

Biodiversity Loss and Emergence of Infectious Diseases

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Editor's Note: In an informal Zoom conversation in the first week of April 2020, the Editor learned from his fellow Rockefeller Bellagio Centre Resident, Dr Chris Breyer, Professor of Epidemiology at the Johns Hopkins University, USA, that there has been extensive literature in the public domain, some as far back as 20 years ago, warning of wild-life habitat destruction by humans leading to overcrowding of earlier distinct species, leading to viruses crossing over from one specie to another. For example there are 1400 species of bats and they earlier tended to hibernate in their own colonies, one specie at a time. But due to habitat destruction, different bat species started hibernating together and this led viruses to crossover from one bat specie to another. Once they survived that jump, they these viruses were able to jump to non-bat species like pangolins. After that it was a matter of time till some of these viruses crossed over to humans.

The titles of the first two references in the article below summarise it all. The first one's (Bell, et al. 2004), title is "Animal origins of SARS coronavirus: Possible links with the international trade in small carnivores." The second article's (Carrasco-Hernandez, 2017) title is even closer to COVID's cause: "Are RNA Viruses Candidate Agents for the Next Global Pandemic? A Review". The fact that this was well known to professionals in the public health field and indeed to higher authorities raises questions about how responsive is our public policy to a possible threat, with low probability but high impact. The article below by Sahibpreet Kaur goes into the details and also covers some recommendations of experts.

The emergence of the current global pandemic caused by the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) or COVID-19 has brought the attention to the role of biodiversity in the spread of infectious diseases. The COVID-19 is a zoonotic disease, which is speculated to have crossed over to humans from bats in a wet market, where wild meat is traded in Wuhan, China in late 2019. The present COVID-19 is genetically similar to the Severe Acute Respiratory Coronavirus (SARS-CoV) epidemic of 2003 which spread to 26 countries and infected patients with similar symptoms. Both viruses are suspected to be bat-borne viruses which spread to humans via an intermediate animal reservoir, suspected to be pangolins in the case of COVID-19, although this is disputed.

The present pandemic is caused by a single strand RNA virus, originated from a wildlife reservoir, a characteristic which it shares with all recent epidemics in the past century such as the Human Immunodeficiency Virus (HIV), H1N1 influenza, the highly pathogenic H5N1 avian influenza

Nipah, Hendra, the Severe Acute Respiratory Syndrome Coronavirus and the recent Ebola virus (Feldmann 2014; Jones et al. 2008; Joseph et al. 2016). In fact, it has been estimated by the US Centre for Disease Control and Prevention that three quarters of the new and emerging infectious diseases in humans originated from 'non-human' animals. The increasing interaction with wildlife which was earlier isolated from humans due to deforestation, urban and agricultural expansion and land use change has brought upon a greater risk of transmission of unknown parasites.

Various studies have been conducted on the link between biodiversity loss and emergence of infectious diseases, establishing the importance of biodiversity in reducing the risk of infectious diseases from transmitting to humans. A study by Keesing and others (2006) states that biodiversity can buffer disease transmission by certain mechanisms- the population density of important natural reservoirs for pathogens can be reduced in high biodiversity; the population of arthropod vectors is reduced and, encounter rates between vectors and reservoirs or among reservoirs would be lesser in an region of higher biodiversity. This phenomenon of high diversity reducing disease risk is known as the dilution effect. A study by Ostfeld (2009) establishes the occurrence of dilution effect by taking the case studies of two zoonotic diseases- the Lyme disease and the West Nile virus (WNV).



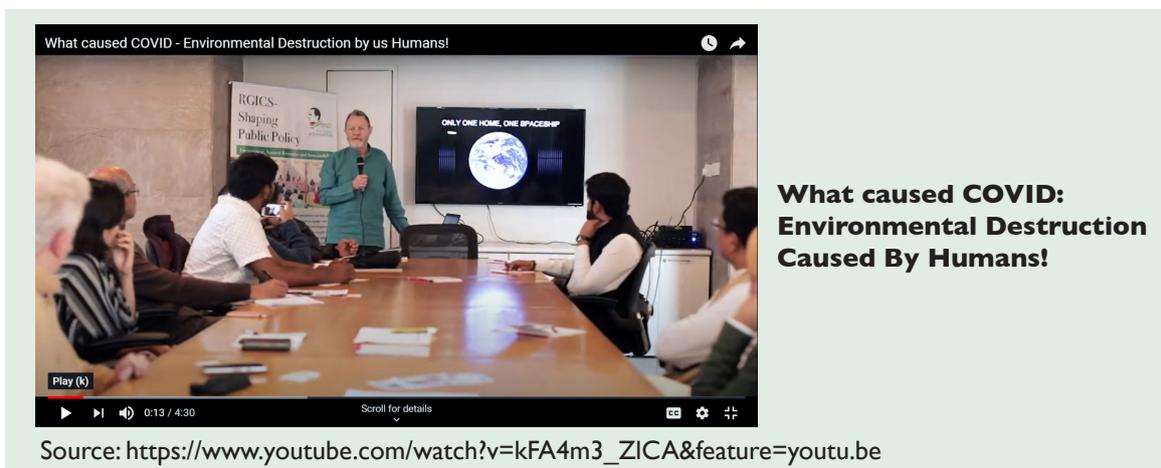
The samples from North Eastern USA on ticks occurring in high vertebrate diversity communities and low vertebrate diversity communities supported the hypothesis that high vertebrate diversity is linked to lesser incidence of Lyme disease outbreak in humans. In the case of WNV, predominant vectors are *Culex* mosquitoes and major reservoirs are passerine birds. The study hypothesized that mosquitoes found in areas of high avian diversity would be less likely to have blood meal on a competent reservoir of WNV whereas mosquitoes occurring in habitats of low avian diversity

would be more likely to get infected from a bloodmeal on a competent reservoir of the WNV. The data collected from all counties of continental USA where the WNV outbreak occurred, showed a strong negative correlation between WNV incidence in humans and bird diversity in those counties, upholding the dilution effect hypothesis.

Biotic homogenisation is also linked to increasing incidence of infectious diseases. Globalization has led to the transfer of exotic organisms from their native habitats to newer ones. These species can often be invasive and outcompete the local taxa causing a reduction in diversity of species leading to biotic homogenisation. Malaria, an infectious disease transmitted by the female anopheles mosquito, continues to infect millions in Africa and India every year. Studies have shown the impact of ecology on the mosquito. According to Yasuoka and Levins (2007), mosquito survival, density and distribution is greatly impacted by changes in plant diversity, especially through deforestation, fragmentation and habitat alteration and this may increase the risk of malaria transmission. Disease transmission is also impacted by land use change as according to a study by Walsh et al. (1993) the risk of malaria can increase with land use changes that can lead to the migration of people who are not immune to the disease, arrival of competent vectors and adaptation of vectors to newly created niches.

A study by Vittor and colleagues (2006) in Amazonian Peru showed the impact of deforestation on malarial incidence. Anopheles darlingi, the most efficient vector of malaria in the region was found in higher densities in deforested sites as compared to forested areas. The Hantavirus Pulmonary Syndrome (HPS), is caused by hantaviruses which are found in Europe, Asia and the Americas, is transmitted via rodents, with each virus species carried by a specific rodent host. A study by Ruedas and colleagues (2004) in South-eastern Panama showed that periods of unusually high rainfall and anthropogenic activities that lead to decline in biodiversity could increase the occurrence of HPS outbreaks. Other studies have also shown that in more diverse communities, with the presence of other rodent species, the hantavirus transmissions are lowered (Peixoto and Abramson, 2006; Suzan et al; 2009). In the case of WNV, a study in the Gulf Coast of Louisiana by Ezenwa et al. (2007) showed that as wetlands declined, the prevalence of WNV mosquitoes grew. As the wetlands declined, the bird composition of the area also changed, making way for more passerine birds that carry the virus. Thus, any changes in the biodiversity of an area can greatly impact the spread of viruses.

A macro study on the outbreaks of infectious diseases in Asia-Pacific by Morand et al (2014) suggested that while on one hand the region is a biodiversity hotspot from which more than a few infectious diseases emerged such as the Nipah virus, new cholera and dengue variants, on the other hand, the loss of biodiversity has further increased the number of outbreaks of infectious diseases. Thus, preserving biodiversity may moderate the spread of infectious diseases by containing pathogens and limiting interaction with humans.



Wildlife markets have emerged to be a major hotspot for spreading viruses as per the outbreak of SARS-CoV and the present COVID-19. It is suspected that the COVID-19 is a bat-borne virus. The genome of the COVID-19 virus has been found 96% identical to the virus RaTG13 which is carried by the intermediate horseshow bat as per a study published in Nature Medicine. However, it is not clear how the virus jumped to humans. Since wet markets host a number of different wild animals, in unsanitary conditions, which come in contact with each other and humans, the virus may have jumped hosts and crossed over to humans. It is suspected the same may have been carried over by pangolins who carry viruses with similar binding sequences to those in humans. Pangolins are one of the world's most trafficked mammals as their meat is consumed in many south-east Asian countries and their scales which are used in Chinese traditional medicines (Marshall 2020).

The international wildlife trade was also in part responsible for spreading SARS-CoV which emerged in China, to Vietnam and Laos (Bell et al. 2004; Grottrex et al. 2016). While wild meat consumption has been in practice in many communities living close to forests, wild meat capture took momentum as international trade commenced. The demand of wild animals is not just for meat but also for traditional medicinal purposes. Grottrex et al (2016) in their study in markets in Laos noted certain risk factors like wildlife-human contact, trade of animals carrying potential zoonotic diseases, poor biosafety and potential of diseases to spread from markets to wider population. Wildlife markets thus, could have the potential to be spaces of future epidemic outbreaks as well and need to be regulated to prevent over exploitation and limit contact between humans and disease-causing pathogens. COVID-19 is speculated to have started spreading from a wet market in Wuhan which was shut by the Chinese authorities as the virus spread rapidly in mainland China. However, as the situation came under control, the same market the virus seems to have spread from is open again.

Preventive Measures

The present pandemic has brought the world to a standstill and has had a huge impact on all major world economies. Unexpectedly, the marginalized and poor have been hit the hardest. The pandemic has made one and all introspect on the way the world functions. The SARS-CoV 2 has shown the negative impact of a globalized world, where an infectious disease starting from a market in Wuhan has spread to 126 countries within a few months, bringing almost all economic activity to a halt, with the most deleterious impact on so called developed nations. The present pandemic is not the first or last and many such infectious diseases are expected. However, the rate at which these diseases spread and affect human life have worsened as they travel faster and wider.

As stated, many of these infectious diseases emerge from our interactions with biodiversity. Anthropogenic activities such as deforestation, monoculture cultivation, migration, urban expansion and overfishing have brought pathogens closer to spaces where they can spread as infectious diseases. Pongsiri and colleagues (2009) note how global disease ecology is being driven by biodiversity loss and stress on the need for acknowledging the impact of biodiversity loss on human health while implementing policies. Below are some preventive measures in this regard-

Preservation of Biodiversity

With mounting evidence on the role of biodiversity and spread of zoonotic diseases, conservation policies need to be strengthened to avoid the risk of newer infections spilling over to humans. Global demand for resources such as minerals, wood, and clearing of forests for agriculture and cattle ranching

lead to ecological disruption and degradation of landscapes. Importance of preserving ecosystems in order to prevent the spread of zoonosis should be made a priority in national targets for the Convention of Biodiversity and part of the Sustainable Development Goals. Ecological restoration of degraded landscapes can also help in increasing biodiversity and prevention of certain diseases. Control of invasive species is also crucial in this aspect as their spread can lead to homogenization reducing diversity in the ecosystem.

Land Use Policy to Limit Interaction

Certain types of land use changes such as habitat alteration and human settlements can affect the distribution and abundance of important vector species differently. Understanding this pattern can help in recognizing landscape features and human activities such as resource extraction and outdoor recreation, that may predict risk of diseases (ibid). Land use policies should be designed to minimize interaction of important vectors and humans. For instance, in the case of Lyme disease, large forested areas could be protected in the vicinity of residential areas to reduce risk. Spatial aggregation to cluster settlements in non-forested areas and maintain contiguous forests could reduce risk of diseases that spread from small fragmented forests.

Regulation of Wet Markets and Wild Meat Consumption

Since wild meat forms an important part of people's diets and the wet markets in several countries like China, Laos, and several African countries cater to livelihood and food security of many, they need to be handled in a sensitive manner. Biosafety equipment should be made available in these markets to ensure a safe and sanitized environment. People involved in the hunt, trade and consumption of such meat such be made aware of the potential risk of zoonosis. Certain meats such as bats and rodents should be banned as research has shown they are huge reservoir hosts for various viruses as compared to other host species (Luis et al 2013; Shea et al. 2014). International trade should be discouraged as it can lead to spread of zoonosis and moreover reduces the abundance of those animals from the ecosystem, causing greater repercussions on the food web and diversity.



Behavioural Change

The prevention of infectious diseases originating from the wild also requires behavioural change of communities that reside close to buffer areas. Along with landscaping, efforts at a smaller scale such as building closed wells to prevent breeding of mosquitoes. Environmental based strategies such as applying bio controls may also help reduce risk in vector breeding sites. Biocontrols can be used specific to local ecology and can prove sustainable and cost-effective against some vectors. The dengue transmitting *Aedes aegypti* mosquito has been brought under control by using predatory fish as biological controls in Australian wells (Russell et al. 1996). In Nicaragua, China and Cameroon, incidence of malaria has been reduced with the application of the bacteria *Bacillus thuringiensis* and *Bacillus sphaericus* (Sutherst 2004).

People's use of natural areas and how their activities may expose them to disease carrying vectors should be understood to guide policies for behavioural change. Reducing access and dependence on such areas by providing substitute resources and alternate livelihoods may help in lowering risk of infections.

Economic and Political Policies for Epidemic Preparedness

While there is ongoing scientific effort on prevention control of zoonotic diseases, there is a need of simultaneous economic and political action in the same regard. Hotez (2017) suggest setting up a global fund, such as the Coalition for Epidemic Preparedness Innovations, alongside national funds from wealthy countries (G20 nations), to ensure that there is adequate funding for timely action and pharmaceutical response.

Development policies must consider the impact of human activities on biodiversity. The increasingly complex ways in which humans, domestic animals and wildlife intermingle has led to the emergence of highly infectious diseases which have cost millions of lives and multitudes of resources. The pandemic caused by COVID-19 has spread in an unprecedented manner and impacted lives unlike before and has reiterated the importance of conserving biodiversity and practising preventive measures on spreading of zoonotic diseases.

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