American Journal of
Biomedical Science & Research

www.biomedgrid.com
ISSN: 2642-1747

Mini Review

How Diseases Help Telling the Story of Changes in the Environment

Natalia Lemos Chaves*

University of Brasília, Electron Microscopy Laboratory, Brazil

***Corresponding author:** Natalia Lemos Chaves, University of Brasília, Electron Microscopy Laboratory, Brazil.

To Cite This Article: *Natalia Lemos Chaves*. How Diseases Help Telling the Story of Changes in the Environment. Am J Biomed Sci & Res. 2024 22(6) AJBSR.MS.ID.003015,* DOI: 10.34297/AJBSR.2024.22.003015

Received: May 23, 2024; **Published:** June 10, 2024

Introduction

Social and environmental characteristics are linked to the pattern of human disease. One thing we are certain of is that no matter how much we evolve technologically and scientifically in the biomedical field, we will still not completely eliminate human disease. Perhaps, unlike the historical major health problems that almost decimated the population, with current awareness, we will be able to better deal with the next pandemics and epidemics by using and improving the signals provided by epidemiological and health surveillance systems and prepare ourselves in the best possible way to the next "new "unknown.

It is known that the human lice evolved along with its human host from the species that parasitized chimpanzees. And its horizontal contagion is favored when man leaves a more solitary lifestyle, coexistence begins in the form of community and caves [1,2]. Still marked by these new human habits, the advent of agriculture was not only marked by demographic increase but also may have altered the ecological transmission of pre-existing human pathogens, increasing the success of vectors of pre-existing pathogens and resulting in new interactions between humans and wildlife. Still for convenience and protection, in an agricultural society the habit of domesticating and living with other animals such as dogs arises, coinciding with records of zoonoses [3].

Following this line, it is possible to draw a parallel between respiratory diseases such as the Spanish flu and the period of the Industrial Revolution. We noticed a strong relationship between the form of transmission (respiratory) and the social characteristics of that period that favored contagion, such as large clusters of families and workers sharing the same enclosed space. In addition, the poor working conditions and few hours of sleep impacted the immune system's ability to fight the disease in the body [4].

The discussion exposed so far highlights the main vulnerable points that, in some way, due to social and cultural characteristics, open doors to the development of diseases that best develop under the conditions of the period in question. This relationship becomes clearer in a retrospective analysis than in a current one in which we are still understanding the course and biological characteristics of the disease. In other words, it is necessary to have both knowledge of the characteristics of the environment and the disease if one wants to analyze it from this perspective. In this context, we have recently seen that a new disease could cause an unprecedented global outbreak comparable to the 1918 influenza pandemic in terms of socioeconomic and political impacts on our global society, the COVID-19 pandemic, caused by SARS-CoV-2 [5,6]. We are still in the phase of understanding the characteristics of the pathogen that causes COVID-19 and its pathophysiology to understand how the environment was related to its establishment. However, we already have good tips pointing out that globalization and its consequent ease of crossing world borders favored the initial spread of COVID-19 and that this is a factor that we will have to deal with from now on. Furthermore, the worse prognosis in older people, those with cardiovascular diseases, diabetics and smokers coincides with the demographic increase in the profile of these people, a result of various characteristics of the environment and habits of society [7-10]. Scientists point out the predictability of the emergence of this pandemic with spoilers including its characteristics such as non-human origin and supported their hypothesis based on the increased rate of appearance of new Emerging Infectious Diseases (EIDs), with the majority of them having wildlife as their origin [11] and including H5N1 [12], MERS-CoV [13], Zika [14] and Ebola [15] in recent decades. More specifically, experts have been raising warnings for years about the potential for contagious bird

flu or coronavirus repercussions [16] to become the next pandemic, because they are often found in animals domestic and wild. Another alarming point was the fact that they also could infect humans. SARS-CoV-2 is the perfect example of zoonosis spreading from wildlife that then established itself in human populations [17]. Smallpox, bubonic plague and cholera are marked by their introduction to the Americas and Africa and the extinction of indigenous populations, but initially also had animal origins. Furthermore, Yellow Fever, HIV/AIDS, dengue fever, and Zika all emerged from non-human primates [18]. Although we have already encountered these forms of disease, what is different now is the level of modern connection of commerce, advances in transportation systems with exponential population growth and the highest rates of urbanization in history [19]. Furthermore, it is believed that the volume of these events is also increasing due to global environmental changes [20].

Recently, even before the coronavirus but still in force, we have experienced a profile of chronic non-communicable diseases, such as cardiovascular diseases, diabetes, obesity and cancer. This type of pathology of modernity, again, coincides with modern habits in terms of its form of development [21]. In these cases, they are not transmissible horizontally, that is, from one person to another through air, blood, etc., but they are highly related to unhealthy lifestyle habits such as a sedentary lifestyle, unhealthy diet, stress, smoking and alcoholism, among others. There is a genetic predisposition factor that can be inherited vertically, however, it is already known that this gene predisposition is not paramount in the importance of the development of the disease phenotype [22]. With a deeper and more focused look at the favorable conditions that would sustain the high incidence rates of cancer in the population, we find explanations from molecular evolution, in which the origin of self-replicating molecules 4 billion years ago formed the basis of life, but also the root of diseases. The evolution of multicellularity allowed complex body plans with trillions of cells, involving innovations associated with the cells' ability to regulate their cell cycles, modulate their growth and form intricate communication networks, fundamental for cells to renew themselves and adapt to organic demand, but it also laid the groundwork for cancer [23,24].

Obviously, the appalling statistics of persistently high cancer cases over the years are a reflection of greater capacity and access to diagnosis, however, there is still a lot to improve about the treatment and prevention of this disease [25]. The main challenge here is to understand the tumorigenic process, which is quite complex and multifactorial. In addition, there is a universe of diversity of patterns between types of cancer, location, and within the same group and sub-group of cancer, thus making a universal anti-tumor approach difficult [26]. The current point we are at depends on the combination of the environment, biomolecular evolution and prevalent diseases and is the result of a natural and irreversible flow. What remains for us is to understand as much as possible about these components to manage their damage until other standards are established and the targets of the challenges are different. However, tools for studying this relationship may be more powerful to provide information that is so valuable for reducing harm.

Acknowledgement

None.

Conflict of Interest

None.

References

1. Reed DL, Vincent S Smith, Shaless L Hammond, Alan R Rogers, Dale H Clayton (2004) Genetic analysis of lice supports direct contact between modern and archaic humans. PLoS Biol 2(11): e340.
2. Amanzougaghene N, Florence Fenollar, Didier Raoult, Oleg Mediannikov (2020) Where are we with human lice? A review of the current state of knowledge. Front Cell Infect Microbiol 9: 474.
3. Pearce Duvet JM (2006) The origin of human pathogens: evaluating the role of agriculture and domestic animals in the evolution of human disease. Biological Reviews 81(3): 369-382.
4. Tomes N (2010) "Destroyer and teacher": Managing the masses during the 1918–1919 influenza pandemic. Public Health Rep 125(3_suppl): 48-62.
5. Taubenberger JK, JC Kash, DM Morens (2019) The 1918 influenza pandemic: 100 years of questions answered and unanswered. Sci Transl Med 11(502): eaau5485.
6. Roche B, Andres Garchitorena, Jean François Guégan, Audrey Arnal, Serge Morand, et al. (2020) Was the COVID-19 pandemic avoidable? A call for a "solution-oriented" approach in pathogen evolutionary ecology to prevent future outbreaks. Ecology letters 23(11): 1557-1560.
7. Lagunas Rangel FA, V Chávez Valencia (2021) Laboratory findings that predict a poor prognosis in COVID-19 patients with diabetes: a meta-analysis. Endocrinol Diabetes Nutr (Engl Ed) 68(7): 520-522.
8. Espejo Paeres C, Iván J Núñez Gil, Vicente Estrada, Cristina Fernández Pérez, Giovanna Uribe Heredia, et al. (2021) Impact of smoking on COVID-19 outcomes: a HOPE Registry subanalysis. BMJ Nutr Prev Health 4(1): 285-292.
9. Choi YJ, Joon Young Song, Hakjun Hyun, Eliel Nham, Jin Gu Yoon, et al. (2022) Prognostic factors of 30-day mortality in patients with COVID-19 pneumonia under standard remdesivir and dexamethasone treatment. Medicine 101(38): e30474.
10. Pepera G, Marina Sofia Tribali, Ladislav Batalik, Ivo Petrov, Jannis Papathanasiou (2022) Epidemiology, risk factors and prognosis of cardiovascular disease in the Coronavirus Disease 2019 (COVID-19) pandemic era: a systematic review. Rev Cardiovasc Med 23(1): 28.
11. Jones KE, Nikkita G Patel, Marc A Levy, Adam Storeygard, Deborah Balk, et al. (2008) Global trends in emerging infectious diseases. Nature 451(7181): 990-993.
12. Vijaykrishna D, Justin Bahl, Steven Riley, Lian Duan, Jin Xia Zhang, et al. (2008) Evolutionary dynamics and emergence of panzootic H5N1 influenza viruses. PLoS pathogens 4(9): e1000161.
13. Cauchemez S, Pierre Nouvellet, Anne Cori, Thibaut Jombart, Tini Garske, et al. (2016) Unraveling the drivers of MERS-CoV transmission. Proc Natl Acad Sci U S A 113(32): 9081-9086.
14. Musso D, AI Ko, D Baud (2019) Zika virus infection—after the pandemic. N Engl J Med 381(15): 1444-1457.
15. Team WER, Bruce Aylward, Philippe Barboza, Luke Bawo, Eric Bertherat (2014) Ebola virus disease in West Africa—the first 9 months of the epidemic and forward projections. N Engl J Med 371(16): 1481-1495.
16. Cheng VC, Susanna KP Lau, Patrick CY Woo, Kwok Yung Yuen (2007) Severe acute respiratory syndrome coronavirus as an agent of emerging and reemerging infection. Clin Microbiol Rev 20(4): 660-694.

17. Lloyd Smith JO, Dylan George, Kim M Pepin, Virginia E Pitzer, Juliet RC Pulliam, et al. (2009) Epidemic dynamics at the human-animal interface. Science 326(5958): 1362-1367.

18. Weiss RA, N Sankaran (2022) Emergence of epidemic diseases: zoonoses and other origins. Fac Rev 11: 2.

19. Anugwom EE, KN Anugwom (2022) Urbanization and the Epidemiology of Infectious Diseases: Towards the Social Framing of Global Responses, in Integrated Science of Global Epidemics. Springer: 307-328.

20. Baker RE, Ayesha S Mahmud, Ian F Miller, Malavika Rajeev, Fidisoa Rasambainarivo, et al. (2022) Infectious disease in an era of global change. Nat Rev Microbiol 20(4): 193-205.

21. Organization WH (2022) Noncommunicable diseases: progress monitor 2022. World Health Organization.

22. Yoon PW, Maren T Scheuner, Cynthia Jorgensen, Muin J Khoury (2009) Developing Family Healthware, a family history screening tool to prevent common chronic diseases. Prev Chronic Dis 6(1): A33.

23. Albuquerque TA, Luisa Drummond do Val, Aoife Doherty, João Pedro de Magalhães(2018) From humans to hydra: patterns of cancer across the tree of life. Biological Reviews 93(3): 1715-1734.

24. Benton ML, Abin Abraham, Abigail L LaBella, Patrick Abbot, Antonis Rokas, et al. (2021) The influence of evolutionary history on human health and disease. Nat Rev Genet 22(5): 269-283.

25. Siegel RL, AN Giaquinto, A Jemal (2024) Cancer statistics, 2024. CA Cancer J Clin 74(1): 12-49.

26. Mroz EA, JW Rocco (2017) The challenges of tumor genetic diversity. Cancer 123(6): 917-927.