To what extent are humans responsible for the rise in transmission and emergence of zoonotic diseases, through the domestication of animals and increased association with the natural wildlife?

Abstract

In recent generations, there has been a dramatic rise in the number and frequency of zoonotic diseases across the world, almost quadrupling over the last century, with 60% of all current infectious diseases and viruses having originated in an animal host (Rozenbaum, 2020). The aim of this paper is to explore the ways in which humans are responsible for this rise, in terms of the factors increasing transmission and the mitigation methods to reduce it in the future. The topic has been split to look into the transmission of domestic and wild diseases separately, as they often have differing mitigation methods and factors causing them. However, as the paper progresses, it becomes clear that the two topics aren't as separable as first imagined and that they are intrinsically linked, as the global system continues to domestic animals into our homes and livestock. This has allowed me to form a clear conclusion which suggests that humans are almost entirely responsible for the increase in zoonotic diseases, and that the mitigation methods are due to a cause and effect idea where we wouldn't need to increase our efforts, if we hadn't already allowed the damage of disease spread in the first place. There are a number of potential ideas to be considered at the end of this paper (in ones daily life, as well as on a larger scale) such as veganism, which if implemented successfully, would result in a world with fewer zoonotic diseases and a decreased need for land and meat, which currently acts as a major cause of disease spread.

Introduction

A zoonotic disease is an infectious disease that is transmitted between species from animals to humans or visa versa and can be spread via a number of methods, including direct or indirect contact (One Health CDC, 2017), such as the recent COVID-19 pandemic, which jumpstarted my research into this interesting topic[1]. Animal pathogens can infect humans directly through wild or domestic animals, or they can be transmitted indirectly through a number of animals acting as intermediate hosts, which can amplify the effects or cause variations in the virus, so that it is transmissible to humans (Cui, Chen and Fan, 2017). Humans are at the root of many of the problems that are causing zoonotic diseases to spread, such as the ever increasing globalisation which brings people and trade from all across the world into new areas, subsequently risking the introduction of these diseases into the countries. Throughout this paper, I will investigate a range of different human factors which are giving rise to the increasing emergence of zoonotic diseases, as well as the methods by which we hope to reduce this risk and maintain the diseases within the animal population.

The Impacts of Human Interactions within the Wild Animal Kingdom

The transfer of zoonotic diseases from animals to humans is not a process that occurs in one motion, due to there being a plethora of different routes which such diseases can take. There are often several different stages that diseases transfer between which are dependant on the drivers, most significantly environmental (climate change), political (conflict and famine) and socio-economic (urbanisation and food preferences), causing them to pass over between different hosts. Intermediate hosts, which are organisms that harbour the parasite and allow the diseases to mutate

---

[1] Despite the COVID-19 pandemic being an excellent example of the problems that can occur as a result of wet food markets acting as a vector for zoonotic diseases, the research is new and still uncertain, with many sources stating differing statistics and explanations.

and develop, play a crucial role as they involuntarily facilitate the transfer of the pathogens and parasites between the animal ecosystems, by acting as mixing vessels for the diseases.

Figure 1 represents an overview of the driver-pathogen interactions that contribute to the emergence of infectious zoonotic diseases (Keusch et al., 2009), and signifies the important notion that there is not one sole cause for the spread of diseases across animal kingdoms.

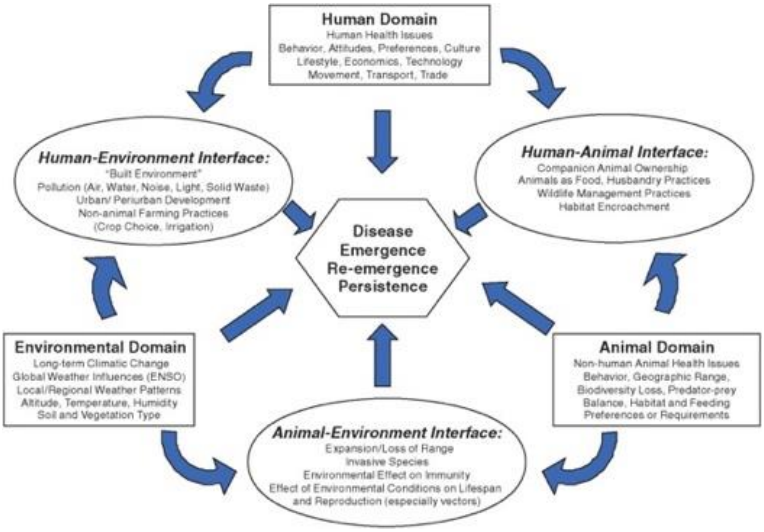

Fig.1. Disease emergence, re-emergence and persistence.

Despite there being a vast number of transmission routes and causes that result in the spread of diseases between humans and wildlife, to investigate all of these would be beyond the scope of this project, and therefore I will first look into urbanisation as I believe it is the most significant factor. Then, I will briefly look into the culture and wild animal food preferences of some societies around the world which have caused diseases, such as Ebola, to develop.

<u>Urbanisation</u>

Populations in urban areas typically have less contact with wild animals than rural populations, due to the nature of their culture, but there are some factors that will cause these groups to become more exposed to animals, via urbanisation and globalisation (*ibid*.). Globalisation is a modern process through which countries are becoming more interdependent and interlinked, creating far greater network systems of transport to countries across the world. This, therefore, brings different populations in contact with each other which causes, causing the possibility of new vectors in these densely packed regions. This is emphasised in the report of the 'Drivers of Zoonotic Diseases' which states that "Once a zoonotic disease has emerged, its spread in the human population is likely to be facilitated by the population movements" (*ibid*). For LIDC (low income developing countries)or EDC (emerging developing countries) urbanites, where they have many informal settlements and poor healthcare systems, the risk of this spread is substantial because they lack protection from common infections due to the absence of vaccinations (Naicker, 2011). According to the United Nations, the global population is increasing at an annual rate of 1.72%, with the population more than doubling in the past fifty years (United Nations, 2007). As a result, there has been significant encroachment into wildlife habitats in order to home the ever-increasing population, which in return escalates the contact that these areas are having with the natural wildlife (Naicker, 2011). This has been seen in Malaysia, where the transmission of Plasmodium Knowlesi from macaques to humans has risen dramatically due to deforestation and urban expansion (Singh et al., 2004). Although it may be assumed that logging decreases the biodiversity, thus also decreasing the risk of disease spread, it in fact alters the ecosystems' natural balance between diverse species, which creates new ecological niches where certain vectors can thrive (Naicker, 2011). For example, large water puddles that are created in areas with lack of tree cover, naturally have lower acidity levels due to infiltration with the soil minerals, causing hotspots for vector breeding grounds (Vora, 2008).

Moreover, culture, society, and religion all influence the kinds of foods that people eat across the world, how the food is prepared, and also the demand for these particular foods at different times (e.g., fasting or Ramadan). For example, in both China and Indonesia, a preference for the consumption of freshly slaughtered local animals such as chickens, has drawn people to "wet markets" that vend live poultry (as well as many other wild animals such as pangolins, Komodo dragons and other reptiles), with many of them being slaughtered within the buyers' home (Liu, 2008). The contact between freshly killed animals, live fowl, and their faeces (which can be contaminated with pathogens) contributes to the transmission of diseases such as SARS and Avian influenza such as H5N1 (Keusch et al., 2009). As well as the use of wet markets in these countries, bushmeat consumption, most significantly of primates, has been tied to zoonotic diseases such as HIV and Ebola (Peeters et al., 2002). Bushmeat is an essential component in many societies around the world, due to it being an inexpensive source of protein in many LIDC or indigenous areas, as well as the cultural significance of some animals which means that they are a sought-after delicacy among the tribes (Keusch et al., 2009). However, 90% of all bushmeat moves through an organised chain of supply, with numerous interchanges, causing the meat to be in contact with many different groups of people such as hunters, bicycle traders and wholesalers who are exposed to the pathogens present from the animal's death and faeces (de Merode and Colishaw, 2006). Due to food security and preferences being a major factor in zoonotic disease spread, this is an element that I will explore in greater depth when discussing the role of domestic animals.

Ebola is an example of a zoonotic disease which was caused by the increased contact between indigenous groups and wild animals, most significantly bats and apes, in countries across Africa. It is a highly pathogenic filo virus, which causes severe hemorrhagic fever (with high mortality rates), that has been massively influenced by the use of bushmeat hunting. Upon first being discovered in 1976, it has killed almost 11,300 people with a death rate of 74.2%, despite it being extremely geographically dense within 6 main countries including Liberia, Guinea and Cameroon (Wong et al., 2016). In 2005, it was found that the fruit bat was the natural reservoir for the disease after testing was done on over 1000 small vertebrates, which found a detection of the viral RNA and anti-EBV antibodies in the bats, suggesting that they had already fought against the virus (Leroy et al., 2005). Surveys were conducted in 11 villages in Southern Cameroon which looked into the contact with bats, and it showed that 40% of correspondents consume bats with an average annual intake of 3 or more and 28% of people hunt them regularly (Baudel et al., 2019). On top of this, scavenging meat from apes in these regions was regarded as the key process of transmission from the animal kingdom to humans, showing that bushmeat consumption is a major contributor to the emergence of Ebola.

The Impacts of increased domestication on zoonotic disease transmission

Although there are still several hunter-gatherer societies around the world, there has been a modern change in agricultural systems which was accelerated by the growth of large urban areas, in addition to the 'green revolution' which further increased crop yields. (Keusch et al., 2009). Since the 1960s, the global milk production has doubled, meat production has tripled and egg production has quadrupled, indicating the extent to which we rely on livestock farming which has been caused by the introduction of large-scale corporate businesses to mass supply animal produce, further distancing us from the 'perfect' civilisations by which many generations used to live (*ibid*.). In this chapter I will focus on the impacts of intensive livestock farming, as I believe this is the greatest factor influencing transmissions of diseases between domestic animals and humans, as well as investigating the H1N1 virus which is a great example of the problems caused by livestock farming.

The explosion of the human population over the past 100 years has created an increased demand for food and caused greater land usage for livestock farming, which has disrupted the natural ecosystems by further domestication (Naicker, 2011). Furthermore, industrial farming practices have risen to compensate for this consumer demand, causing many animals (of varying species) to be farmed together. This facilitates the cross-species transmission of pathogens in these livestock areas, due to the extremely dense and compact living conditions, causing many diseases to spread exponentially (Cutler et al., 2010). These intensive methods of farming have been seen in the creation of feedlots which are used to fatten beef cattle prior to slaughter. They create high stocking areas which are home to extremely warm and crowded conditions, causing an increase in the shedding of bacteria in their faeces, further risking the spread of pathogens between animals (SaveOurAntibiotics, 2013). These living conditions create 'mixing vessels', where large number of animals, potentially of different species, remain in close contact and allow the genetic mutation of the disease, allowing it to spread to other species and humans.

Cattle, sheep, and pigs can all carry diseases such as E. coli without developing the disease themselves, which is caused by bacteria contaminating the products from faecal material in the lower gut or on the hide of the animal at slaughter (*ibid*.). Additionally, due to the use of antibiotics in livestock farming to create growth and treat infection, they are incidentally applying selective pressure, leading to the emergence of anti-microbial resistant strains, which are more dangerous if transmitted to humans as the treatment solutions are much harder to create (Schlundt et al., 2004). The greatest example of this would be the development and spread of livestock associated Methicillin-resistant Staphylococcus aureus (MRSA) throughout Europe, which was due to the porcine ST398 strains of the disease in pigs becoming resistant to the antibiotics used to prevent the illness (Naicker, 2011).

Swine flu, similarly to MRSA, clearly demonstrates the idea that domestic animals, for the most part, act as mixing vessels for disease, but also can be the initial host, due to mutations within the animal. It is a novel influenza (H1N1) virus that emerged in 2009, which has become a seasonal flu, infecting over 60 million people, and further killing just over 12,500 people (Miller, 2020). H1N1 causes upper and potentially lower respiratory tract infections in hosts, resulting in symptoms such as nasal secretions, chills, fever etc. Domestic animals normally do not act as the source of diseases, but instead they act as the intermediate host mixing vessels causing mutation and increased cross-species transmission. However, H1N1 is an example of a disease where the source animal is the domestic pig population, while also still acting as the mixing vessel for mutations and variation (Jilani, Jamie and Siddiqui, 2020). The HA and NA surface glycoproteins are the variable unit which differentiates it from other strains and diseases such as Avian flu (H5N1). The HA protein has 16 variations and the NA has 9 subtypes which is the reason for it being referred to as a reassortment virus, because it has the ability to mutate and become compatible with a large array of different species, giving way to many different strains (*ibid*.). Swine Flu has established a stable lineage in pigs due to the receptors of the virus being found in the porcine epithelium, but it has also found a genetic mutation subtype of H1N1 that is transmissible to humans, which is why swine flu is a highly infectious virus, infecting millions worldwide (*ibid*.).

The Mitigation of Transmission from Wild Animals to Humans

When an emerging wild zoonotic disease is first detected, scientists can undertake preliminary studies into the epidemiology and ecology of the new zoonotic pathogen, by first using data and understanding from species which have similar patterns and genetics to that of the infected (Shiferaw et al., 2017). Research and surveillance can commence in this field; after identifying techniques such as sampling collection, processing and diagnostics, scientific partners can collaborate with other ministries and colleagues to create a broader spectrum of knowledge and experience across fields (*ibid.*). As a result of this initial surveillance, they should understand the geographical distribution of the disease in differing mammalian species which they can compare with the initial host, to confirm ideas on how it is transmitted and which species are most vulnerable to becoming intermediate hosts (*ibid*). Success can come in any of these approaches due to the fact that there is often no right or wrong technique during the early stages of disease identification, but many of them have their pros and cons. The key Idea that I have seen throughout my research of this project is that 'multi-sectorial' collaboration is crucial, such that the ideas of professionals in a wide range of fields can be combined to put a stop to, and find the source of, zoonotic diseases. In this chapter I will explain how the collaboration of ideas has been massively important, as seen in the prevention of monkeypox in the DRC, despite this unfortunately not being possible in many countries across the world.

Although these collaborative methods have been massively important, they are often hard to implement in wild biomes such as forests or grasslands, because these civilisations often have differing cultural beliefs and priorities, disparate legal authorisations and lack of resources which can put a halt to the development and implementation of formal techniques, which are needed in control programmes (Shiferaw et al., 2017). In addition to this, due to the lack of funding and legal schemes in these remote areas, basic necessities for these techniques such as medical and veterinary services are hard to come by, further weakening their chances of control (*ibid*). The transmission from wildlife to humans is clearly harder to regulate than that of domestic animals, as the ongoing movements of species within their ecosystems are impossible to survey at all times, even if extensive surveillance has been applied, simply due to the fact that wild animal behaviours are complex and differing. Therefore, due to the extent of the operations required, alternate options such as zoning of the most important areas (e.g. highly populated spaces) or in fact no action at all should be considered, especially in the view of cost benefit assessments of these poorer areas, despite being potentially controversial (Gortazar et al., 2015). However, I believe that disease and animal population monitoring of remote areas is still crucial, however small it may be, due to the fact that many of the modern pandemics and epidemics across the world have originated in these wild animal reservoirs, causing complex understanding of where the diseases originated and the chains of transmissions by which they have taken.

An example of a scheme which was effective in the control of zoonotic disease was the stepwise prevention of monkeypox in the Tshuapa province of DRC in 2008, which infected only 470 people (Shiferaw et al., 2017). The programme provided data collection methods and tools for monkeypox, which included training sessions for 60 local animal and human health workers for testing (Bass., et al 2013). This was extremely effective, providing 16x the amount of testing than in the initial detection, which increased the number of confirmed cases in the area by 2.5x, demonstrating how successful the scheme was, by allowing them to control the spread in infected areas (Shiferaw et al., 2017). Due to multi-sectorial relationships in this scheme, the ministry of agriculture and the ministry of health worked together to implement a ban on the sale of animal carcasses due to the idea that they were a key factor in the disease spread - information which was provided by the research (*ibid.*). As a result of this comprehensive scheme, including lab setup and sector collaboration, during the 2014 outbreak of Ebola which had major impacts across Africa, they were far more suited to the problems that arose and were much quicker in starting the defensive systems, providing long-term protection (*ibid.*). This demonstrates the mitigation of a wild disease, which has similarities to the strategies of domestic animal disease mitigation, as I will investigate in the next section

The Mitigation of Transmission from Domestic Animals to Humans

Early detection of disease within the livestock or companion animals sector, through the implementation of detection or prevention strategies, can trigger a collaborative response with the public health authorities to control the spread and stop it from moving to the human population. This collaboration is most significant in areas where humans are heavily dependant on livestock production such as the African countries of Niger, Madagascar and Malawi, with 44-79% of households keeping livestock in 2013 (Quick facts about the world's livestock economy, 2016). In addition, countries such as Argentina and Mexico, which have household ownership rates of 81.5% for domestic animals or pets, should also be considered, as the probability of infection from diseases common in domestic animals is heightened (Petfoodindustry, 2016). As briefly discussed before, the transmission of disease in domestic animal populations is clearly easier to regulate than the wildlife due to the contained and controlled methods of handling the livestock/pets, which provides opportunities for the public health and veterinary scientists to give input into the course of action such as vaccination or measures to stop the spread (Gortazar et al., 2015). In this chapter, I will discuss how a number of techniques such as farm-bio security and small-scale fencing are important in livestock control, as well as the methods which were used to control rabies in Ethiopia.

Farm-bio security is becoming an important and more widely implemented method of prevention for infectious disease transmission, as well as cross-species interactions (Engeman et al., 2011). For example, industrial poultry farms continue to maintain a relatively low level of disease due to the fact that they are effectively separated from the, possibly infected, wildlife by physical barriers such as fencing (Gortazar et al., 2015). In recent years, the UK have introduced simple exclusion measures such as sheet-metal gates, fencing and feed bins which have been 100% effective in preventing the Eurasian badger species from entering the buildings and farm areas, which had previously been a major transmission route for diseases entering the livestock vessels (*ibid.*). This demonstrates how simple it is to implement these defensive systems and how effective they are in halting the disease at the source and preventing spread. The dispersal or modification of current feeding systems in farms, which are the key areas for mixing of animals due to saliva residue and faeces, is another simple method that can be used to create 'selective feeders', which are only accessible to certain species (*ibid.*). By doing this, it will reduce the amount of contact between the animals, which subsequently reduces the threat of disease spread into different hosts, allowing specific species to be isolated rather than the whole farm, which would cause a major decline in income. Changes in husbandry can provide many possibilities in dealing with bio security, because veterinary agencies can substitute animals which are less susceptible to specific diseases into farms where it is endemic, to reduce the risk for other species (Ward et al., 2009) – for example, horses are far less likely to contract TB than sheep and other cattle, so therefore they can relocate horses into these areas or breed species together, to minimise disease spread (Gortazar et al., 2015).

One-sided disease retention, which is when the control and prevention process only focuses on one area of concern, is often an insufficient approach because in many developing countries where diseases such as rabies are still endemic, they often only look into human vaccination as it's the most obvious way to prevent human death (Shiferaw et al., 2017). However, the most successful and cost-effective method would be to create vaccines for domestic dogs, because they wouldn't need as much and this would eliminate the disease at the source (Lembo, 2012). This was achieved in Ethiopia in 2015, where a comprehensive scheme was made which involved a number of different groups such as the Ethiopian public health institute, the ministry of livestock and fisheries and the US centre for disease control, which provided a more rapid roll out of vaccinations (Shiferaw et al., 2017). The programme covered over 10.5 million people and incorporated lab-based surveillance, by sustained canine mass vaccine programmes and greater efforts surrounding the education of diseases, which was heavily supported by the government (*ibid.*). Due to this scheme and the associated international investments made, Ethiopia have created a platform to save lives in the future which has already been seen as only 1.7 people/100,000 now die of rabies each year (*ibid.*).

So, which transmission is more dangerous?

Despite the routes of transmission seeming very different at first glance, as I have worked through this project I have discovered that they aren't as separable as I imagined due to the fact that more and more animals are becoming 'domesticated' across the world, causing crossovers into the wildlife. As a result, it is not as simple as just one or the other. Many of the zoonotic diseases that we are experiencing are not originating in the livestock or pet populations, but rather they are picking up the disease from a wild animal or an area which has been contaminated by wildlife. As briefly mentioned in my second chapter, domestic animals often act as mixing vessels for the diseases, rather than the hosts themselves, creating a more direct route of transmission to humans. But this certainly poses the question of what 'wild' really means, as many people would instinctively think of the desert or forest biomes due to their stereotypical characteristic and exotic animals. As I found from one source, wildlife is normally described as "free-roaming animals (mammals, birds, fish, reptiles and amphibians)", showing how broad and undefined the word really is (Kruse, Kirkemo and Handeland, 2004). Rodents such as mice and rats are kept as pets by many but are also found in their own 'wild' environments, which includes man-made areas such as houses or garden borrows, and they are the main spreaders of Hantaviruses which are transmitted via aerosols in dust from rodent excreta (*ibid.*). This is a prime example of the confusions that can be made between domestic and wild animals, which could cause serious problems in the future as we bring, potentially dangerous, animals into our homes. Although the transmissions are hard to differentiate, in this brief chapter I will separately discuss the arguments for why each transmission is more significant.

The obvious argument for why wildlife is the most significant transmission, which I have mentioned throughout this paper, is that hundreds of pathogens and many different transmission modes are involved and there are a large array of factors which influence the epidemiology of various zoonotic diseases (*ibid.*). Also, there are several zoonotic agents (genetic variations of the zoonotic disease) which can be transmitted directly from wildlife to humans due to the spread of disease from different species in the wild, which creates a greater opportunity for uptake in the human host without the need for mixing in domestic animals (*ibid.*). An example of this is the pathogen F. *tularensis,* which is the causative agent for tularemia, and is primarily transmitted by the wild hare, causing hunters to be the most affected group (*ibid.*). However, it can also move by tick and mosquito bites, as well as infecting the water sources of nearby regions, which gives rise to disease spread for the nearby communities, showing how difficult it is to identify the sources and transmission routes for diseases, as they can move by numerous nodes (*ibid.).*

In 2017, it was estimated that 44% of households worldwide have ownership to at least one pet, increasing by 4% just one year before, indicating how much domestic animal ownership is rising, which will certainly have implications for disease spread as they interact with the wild everyday via walks or vets etc (Pet Population 2017, 2017). In addition to this, domestic animals are generally raised in relatively small and much more densely packed areas than their wild counterparts, which means that if a disease is present, it will spread much quicker e.g. livestock settlements and breeders (Murcia et al., 2009). This is particularly the case in the more industrialised countries around the world which are invested in modern intensive farming, which brings together thousands of animals in the same location, meaning that disease spread is rampant (*ibid.*). However, it is still much easier to control the whereabouts of these domestic animals/pets, and in the long term, I believe that it will be more sustainable and simple to reduce the amount that we use domestic animals, rather than trying to control the unpredictability of wild animal movements and nature, which is out of our hands.

Conclusion

It can be concluded that humans are almost wholly responsible for the increasing emergence and transmission of zoonotic diseases, from both wild and domestic animals, due to the direct link of expanding population sizes and the knock on effects such as food demand and globalisation. After all humans are the dominant species on earth, so our everlasting desire for meat, and greed for what isn't rightfully ours, has been accentuated to the point of extinction for many animals. Animals cannot be 'responsible' as such, for the spread of disease due to their lack of understanding of infection[2], which therefore means that it has little to no effect on their natural behaviours and movements. When a disease is identified within the human population, one can simply isolate them-self from the activities of daily life or seek medical help, such as medication or a check-up, whereas animals do not have this ability and subsequently spread the disease unknowingly. In addition, while researching this topic I have found a number of environmental factors which are at play, such as climate change and the recent changing weather patterns[3], but I have struggled to identify these as solely 'environmental factors', because once simplified to their roots they are often human factors once again. One example of this would be the rise in the number of rainstorms and floods across temperate grassland biomes, due to greater global temps, which is breeding perfect conditions for mosquito life and therefore creating new diseases – However, this increased global temp is as a result of the modern climate change which has occurred due to the actions of humans, in releasing lethal greenhouse gases into the atmosphere. As well as this, two of my biggest arguments for humans being responsible were the over-domestication of animals and intensive agriculture practices, which are directly causing the increased production of methane and other greenhouse gases, causing a feedback loop of human-invoked climate change (But to explain the ins and outs of climate change is a whole other topic completely).

Although I have argued in the final chapter that the human impacts on the transmission from wild animals to humans is more significant than domestic animals, it is impossible to tell which really has a greater influence on disease spread, due to the multitude of factors which are at play, and the fact that they are constantly changing over time. If this question were to be posed 100 years ago, maybe the answer wouldn't have been so straight forward, because domestication hadn't reached the heights that is has during the 21st century. Moreover, the control and prevention methods that have been introduced in recent years perhaps wouldn't have even been considered, because zoonotic diseases just weren't a massively researched problem. However, I cannot be certain of this, as the data from recent centuries is scarce and some of it is conflicting. I believe that the zoonotic disease spread within domestic hosts is an issue that we can work to prevent by controlling the flow of movement into livestock farms, which will prevent many of the diseases from entering these new species in the first place. However, I am not of the opinion that we can work to prevent zoonotic disease from wild animal hosts, and that it may be something that we have to learn to live with, due to their unpredictable nature. This would be done by instead focusing on the control methods such as vaccination and surveillance, which would hold the disease at bay and slow the spread, because trying to prevent wild animals from transmitting disease across the animal kingdom is unrealistic. On a smaller scale (the average person for example), more can be done to reduce the interactions that we are having with animals and the implications that follow with this. For example, a global switch from meat-based to vegan-based diets would massively reduce the reliance on livestock, which would cause this sector to fall, and slowly minimise the chances of disease being spread to humans via meat produce. Although this is obviously not going to happen overnight, there has been encouraging

---

[2] Although animals do not have the mental capacity to understand disease and the effects of them, they certainly still have a role to play within disease spread, because this naïve (NOT SURE) way of life is one of the key reasons by which disease is spread across the world and cross-species.

[3] The range of environmental factors that are relevant to this topic can be summarised in figure.1, which is found in the first chapter of this paper.

progress over recent years. This would have a major importance in the prevention of larger epidemics occurring in the future, as we have seen the consequences of COVID-19 for example, ripping through the world. Less expansion into the wild will inevitably reduce the contact that we have with these animals and cut the risk of disease spread from the source.

Bibliography:

Naicker, P., 2011. The Impact of Climate Change and other Factors on Zoonotic Diseases. [online] Acmicrob.com. Available at: <https://www.acmicrob.com/abstract/the-impact-of-climate-change-and-other-factors-on-zoonotic-diseases-220.html>

Vora N (2008) Impact of anthropogenic environmental alterations on vector-borne diseases. Medscape J Med 10(10):238

Singh B, Sung LK, Matusop A, Radhakrishnan A, Shamsul SSG et al. (2004) A large focus of naturally acquired Plasmodium knowlesi infections in human beings. Lancet 363:1017-1024

Keusch, G., Pappaioanou, M., Gonzalez, M., Scott, K. and Tsai, P., 2009. Drivers of Zoonotic Diseases. [online] Ncbi.nlm.nih.gov. Available at: <https://www.ncbi.nlm.nih.gov/books/NBK215318/>

United Nations. 2007. World population prospects: The 2006 revision, medium variant . Department of Economics and Social Affairs, Population Division. New York: United Nations.

de Merode, E., and G. Cowlishaw. 2006. Species protection, the changing informal economy, and the politics of access to the bushmeat trade in the Democratic Republic of Congo. Conserv Biol 20(4):1262–1271.

Peeters, M., V. Courgnaud, B. Abela, P. Auzel, X. Pourrut, F. Bibollet-Ruche, S. Loul, F. Liegeois, C. Butel, D. Koulagna, E. Mpoudi-Ngole, G. M. Shaw, B. H. Hahn, and E. Delaporte. 2002. Risk to human health from a plethora of simian immunodeficiency viruses in primate bushmeat. Emerg Infect Dis 8(5):451–457.

Liu, T-S. 2008. Custom, taste and science: Raising chickens in the Pearl River delta region, South China. Anthropology & Medicine 15(1):7–18.

Peiris, J., de Jong, M. and Guan, Y., 2007. Avian Influenza Virus (H5N1): a Threat to Human Health. Clinical Microbiology Reviews, 20(2), pp.243-267.

Sturm-Ramirez, K., Ellis, T., Bousfield, B., Bissett, L., Dyrting, K., Rehg, J., Poon, L., Guan, Y., Peiris, M. and Webster, R., 2004. Reemerging H5N1 Influenza Viruses in Hong Kong in 2002 Are Highly Pathogenic to Ducks. Journal of Virology, 78(9), pp.4892-4901.

Who.int. 2004. WHO | Avian influenza: H5N1 detected in pigs in China. [online] Available at: <https://www.who.int/csr/don/2004_08_20/en/>

WONG, J., ZHANG, W., KARGBO, D., HAQUE, U., HU, W., WU, P., KAMARA, A., CHEN, Y., KARGBO, B., GLASS, G., YANG, R., COWLING, B. and LIU, C., 2016. Assessment of the severity of Ebola virus disease in Sierra Leone in 2014–2015. Epidemiology and Infection, 144(7), pp.1473-1481.

Baudel, H., De Nys, H., Mpoudi Ngole, E., Peeters, M. and Desclaux, A., 2019. Understanding Ebola virus and other zoonotic transmission risks through human–bat contacts: Exploratory study on knowledge, attitudes and practices in Southern Cameroon. Zoonoses and Public Health, 66(3), pp.288-295.

Bharat, T., Noda, T., Riches, J., Kraehling, V., Kolesnikova, L., Becker, S., Kawaoka, Y. and Briggs, J., 2012. Structural dissection of Ebola virus and its assembly determinants using cryo-electron tomography. Proceedings of the National Academy of Sciences, 109(11), pp.4275-4280.

Leroy, E. M. , Kumulungui, B. , Pourrut, X. , Rouquet, P. , Hassanin, A. , Yaba, P. , … Swanepoel, R. (2005). Fruit bats as reservoirs of Ebola virus. Nature, 438(7068), 575–576. 10.1038/438575a

Hanbury-Tenison, R., 2020. Taming the four horsemen.

Cutler SJ, Fooks AR, van der Poel WHM (2010) Public health threat of new, reemerging, and neglected zoonoses in the industrialized world. Emerg Infect Dis 16(1):1-7

Schlundt J, Toyofuku H, Jansen J, Herbst SA (2004) Emerging food-borne zoonoses. Rev sci tech Off IntEpiz 23(2):513-533

Saveourantibiotics.org. 2013. [online] Available at: <https://www.saveourantibiotics.org/media/1496/zoonotic-diseases-human-health-and-farm-animal-welfare-16-page-report.pdf>

Peiris, J., de Jong, M. and Guan, Y., 2007. Avian Influenza Virus (H5N1): a Threat to Human Health. Clinical Microbiology Reviews, 20(2), pp.243-267.

Miller, K., 2020. Swine Flu vs. Covid-19: Here's How the Two Pandemics Compare, According to Experts. [online] Health.com. Available at: <https://www.health.com/condition/infectious-diseases/swine-flu-vs-covid-19>

Jilani, T., Jamil, R. and Siddiqui, A., 2020. H1N1 Influenza. [online] Ncbi.nlm.nih.gov. Available at: <http://www.ncbi.nlm.nih.gov/books/NBK513241/>

Gortazar, C., Diez-Delgado, I., Barasona, J., Vicente, J., De La Fuente, J. and Boadella, M., 2015. The Wild Side of Disease Control at the Wildlife-Livestock-Human Interface: A Review. Frontiers in Veterinary Science, 1.

Shiferaw, M., Doty, J., Maghlakelidze, G., Morgan, J., Khmaladze, E., Parkadze, O., Donduashvili, M., Wemakoy, E., Muyembe, J., Mulumba, L., Malekani, J., Kabamba, J., Kanter, T., Boulanger, L., Haile, A., Bekele, A., Bekele, M., Tafese, K., McCollum, A. and Reynolds, M., 2017. Frameworks for Preventing, Detecting, and Controlling Zoonotic Diseases. Emerging Infectious Diseases, 23(13).

Bass J, Tack DM, McCollum AM, Kabamba J, Pakuta E, Malekani J, et al. Enhancing health care worker ability to detect and care for patients with monkeypox in the Democratic Republic of the Congo. Int Health. 2013;5:237–43.

Boadella M, Gortazar C, Acevedo P, Carta T, Martín-Hernando MP, de la Fuente J, et al. Six recommendations for improving monitoring of diseases shared with wildlife: examples regarding mycobacterial infections in Spain. Eur J Wildl Res (2011) 57(4):697–706.

Vicente J, Carrasco R, Acevedo P, Montoro V, Gortázar C. Big game waste production: sanitary and ecological implications. In: Kumar S, editor. Integrated Waste Management. II. Rijeka: InTech (2011). p. 97–128.

Downtoearth.org.in. 2016. Quick facts about the world's livestock economy. [online] Available at: <https://www.downtoearth.org.in/news/economy/quick-facts-about-the-world-s-livestock-economy-54826>

Engeman R, Betsill C, Ray T. Making contact: rooting out the potential for exposure of commercial production swine facilities to feral swine in North Carolina. Ecohealth (2011) 8(1):76–81. doi:10.1007/s10393-011-0688-8

Ward AI, VerCauteren KC, Walter WD, Gilot-Fromont E, Rossi S, Edwards-Jones G, et al. Options for the control of disease 3: targeting the environment. In: Delahay RJ, Smith GC, Hutchings MR, editors. Management of Disease in Wild Mammals. Tokyo: Springer (2009). p. 147–68.

Petfoodindustry.com. 2016. INFOGRAPHIC: Most of world owns pets; Dogs are tops. [online] Available at: <https://www.petfoodindustry.com/articles/5845-infographic-most-of-world-owns-pets-dogs-are-tops>

Lembo T; Partners for Rabies Prevention. The blueprint for rabies prevention and control: a novel operational toolkit for rabies elimination.PLoS Negl Trop Dis. 2012;6:e1388.

Meslin FX, Briggs DJ. Eliminating canine rabies, the principal source of human infection: what will it take? Antiviral Res. 2013;98:291–6

Kruse, H., Kirkemo, A. and Handeland, K., 2004. Wildlife as Source of Zoonotic Infections. Emerging Infectious Diseases, 10(12), pp.2067-2072.

Walden, L., 2017. Worldwide Pet Ownership Statistics | Most Common Pets Around the World - PetSecure. [online] PetSecure. Available at: <https://www.petsecure.com.au/pet-care/a-guide-to-worldwide-pet-ownership/>

Pfma.org.uk. 2017. Pet Population 2017. [online] Available at: <https://www.pfma.org.uk/pet-population-2017>

Murcia P, Donachie W, Palmarini M. Viral Pathogens of Domestic Animals and Their Impact on Biology, Medicine and Agriculture. Encyclopedia of Microbiology. 2009;805-819. doi:10.1016/B978-012373944-5.00368-0

Cdc.gov. 2017. Zoonotic Diseases | One Health | CDC. [online] Available at: <https://www.cdc.gov/onehealth/basics/zoonotic-diseases.html>

Cui, J., Chen, F. and Fan, S., 2017. Effect of Intermediate Hosts on Emerging Zoonoses. Vector-Borne and Zoonotic Diseases, 17(8), pp.599-609.

Rozenbaum, M., 2020. The increase in zoonotic diseases: the WHO, the why and the when?. [online] Understanding Animal Research. Available at: <https://www.understandinganimalresearch.org.uk/news/research-medical-benefits/the-increase-in-zoonotic-diseases-the-who-the-why-and-the-when/>

Sandoiu, A., 2020. Why are infections from animals so dangerous to humans?. [online] Medicalnewstoday.com. Available at: <https://www.medicalnewstoday.com/articles/zoonotic-diseases-why-are-infections-from-animals-so-dangerous-to-humans>