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Chapter 6. Origin of New Emergent Coronavirus and Candida Fungal Disease– Terrestrial or Cosmic? ver#4 16.2.20

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Abstract: We analyse the relevant genetic and epidemiological data of two recent and suddenly emerging diseases- the fungal disease due to *Candida auris*, and the common cold causing viral disease due to Coronavirus COVID-19. Analysis of all genetic, epidemiological and geophysical and astrophysical data suggest the alternate hypothesis of cosmic origins in both cases. The in-fall “signatures” are different yet distinctive implying clear Panspermic arrival of micro-organisms and viruses from space. For COVID-19 the evidence is now compelling that it arrived as a ‘pure culture’ via a meteorite, presumed carbonaceous meteorite, that struck North East China on October 11 2019. We also assume the viral dust debris carrying trillions of COVID-19 particles then made land fall in the Wuhan and related regions about a month to six weeks later. This resulted in first cases of the viral pneumonia due to COVID-19 emerging in Wuhan regions late November 2019-early December 2019. For COVID-19 the entire central region of China has been heavily physically contaminated, and that is why it has been described as a “Chernobyl-like” event. We make a number of future predictions – e.g. fragments of the meteorite viral dust cloud we think is now (February 16 2020) on the move into the South China Sea and making spot land fall over Japan.

1.Introduction

In the past 40 years there have been a number of suddenly emerging epidemic viral diseases.

Many were self-limiting and “went away “ or “disappeared” almost as quickly as they appeared

(SARS,MERS,ZIKAV). The origins in all cases were a mystery, and very controversial. Others such as the far more deadly HIV retrovirus has finally succumbed to highly effective antiretroviral therapy (HAART) making life bearable for infected HIV+ people. However it has integrated into the human germline in many cases and is likely to be a permanent “endogenized retroviral signature” in the human germline, joining the many thousands of other HERVS , human endogenous retrovirus sequences, that litter the human genome as fragments or potentially active retroviruses (Wickramasinghe 2012, Wickramasinghe & Steele 2016).)

Arguably the best example of the emergence of a new pandemic disease of considerable virulence and pathogenicity was the Spanish Flu Pandemic1918-1919. That pandemic has been analysed in great detail by Hoyle & Wickramasinghe (1979), where the argument is made that the best interpretation of the epidemiology of the Spanish Flu in an era without massive human air travel is that the disease originated and was transmitted predominantly “extra-terrestially”, an example of panspermia.

We do not intend to review again these earlier epidemics and pandemics, which have been covered in many previous papers (some cited here). We will instead focus our analysis on the origins of two recently emergent epidemics: a fungal disease caused by *Candida auris* and the current coronavirus “common cold” epidemic caused by the COVID-19 virus. These two epidemics display distinctive features and clear evidence that they may have come from a space in-fall of infectious viruses and micro-organisms in cometary dust or meteorite-derived dust particles.

2. Sudden Simultaneous Emergence of *Candida auris* Infections in Separate Global Regions

Candida species are well-known yeasts that can cause a variety of cutaneous and invasive infections. However, they had never been considered a serious global health threat until the recent emergence of *Candida auris*. This was first reported in the ear canal of a patient in Japan in 2009. Since then, cases have been recorded on all continents except Antarctica (Rhodes and

Fisher 2019). It can cause a variety of invasive infections with a mortality rate of up to 60%, typically infecting susceptible hosts, namely those with long hospitalisations, many illnesses and impaired immunity (Bradley, 2019). In addition, it can be resistant to multiple antifungals and has the capacity to cause outbreaks within healthcare facilities (Chow et al., 2018). Its ability to colonise and persist for a long time on human skin, tolerate some disinfectants that are commonly used in healthcare settings, and to survive on inanimate surfaces for many weeks, all contribute to its effectiveness as an outbreak agent (Jackson et al., 2019).

Equally remarkable is the data detailing the epidemiology of the emergence of this infection. An analysis of whole genomic sequencing from fifty-four isolates of *C. auris* from four regions around the world revealed four major clades or genetically distinct populations. This finding supports the hypothesis of the nearly simultaneous and independent emergence of these clades in geographically separate human populations. The SENTRY Antifungal Surveillance Program is a global system that has continued for 20 years (1997–2016). It collects consecutive invasive *Candida* isolates from medical centres located in four regions during each calendar year, namely: North America, Europe, Latin America, and the Asia-Pacific (Pfaller et al., 2019). Despite going back to 1997, the SENTRY data did not identify *C. auris* until 2009 (Jackson et al., 2019). In fact, the earliest *C. auris* isolates were found in South Korea in 1996 and Japan in 1997 (Forsberg et al., 2018).

Although it is a *Candida* species, *C. auris* is quite distinct from its *Candidal* relatives. The genus consists of >500 species, many of which greatly differ from each other. *C. auris* comes from the *Clavispora* clade of the *Metschnikowiaceae* family. It has not been identified in any natural environments (Jackson et al., 2019). It is relatively thermotolerant, and has been shown to survive and grow at temperatures as high as 42 degrees Celsius. Such thermotolerance could potentially allow it to infect avian hosts (Chatterjee et al., 2015).

Infections caused by the fungus *Candida spp* have been recognised for many years. However, what is of most interest here is the **abrupt** emergence of a new strain *Candida auris* which

presents a profound puzzle (Lockhart et al, 2017). This new strain is multi-drug resistant and has emerged as a major cause of mortality, posing a serious challenge for health officials the world over (Lockhart et al., 2017, Chowdhary, et al., 2017,3 Jeffrey-Smith et al., 2018, Cortegiani et al., 2018). While *Candida auris* was reported for the first time in Japan in 2009 it appears to have been *isolated more or less simultaneously* in many widely separated locations across the world.

Phylogenetic analysis by Lockhart et al (2017) has identified 4 distinct clades separated by tens of thousands of single nucleotide polymorphisms (SNPs) each of which is geographically localised. A large number of SNPs have been discovered in isolates that were recovered from four widely separated locations (South Asia, East Asia, South America, and South Africa). Whole genome sequencing of these isolates has revealed an exceedingly low genetic diversity within individual regions even across the largest clade involving some 36 isolates from surveys over as wide a field as India and Pakistan. The conclusion reached by Lockhart et al (2017) is that *C. auris* likely arose almost simultaneously in multiple four different global locations. Using isolates of *Candida* from four continents Lockhart et al., (2017) could find no evidence for *C. auris* before 2009, confirming that this pathogen had not simply been misidentified in previous analyses. Thus, it seems reasonable to conclude that a 2009 date for the origin *Candida auris* is fairly secure (Cortegiani et al, 2018).

Since global cross-infection over such a short timescale (< 1 year) appears very unlikely one possibility is to consider independent multiple origins of *Candida auris* from a widely dispersed *Candida* ancestor. A fungicide driver model has been advanced to partly explain the phenomenon (Lockhart et al, 2017). However this vague model does not fit the available data in our opinion. We thus argue alternatively that a panspermic in-fall model should be considered as a plausible and better alternative.

Using this hypothesis as a starting point, given all of the available data, we suggest that *C. auris* first arose in 2009 from several environmentally-induced hypermutation events that occurred

after in-fall from cosmic (cometary) dust clouds through which the Earth passed sometime during or before 2009. Thus this new *C. auris* would appear simultaneously in many widely separated places on the Earth. As another viable (though we think less likely) alternative, a genetic hybridisation event may have taken place at this time involving a globally distributed set of comet-borne gene segments that were themselves genetically diverse.

How could this have occurred? We evaluate the data in the following from a genetic point of view. The data demands that there are at least four pre-existing clades ($\geq 10,000$ SNP differences) in an external non-terrestrial source (cometary dust tails) and these came down separately in separate regions and thereafter spread clonally (Lockhart et al., 2017). The other alternative is to consider the existence of a single “mother” or “parent” *C. auris* clade in the cometary dust source, which upon landing and infection of susceptible hosts is induced into a hypermutation-adaptation sequence via a fast, essentially Lamarckian, Adaptive Mutation strategy (Rosenberg 2001, Chapter 3) thereby generating in excess of 10,000 new SNP differences from the parent orbiting cosmic strain. The final step that can be envisaged is the dispersal of a successful adaptive variant in a particular region to other hospitals in that region. Thus on the basis of a Panspermic model there are two possible explanations for the strange and striking *C. auris* patterns of genome diversity. The Lamarckian hypermutation strategy at each separate in-fall location (susceptible hospital patients) from a pure line “mother” strain is, on parsimony grounds, preferred.

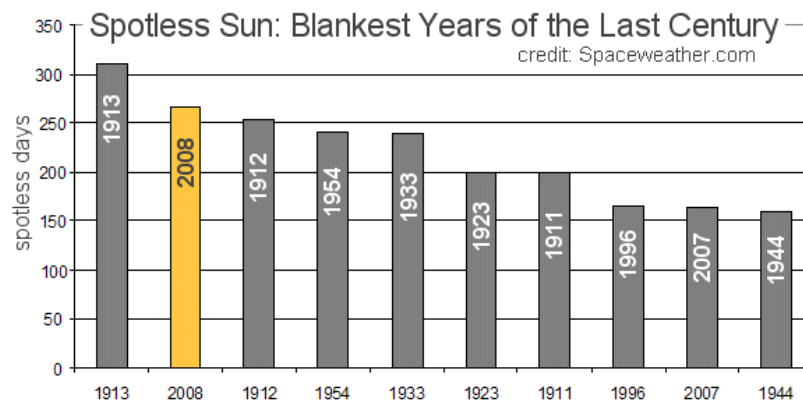


Figure 1. The distribution of the number spotless days in the Sunspot cycle, showing the period 2008/2009 to be the lowest on record for a century. Exceptionally low sunspot activity in solar minima open the floodgate to interstellar and comet dust.

We have previously argued that a sudden emergence of new pathogenic variants of circulating viruses could be linked to cosmic events related to the well-known 11-year sunspot cycle (Qu & Wickramasinghe 2017, 2018, Wickramasinghe et al., 2017, 2019). The Earth's magnetosphere, and the interplanetary magnetic field in its vicinity, are both modulated by the solar wind that controls the flow of charged particles onto the Earth. During times of sunspot minima, a general weakening of magnetic field occurs and this would be accompanied by an increase in the flux of cosmic rays (GCR's) and also of charged interstellar and interplanetary dust particles. Since the latter could, in our view, include biological entities such as bacteria, viruses and other eukaryotic microorganisms including *C. auris*, an increase in their incidence on the Earth would be expected at such times. It is interesting to note that in 2008-2009 (the solar minimum under discussion) the interplanetary magnetic field was the lowest on record since the beginning of the space age. We would therefore expect a significantly enhanced flux of both cosmic rays as well as electrically charged biological entities at this time, so the possible arrival of a new clade of *C. auris* from a space source would not be surprising.

A crucial fact relating to the first appearance of *Candida auris* in 2009 is that this time point marks not merely a solar minimum but *the lowest minimum* of the sunspot cycle in 100 years (See Figs. 1, Fig 2). This particular minimum was all the more remarkable because the sun was spotless (devoid of spots) for more than 70% of the time. The opportunity of the transference of both Galactic Cosmic Rays (GCR's) and charged molecular structures (e.g. *C. auris*) thus remained continuously optimal over extended periods. At the present time (Feb 2020) as we approach a new sunspot minimum the sun continues to be exceedingly "quiet" and the expectations are that we are heading for an even deeper minimum than before. We would hypothesize further then, given past evidence, that epidemiological vigilance for the emergence of novel microbial and viral pathogens should be even greater at the present time.

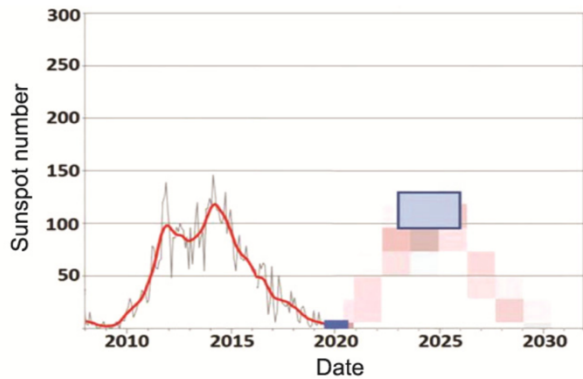


Figure 2 Current Sunspot Cycle 24 and Predicted Cycle 25 (Wickramasinghe et al., 2019). From Term Solar Observations-World Data Center, Royal Observatory of Belgium, Brussels (<http://www.sidc.be/silso/home>).

3. Sudden Emergence new Coronavirus (COVID-19) Causing Respiratory Infections in Wuhan, China and neighbouring regions

We now turn to our critical analysis to the origin of the COVID-19 epidemic, which is underway at the time of writing.

3.1. Overview of the COVID-19 Epidemic The global extent of the emotion around this epidemic in the mainstream popular media, and even the scientific press (*Science* magazine) is disturbing. It is without parallel in our experience in this social media internet age. However it does approach the justified hysteria around the far more serious, and initially more lethal, HIV epidemic/pandemic that suddenly emerged 40 years ago.

The actual COVID-19 viral disease itself causes respiratory “common cold-like” illness in most people with symptoms – and like many respiratory viruses often potential carriers of the diseases are asymptomatic. The infection can progress to severe pneumonia in elderly and already medically-compromised patients with other conditions (diabetes, coronary disease, etc). About 2% of all COVID-19 cases have died from pneumonia (Figure 4). Vaccines and antivirals at this time are either not yet available or have not proven very effective, but standard supportive medical care for the respiratory crisis often associated with the life-threatening pneumonia and inflammatory bronchial symptoms, allows for recovery in most patients. The fact that “Recoveries” far exceed “Deaths” (Figure 4) indicates that timely medical care for this otherwise “common cold” respiratory illness must be the medical priority in the

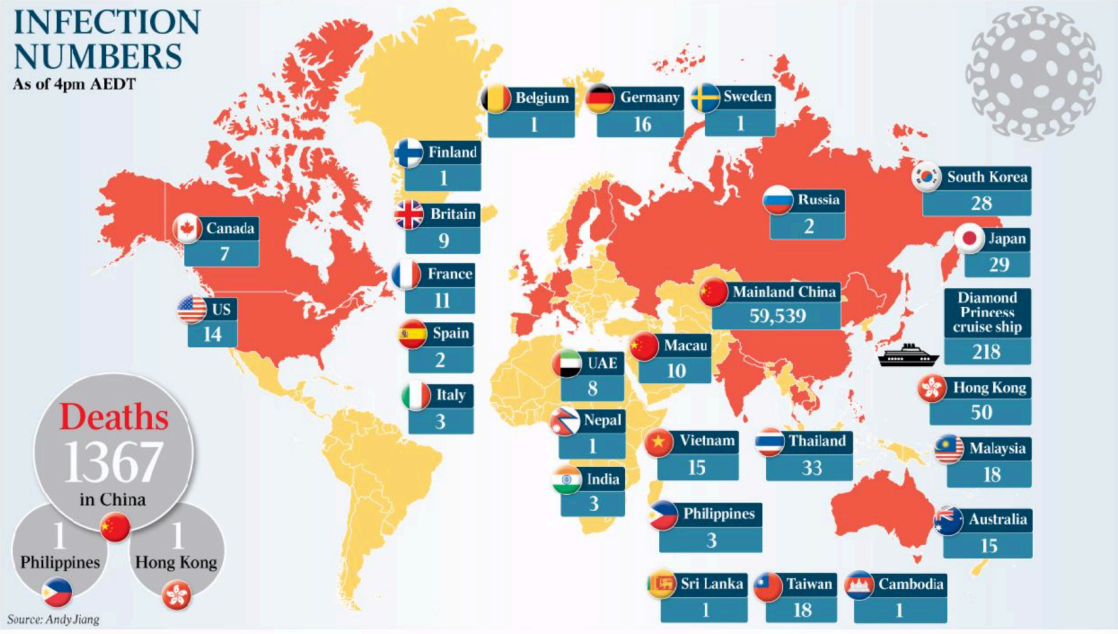


Figure 3. The Australian newspaper as 14. 2.20 page 8

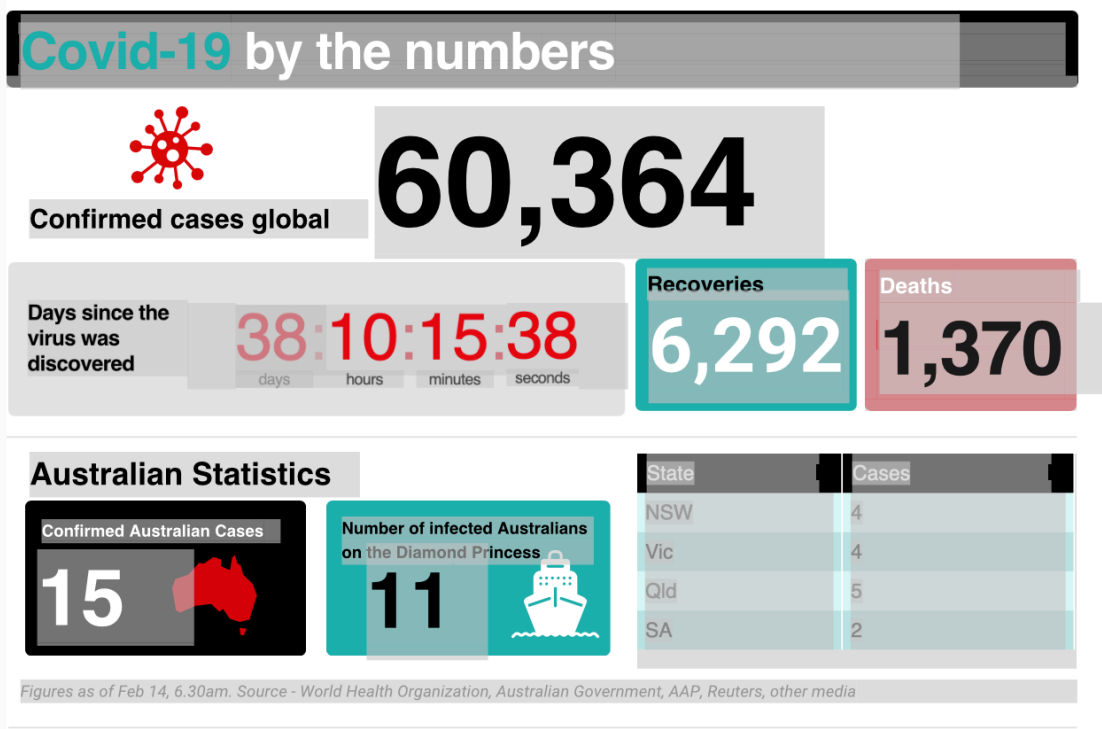


Figure 4. COVID-19 by Numbers , in The Australian newspaper 14 February 2020 p.8. Figures as of Feb 14, 6.30am. Source - World Health Organization, Australian Government, AAP, Reuters, other media. However sorting out what is true from what is untrue is a challenge. The current distribution

epicenter of the infection in Wuhan and nearby regions in China. We believe this medical care is being implemented throughout China. But it is the origin of this new emergent virus disease which has raised the most angst. It is explosively centred on Wuhan, which appears to be the epicenter. And it appeared suddenly without warning. The theory that it jumped from bats via snakes to humans is implausible (below). The same angst over viral origins was also evident when HIV, SARS, MERS, Ebola, and ZIKAV suddenly appeared on the scene. We will not deal with these earlier diseases as their origins, in our considered opinion, are far less clear cut than COVID-19 and case numbers for COVID-19 as of February 14 2020 are shown in Figures 3 and 4. The epidemic is centred on the city of Wuhan, in the central Hubei province of China.

From about mid-January the Chinese government ordered the complete quarantine and lockdown of Wuhan and wider region around the city in Hubei province, affecting 50-100 million people. *ABC News* in Australia estimates Coronavirus COVID-19 has affected 500 million people in China under lockdown (Updated Sat 15 Feb 2020, 1:29am). A problem with all these reports is the lack of detailed information that led officials to such an extraordinary quarantine decision. We speculate later on this.

At the time of writing, the case incidence of this newly discovered Coronavirus is passing through 60,000 and > 99.99% of all cases, almost exclusively, are Chinese. From reports of cases that exited Wuhan by aircraft in late January to other countries, including Australia, the disease does not appear to be spread in a sustained by person-to-person infection, although there are clearly apparent cases of person-to-person spread elsewhere (in UK and Europe, BOX1). Nevertheless, there is clear consensus that this disease is centred on China. The Johns Hopkins University COVID-19 case density maps are extremely informative. These are in Figures 5,6 and 7.

To put one interpretation on the striking case patterns in Figures 5-7, particularly the symmetrical pattern in Figure 7, one could liken the image to that of a viral bomb explosion which took place near or over Wuhan, with subsequent fall-out of the disease causing viral

particles to land on millions of people either laterally or from above. Some of those infected would, by virtue of age/comorbid factors, be susceptible and succumbed to respiratory illness.



Figure 5. Case density map- South East Asia region wide . Johns Hopkins University as February 7 2020
Johns Hopkins University's Centre for Systems Science and Engineering

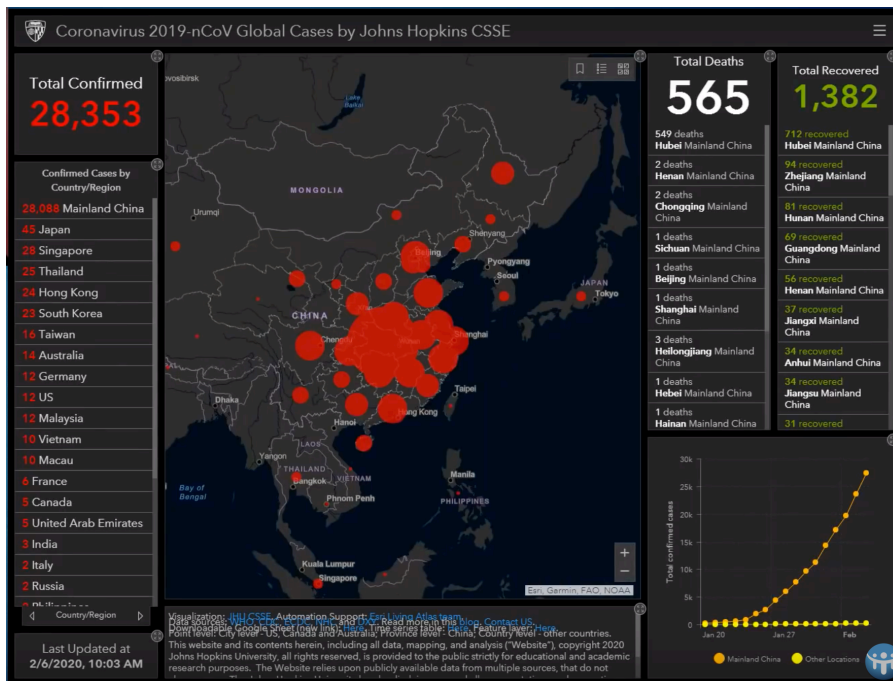


Figure 6 Case density map –China and nearest neighbours. Johns Hopkins University as February 7 2020
Johns Hopkins University's Centre for Systems Science and Engineering

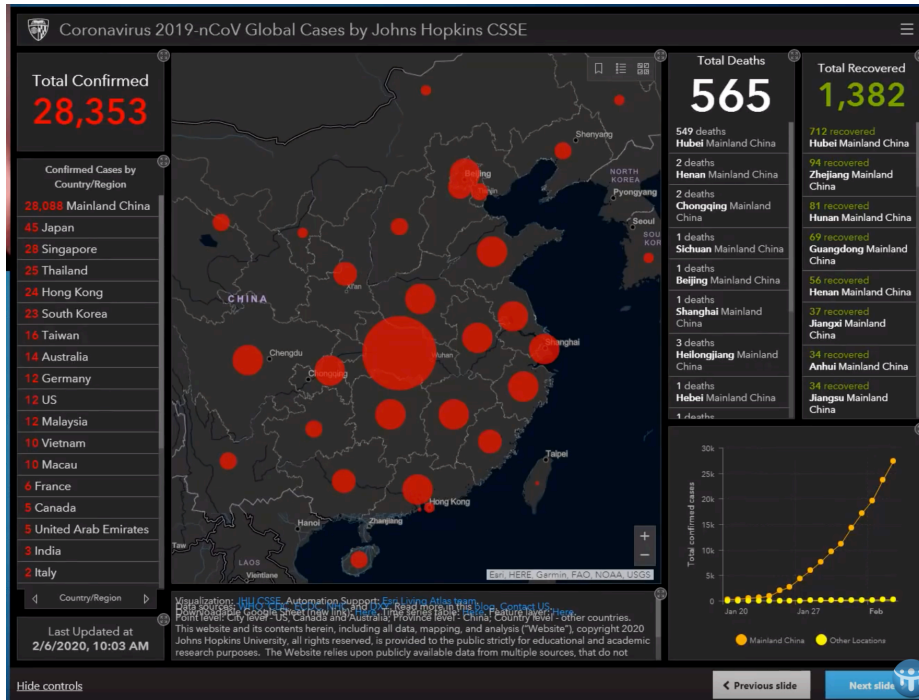


Figure 7 Case density map –China itself. Johns Hopkins University as February 7 2020
Johns Hopkins University's Centre for Systems Science and Engineering

Paradoxically, asymptomatic patients can be efficient “spreaders” of the disease. This is contrary to normal expectations as usually the infected potential spreader would display overt and full blown disease (and the coughed-up aerosols from such a patient would be dense with viral particles).

3.2. Detailed Analysis of COVID-19 Epidemic We now analyse all reliable genetic, epidemiological and geophysical and astrophysical data. This data supports our hypothesis that COVID-19 arrived via a meteorite, a presumed relatively fragile and loose carbonaceous meteorite, that struck North East China on October 11 2019. This is at odds with the main stream expert “Infectious Disease” opinion of traditional person-to-person spread of an infectious endemic disease such as, for example, Cholera (*Vibrio cholerae*).

We assume the viral debris and particles made land fall in the Wuhan and related regions about a month to six weeks later resulting in first cases of the viral pneumonia caused by COVID-19 emerging in Wuhan regions late November 2019-early December 2019 (Huang et al, 2020,

Cohen 2010) . This hypothesis is consistent with the patterns shown in Figure 7. Moreover, our hypothesis makes a discrete set of predictions, that are explored in our conclusions.

We argue first that massive region-wide physical contamination with potentially trillions of infective COVID-19 viral particles occurred in central China- contaminating buildings, roadways, cars and factory equipment, vegetation, surface water pools, people (and their clothes, body parts such as hair, skin, personal affects, mobile phone, keys , wallets etc) as well as wild and domestic animals, etc. This explains the actions of the Chinese Government who are acting in a manner consistent with their being in receipt of information from region-wide sampling to detect COVID-19 RNA sequences in swabs from physical objects, people and animals (via Real time PCR).

The recent paper by Huang et al., (2020) and the extremely important news commentary by Cohen in *Science* (Cohen 2020) highlights many unusual aspects of the outbreak of COVID-19. The evidence demonstrates that many cases of disease (about 30% of case reports) arose in locations unconnected with the Wuhan seafood and meat market, and the total tally continues to increase. Phylogenetic analyses of COVID-19 (previously named nCov-2019) sequences show little by way of sequence variation indicating low mutation rates, closely approximating what would be expected for a pure culture of a single infecting and replicating sequence affecting disease cases (Andersen 2020, Lu et al 2020). These facts, combined with the global epidemiological data, suggests little or no really sustained human-to-human transmission thus far (e.g. latest reports by the Australian Department of Health). We acknowledge that there are apparent exceptions e.g. the “super-spreader” from Singapore, via the French Alps, and then to a UK GP surgery reporting mild symptoms, resulting in the GPs also getting the disease (BOX 1). Even this data can be explained as evidence of spread mainly by viral contamination of physical objects rather than direct “cough in your face” human to human spread.

Thus current data suggest that the human-to-human spread rate is unusually low, and likely depends on close proximity and a high dose of virus delivered at very close quarters. The

“lethality” or “death rate” from this or any other epidemic disease increases in older patients with pre-morbid factors, so wider global estimates yield a death rate at 2% of infected (Figure 4) . All these basic facts now appear agreed.

The initial traditional explanation of the new epidemic of COVID-19 is that it jumped from bats (possibly via snakes) to humans and then spread by human-to-human infection contact, mutating at a high rate. This explanation is inconsistent with the current data. Indeed Jon Cohen the respected *Science* magazine journalist reports that the head of the Huang et al (2020) study when interviewed said:

“ Bin Cao of Capital Medical University, the corresponding author of *The Lancet* article and a pulmonary specialist, wrote in an email to *ScienceInsider* that he and his co-authors “appreciate the criticism” from Lucey (Daniel Lucey, an infectious disease specialist at Georgetown University confirmed the epidemic could not possibly be caused by visits to the Wuhan seafood and meat market).

“Now It seems clear that [the] seafood market is not the only origin of the virus,” he wrote. “*But to be honest, we still do not know where the virus came from now.*” (our italics)

Indeed Dr Bin Cao speaks for all mainstream medical and epidemiological professionals around the world - no formal traditional explanation can be provided for the origins of COVID-19. Thus Andrew Rambaut, Professor of Molecular Evolution at the University of Edinburgh tweeted: “Don’t think any epidemiologist is still thinking that a non-human animal reservoir has had anything to do with the nCoV-2019 epidemic since December. Certainly the genome data doesn’t support that.” (reported in (Heidi Han and Kieran Gair, Associated Press, *The Australian* newspaper Jan 27 2020).

Thus, when we combine all the available facts we cannot rule out a viral in-fall event targeting the Wuhan province and the wider region around it as an equally viable, indeed to our mind preferable, explanation as the primary cause of the epidemic. This would fit with the admittedly heterodox view of viral pandemics first proposed by Hoyle and Wickramasinghe as far back as

1978 (Hoyle & Wickramasinghe 1979, Hoyle & Wickramasinghe 1990, Wickramasinghe et al 2003, Wickramasinghe et al., 2019). This concept accords with the theory of cosmic biology for which growing evidence have recently been presented in the Chapters of this book and in recent peer-reviewed papers where all the main extant evidence has been reviewed. It is consistent with the Hoyle-Wickramasinghe thesis (Steele et al., 2018, 2019a,b). Our theory thus posits a sporadic input of cosmic bacteria, viruses and other micro-organisms that has the potential to interact with evolving terrestrial life forms, causing terrestrial diseases and further adaptive evolution on Earth.

3.3. Link with a Direct Strike of Meteorite Over Central- North East China, October 11 2020

In the case of the current coronavirus epidemic in China it is interesting to note that an exceptionally bright fireball event was seen on October 11 2019 over Sonjyan City in the Jilin Province of NE China (See Figure 8). It is tempting to speculate that this event had a crucial role to play in what is now unfolding in and throughout China. Indeed, the match with the Johns Hopkins University case incidence patterns is so striking it is difficult to easily dismiss this as a chance correspondence of patterns, in both time and place. e.g. Figure 7.

If a fragment of a fragile and loosely held carbonaceous meteorite carrying a cargo of trillions of viruses/bacteria and other primary source cells (for the cosmic replication of the COVID-19 virus), entered the mesosphere and stratosphere at high speed $\sim 30\text{km/s}$, its inner core which survived incandescence would have been dispersed in the stratosphere and troposphere. Indeed, it could easily have been fragmenting and dispersing its contents before the ignition of the fireball event. The fall time through the atmosphere of 1-10 micrometre-sized solid particles could range from a few months to well over a year on the basis of straightforward calculations (e.g. in the Appendix of Hoyle & Wickramasinghe 1979 "Diseases from Space"). Because dispersal at ground level depends on the vagaries of meteorology and precipitation the deposition of virus at ground level is expected to be patchy in regard to both time and place. This is certainly consistent (thus far) with what has happened in relation to the new COVID-19 coronavirus epidemic between November 2019 and the present day (15 February 2020).

Following the initial deposition of infective particles in a small localised region (e.g. Wuhan, Hubei province, China) particles that have already become dispersed over a wider area in the troposphere will fall to ground in a randomized manner, a process possible occurring over a timescale of 1-2 years, until the initial inoculant of the infective agent is drained. This accords well with many new strains of viruses including influenza that have appeared in recent years (Wickramasinghe et al., 2019).



Figure 8. The public record of this meteorite strike can be found at the Space.com website in an article by Tariq Malik, on October 13 2019 “Brilliant Midnight Fireball Lights Up Sky Over Northeast China” . The October event is described at :

<https://www.space.com/china-midnight-meteor-brilliant-fireball-october-2019.html>

The possible link of sunspots with pandemics has been discussed over many years (Wickramasinghe et al., 2017, 2019, Qu & Wickramasinghe 2017, 2018) and is worthy of brief further discussion. The present cycle (interface between cycles 24 and 25, Figure 2) has seen the lowest minimum for well over a century with many sunspot free days recorded in the last months of 2019. Sunspot minima are associated with a weakening of the interplanetary magnetic field near the Earth, which in turn allows easy ingress of Galactic Cosmic Rays (GCRs) and electrically charged bacteria and viruses to the Earth. The mutagenic role of GCRs can cause genetic changes in already circulating viruses. But in respect of COVID-19, it is primarily an enhanced flux of new infective particles released by the exploding meteoroid that may follow this particular sunspot minima that is of importance. We argue that a perfect storm over China

is paying out before our eyes, a meteorite delivering COVID-19 particles corresponding with a very significant Sunspot Minimum cycle. It raises the important issue: “How would other densely populated countries have reacted to, and handled, this event involving COVID-19?” Only the vagaries of chance caused this meteoroid to explode over China.

4. Conclusions

We conclude by noting some predictions and expectations:

- We expect the pattern of further spread of the new coronavirus COVID-19 to be dictated mostly by primary in-fall until a high level of person-to-person infectivity might *possibly* be achieved and the virus then acquires the status of an endemic virus.
- Viral contamination of the “environment” in the most general sense explains most of the apparent contagion e.g. news reports like in BOX 1 (below).
- The possibility cannot be ruled out that the *Diamond Princess* cruise ship in the South China Sea was contaminated by a fragment of the main COVID-19 dust cloud. Similar inexplicable events appeared to happen for ships at sea during the 1918-1919 Spanish Flu Pandemic (Hoyle & Wickramasinghe 1979).
- Furthermore, other drifting COVID-19 smaller dust clouds that have not as yet made land fall may target remote island and other communities, as was also the case during the 1918-1919 Spanish Flu Pandemic (Hoyle & Wickramasinghje 1979, and see Appendix report on Japan cases)
- Given the low mutation rate and the very wide apparent in-fall infectivity pattern (Figure 7), we predict is this pure viral culture has already inoculated millions of Chinese citizens (as well as potentially millions of wild and domestic animals in China) inducing protective adaptive immune responses (Acquired Herd Immunity) on a very large scale.
- Accordingly, development of a so called “COVID-19 vaccine” which is much in the news at the time of writing would be a waste of public tax-payer funds if mounted on the scale envisaged by governments and national centers for disease control.
- We thus expect the decline of the epidemic (peaking and declining at time of writing) to be driven by this mass natural vaccination process now underway in China. So the suddenly

emerging COVID-19 epidemic, like many similar suddenly emerging human epidemics in the past (SARs, MERs, ZIKAV), is expected to rapidly end by the self-limiting process of wide spread herd immunity.

- We predict that the incidence of serum antibodies specific for COVID-19 will be wide-spread in the Chinese population in the coming months. Millions will be potentially immunised for life against future infections with COVID-19.
- How long will COVID-19 remain potentially infective in the physical environment? Clearly for some time - given that over the space of a month or so many cases appeared rapidly, spread by environmental contamination in our view, and not by traditional person-to-person generated aerosols at the height of the donor's infection. This is consistent with those news reports out of China: “ As the death toll rose to 80, China said , increasing concerns about the potential the virus was infectious even before symptoms were visible rapidity of its spread.” (Heidi Han and Kieran Gair, Associated Press, *The Australian* newspaper Jan 27 2020)

Postscript:

As this Chapter was submitted to the publisher an authoritative news despatch from Japan reports sporadic outbreaks across the country with *no direct link* with China (Appendix). Further, in early February we tried to alert the world on our interpretation of the origins of COVID-19 with many of the same arguments and analyses listed in this Chapter. One succinct letter was sent to *The Lancet*, and the other was a more general article for a wider lay readership , to *The Australian* newspaper – both articles were rejected by the editors . The archived PDFs of both articles can be found at the viXra.org site under accession numbers URLs [viXra:2002.0039](http://viXra.org/abs/2002.0039) and <http://viXra.org/abs/2002.0039?ref=11076818> , and <https://vixra.org/abs/2002.0118>

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REFERENCES

- Andersen K. Clock and TMRCA based on 27 genomes (2020). Novel 2019 coronavirus <http://virological.org/t/clock-and-tmrca-based-on-27-genomes/347>
- Bradley, S.F. (2019). *Candida auris* infection. *JAMA* 322:1526.
- Chatterjee, S., Alampalli, S.V., Nageshan, R.K., Chettiar, S.T., Joshi, S., & Tatu, U.S. (2015). Draft genome of a commonly misdiagnosed multidrug resistant pathogen *Candida auris*. *BMC Genomics*. 16, 686.
- Chow, N.A., Gade, L., Tsay, S.V., Forsberg, K., Greenko, J.A., Southwick, K.L, et al., (2018). Multiple introductions and subsequent transmission of multidrug-resistant *Candida auris* in the USA: a molecular epidemiological survey. *Lancet Infectious Diseases*. 18, 1377-84.
- Chowdhary, A., Sharma, C., & Meis, JF. (2017) *Candida auris*: A rapidly emerging cause of hospital-acquired multidrug-resistant fungal infections globally. *PLoS Pathog*. May 18;13(5):e1006290. doi: 10.1371/journal.ppat.1006290.
- Cohen, J. (2010) Wuhan seafood market may not be source of novel virus spreading globally *Science* Jan 26 2020. doi:10.1126/science.abb0611
- Cortegiani, A., Misseri, G., Fasciana, T., Giammanco, A., Giarratano, A., & Chowdhary, A. (2018) Epidemiology, clinical characteristics, resistance, and treatment of infections by *Candida auris*. *J. Intensive Care* 6:69. doi: 10.1186/s40560-018-0342-4.
- Forsberg, K., Woodworth, K., Walters, M., Berkow, E.L., Jackson, B., Chiller, T., et al. (2018). *Candida auris*: The recent emergence of a multidrug-resistant fungal pathogen. *Medical Mycology*. 57, 1–12.
- Hoyle, F., & Wickramasinghe, N.C. (1979) *Diseases from Space*, (J.M. Dent & Sons, Ltd, London)
- Hoyle, F., & Wickramasinghe, N.C. (1990) Influenza – Evidence against contagion, *J. Royal Soc.Med.*83(4), 58
- Huang, C., Wang, Y., Li, X., Ren, L., Zhao, J., Hu, Y., et al. (2020) Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China . *The Lancet* Published online January24,2020 [https://doi.org/10.1016/S0140-6736\(20\)30183-5](https://doi.org/10.1016/S0140-6736(20)30183-5)
- Jackson, B.R., Chow, N., Forsberg, K., Litvintseva, A.P., Lockhart, S.R., & Welsh R. (2019). On the Origins of a Species: What Might Explain the Rise of *Candida auris*? *Journal of Fungi*. 5: 58.
- Jeffery-Smith, A., Taori, S.K., Schelenz, S., Jeffery, K., Johnson, E.M., Borman, A., et al. (2018)

Candida auris: a Review of the Literature. Clin. Microbiol. Rev. 31(1). pii: e00029-17. doi: 10.1128/CMR.00029-17

Lockhart, S.R., Etienne, K.A., Vallabhaneni, S., Farooqi, J., Chowdhary, A., Govender, N.P., et al., (2017) Simultaneous emergence of multidrug-resistant *Candida auris* on 3 continents confirmed by Whole-Genome Sequencing and Epidemiological Analyses. *Clinical Infectious Diseases* 64, 134-140 DOI: 10.1093/cid/ciw691

Lu, R., Zhao, X., Li, J., Niu, P., Yang, B., Wu, H., et al, (2020). Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *The Lancet* published Online January 29, 2020 [https://doi.org/10.1016/S0140-6736\(20\)30251-8](https://doi.org/10.1016/S0140-6736(20)30251-8)

Pfaller, M.A., Diekema, D.J., Turnidge, J.T., Castanheira, M., Jones, R.N.(2019). Twenty Years of the SENTRY Antifungal Surveillance Program: Results for *Candida* Species From 1997–2016. *Open Forum Infectious Diseases*. 6(S1):S79-94.

Qu, J., & Wickramasinghe, C. (2017) SARS, MERS and the sunspot cycle. *Current science*. 113(8),1501- 1502.

Qu, J., & Wickramasinghe C. (2018) Weakened magnetic field, Cosmic rays and the Zikavirus outbreak. *Current science*. 115(3), 382-383

Rhodes J., & Fisher MC.(2019). Global epidemiology of emerging *Candida auris*. *Current Opinion in Microbiology* 52: 84-89.

Rosenberg, S.M. (2001). Evolving responsively: adaptive mutation. *Nat. Rev. Genet.* 2, 805-815.

Steele, E.J., Al-Mufti, S., Augustyn, K.A., Chandrajith, R., Coghlan, J.P., Coulson, S.G., et al (2018) Cause of Cambrian Explosion - Terrestrial or Cosmic? *Prog. Biophys. Mol. Biol.* 136, 3- 23. <https://doi.org/10.1016/j.pbiomolbio.2018.03.004>

Steele, E.J., Al-Mufti, S., Augustyn, K.A., Chandrajith, R., Coghlan, J.P., Coulson, S.G., et al., (2019a). Cause of Cambrian explosion - terrestrial or cosmic? - reply to commentary by R Duggleby. *Prog. Biophys. Mol. Biol.* 141, 74-78.

Steele, E.J., Gorczynski, R.M., Lindley, R.A., Liu, Y., Temple, R., Tokoro, G., Wickramasinghe, D.T., Wickramasinghe, N.C.(2019b) Lamarck and Panspermia - On the Efficient Spread of Living Systems Throughout the Cosmos. *Prog. Biophys. Mol. Biol* 2019 149, 10-32 . pii: S0079-6107(19)30112-9. doi: 10.1016/j.pbiomolbio.2019.08.010

Wickramasinghe, N.C. (2012) DNA sequencing and predictions of the cosmic theory of life. *Astrophys Space Sci* 343: 1-5.

Wickramasinghe, N.C., & Steele, E.J. (2016). Dangers of adhering to an obsolete paradigm: could Zika virus lead to a reversal of human evolution? *J. Astrobiol. Outreach* 4 (1). <https://doi.org/10.4172/2332-2519.1000147>.

Wickramasinghe, N.C., Steele E.J., Wainwright, M., Tokoro, G., Fernando, M., Qu., J (2017) Sunspot cycle minima and pandemics: the case for vigilance. *J. Astrobiology and Outreach* 2017, 5:2 DOI: [10.4172/2332-2519.1000159](https://doi.org/10.4172/2332-2519.1000159)

Wickramasinghe, N.C., Wainwright, M., & Narlikar, J. (2003) SARS--a clue to its origins? *The Lancet* 361: 1832.

Wickramasinghe, N.C., Wickramasinghe, D.T., Senananyake, J., Qu, J., Tokoro, G., Temple, R., & Steele, E.J. (2019) Space weather and pandemic warnings? *Curr. Sci.* 117, 1554 (Issue 10, 25 Nov 2019)

BOX 1 - SUMMARY OF UK CASES (N. C. Wickramasinghe email report to Edward J Steele)

- 21 January 2020

CDC confirms 1 case of transmission between person who returned from Wuhan, and a person who shared accommodation in the US.

Via a ski resort in the French Alpine town of Les Contamines-Montjoie, near Switzerland, late last month.

- 28 January 2020

A cluster linked to an Alpine chalet:

A British man (Mr Walsh) from Brighton, was found to have the virus when he returned to the UK (London Gatwick Airport) from Geneva on 28 January on an EasyJet flight. A total of 6 people in Britain, including Mr. Walsh, and 5 Britons in France who have the virus have been staying in two apartments in a ski chalet in the Alpine resort area near Mont Blanc when they were visited by Mr Walsh on 24 January *who had attended a business conference at the Grand Hyatt Hotel Singapore, where he is believed to have contracted the virus.*

Mr Walsh is *thought* to have passed the virus onto eleven confirmed cases while he was at the Ski resort. But he is thought to have come into contact with scores of people after leaving Singapore and no others have yet succumbed.

All the supposed transmissions of the virus from Mr Walsh to the others were whilst they occupied the Chalets in France.

Four are from Brighton and Hove. They are Dr Greenwood and three men, one of whom is a healthcare worker. He also passed it to one other person in the UK, one person who is now in Mallorca and five UK nationals in France – one of which is Dr Greenwood's husband Bob Saynor and another their nine-year-old son. None are said to be in a serious condition.

So far, the places in Brighton and Hove being quarantined are:

- County Oak Medical Centre, where Dr Catriona Greenwood worked one admin day last week, and its branch surgery at Deneway.
- Grenadier Pub in Hangleton, which was visited by Steve Walsh on February 1.
- Cornerstone Community Centre, where a yoga teacher came into contact with Steve Walsh on February 3. No other people have been advised to self-isolate.
- Easyjet flight EZS8481 to Gatwick from Geneva on January 28, which is believed to be the flight Mr Walsh took back to the UK
- Bevendean Primary School, where a staff member has been in close contact with someone who has been advised to self-isolate (but is not themselves diagnosed)
- Portslade Academy, which told parents on Friday one of its pupils has been advised to self-isolate for a fortnight after coming into contact with the Hove father. It's believed pupils at other schools have been given the same advice.
- Patcham Nursing Home, which has closed its doors to all visitors after being visited by one of the medics now confirmed as having the virus.

The cluster associated with Mr Walsh could have been coinfecting from a common source, with Mr W showing symptoms first."

Appendix as February 15 2020

Headline: None of Japan's new coronavirus patients had direct China links.

First death raises fear that virus is quietly spreading

By Yusuke Kurabe, Nikkei staff writer , in Nikkei Asian Review

February 13 13, 2020 22:37 JST ● Updated on February 14, 2020 04:52 JST

<https://asia.nikkei.com/Spotlight/Coronavirus/None-of-Japan-s-new-coronavirus-patients-had-direct-China-links>

- “ A Kanagawa Prefecture woman in her 80s died from the coronavirus. Her son-in-law also tested positive for the disease. A doctor in Wakayama Prefecture and a man in Chiba Prefecture are confirmed to have the virus. None of them traveled to China recently or had contact with people who visited Hubei Province, the epicenter of the outbreak. .. The 80 year old woman's symptoms began Jan. 22 when she felt fatigue, the health ministry said. Symptoms worsened on Jan. 25, prompting her to see a doctor three days later. She was placed under observation. .. The victim was hospitalized Feb. 1, diagnosed with pneumonia. She underwent screening for the coronavirus Wednesday. The test results came back positive Thursday, the day she died.. Her son-in-law also tested positive for the coronavirus. The man, a taxi driver in his 70s living in Tokyo, has been hospitalized since Feb. 6, but the symptoms are reportedly mild. He developed a fever Jan. 29.
- “ A doctor in Wakayama Prefecture south of Osaka has been infected with the virus, prefectural officials said Thursday .. The man, in his 50s, has been hospitalized with symptoms of pneumonia, but is otherwise in stable condition. The doctor did not travel outside the country in the 14 days prior to the onset of symptoms, nor can any contact with people coming from China be confirmed. Wakayama officials suspect the infection had domestic origins.
- ” Elsewhere, a man in his 20s from Chiba Prefecture near Tokyo is also confirmed to have the virus. He developed a fever and other symptoms Feb. 2. The man reportedly has not travelled overseas or had contact with other infected individuals.
- “ Besides the outbreak on the Diamond Princess cruise ship, which has infected over 200 people aboard the vessel quarantined in Yokohama, 29 cases of coronavirus had been confirmed inside Japan through Wednesday.
- “These cases raise new challenges for health officials, who until now had been trying to contain the virus by closely monitoring people with the possibility of contracting the disease. If more people with no direct links to China become sick, determining infection routes will become impossible. Instead of containment, treating seriously sick people may have to become the priority. “