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Evolution of Ecosystems and Biological Diversity

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Abstract

The most important advances in science related to infectious agent transmission in multi-host systems over the past ten years. Nearly 60% of the diseases that have appeared in humans during the past 30-40 years are of animal origin, and 60% of them have a significant range of hosts outside of humans. We concentrate on zoonotic illnesses with vector-borne transmission and analyse the divergent influences that a variety of host reservoirs and vectors may have on their disease dynamics. Three or more potential host species. We explore the reduction, including the dilution impact, or amplification of pathogen prevalence caused by the richness and mix of host and vector species. In this work, we will use the term "parasite" to refer to carriers of infectious diseases because the majority of significant infections and parasites that influence human populations are zoonotic.

Keywords: Transmission; Parasite; Amplification; Species

Introduction

The significance of having a better understanding of animal species as possible hosts and suppliers of novel contaminations in humans is thus readily apparent. The recent emergence and spread of highly pathogenic animal-derived diseases like Severe Acute Respiratory Syndrome (SARS), West Nile fever, Lyme disease, and rabies as well as the highly pathogenic H5N1 avian influenza (bird flu), all of which are highly contagious, have brought to light the importance of animal species as major reservoirs for (new) human infections. To reduce, it is crucial to understand how they are spread among animal species populations and to pinpoint the underlying ecological and evolutionary factors [1, 2].

An "ecological community" can be defined in a variety of ways. The abundance of definitions does not make communication within this field of study any easier. In this article, we have opted to utilize Putman's definition, which is somewhat neutral but also ambiguous. Thus, "a group of species that interact in a certain geographic area and whose functions and dynamics are somehow linked" is the definition of an ecological community. Infectious disorders that impact human populations are frequently caused by pathogens that are not absolutely exclusive to our species. Around 58 to 61% of the approximately 1415 infectious illnesses that affect humans have a known animal origin. Ruminants, carnivores, rodents, birds and primates constitute, in the order, the five major animal categories that have transmitted pathogens to human populations. This percentage increases to 73–75% if only the "emerging" or "re-emerging" diseases, which have appeared in the last 30 to 40 years, are considered [3].

These species abundance/richness relationships represent the outcomes of all interactions that take place within local communities, such as preys/predators and competition, and as such they may serve as an effective integrator of all these relationships. Trophic networks should not be discounted in light of the fact that they may represent another significant contributing mechanism to the dynamics of ecological communities, despite the fact that they are insufficient to explain the observed community structure. Although the fundamental function of parasites in ecosystems is effectively illustrated by this example, it is still important to distinguish between the impacts of generalist (nonspecific) and host-specialized parasites on host species communities. A generalist parasite that can infect a wide variety of host species would typically have disruptive effects on the host communities. In fact, if a parasite species can attack multiple host species at once, the

more tolerant hosts those that can support the parasite's reproduction while suffering little damage will engage in "apparent" competition with the less tolerant hosts, bearing the burden of the parasite's virulence. Both pheasants in Scotland are infected by the parasitic worm *Heterakis gallinarum* [4].

Pheasants have a high tolerance for this parasite since it multiplies very well in them without affecting the size of their population. The scenario is different for partridges because a significant majority of partridges afflicted by this worm will pass away quickly. The degree of pheasant abundance in the area has the effect of raising local nematode incidence, which will have an immediate impact on the quantity of partridges because they are more vulnerable to the parasite. Although we are unable to offer any further examples that are as illustrative as this one, such circumstances must occur regularly in nature. The complexity of the commonly employed epidemiological models makes it challenging to incorporate the significant interspecies heterogeneity that can be found within a host (reservoir or vector) species [5-7].

Discussion

A number of laboratory and field investigations that focused on the interspecific variability of susceptibilities have been conducted, and they have shown the significance of the local composition in reservoir host species on the transmission of the bacterium that causes Lyme disease. These pathogen dynamics are typically the consequence of a balance between effective transmission by competent hosts and unsuccessful transmission by under-competent hosts, which may result in a dilution effect. Actually, the proportion of reservoir species with low susceptibility, which tends to increase in communities with a variety of species, is what actually affects the level of pathogen prevalence in the vectors, not strictly speaking the local richness in reservoir species,

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which tends to reduce the intensity of vector-borne transmission. The "take home" lesson from the multi-host/multi-vector models for the West Nile virus is that the local diversity and composition of host reservoirs and vectors may result in various combinatorial effects on disease transmission. The prevalence of West Nile virus is extremely sporadic in Southern Europe, such as the Camargue region, where the bird reservoir species are poorly to moderately susceptible to infection and only two vector species, one of which is moderately and the other of which is poorly susceptible, are present [8].

Conclusion

It is still early days for community epidemiology. The development of natural communities in the coming years should result from collaboration between experts in complex systems, especially those working on multi-agent systems, ecologists, evolutionary biologists, and epidemiologists. Up to this point, it has been constrained by an overly simplistic perspective (the triad "one agent, one vector, one reservoir") on the complexity of natural communities. We end this review by reiterating a theme that has run through the entire piece: different epidemiological and ecological outcomes for the same disease can occur in various locations. The role of biological diversity and its heterogeneity in space and time is one crucial and likely overlooked component in the understanding of emerging infectious disease [9, 10].

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Conflict of Interest

None

References

- Fawzy S, Osman AI, Doran J, Rooney DW (2020) Strategies for mitigation of climate change: a review. Environ Chem Lett 18: 2069-2094.
- Ricke K, Millar R, Macmartin DG (2017) Constraints on global temperature target overshoot. Sci Rep 1-7.
- Bustreo C, Giuliani U, Maggio D, Zollino G (2019) How fusion power can contribute to a fully decarbonized European power mix after 2050. Fusion Eng Des 146: 2189-2193.
- Goglio P, Williams AG, Balta-Ozkan N, Harris NR, Williamson P, et al. (2020) Advances and challenges of life cycle assessment (LCA) of greenhouse gas removal technologies to fight climate changes. J Clean Prod 244: 118896.
- Khalidy R, Santos RM (2021) The fate of atmospheric carbon sequestrated through weathering in mine tailings. Miner Eng 163: 106767.
- 6. Lezaun J (2021) Hugging the shore: tackling marine carbon dioxide removal as a local governance problem. Front Climate 3: 684063.
- Lockley A, Mi Z, Coffman DM (2019) Geoengineering and the blockchain: coordinating carbon dioxide removal and solar radiation management to tackle future emissions. Front Eng Manag 6: 38-51.
- Osman AI, Hefny M, Maksoud MA, Elgarahy AM, Rooney DW (2020) Recent advances in carbon capture storage and utilisation technologies: a review. Environ Chem Lett 19: 797-849.
- 9. Allen JC, Komar PD (2006) Climate controls on US west coast erosion processes. J Coast Res 22: 511-529.
- 10. Meehl GA, Washington WM, Collins WD, Arblaster JM, Hu A, et al. (2005) How much more global warming and sea level rise? Science 307: 1769-1772.