ECOLOGY OF DISEASE TRANSMISSION IN MULTI-HOST SYSTEMS

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Abstract

Emerging infectious diseases (EIDs) result from the spill-over of pathogens to new species within multi-host systems [2,6,9]. The current disease surveillance systems cannot anticipate emergences because they fail to identify future culprits (pathogens and reservoir or spreader hosts) in these complex systems [15]. The actions of public health officers and veterinarians are restricted to later stages of epidemics once the severity of outbreaks can be much higher [14]. However, recent advances in community ecology [11,13], molecular ecology [3,5,7] and network analysis [10] open new perspectives for the integration of epidemiology and ecology [4,8] and for the understanding of disease transmission in multi-host systems. Shifting the focus from host-pathogen relationships to transmission processes, we develop a framework building networks of epidemiological interactions [1] between host populations (of the same species or from different species) at the ecosystem level. These networks use two types of data: 1) Host movement and contact data (e.g., direct observation, telemetry as a proxy of disease transmission); 2) Parasite community data from different host populations, assuming that past transmission pathways inferred from this data are the most likely transmission pathways for emerging pathogens. The field of parasite community ecology has provided analytical tools to compare parasite communities by controlling for confounding factors (e.g., phylogenetic distance) [12]. We define also the concept of epidemiological functional groups to which host populations can be allocated according to their potential role in epidemiology of parasites, drawing a parallel with the approach adopted by community ecologists to assign species to functional groups. Hosts are grouped together when sharing a similar role in the transmission of a parasite or a group of parasites (e.g., reservoir, spreader, dead-end host). We explore the relevance of this approach to identify the most likely future transmission pathways between host populations in a given ecosystem. Once identified, these transmission pathways can be targeted by disease surveillance and control to prevent the next pathogen emergence. The epidemiological interaction network framework that we present could achieve two objectives: increasing theoretical knowledge on the ecology of disease transmission and on multi-host multi-pathogen interactions and providing a tool for EIDs early detection.

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