and low UV radiation in the Continents		
4	High aeolian desert dust	The Arabian Desert and Shamal wind enriched with sulfur		
5	Low rice/wheat	Less route of migratory flyways		
6	Low waters	Less drinking water in the Arabian Desert with annual rainfall less than 100 mm		
7	High temperature	~38°C in the Arabian Desert		
8	High relative humidity	85% - 100%		
9	High salinity	In the Persian Gulf, 40 parts per thousand		
10	Non-migratory humpback whales	Populations of 100 to 400		
11	Dromedary camel	In the Arabian Desert		

Table 4. Environments for outbreak of MERS-CoV in the Arabian Peninsula between September2012 and peak in 2014.

the Arabian Desert. The UAE is mostly covered with the Arabian Desert and the Persian Gulf, whereas Jordan is mostly covered with the Arabian Desert and connected to the Red Sea through Aqaba while Kuwait and Oman are surrounded by the Arabian Desert and the Persian Gulf (Table 4).

8. CO₂ EMISSIONS IN THE MIDDLE EAST

Qatar is the exception among the GCC countries with its massive gas production and LNG facilities giving the country a distinct advantage over its neighbors. Qatar holds the world's third largest stock of reserves and is the largest LNG exporter (Table 5). LNG composition is 90% CH₄, 6% C₂H₆, 2% C₃H₈, CO₂ and H₂S. For production of LNG, CO₂ has to be removed. The primary greenhouse gases in the Earth's atmosphere are water vapor, CO₂, CH₄, nitrous oxide (N₂O) and O₃.

Therefore, it is expected that GCC countries have extensive CO_2 emission effects, causing the strong UV radiation mutating the worst virus of MERS-CoV in the Persian Gulf during the maximum sunspot number.

From 2010 to 2013 there were abrupt increases of gas supply in Qatar, as shown in **Figure 11**. Coincidentally, there was the outbreak of MERS-CoV in September 2012 to 2014 with their peak in Saudi Arabia.

As shown in **Figure 12(a)**, the Qatar oil and natural gas fields are distributed in the Persian Gulf, presumably to impact the non-migratory Arabian Sea humpback whales with steps as below,

1) Viruses in the Poles are mutated by the strong UV radiation during maximal sunspot number and become more powerful.

2) The mutant virus is transmitted by migratory humpback whales in Madagascar.

3) Non-migratory humpback whales in the Arabian Sea are infected during possible mating with

migratory humpback whales in Madagascar.

4) Infected non-migratory humpback whales in the Persian Gulf are involved in virus evolution [25] in environments (Table 2) transmitting the mutant virus to coastal animals such as dolphins, whales, and bats to infect the dromedary camel as the animal source of MERS-CoV.

There have been an abrupt increase of Saudi crude burn in power plants since 2009 till now with coincidental outbreaks of MERS-CoV mainly in Saudi Arabia (Figure 12(b)) since 2012 with their peak causing in 2014.

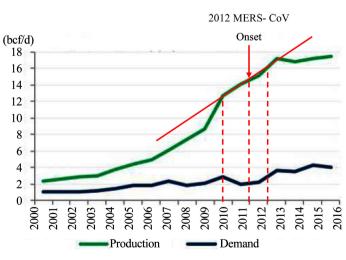
Oil and natural gas field in the right side of the Arabian Desert and the Persian Gulf are partially transported to the Red Sea and the Mediterranean Sea across Saudi Arabia with possible leakages throughout Saudi Arabia to infect the dromedary camel with MERS-CoV, as shown in Figure 12(c).

Camel trails crisscross the surface between watering places, as shown in **Figure 6**. It is possible that the waters for dromedary camels are infected by MERS-CoV in Saudi Arabia.

The UAE depends almost 100 percent on natural gas for power generation, with gas imports via

	Estimated Reserves	Share of GCC	Share of World
Qatar	858	58.6%	13.0%
Saudi Arabia	298	20.3%	4.5%
UAE	215	14.7%	3.3%
Kuwait	63	4.3%	1.0%
Oman	25	1.7%	0.4%
Bahrain	6	0.4%	0.1%
GCC Total	1464	100%	22.2%
Iran	1183	-	18.0%
Russia	1140	-	17.3%
Turkmenistan	617	-	9.4%
United States	308	-	4.7%
Rest of World	1877	-	28.5%
Total World	6589	_	100%

Table 5. World Gas Reserves (in tcf) [46].





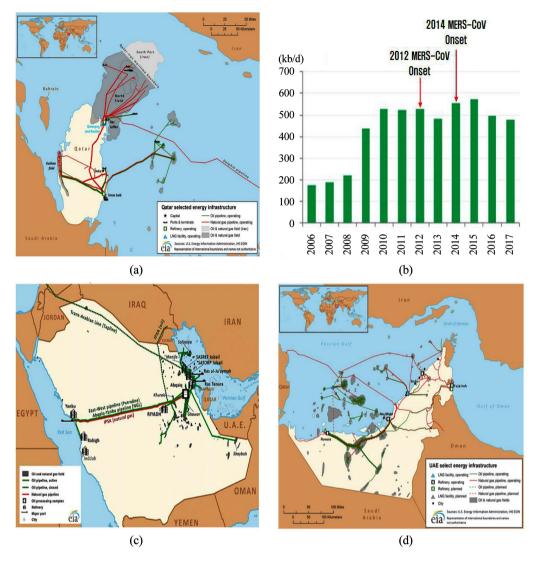


Figure 12. (a) Qatar selected energy infrastructure. (b) Saudi crude burn in power plants. (c) Saudi Arabia major oil and natural gas infrastructure. (d) UAE select energy infrastructure [46].

pipeline from Qatar and LNG cargoes filling a widening supply gap [46]. The UAE has the second largest outbreak of MERS-CoV. In addition, it has the second longest coastline in the Persian Gulf and the wide spread oil and natural gas fields in the Persian Gulf (Figure 12(d)), which may have more chances to decrease the immunity of non-migratory humpback whales in the Persian Gulf.

Saudi Arabia's carbon dioxide (CO_2) emissions have considerably increased over the last years. Saudi Arabia is the largest country in the Arabian Peninsula, bordering the Red Sea, the Persian Gulf, and lying to the North of Yemen. It is also among the world's largest oil-producing countries with over 63% of the world's oil production. According to reports in November 2012, Saudi Arabia produced 9.9 million barrels of crude per day.

Climate change, global warming, biodiversity, acid rain, desertification and deforestation have been caused by fossil fuel emissions. Many researchers have determined there is a relationships between growth and gaseous emissions in the last few decades.

Higher economic development needs a higher amount of energy use and this determines amounts of CO_2 emissions. This notion attracted the world's attention in the 1990s because of the potential threats to the ecosystem. Among the variety of polluting substances, CO_2 is a major one and represents 58.8 percent

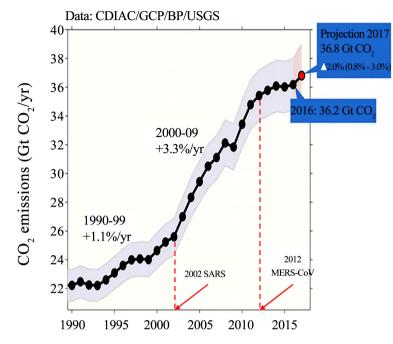


Figure 13. Global CO_2 emissions from 1990 to 2017. After a brief plateau, 2017's emissions are forecast to hit a new high. Credit: Global Carbon Project, Author provided. Global greenhouse emissions from fossil fuels and industry are on track to grow by 2% in 2017, reaching a new record high of 37 billion tonnes of carbon dioxide [49].

of greenhouse gas emissions (Figure 13). Saudi Arabia is the largest oil producer and exporter of total petrolcum liquids in the world and being a faster developing country that utilizes energy more than the other developing countries in Asia or other continents. Saudi Arabia's emissions are 118 million metric tons of carbon [47].

The Earth recently experienced its largest annual increases in atmospheric carbon dioxide levels in at least 2000 years. Data from NASA's Orbiting Carbon Observatory-2 (OCO-2), which was launched in 2014, are helping scientists understand why [48].

9. DESALINATION OF THE ARABIAN GULF

With extremely low and unreliable precipitation [50], desalination is the main source of freshwater in the Middle East. The cumulative desalination capacity of the countries in the Arabian Gulf is around 11 million cubic meters (MCM) per day [51] including Kuwait, Saudi Arabia, Bahrain, Qatar, the United Arab Emirates and Iran is approximately 11 MCM constituting some 45% of the total desalination activity of the world [51]. The main producers of desalinated water in the Arabian Gulf are the United Arab Emirates with a combined daily capacity in excess of 6.278 MCM/d, Saudi Arabia 2.318, Kuwait 1.69, Qatar 0.917, Bahrain 0.358 and Iran 0.205 [52]. Seawater desalination constitutes an important source for water supply to the population bordering the Arabian Gulf. The amount of desalinated water in the Arabian Gulf accounts for over 60% of the world's total production [53]. In the reverse osmosis desalination plants (RODP), the total water is taken from the sea and the brine is discharged back to the same medium, where salinity will increase by 70% [54]. The Arabian Gulf is a shallow semi-enclosed marginal sea, less than 100 m in depth over its entire extent and with a mean of only 35 m [55]. There are freshwater inflows from the Tigris, the Euphrates, and the Karun at the delta of the Shatt al Arab. The main producers in the Gulf region are the United Arab Emirates, Saudi Arabia (9% from the Gulf region and 13% from the Red Sea), Qatar and Kuwait [51, 56].

10. CONCLUSIONS

Spanish flu in 1918, SARS in China in 2002, and MERS-CoV in Saudi Arabia in 2012, have the following features; 1) the induction by viruses (Spanish flu; avian influenza virus (AIV), SARS and MERS; coronavirus), 2) the outbreak during the maximal sunspot number, 3) the aeolian desert dust region (Spanish flu; Saharan, SARS; Asian, MERS-CoV; Arabian), 4) similar incubation period (AIV; 5, SARS; 2 -7, MERS-CoV; 5 days), and 5) different transmission reservoir (Spanish flu; aquatic birds/swine, SARS; bat, MERS-CoV; bat/dromedary camel). The abrupt increase of global CO_2 emissions from fossil fuel combustion causes the thin ozone hole while the maximal sunspot number allows the extensive UV radiation in the Poles. When carbon dioxide combustion emission was high simultaneously at the maximal sunspot number, the UV radiation on the surface of the Poles was so extensive as to mutate the aquatic virus through the food web eventually reaching poultry and humans, which could be the fundamental reason for the 1918 Spanish flu. Guangdong Province and Hong Kong in China are favorable environments for the habitats of migratory birds. These locations are ideal stopovers for migratory birds flying from the Antarctic via Australia. Since Guangdong Province and Hong Kong are located on the long coastline of the South China Sea and have mild temperatures, high relative humidity and ideal habitats with small islands for migratory birds and humpback whales, such locations could be the source of 2002-2003 SARS.

The reduction of CO₂ emissions by nuclear power plants is a unique solution to decrease MERS-CoV outbreaks, especially in Saudi Arabia, UAE, and Qatar with the largest outbreaks of MERS-CoV due to factors such as Arabian Desert area, coastline length of the Persian Gulf, and CO_2 emissions by combustions of crude oil and natural gas. Stranding and subsequent deaths of whales and dolphins along the coast of the Persian Gulf are caused by infection by the worst virus from the Antarctic. They may be fed on by coastal animals from the Arabian Desert, where bats and dromedary camels are present to transmit the evolutionary virus in the form of MERS-CoV under various environments such as high sulfur, high temperature, and low water in the Arabian Desert, high relative humidity and high CO₂ emissions in the Persian Gulf. Migratory Madagascara humpback whales may mate with non-migratory Arabian Sea humpback whales and become infected by the Antarctic aquatic virus without movement to the Antarctic. Aquatic virus infected humpback whales releases feces in the Arabian Sea and the Persian Gulf, which is transmitted to coastal animals such as birds, bats, seals and whales. Dromedary camel contaminated by waters in the Arabian Desert may evolute the virus to be mutated as MERS-CoV and transmitted to humans. Arabian Sea humpback whales may enter the Persian Gulf with some regularity. The non-migrating population of humpback whales inhabits the northern Arabian Sea year round. The evidences for humpback whale presence in the Persian Gulf were confirmed in the period from 1883-2017. There has been an abrupt increase of Saudi crude burn in power plant since 2009 till now with coincidental outbreaks of MERS-CoV mainly in Saudi Arabia since 2012 peaking in 2014.

Serious diseases such as Spanish flu, SARS, and MERS-CoV have occurred by mutant viruses initiated from the Poles during both the abrupt increase of CO_2 emissions and the maximal sunspot number. The sunspot number is a good index to predict the scope and the extent of serious diseases for humans during the maximal sunspot number.

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CONFLICTS OF INTEREST

The authors declare no conflicts of interest regarding the publication of this paper.

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