Impact of environmental changes on the pathogens transmission: Modelization and Mathematical Analysis

Location: Laboratoire de Mathématiques Appliquées du Havre (LMAH), Université Le Havre Normandie.

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Context of the thesis:

Infectious diseases are due to the transmission of a pathogen such as bacteria, viruses, parasites, etc. According to the OMS, 17% of them are vector-borne diseases, i.e. diseases in which the pathogen is transmitted from one host (human or animal) to another via a vector (essentially insects and haematophagous mites, for example mosquitoes and ticks). For a majority of these vector-borne diseases, the pathogen is naturally transmitted from vertebrate animals to humans, these are zoonoses. Examples include dengue fever, Zika, malaria or Lyme disease. Among infectious diseases in humans, zoonoses represent 60% of them and 80% of emerging infectious diseases.

Global warming favors the extension towards temperate regions of vectors of diseases, formerly confined to hot regions. What modifies the balances and the biodiversity of environments, increasing the risk of the appearance of emerging diseases and the transmission of infectious diseases. On the other hand, the modification of regions by deforestation, or by conversion of land for ranching, agriculture or construction increases the frequency and intensity of contacts between humans and wildlife, increasing the risk of viral transfers. Thus, the variety of vector populations or reservoirs of pathogens are multiplied by the intensity of international mobility. Indeed, maritime transport multiplies the proliferation of invasive species. Let us cite, for example, the case of reservoir hosts with rodents, bats or the case of vectors such as mosquitoes or ticks. Moreover, taking into account the changes in the range of reservoir or vector hosts and habitats of the human population is represented by non-coincident time-dependent domains.

The objective of this thesis is to propose and study non-autonomous reaction-diffusion systems modeling the dynamics of transmission of an infectious disease through different populations living in non-coincident domains and evolving over time. Therefore, the spatial domains in which populations interact change over time.

We will endeavor to describe several situations:

1. The case of transmission of a vector-borne disease in the presence of an invasive vector population.

2. A second case will be the modeling and qualitative study of direct transmission of a zoonosis when the distribution area of the host populations extends over that of the disease reservoir. Typically this case corresponds to questions of urban extensions, peri-urban areas or increases in agricultural land, which favor contacts with animal populations, possibly carriers of pathogens.

Requested skills: The candidate must have a solid backround on mathematical analysis of PDE with a strong interest in biology.

To apply, contact A. Ducrot and D. Manceau with a CV, a recommendation letter and the transcript of the Master.

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