

Dynamic modeling of a vector-borne disease, from an individual to a metapopulation perspective. Application to plague in central Asia.

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ABSTRACT

Context and objective

Bubonic plague, a zoonotic infection that circulates in wild rodents but is transmissible from them to humans through the bites of infected fleas, is not merely of historical interest. It is widespread in the world today and a continuing threat (Stenseth et al. (2008)). In the Pre-Balkhash autonomous focus (Kazakhstan, central Asia), the great gerbil *Rhombomys opimus* is the main reservoir host (Gage and Kosoy, 1995). Davis et al. (2004, 2007) proposed that the family-oriented population structure of the great gerbil and its associated ectoparasite fleas of genus *Xenopsylla*, along with their seasonally constrained weather-dependent dynamics, is a key factor that determines plague epizootics and plague long-term persistence in rodents in this focus. Yet, the question of the geographical level of plague endemicity, i.e. whether plague can persist in a local autonomous “micro-focus” of minimum size to be determined, or necessarily operates at a larger level, remains poorly understood (Schmid et al., 2012). A knowledge-driven dynamic modeling framework is developed to help answering this question.

Methods

Individual-based and population-based approaches are often employed alternatively in eco-epidemiological modeling. We propose to combine these two approaches, though not in a dynamical way. A spatially explicit agent-based model is first developed, based upon finely described individual processes and interactions rules in the host-vector parasitoid system, derived from literature. From individual-based simulations, we compute population parameters that are used in a second ODE-based model, representing a specified metapopulation structure of burrow systems, each of one inhabited by family groups of great gerbils and their ectoparasites. The individual-based model integrates the seasonality of fleas and great gerbils’ reproduction and daily foraging activity, whereas the second captures the permanent dispersal movement of juvenile great gerbils to form new family groups, through which plague propagates.

Results and discussion

One of the main drawback of the use of compartmental models in epidemiology is that they rely on an incidence function that is difficult to parameterize. On the other hand, agent-based epidemic models are very cumbersome and can hardly be extended to large populations over long periods of time. By combining the two approaches, we overcome these two limitations. From a series of individual-based simulations with plague

introduced at initialization, we derive the host and vector incidence functions for plague within burrow dynamics that is used in the metapopulation model. Further analysis is required to assess the extent to which the between-patch dynamics, related to the host dispersal between burrow systems, is important for the persistence of the infection, among some other aspects.

KEYWORDS

Plague, *Rhombomys opimus*, agent-based / ODE-based modeling, metapopulation structure, incidence function

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