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Overview SARS-CoV-2 Pandemic as January 2022: Cometary Origin, Global Spread, Prospects for Future Vaccine Efficacy

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Abstract (461 words**)**

As the SARS-CoV-2 pandemic is nearing its eventual end we focus on what we believe are two key omissions from the mainstream scientific literature and which have significant implications for how mankind manages the next global pandemic. We therefore review data, observations, analyses and conclusions from our series of papers published through 2020 and 2021 on its likely cometary origin and global spread. We also revisit our long held understanding of the superior effectiveness of intra-nasal vaccines against respiratory tract pathogens that involve induction of dimeric secretory IgA antibodies. While these two oversights seem disparate, together they provide us with new insights into our collective awareness of how we might view and address the next global pandemic. We begin with our hypothesis of its likely cometary origin via a bolide strike in the stratosphere on the night of October 11 2019 on the 40º N line over Jilin in NE China. Further global spread most likely occurred via prevailing wind systems transporting both the pristine cometary virus followed by continuing strikes from the same primary source as well as prior human passaged virus transmitted by person to person spread and through contaminated dust in global wind systems. We also include a discussion of our prior work on data relating to vaccine protective efficacy. Finally we review the totality of evidence concerning the likely origin and global spread of the predominant variants of the virus 'Omicron' (+ Delta mix?) from early to mid-December 2021 and extending into the first week January 2022. We describe the striking data showing the large numbers of infectious cases per day and outline the scale of what appears to be a global pandemic phenomenon, the causes of which are unclear and not completely understood. First, these essentially ***simultaneous and*** **sudden** global-wide epidemic COVID-19 outbreaks, appear to be *largely correlated with events external to the Earth, probably causing globally correlated precipitation events.* They appear related broadly to "Space Weather" events that render the Earth vulnerable to cosmic pandemic pathogen attack particularly during times of the minima of the Sunspot Solar Cycle which we are now currently passing through. Second, we argue that these sudden global-wide epidemic outbreaks of COVID-19 are specifically largely influenced by global wind transport and deposition mechanisms. We conclude with an optimistic note for mankind. Given our prior knowledge on the effectiveness against

respiratory tract pathogens of mucosal immunity involving induction of dimeric secretory IgA antibodies, we consider the recently published intra-nasal vaccine data from laboratories based at the University of California, San Francisco and, independently at Yale University, holds great promise for the future development of both *pan-specific and specific* immunity against future pandemics caused by suddenly emergent respiratory pathogens, whether viral and bacterial.

1.Introduction

The authors encompass a multi-disciplinary team across the scientific disciplines of Biology, Medicine and Physics in the broadest meaning of those categories of scientific understanding. We follow in the footsteps of the prior foundation studies published in many key books on Astronomy, Astrophysics and Astrobiology incorporating references to many peer reviewed papers (mainly in the journal *Nature*) by Fred Hoyle and N. Chandra Wickramasinghe (Hoyle and Wickramasinghe 1978, 1979, 1981, 1985, 1991, 1993, 1999, Wickramasinghe 2020). Many on the current list of co-authors have made significant contributions to recent publications on these matters, and some presciently just prior to the emergence of the COVID-19 pandemic (Wainwright et al 2015, Wickramasinghe et al 2017, 2019, Steele et al 2018, 2019). This previous experience has heightened our analytical ability to scientifically track and plausibly explain the cometary origin and global spread of COVID-19. A number of reviews of the relevant datasets and conclusions therefrom have been published through 2020 and 2021 (Steele et al 2020a, Steele et al 2020b, Steele et al 2021a), including a compendium of chapters on 'Cosmic Genetic Evolution' that places the COVID-19 pandemic in its appropriate cosmic perspective (Steele and Wickramasinghe 2020). Thus, a number of papers submitted by us since February 14 2020 review the data supporting our first claims of COVID-19's putative meteorite origins over China, following a meteorite strike on the 40^{o} N Latitude line over Jilin, NE China on the night of October 11, 2019 (Wickramasinghe et al 2020a). We note here that the causative meteor may not have arrived at the top of the Earth's atmosphere as a cohesive body, but an aggregation of dust particles, with individual radii ~ micro meters. Past work shows that around 60 tonnes of such material are incident on the upper atmosphere daily. Approximately two thirds of micron sized meteors are of cometary origin. Modelling of their dynamics in the atmosphere shows that a significant fraction of these particles reach the surface of the Earth without experiencing intense heating (Coulson and Wickramasinghe 2003).

Subsequent publications in the early weeks of the pandemic focused on the relative lack of evidence for person-to person transmission as the primary infection mechanism for COVID-19 (Wickramasinghe et al 2020b). Indeed detailed analyses of the active region-wide epidemic episodes around the globe during 2020 and 2021 occurred initially (late 2019 to March through April 2020) mainly on the 30-50^{o} N latitude band with limited outbreaks outside this band (Wickramasinghe et al 2020c). We developed evidence-based explanations of what engulfed the world since the later months of 2019, with regard to genetic, immunologic and epidemiologic evidence, and

geophysical and atmospheric wind systems, with regard to possible astrobiological input of the virus. In summary, the main analyses were as follows:

a. The genetic analysis of the SARS-CoV-2 viral genomes and the deaminase-mediated haplotype variation and adaptation strategy of the coronavirus as it navigated infections in different susceptible/vulnerable human hosts and genetic backgrounds first in China, then Spain, to New York then France, Australia January through April May then to September 2020 (Wickramasinghe, et al 2020a, Steele and Lindley 2020, Steele et al 2020b, Lindley and Steele 2021).

b. The immunologic analysis of the host-parasite relationship and vaccine efficacy of systemic versus mucosal-local antigen routes of immunization (Steele and Lindley 2020, Lindley and Steele 2021, Gorczynski et al 2021).

c. The epidemiologic analyses of both the temporal order of epidemics and their global location, including the role of prevailing winds systems, remote outpost strikes (O'Higgins Chilean Army outpost in Antarctica), sudden island strikes and strikes on ships at sea (Howard et al 2020, Wickramasinghe 2020c, Wickramasinghe et al 2020d, Steele et al 2020b, Steele et al 2021a.).

d. The geophysics and atmospheric physics of the major convection cells plus jet streams sweeping up and depositing virus-bearing dust, including human-passaged aerosol transferring them in the northern hemisphere with limited connection to the south (Wickramasinghe et al 2020c, Wickramasinghe et al 2020e, Steele et al 2021b). Global connectivity is effective on the 10-day time-scale. The evidence of long distance tropospheric transportation in the Northern Hemisphere is provided by the COVID-19 genomic sequence data from the *Grand Princess* cruise ship off San Francisco (engaged late February 2020) which displayed the exact same largely unmutated genomic sequence (Hu-1) as determined in China during December 2019 and January 2020 (Steele and Lindley 2020, Steele et al 2021a).

e. The role of human-passaged (and created) regional variants lofted or plumed attached to microdust particles into the troposphere and the global wind systems, in likely attenuated form (Steele et al 2021b, Steele et al 2021c) – cf. independent assessment of the role of global wind transportation systems in past influenza pandemics in Hammond et al 1989.

All of our prior analyses and conclusions and its relation to the wider scientific literature on SARS-CoV-2/COVID-19 can be found in our past publications, which can be accessed at https://www.academia.edu/50814212/Papers_and_Summary_Interviews_on_Origin_and_Global_Spread_of_COVID_19_Wickramasinghe_and_colleagues. The URL links to all relevant video interviews involving N. Chandra Wickramasinghe and Edward J Steele can be found in this list and at *The Cosmic Tusk* website of George Howard. https://cosmictusk.com

We have also considered and refuted the main popular explanations that were spreading uncritically abroad in both the scientific and popular media, concerning the protective efficacy of all systemic delivered vaccines and the putative origins of COVID-19, the latter as either a jump from a latent SARS-CoV-1 animal reservoir (bat, pangolin, cat) or as a human-engineered COVID-19 genome. In the latter case this infection, identical in genomic sequence to the original Hu-1 reference (isolated in China in December 2019, NC_045512.2), was postulated to have been released from a Chinese laboratory (Wuhan Institute of Virology,) either accidently or deliberately. We show both these origin explanations are scientifically implausible or impossible on genetic grounds (Steele et al 2020b, Steele et al 2021c). Indeed, the Wuhan Lab Leak and related narratives are clearly implausible and simply do not explain *what was actually observed* in the first month or two of the pandemic.

Armed with this background and knowledge, we have analysed a putative "Space Weather" and "solar wind pulse" -like event (Wickramasinghe et al 2017, Wickramasinghe et al 2019) which we argue in part is currently contributing to the manner in which the pandemic signature is evident globally, as it peters out in severity via the natural processes of Herd Immunity, attenuation of human passaged variants and viral decay in the environment (Hansen et al 2021, Steele et al 2021d). From the Cases Per Day Curves (Figures 1-5) we think this has been the major new phenomenon of this pandemic evident from the middle of December 2021.

2. Omicron/Delta Outbreaks in Global Synchrony

Cases per Day plots for selected locations (captured as screen shots on January 3 2022) are shown in Figures 1-5 to illustrate the extreme synchronous or simultaneous eruptions of COVID-19 epidemics (Omicron/Delta mix?) in the Northern Hemisphere regions Figures 1-3 (United Kingdom, Denmark, France, Italy, Ontario, Quebec, New York, Florida, Hawaii, Aruba), and in The Southern Hemisphere, Figs 4-5, embracing populated regions in South America , Africa and Australia (Buenos Aires, Angola, Kenya, Mozambique, and in Australia : South Australia, Victoria, New South Wales and Queensland). In Table 1 we list all regions of the world that display *identical* exponential rising cases per day curves over the *same* time interval as illustrated by the selected examples in Figures 1-5. Countries or regions with low or equivocal rises are listed in Table 2. In some regions there was a clear peak of assumed Omicron initiating about a week or two earlier and case numbers per day are coming down in those regions (Table 3). However, many countries are 'null zones' with respect this time period experiencing no rising epidemic (Table 4).

The reader can scrutinise the data at the URL site for '*Coronavirus disease statistics'* shown in the legend to the figures. The predominant pandemic 'strain' evident in most regions of the world prior to these extraordinary

explosive and coordinated-in-time epidemic outbreaks was the 'Delta' strain (and related Indian plumed strains) from the massive Indian epidemic of April-May 2021, which we hypothesized was released as a very large aerosol of many millions of trillions of virions into the troposphere for distribution to global regions via prevailing W-E, E-W and N-S wind systems (Steele et al 2021b). The Omicron variant was found first in Botswana on November 2, 2021 and was widely assumed to have emerged first in South Africa. We discuss speculative causes of the emergence of the Omicron variant and origin region in Section 3.

What plausible explanations can be provided for the data in Figure 1-5 and Table 1-4, and in particular the essentially simultaneous eruptions of region-specific epidemics of COVID-19 in so many different regions globally? This is not a question that can be easily resolved. The strong indications are of a globally correlated phenomenon that we do not fully understand. One explanation could be connected to space weather events associated with the deep Sun Spot minimum between Solar Cycles 24 and 25 (Wickramasinghe et al 2017, 2019). Unseasonal weather that has been reported both in the Northern and Southern hemispheres (eg. UK and Australia) during this time period may give a hint in this direction. The sheer numbers and global coverage of infection essentially eliminates Person-to-Person spread as the sole causative explanation.

A more plausible scientific explanation lies in massive region wide in-falls from the sky (the troposphere) of prior human-passaged then aerosol-plumed COVID-19 virions lofted into the troposphere and introduced into prevailing wind systems. Given current Omicron case densities, we tentatively assume a northern European origin followed by transport of viral aerosol-clouds across the Atlantic from an origin in the UK/North Europe (?), into the Pacific and Atlantic prevailing winds onto to Africa and thence to Australia.

We are still left with the conundrum of why now, and why at the same time all over the globe? The data in Figures 1-5 is but a small subset of the large number of global-wide regions in the Northern Hemisphere, Equatorial Regions, Island States, and Southern Hemisphere *all struck like this at the same time* (Table 1, 2). In addition, over this time period many Atlantic cruise ships with double vaccinated and pre-screened passengers also became suddenly engaged with COVID-19 (assumed Omicron , see Lee 2021, Khalip and Pereira 2021) including a fully vaccinated US Navy ship (AP|Washington Dec 25 2021) and the sudden outbreak from December 14 of large numbers of fully vaccinated personnel at a remote Belgian Research Station in Antarctica thousands of miles from civilization (BBC News) - this is indeed all reminiscent of similar strikes on ships at sea and remote locations during the early phases of the pandemic in 2020 (Steele et al 2020b, Howard et al 2020, Steele et al 2021a), including the sudden strike on the island of Sri Lanka Oct 4-5 2020 (Wickramasinghe et al 2020d) and more

recently Taiwan by Indian-plumed Delta struck suddenly for first time from 14 May 2021. All indications are of a globally correlated environmental trigger that we cannot fully understand.

One possibility is that globally dispersed viral aerosol-clouds (Omicron/Delta variant mix?) were released, following human passage, and were widely distributed in the troposphere remained viable although not immediately falling to Earth or ocean over many different regions of the world. A putative global trigger in mid-December 2021 might be postulated that brought such viral particles to earth virtually simultaneously around the world. This may have been ultimately facilitated by, but not been dependent upon, rain/precipitation (Steele et al 2021b, Steele et al 2021c). The resulting viral contaminated environments would then ignite outbreaks of mystery unlinked Omicron/Delta cases on a large scale giving the appearance of superfast infective spreading in a given populated viral-contaminated region as we have previously discussed in detail for the outbreaks of mystery infections in Victoria, Australia (Steele et al 2021b, Steele et al 2021c). This is a plausible explanation for the synchronous sudden rises of COVID-19 globally. The fact there are many "null" zones (Table 4) and 'low' or equivocal regions (Table 2) adds to the patchy cloud -like nature of the viral distribution in the troposphere prior to and coinciding with the solar cycle minimum. That is, it arises as deposition from the convection-driven upper troposphere which is patchy.

Another possibility given the global nature of the present observations, and thus cannot be avoided as a causative factor, is the known vulnerability of the earth to pandemics during the minima of the sunspot Solar Cycle (Wickramasinghe et al 2017, 2019). Thus it could be an ill-defined and poorly understood physical event broadly classed as a "Space Weather" event associated with the Sunspot Minimum cycle, particularly now between cycles 24 and 25, where we are most vulnerable to "pathogen attack" from the sky : viz.

> "..the Earth's magnetosphere, and the interplanetary magnetic field in its vicinity, are modulated by the solar wind that in turn controls the flow of charged particles onto the Earth.[4] During times of sunspot minima, particularly deep sunspot minima, a general weakening of magnetic field occurs which would be accompanied by an increase in the flux of cosmic rays (GCR's) and also of electrically charged interstellar and interplanetary dust particles"… bringing charged particles (virus-laden dust particles) to earth. Wickramasinghe et al 2019 .

Getting back to the original events in late 2019 we can advance another specific scenario on what *actually happened* across N-E China in late Dec 2019 and early Jan 2020 after the initial input of cometary virus-carrying dust. The virus became strongly amplified in humans until lockdown. Despite efforts to wash down the streets, the virus's long lifetime on dust particles spread it widely in the environment. When appropriate wind conditions arrived, the infection-carrying dust was swept up in tropospheric winds into the East Asian subtropical jet stream, taking it across the Pacific to southern USA and western Europe. Precipitation into local wind systems caused

infection on the state and country scale. In 2021 similar wind-borne viral-laden dust spread over the entire sub-continent of India causing sudden eruptions of COVID-19 infections (via PANGO variants Alpha, Kappa, and Delta at least). These country-wide sudden eruptions have been noted before but not fully understood (Steele et al 2020a, Steele et al 2021a, Steele et al 2021b, Steele et al 2021c).

Finally, we should ventilate another putative "pulse-like" causative factor contributing to the synchronous nature of the sudden global outbreaks of Omicron/Delta infections. This was not previously considered in our thinking, except in broad terms (Steele et al 2018, 2019). It is related to fact that most viruses in their cell-to-cell infection cycle do so as an enveloped *cluster* of mature virions (Combe et al 2015). This may be important if an influence associated with "Space Weather" external to the Earth somehow triggered the liberation of smaller clusters of virions associated with tropospheric dust clouds over a given region. A dust particle of 2-3 microns (mu) could theoretically envelope 40-60 COVID-19 virions. If these were suddenly liberated as smaller clusters (doubletons or triplets) that would result in a ten-fold sudden increase in putative infective virion clusters floating down to contaminate the immediate terrestrial environment below in that time interval. The nature of this virion liberation "trigger" is unknown (temp/pressure/radiation?), so this is a speculative scenario.

However we can now add another observation, as the manuscript was readied for submission to the commissioning editor. This is consistent again with a power series "pulse-like" set of infection events engaging a large cross section of the globe at the same time. This has been noted as January 14 2022 from the "**Coronavirus disease statistics**" database. This involved the following countries all engaged in an exponential sharp rise in COVID-19 new cases per day not evident in the earlier survey of January 3 2022. These countries are: Pakistan, India .Nepal, Bhutan, Kyrgyzstan, Uzbekistan, Philippines, Japan, Taiwan, Thailand, Mongolia.

We have laid out here a range of explanations, some over-lapping, because we are dealing with a "globally correlated phenomenon that we do not fully understand." We have done this to ensure as many plausible alternatives are available for discussion and consideration to understand what has happened.

3. Speculations how Omicron may have arisen and where

All news reports in Australia, USA, South Africa and European countries, that are engaged with the synchronous exponential eruptions, the main variant is Omicron which is rapidly replacing Delta. From all news reports the respiratory disease severity of Omicron is less than Delta. This is consistent with all Death rate data (this can be confirmed at URL links in Figs 1-5) which is very low, and is approaching or below other estimates of death rates

caused by COVID-19 (whether Original Hu-1, Alpha, Delta and now Omicron) as about 0.1% of all COVID-19 exposed cases (Steele et al 2021c) death being the serious outcome in the 'Immune Defenseless Elderly Co-Morbid' patient group. These patients require immediate respiratory therapies to navigate the respiratory crisis. These patients display clear deficits in innate immunity (Acharya et al 2020, Blanco-Melo et al 2020, Hadjadj et al 2020, Netea et al 2020, Zhang et al 2020) and also feeding into deficits in adaptive immunity (Moderbach et al 2020, Sette and Crotty 2021). Further, longitudinal studies (Lucas et al 2020) show that patients in this subgroup specifically display deficits in Type I and type III interferon (IFN) inducible anti-viral immunity and thus appear 'immune defenceless' to coronavirus respiratory tract infections and are at a very high risk for severe outcomes including death.

How could a human-passaged variant like Omicron arise? Omicron is clearly a derivative of "Delta" a PANGO lineage name of the L241f haplotype of the Steele-Lindley replicative-haplotype scheme (Steele and Lindley 2020) with many changes in the mRNA encoding the spike protein suggestive of mutation accrual via human passage (person to person spread, P-to-P). The analysis of how a single putative cloned variant we named "L241f.1vic" spread through aged care and nursing facilities in Melbourne, Australia beginning from about 10 May 2020 through June 2020 then erupting on scale in such facilities through July and August 2020 is very informative (Lindley and Steele 2021). From the full-length genomic analysis of many thousands of publicly available genomes (> 12,000 made available by the Victorian Dept of Health through The Peter Doherty Institute) we showed previously that there were two types of clearly identifiable patients. The first displayed *unmutated* versions of the virus over the entire 29903 nt genomic length. These types were particularly evident in the last two weeks of June 2020 through most of July 2020. It appeared very much like the virus was being amplified on scale in hosts that were *unable to mutate* the RNA virus genomes at APOBEC (cytosine to uracil) and ADAR (adenosine to inosine) deamination sites (Steele and Lindley 2020, Lindley and Steele 20121). The second group of patients, clustering in a late August time window, displayed mutated versions of the virus, again largely at APOBEC and ADAR cytosine and adenosine deamination motifs. It was concluded thus (Lindley and Steele 2021):

"The data reported herein are thus consistent with the following P-to-P infection model which is also the operational hypothesis under test: clusters of immune defenceless elderly co-morbid citizens in many aged care and nursing facilities were all systematically struck with devastating force (high infection rates and death rates), with a single unmutated (or lightly mutated) SARS-CoV-2 haplotype variant (L241f.1vic). Through late June, July, August and September in 2020, this putatively cloned variant must have been spread unimpeded by carriers who were asymptomatic or lightly symptomatic infected health- care professionals and carers working across multiple age care institutions.[30-33] The large-scale amplifications of the L241.1vic variant—instanced by the size of the multiple 'New case' spikes (shown in Figure 1), particularly through July 2020—could have produced many trillions of L241f.1vic virions in each location thus contaminating numerous surfaces (fomites, personal effects of all types) and could have contaminated or infected human carriers in each institution. This then fuelled the further putative quantitative dominant rapid spread of this apparently capricious L241f.1vic variant into the local community and particularly to other aged care facilities leading to further putative viral amplifications in elderly co-morbid subjects. If anything, the Victorian experience underlines why elderly co-morbid citizens require very special care, protection and therapies during cold and flu seasons.[31,32]

It was then speculated that the putative highly contagious, yet clearly attenuated, "UK Mutant" (Alpha) that emerged in September in 2020 in parts of southern England was generated the same way. We also think Omicron arose by similar cycles of deaminase-mediated mutagenesis in healthy almost asymptomatic carriers, then amplified (cloned unmutated) in Immune Defenseless Elderly Co-morbids – then after one or two more cycles via healthy intermediate 'vectors' infecting Immune Defenseless Elderly Co-morbids where it was amplified and cloned. A plumed aerosol of literally millions on trillions of Omicron virions into the immediate troposphere and prevailing wind transportation could have easily distributed Omicron in the prevailing wind systems (e.g. from Northern Europe to South Africa where first detected). This model of alternating cycles of deaminase-mutagenesis and cloning amplification could have created a plume in a real high-density hotspot. Was it around or near UK where most Omicron have been recorded initially? At the present time we acknowledge these are speculations, but given the existence of detailed genomic records from the millions of genomes now sequenced and in computer databases, these speculations can, and will be tested in the fullness of time.

4. Future vaccine developments for next Pandemic of cold or flu respiratory tract pathogens?

There are many public health lessons to be learnt from the COVID-19 pandemic. Near-Earth balloon launches, stratospheric airplane and orbiting platform sampling of incoming meteorite dust has been stressed on many previous occasions in other places (discussed recently in Wainwright et al 2015, Qu and Wickramasinghe, 2020, Steele et al 2021a, Steele et al 2021c,). But a pandemic public health management strategy employing a more effective vaccination method needs urgent consideration. The aim should be quite different from the current very simplistic strategy of intramuscular "jab-in-the arm" vaccination (irrespective whether traditional antigens are used or the poorly safety tested mRNA expression vector vaccines). Public health vaccination which mimics natural 'Herd' immunity" is the desired outcome, whether to coronaviruses, influenza viruses and many other respiratory tract pathogens including bacterial *ssp*. that cause respiratory pneumonias and severe bronchitis.

Here we review how to optimize intranasal defective /attenuated live virus vaccination for all likely future types of pandemic respiratory viruses and finally discuss promising newly published experimental data which offers some hope for the future. We and many others have discussed the failure of the current jab in the arm intramuscular mRNA vaccines to protect against COVID-19 – yet they have been mandated by many governments and public health bureaucracies (Subramanian and Kumar 2021; Gorczynski et al 2021, Steele et al 2021c). Further, the mRNA vaccines which also have high adverse effect rates are ineffective on first immunological principles because of the *wrong route of delivery*. The current 'jab-in-the-arm' route of immunization cannot possibly protect

against COVID-19 infection gaining entry to and growing in mucosal cells of the respiratory tract. For that the mucosal secretory IgA antibody system needs *local* activation (Lindley and Steele 2021; Gorczynski et al 2021, Steele et al 2021c). In a rush to bring COVID-19 vaccines to market, it seems that science and medicine neglected a large body of work already available on the nature of immunity and host resistance to respiratory viral infections, and how best to mimic this by vaccination, and instead became seduced by advances in 21st century molecular engineering principles into production of a vaccine whose utility and clinical efficacy even now remains unknown- more troubling is that any serious long-term sequalae are entirely unexplored. This is discussed graphically and underlined in recent interviews as well in https://youtu.be/Ijc4mjiIquk and in the *Asia Pacific TV* interview with Mike Ryan https://rumble.com/vmrmmq-the-origins-of-covid-19-and-why-the-vaccines-dont-work..html

Thus, protective vaccination needs to be via the oro-nasal route to activate the mucosal immune response, which is responsible for d Natural Immunity and "Herd Immunity" in the population. The natural decline in the incidence of severe COVID-19 outcomes (COVID-19 associated death) was *well underway before the vaccine roll out* in European and USA Infection zones through 2020 and early 2021 (Steele et al 2021d). This is brought about most effectively by effective 'Herd Immunity' which has been documented in a large longitudinal and population base study, conducted in Denmark through 2020 (Hansen et al 2021).

We have previously discussed the two most important forms of immunity to be activated in the mucosal cells and associated lymphoid cells of the respiratory lining. The first of these is Innate Immunity- a general elevation of these activities would strengthen the "Anti-Viral Wall" in all nasal cells and mucosal lining cells. This barrier is defective in 'Immune Defenseless Elderly Co-Morbids' which are the primary vulnerable group in the COVID-19 pandemic. Note that this group equates to < 1% of all infected patients (Netea et al 2020 discussed in Lindley and Steele 2021 in detail based on data from many clinical studies throughout 2020 : Acharya et al 2020, Blanco-Melo et al 2020, Netea et al 2020, Hadjadj et al 2020, Moderbacher et al 2020, Lucas et al 2020, Zhang et al 2020,and reviewed also in Sette and Crotty 2021). In our analysis of the data >99% of the population handles COVID-19 effectively via natural immune mechanisms- to these patients it is just a "Common Cold". Both Innate Immune Interferon Type I and III anti-viral barriers in all cells would be activated, and then adaptive acquired mucosal immunity.

Secondly, Adaptive Acquired Mucosal Immunity requires, as we discuss, the induction of the dimeric form secretory IgA antibodies – these antibodies are demonstrably highly avid (strong binding and thus neutralizing of toxins, viruses and adhesins preventing cell adherence and cell entry) that do not activate the Complement Cascade thus do not add to "inflammatory cytokine storms" . Indeed secretory IgA is expected to competitively block

antigen binding and thus nullify the antibody-dependent enhancement (ADE) by the blood borne IgG and IgM complement fixing antibodies particularly in advanced COVID-19 infections of the elderly vulnerable group (discussed in Lindley and Steele 2021, Gorczynski et al 2021). This sequelae of ADE pathology in vaccinated individuals who then go on to catch COVID-19 for first time is discussed more fully in Steele et al 2021c.

To ensure that intranasal vaccination is effective it is desirable that activation of the innate immune response via the Toll receptors in addition to induction of secretory IgA against the virus. An agonist, INNA-51 of the Toll-2 receptor, was patented in 2018 (WO2018176099, Treatment of respiratory infection with a TLR2 agonist). It is currently being used in a Phase 2 trial of intranasal vaccination to prevent COVID-19 with the AstraZeneca antigen (Deliyannis et al 2021). A better antigen could be an inactivated virus such as Sinovac as many more epitopes would be delivered than with AstraZeneca's viral vector containing just the SARS-CoV-2 spike protein.

Two recent papers in experiments in mice (a small mammal with an immune system similar to, but not identical to, humans in principle) involving intra-nasal vaccine development and assessment of efficacy in protection from disease, have now been published in December 2021. Xaio et al 2021 created a defective or harmless coronavirus that cannot replicate properly, and delivered it via the intra-nasal route so as to induce both Innate Immunity (to *any other* viral challenge oro-nasal) and Adaptive Immunity (that is antigen specific secretory IgA). In the other study Oh et al 2021 set up intranasal priming with influenza infection or with adjuvanted recombinant neuraminidase flu vaccine. This induced local lung-resident B cell populations that secrete protective mucosal antiviral secretory IgA. In these complimentary studies, using these different intra-nasal, mucosal lining activation strategies the workers induced both elevated *pan-specific* Innate Immunity as recommended by Netea et al 2020 protecting against many other unrelated respiratory track pathogens, but also the necessary dimeric secretory IgA *adaptive specific immunity* akin to more tradition vaccination strategies.

We would argue that studies such as these offer the hope that can now look forward to the production of easily delivered, safe and effective vaccines against many epidemic respiratory viruses, irrespective of variant or viral type, so we will be well armed in advance of the next pandemic of respiratory tract infections. This would represent a real scientific advance and a saving grace for humanity.

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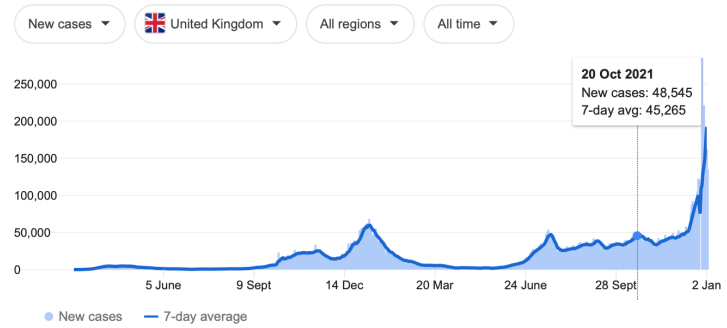
United Kingdom



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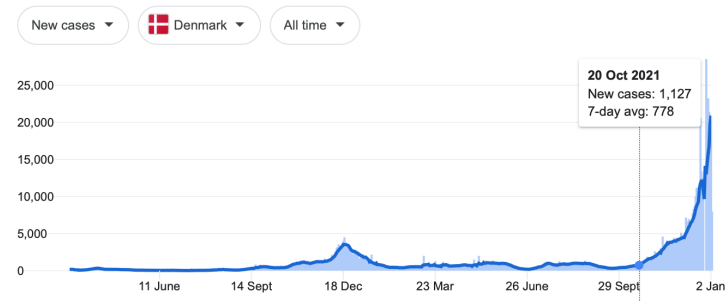

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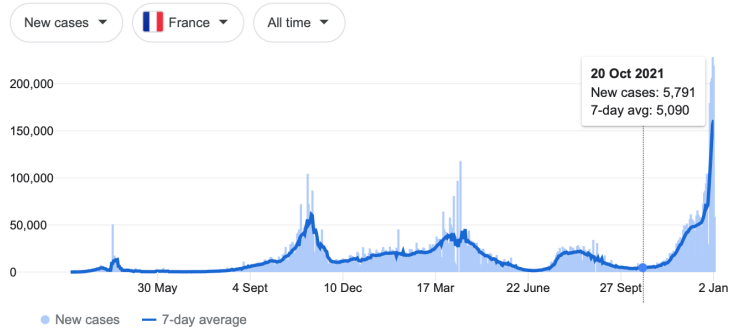

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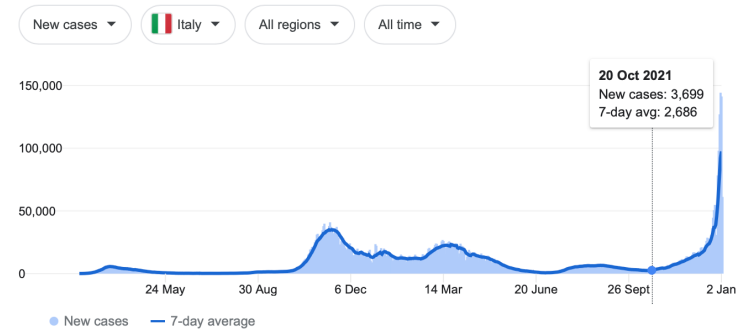
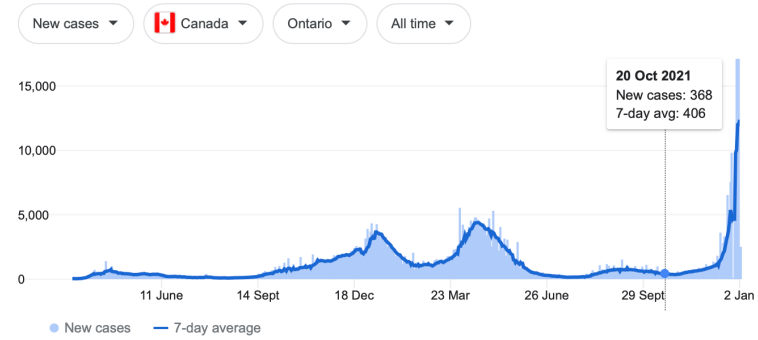


Figure 1 COVID-19 Case Rises in Selected Global Locations- Europe : United Kingdom, Denmark, France, Italy. Exponential rises in new COVID-19 cases per day as captured January 3 2022 from the Google searched site : "**Coronavirus disease statistics**". The URL opens at the Australia dashboard but all countries and regions can be searched via the Cases and Deaths search Menus for that region. Click or copy and paste URL into your browser : https://www.google.com.au/search?hl=en&ei=vWxyX7ipM4-m9QP18If4CQ&q=Coronavirus+disease+statistics&oq=Coronavirus+disease+statistics&gs_lcp=CgZwc3ktYWIQAzICCAAyAggAOgQIABBHOgcIABCxAxBDOgQIABBDULZUWPh1YJF7aABwAXgAgAH2AYgBvA6SAQYwLjEwLjGYAQCgAQGqAQdnd3Mtd2l6yAEGwAEB&sclient=psy-ab&ved=0ahUKEwj4-47e-4zsAhUPU30KHXX4AZ8Q4dUDCAw&uact=5

Canada - Ontario



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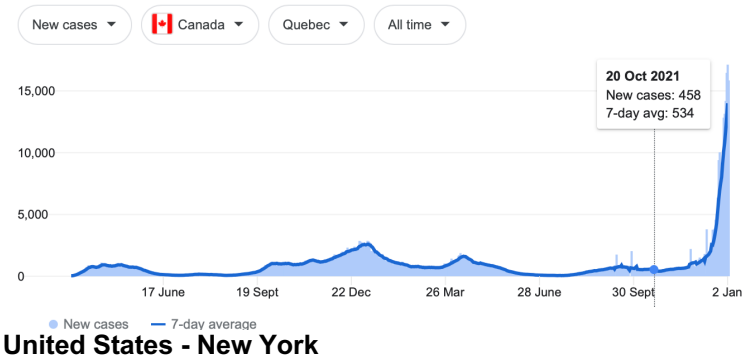


United States - New York

United States - Florida

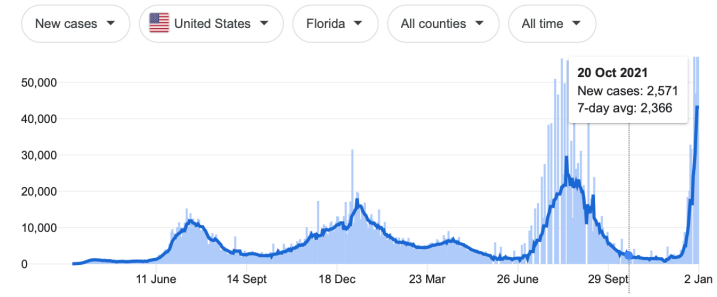
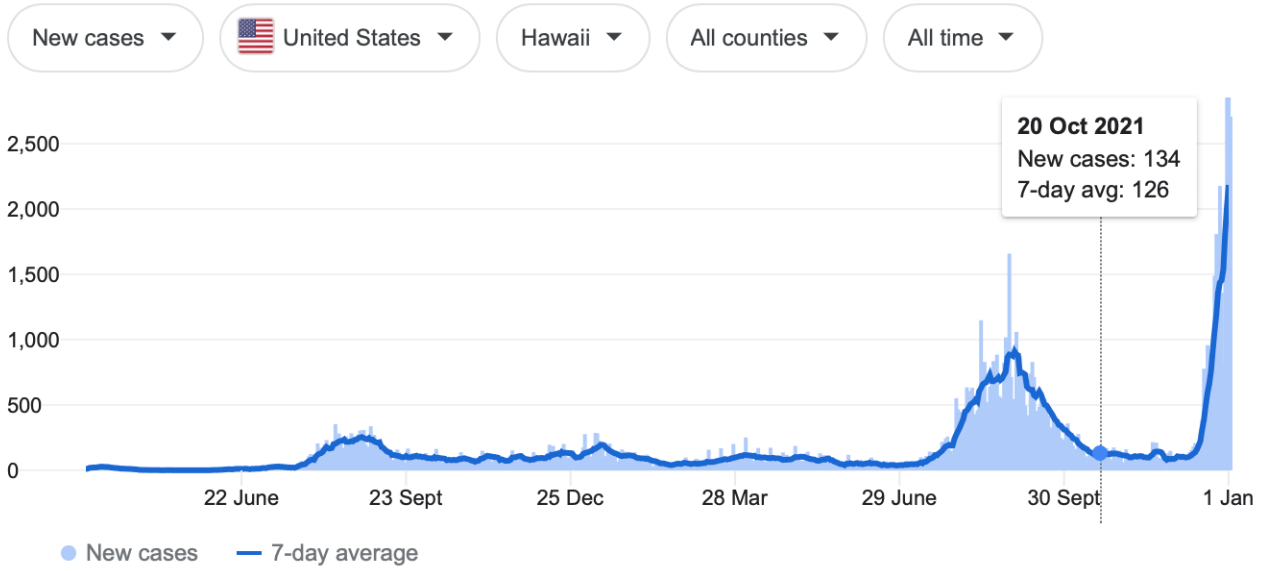


Figure 2 COVID-19 Case Rises in Selected Global Locations- Canada and USA: Ontario, Quebec, New York, Florida . Exponential rises in new COVID-19 cases per day as captured January 3 2022 from the Google searched site : "**Coronavirus disease statistics**". The URL opens at the Australia dashboard but all countries and regions can be searched via the Cases and Deaths search Menus for that region. Click or copy and paste URL into your browser : https://www.google.com.au/search?hl=en&ei=vWxyX7ipM4-m9QP18If4CQ&q=Coronavirus+disease+statistics&oq=Coronavirus+disease+statistics&gs_lcp=CgZwc3ktYWIQAzICCAAyAggAOgQIABBHOgcIABCxAxBDOgQIABBDULZUWPh1YJF7aABwAXgAgAH2AYgBvA6SAQYwLjEwLjGYAQCgAQGqAQdnd3Mtd2l6yAEGwAEB&sclient=psy-ab&ved=0ahUKEwj4-47e-4zsAhUPU30KHXX4AZ8Q4dUDCAw&uact=5

United States - Hawaii



Aruba (island state in Caribbean**)**

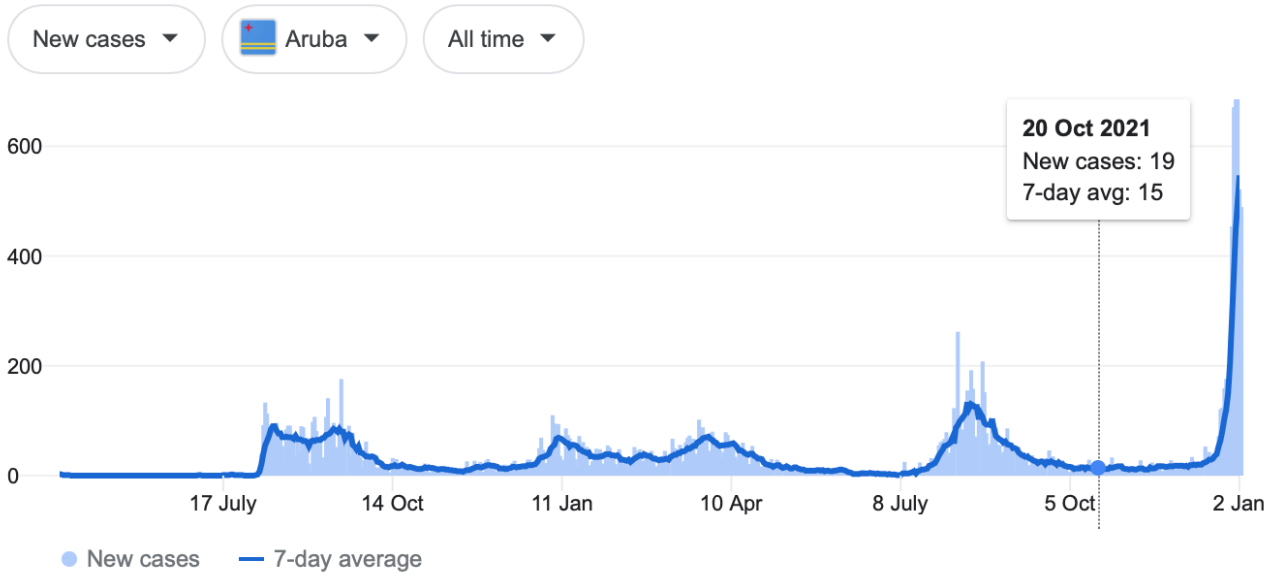
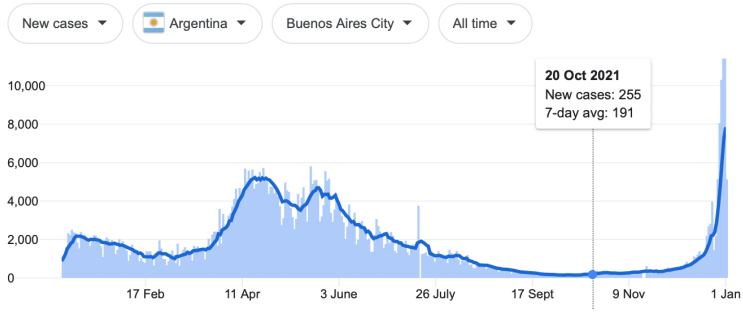
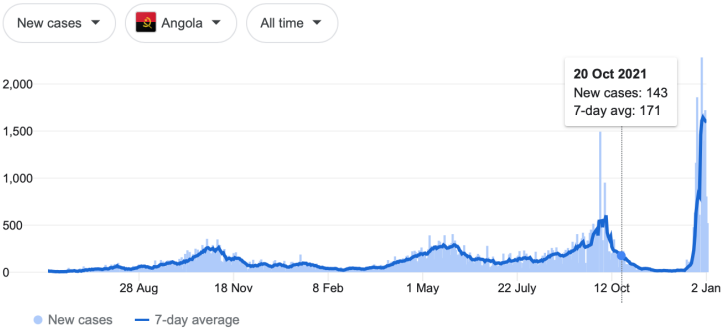


Figure 3 COVID-19 Case Rises in Selected Global Locations- Hawaii and Aruba . Exponential rises in new COVID-19 cases per day as captured January 3 2022 from the Google searched site : "**Coronavirus disease statistics**". The URL opens at the Australia dashboard but all countries and regions can be searched via the Cases and Deaths search Menus for that region. Click or copy and paste URL into your browser : https://www.google.com.au/search?hl=en&ei=vWxyX7ipM4-m9QP18If4CQ&q=Coronavirus+disease+statistics&oq=Coronavirus+disease+statistics&gs_lcp=CgZwc3ktYWIQAzICCAAyAggAOgQIABBHOgcIABCxAxBDOgQIABBDULZUWPh1YJF7aABwAXgAgAH2AYgBvA6SAQYwLjEwLjGYAQCgAQGqAQdnd3Mtd2l6yAEGwAEB&sclient=psy-ab&ved=0ahUKEwj4-47e-4zsAhUPU30KHXX4AZ8Q4dUDCAw&uact=5

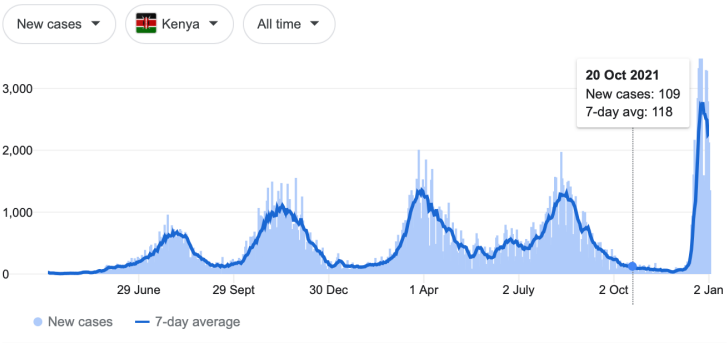
South America- Argentina, Buenos Aires City



Africa - Angola



Africa - Kenya



Africa - Mozambique

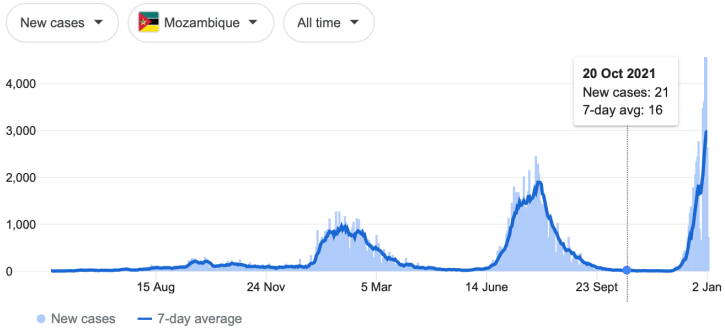
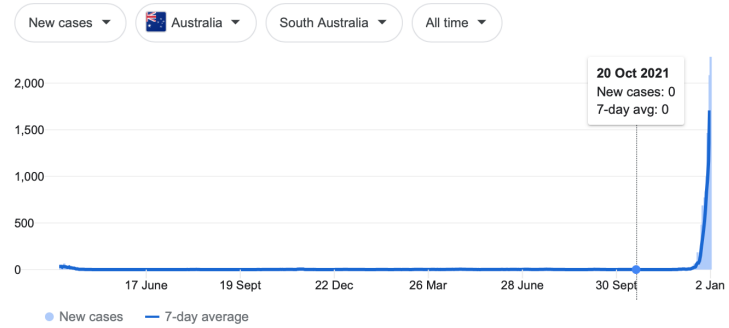
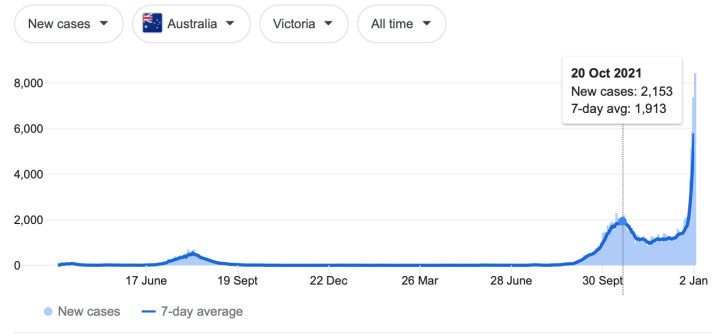


Figure 4 COVID-19 Case Rises in Selected Global Locations- South America and Africa : Buenos Aires, Angola, Kenya, Mozambique. Exponential rises in new COVID-19 cases per day as captured January 3 2022 from the Google searched site : "**Coronavirus disease statistics**". The URL opens at the Australia dashboard but all countries and regions can be searched via the Cases and Deaths search Menus for that region. Click or copy and paste URL into your browser : https://www.google.com.au/search?hl=en&ei=vWxyX7ipM4-m9QP18If4CQ&q=Coronavirus+disease+statistics&oq=Coronavirus+disease+statistics&gs_lcp=CgZwc3ktYWIQAzICCAAyAggAOgQIABBHOgcIABCxAxBDOgQIABBDULZUWPh1YJF7aABwAXgAgAH2AYgBvA6SAQYwLjEwLjGYAQCgAQGqAQdnd3Mtd2l6yAEGwAEB&sclient=psy-ab&ved=0ahUKEwj4-47e-4zsAhUPU30KHXX4AZ8Q4dUDCAw&uact=5

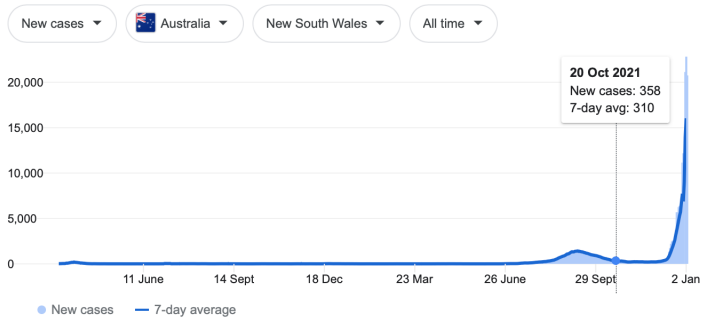
Australia – South Australia



Australia – Victoria



Australia – New South Wales



Australia – Queensland

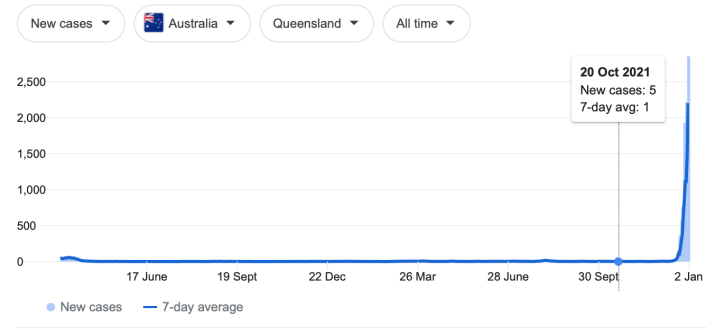


Figure 5 COVID-19 Case Rises in Selected Global Locations- Australia : South Australia, Victoria, New South Wales, Queensland . Exponential rises in new COVID-19 cases per day as captured January 3 2022 from the Google searched site : "**Coronavirus disease statistics**". The URL opens at the Australia dashboard but all countries and regions can be searched via the Cases and Deaths search Menus for that region. Click or copy and paste URL into your browser : https://www.google.com.au/search?hl=en&ei=vWxyX7ipM4-m9QP18If4CQ&q=Coronavirus+disease+statistics&oq=Coronavirus+disease+statistics&gs_lcp=CgZwc3ktYWIQAzICCAAyAggAOgQIABBHOgcIABCxAxBDOgQIABBDULZUWPh1YJF7aABwAXgAgAH2AYgBvA6SAQYwLjEwLjGYAQCgAQGqAQdnd3Mtd2l6yAEGwAEB&sclient=psy-ab&ved=0ahUKEwj4-47e-4zsAhUPU30KHXX4AZ8Q4dUDCAw&uact=5

Table 1. Countries and Regions all showing clear Synchronous Epidemics as shown in Figures 1-5 as captured January 3 2022 (use URL Fig.1-5)

Albania, Angola, Argentina (Buenos Aires City and Region in main), **Aruba, Australia** (SA, Vic, NSW, Tas, Qld but not WA, NT, the latter could be airplane visitors), **Barbados, Belize, Bermuda, Bolivia, Botswana, British Virgin Islands, Burundi, Canada** (Alberta, British Columbia, Manitoba, New Brunswick, Newfoundland and Labrador, Northwest Territories, Nova Scotia, Ontario, Prince Edward Island, Quebec, Saskatchewan), **Cape Verde, Cayman Islands**, **Comoros, Cote d'Ivoire, Croatia, Curacao**, **Cyprus, Denmark, Dominion Republic, Ecuador, Ethiopia, Faroe Islands, Fiji, Finland, France, Gabon, Ghana, Gibralter, Greece, Guinea, Guyana, Iceland, Ireland**, **Israel, Italy, Jamacia, Kenya, Kuwait, Lebanon, Luxemburg, Madagascar, Malawi, Mali, Malta, Mauritania, Mexico, Montenegro, Mozambique, Netherlands, Panama, Peru, Portugal, Qatar, Reunion, Rwanda, Saint Barthelemy, Sait Kitts and Novis, San Marino, Sierra Leone, Sint Maarten, South Sudan** (coming down rapidly)**, Spain, Sweden, Switzerland, Togo, Uganda, United Arab Emirates, United Kingdom** (England, Northern Ireland, Scotland, Wales), **United States** (Alabama, Arkansas, California, Colorado, Connecticut, Delaware, Florida, Georgia, Hawaii, Illinois, Louisiana, Massachusetts, Mississippi, Nevada, New Jersey, New York, North Carolina, Ohio, Oregon, Pennsylvania, Puerto Rico, Rhode Island, South Carolina, Tennessee, Texas, US Virgin Islands, Virginia, Washington, Washington D.C.), **Zambia,**

Table 2. Countries and Regions showing only a Low or Equivocal Synchronous Epidemics as shown in Figures 1-5 as captured January 3 2022 (use URL Fig.1-5)

Andorra, Algeria, Austria, Bahrain, Belgium, Bulgaria, Burkina Faso, Caribbean Netherland,Canada (Nanvut), **Chad**, **Columbia, Estonia, Greenland, Grenada, Hong Long, Latvia, Liberia, Mauritius, Mayotte, Monaco, Morocco, Niger, Saint Lucia, Saint Martin, Sao Tome and Principe, Saudi Arabia, Serbia, Senegal, Seychelles, Suriname, The Bahamas** (Visitors from infected zones?), **Turkey, Turks and Caicos Islands, United States** (Indiana, Kansas, Kentucky, Michigan, Minnesota, Nebraska, New Hampshire, North Dakota, Northern Mariana Islands, Oklahoma, Utah, Vermont, West Virginia, Wisconsin), **Uruguay**

Table 3. Countries and Regions all showing an explosive epidemic begining a week or two earlier relative to those shown in Fig 1-5 as captured January 3 2022 (use URL Fig.1-5)

Namibia, Nigeria, Norway, South Africa, South Korea, Trinidad and Tobago, Zimbabwe

Table 4. Countries and Regions all showing no explosive epidemic or obvious begining a week or two earlier as Fig 1-5 as captured January 3 2022 (use URL Fig.1-5)

Afghanistan ,Anguilla, Antigua and Barbuda, Armenia, Azerbaijan, Bangladesh, Belarus, Benin, Bhutan, Bosnia and Herzegovina, Brazil, Brunei, Cambodia, Cameroon, Central Africa Republic, Chile, China , Dominica, Egypt, El Salvador, Equatorial Guinea, Eswatini, Falkland Islands, French Guinea, French Polynesia, Guadeloupe, Guatemala, Guernsey, Guinea-Bissau, Haiti, Honduras, India, Indonesia, Iran, Iraq, Isle of Man, Japan, Jersey, Jordan, Kazakhstan, Kosovo, Kyrgyzstan, Laos, Lesotho, Libya, Liechtenstein, Lithuania, Macao, Malaysia, Maldives, Martinique, Moldova, Mongolia, Montserrat, Myanmar, Nepal, New Caledonia, New Zealand, Nicaragua, North Macedonia, Oman, Pakistan, Palestine, Philippines, Poland, Republic of Congo, Romania, Russia, Saint Pierre and Miquelon, Saint Vincent and the Grenadines, Singapore, Slovakia, Somalia, Slovenia, Sri Lanka, Sudan, Syria, Taiwan, Tajikistan, Tanzania , Thailand, The Gambia, Timor-Leste, Tunisia, Ukraine, United States (American Samoa, Guam, Iowa-maybe a little earlier?), **Uzbekistan, Venezuela, Vatican City, Vietnam, Yemen.**