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COVID Awareness Issue

Climate Change and Covid-19: is the Pandemic Really a Surprise?

Dr. Ritu Malani*

*Corresponding Author: Dr. Ritu Malani
- Director and Consultant Pulmonologist and Allergy Specialist (MediCasa, New Delhi)
- Consultant Allergy and Asthma Clinic (Max Healthcare, New Delhi). India

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Walking towards the school gate, as I adjusted the N99 mask on my four-year old's face, I felt deeply disturbed. The AQI numbers in New Delhi had soared to hazardous levels and the air pollution was causing worrisome adverse effects on the tiny lungs of our children.

Pollution was not the sole cause of anxiety. The extreme weather conditions, the rise of vector-borne diseases like dengue and chikungunya, the continuing emergence of novel viral infections, the increasing resistance of infectious agents to medications….everything was pointing towards an extremely grim future in the world of health. The thought of our children being the bearers of such a future perplexed me, both as a mother and as a pulmonologist.

Thus, started my exploration of the obvious, yet oft-ignored, changes taking place in our ecosystems and led me to my research on climate change.

According to scientists at NASA's GISS (Goddard Institute for Space Studies, NYC), (NASA, 2020), the average global temperature has risen by 1°C since the pre-industrial era (1890), and with the current rate of rising of 0.2°C per decade, we may soon reach an irreversible level (2.5°C above pre-industrial average). Greenhouse gases like water vapor, carbon dioxide, methane, ozone, fluorinated gases, etc., contribute to 95% of global warming. The levels of these gases in the atmosphere are rising alarmingly

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due to human activities like fossil fuel combustion, waste, and crop burning, biomass burning, etc. **(**Asrar S, 2019; IPCC, 2020; Goosse et al, 2008-2010**)**

The exploitation of land by humans for agricultural expansion, livestock ranching, urbanization, and the lumbar industry is also promoting climate change and global warming in myriad ways - by loss of terrestrial, aquatic, and soil biodiversity, decrease in atmospheric carbon sequestration, change in patterns of precipitation, change in temperature regulation, decrease in albedo effects and so on.

This global warming is causing the melting of ice masses in Greenland, Antarctica, and Arctic regions, the rise of sea levels, and major alterations in regional precipitation patterns the world over, resulting in unprecedented and extreme weather conditions - heat waves, droughts, wildfires, earthquakes, floods, tsunamis, and snow-storms. **(**Goosse et al, 2008-2010**)**. The European heatwave in 2003, which killed 70,000 people, the Indian Ocean earthquake in 2004 that killed 2,27,000 people, Cyclone Nargis in Myanmar in 2008 which killed 1,38,000 people, the earthquake in Haiti in 2010 that killed 3,00,000 people are but a few examples. There have been many more such natural calamities from 2010 until now; Indian floods, Brazilian wildfires, and Australian bushfires being the most recent ones. **(**Ritchie, H et al, 2014; Pedley, D, 2010**)**.

The direct effects of climate change on our health are easy to guess. Natural calamities are leading to deaths and displacements, food-borne, water-borne and vector-borne diseases, malnutrition, mental health issues, etc. Extreme temperatures are causing heat strokes, respiratory, cardiovascular, and renal diseases. Greenhouse effects are leading to air pollution-related diseases. (WHO, 2003; NIEHS; 2019).

But what is more important and less obvious is the gradual and persistent damage that is being caused by climate change to the natural habitats and ecosystems of the world, and its quiet, devastating effects on our health.

Think about it.....why are we having newer and frequent viral infections to deal with? Why are our children falling sick so often? Why is every simple viral cough leading to bronchitis? Why is the prescription of anti-inflammatory inhalers, medicines that should be reserved for asthmatics and patients with bronchitis, increasing rampantly?

CLIMATE CHANGE, HUMAN BEHAVIOUR, AND EMERGING INFECTIONS

Stephen Morse, in the book *Microbial Evolution and Co-adaptation* **(**Institute of Medicine (US) Forum on Microbial Threats, 2009**)** defines "emerging infections" as infections that are rapidly increasing in incidence or geographic range. These include a novel, previously unrecognized infections like HIV/AIDS, SARS, Ebola viral disease, etc, as well as "re-emerging infections", i.e. forgotten infections of the past that reappear, like diphtheria, which re-appeared in Russia in 1990 due to lack of immunization.

Out of the 1399 recognized pathogens that infect humans, 87 species have been recognized since 1980 and are currently designated as the "novel" pathogens. Though novel, they have existed in nature for decades; and it is only now that, due to the disruptive effects of climate change and human behavioural change, they are being forced out of their natural habitats of wild forests and deep seas, to interact with humans and cause sickness.

We now know that 75% of the pathogens which cause emerging infections are zoonotic, i.e they exist in animals but can infect humans. Four characteristics have been found common in them: they are mostly RNA viruses, have non-human animal reservoirs, have a broad host range, and have some potential for human to human transmission; all the attributes that, as we will learn later, give them the ability to cause outbreaks, epidemics or even pandemics. **(**Woolhouse et al, 2009**)**

• Loss of Biodiversity: "The Dilution Effect"

When imbalances in an ecosystem occur through climate change and land loss, there is extinction or relocation of native species, a predominance of invasive species, and loss of biodiversity.

As published in *The Lancet* (Ostfeld, R S, 2017), burgeoning research has shown that high biodiversity in an ecosystem reduces the rates of pathogen transmission. Most pathogens infect more than one species of host. The species that are most likely to acquire and transmit infection (the so-called reservoir hosts) are those that are abundant and resilient to anthropogenic perturbations. Consequently, when diversity is reduced, these reservoir species increase in abundance relative to other species. If multiple species are living in ecological communities with high diversity, they tend to dilute the effect of the reservoir species and thereby reduce disease risk, the so-called "dilution effect".

An article published in *Nature* (Gilbert, N, 2010) reviewed analyses studies of 12 emerging infections in widespread ecosystems. In one study conducted in Oregon in the USA, researchers found that the prevalence of the Sin Nombre hantavirus in the deer mouse (the reservoir host) increased from 2% to

14% as the diversity of the mammalian species declined in the area. In another study conducted in Panama, researchers experimentally reduced the diversity of small mammals on several study plots and found that the number of reservoir host species to hantavirus increased in all plots (65 vs 48%), as also their seroprevalence rate (25% vs 14%) and their seroconversion rate (85%). Similarly, three separate investigations done on the West Nile virus showed strong links between low bird diversity (its reservoir host) and increased incidence of West Nile encephalitis in the USA.

• Migration of Species

Weather pattern changes and global warming cause many wildlife species to migrate away from the equator and toward higher altitudes, bringing them in contact with new pathogens, to which they have not evolved resistance. The migration also causes stress and immunosuppression in these animals and makes them more susceptible to infection. The climate crisis will also force humans to migrate, likely in patterns paralleling other animal species, thereby increasing their interactions with them. (Morse, S, 2009).

• Contact with Humans

The disruption of pristine forests by anthropogenic activities like logging, mining, road building, urbanization, and livestock ranching as well as population growth brings people into closer contact with forest species and increases the interaction between humans, livestock, and wildlife. Major landscape changes also cause animals to lose their habitats and migrate to areas that are closer to human settlements.

Ebola viral disease, Kyasanur forest disease, Lyme disease, Rift valley fever, Schistosomiasis, and Nipah virus encephalitis are some of the infections that have emerged as a result of an increased host to human interactions secondary to such anthropogenic activities. **(**Daszak et al, 2009**)**.

Since the 1970s, there have been sporadic outbreaks of Ebola viral disease in tropical regions of Africa, but epidemiological data suggest that the Ebola virus existed long before these outbreaks occurred. Increased interaction of local population with fruit bats (the reservoir hosts of Ebola virus) due to population growth, encroachment into forest areas, and hunting of wildlife for bush meat consumption have contributed to its emergence. The 2013-2016 epidemic in West Africa represents the largest Ebola outbreak. The index case was believed to be a two-year-old boy who lived in a village in Guinea, and whose house was in the vicinity of a forest that was inhabited by a large colony of Angolan bats.

Kyasanur forest disease (KFD) or monkey fever was once limited to the Western Ghats of Karnataka in India, but, for the last five years, cases have been reported from several adjacent states as well. This has been attributed to deforestation and the conversion of forest land into cashew and coffee plantations and paddy fields, which has brought the locals in closer contact with forest monkeys (the reservoir hosts of the KFD virus). (Morse, S, 2009).

• Intermediate and Amplifier Hosts

Intermediate and amplifier hosts also bring viruses existing naturally in wildlife species into close contact with recipient hosts; this mode of transmission has increased due to the practice of livestock ranching near forest areas and due to the practice of bushmeat consumption. For example, the emergence of the Nipah virus in Malaysia was facilitated by intensive pig farming around forests. Fruit bats, the natural reservoirs of the Nipah virus, were attracted from the forests to the fruit orchards around the piggeries, allowing spillovers of the virus from the bats to the pigs and then to humans. Similarly, the SARS-CoV originated in wild bats and infected humans through the infection of farmed civet cats and civet cats sold for bushmeat consumption. **(**Daszak et al, 2009**)**

• The Market Connection

In informal “wet” markets that provide fresh meat to urban populations around the world, animals are slaughtered, cut up, and sold on the spot. The wet market in Wuhan, believed to be the starting point of the current COVID-19 pandemic, was known to sell numerous wild animals, including live pangolins, wolf pups, salamanders, crocodiles, scorpions, foxes, civets, and turtles. Wet markets in Africa sell monkeys, bats, rats, birds, insects, and rodents. Wet markets are a perfect platform for cross-species transmission of pathogens. Whenever a chance for novel interactions with a range of species in one place is available, whether it is in a natural environment like a forest or a wet market, a spill over event can happen. (Webster, R.G, 2004). This was also the mode of transmission proposed for the SARS outbreak; 39% of the early cases of SARS were wildlife food handlers. **(**Xu et al, 2014**)**.

• Inter-Species Transmission

Significant biological barriers prevent organisms from jumping from one host to another. To infect a new host, a virus must be able to efficiently enter the appropriate cells of the new host and that process can be restricted at many levels like receptor binding at the cell wall, entry into the cell, trafficking within the cell, genome replication, and gene expression. Each host barrier would require one or more corresponding genetic changes in the virus for the virus to overcome it.

RNA viruses, especially single-stranded RNA viruses, a category to which most of the 'novel' viruses belong, are rapidly replicating viruses. This rapid replication is prone to errors due to the lack of a proofreading mechanism, which makes these viruses capable of random mutations and thereby of host shifting. For many such viruses, recombination and re-assortment allow the acquisition of multiple genetic changes in a single step, e.g. the 1957 H2N2 and 1968 H3N2 influenza A pandemic viruses, in which new avian genome segments were imported into the backbone of 1918-descended H1N1 viruses by reassortment. For SARS CoV-2 also, it is believed that the receptor-binding motif, which controls specific ACE2 receptor binding in humans, has been acquired from a group 1 CoV by recombination. **(**Holmes et al, 2009**)**.

The species barrier between humans and other mammals may not, however, be as profound as is sometimes implied, as we share more than half our pathogens with other mammalian species and also some with birds.

The preexisting host range of a virus can also influence its ability to shift to additional hosts. Most of the novel viruses are "generalist" viruses that infect many different hosts, hence jumping into newer species is easier for them.

• Human Transmission

Most viruses transferred to humans from animals are poorly adapted, poorly replicated, and inefficiently transmitted; so fortunately for us, most of them cause limited outbreaks. Out of the 1399 human pathogens that we recognize, about 500 are transmissible between humans; and about 100-150 are capable of being sufficiently transmissible to cause epidemics or pandemics. **(**Woolhouse et al, 2009**)**.

A high level of viral genetic variation is required both for the adaptation of the virus to the new host and for further transmission within the new population. For example, extensive secondary re-assortments in the H3N2 influenza virus occurred after its transfer from avian to human hosts, which facilitated its transmission among humans, leading to the 1968 influenza pandemic. Such similar re-assortments were also seen in the SARS-CoV virus (and now in the SARS-CoV-2 virus), making them highly transmissible between humans. **(**Holmes et al, 2009**)**

• Human behavioral changes

Modern changes in human behaviour and lifestyle, like international travel, urbanization, practices of sexual contact, international trade of wildlife, etc, have further facilitated human transmission. (Morse, S, 2009).

COVID 19: WHAT DO WE KNOW?

On December 30th, 2019, The Wuhan Centre for Disease Control and Prevention detected a novel coronavirus in two hospital patients with atypical pneumonia. It sent the samples to the Wuhan Institute of Virology for further investigation. The genomic sequence of the virus, eventually named SARS-CoV-2, was 96% identical to that of a coronavirus identified in horseshoe bats in a bat-cave in Yunnan during virus-hunting expeditions. It belonged to the SARS group of coronaviruses. (Qui, J, 2020).

The expeditions had been carried out by the Director of the Centre for Emerging Infectious Diseases at the Wuhan Laboratory, Shi Zhengli (nicknamed "China's Bat-woman") and her team, from 2004 for over 16 years, in an attempt to isolate the SARS coronavirus. They had discovered hundreds of bat-borne coronaviruses with incredible genetic diversity in bat-caves deep inside forests. In bat dwellings, the constant mixing of different viruses creates a great opportunity for dangerous new pathogens to emerge and the bats turn into flying factories of new viruses.

But bats were not present at the Wuhan wet market. The wild pangolin sold for its exotic meat and its medicinal scales, became suspect as an intermediate host when a SARS-CoV-2 like coronavirus was discovered in pangolins that were seized in illegal trade markets in Southern China.

Whether or not the SARS-CoV-2 was accidentally or deliberately released from the Wuhan Laboratory is a debate not proven. None of the coronaviruses that were understudy in this laboratory were identical to the SARS-CoV-2 virus. Also, researchers believe that the spike proteins present on the viral surface that target the ACE2 receptors on human cells, are so effective in binding the virus to the cells that they could have developed only by natural selection, and not by genetic engineering. When computer simulations were carried out, the mutations in the SARS-CoV-2 genome did not work well in binding the virus to human cells, leading to the argument that if scientists were to deliberately engineer the virus, they would not choose mutations that computer models suggested did not work.

Whatever the origin of the virus, the response to develop what is needed to control the present outbreak remains the same; as do the policies needed to prevent future such outbreaks.

A recent analysis done in China estimates that there are now more than 30 strains of the virus spread across the globe; meaning that it has already mutated 30 times, which filters down to roughly one mutation every 2 weeks. (Yao, H et al, 2020). More studies are needed to determine the effects of these mutations on the virulence and transmissibility of the virus, but going by the rapidity with which COVID 19 is taking over the world, it should be an easy guess.

So really, is the COVID 19 pandemic a surprise? Not at all …it was coming ….and so will others.

COVID 19 has thrown us into a world of turmoil and uncertainty. The impacts on health and the economy have been devastating. The only thing that is flourishing….is Nature! Maybe Nature will make us see what innumerable climate-related world conferences could not. It is there for us to appreciate in its full glory - the blue skies, the clean air, the blooming flowers, the variety of birds, and the wild creatures returning to claim the land that was once theirs!

Nature is sending us a message. Please heed it!

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