

EDITORIAL

Vector adaptation to microorganisms or adaptation of microorganisms to vectors?

¿Adaptación de los vectores a los microorganismos o adaptación de los microorganismos a los vectores?

Forecasting the emergence of zoonotic infectious diseases and their geographical extent is a challenging task; this is despite recent technical advancements in the development of statistical and mathematical epidemiological tools for understanding disease distribution and dynamics. During the recent Ebola outbreak countries worldwide were concerned with transboundary transmission of infection fueled by enhanced human population mobility originating from infected countries in West Africa. Similarly, transboundary movement of live animals and their products can give rise to the introduction and spread of diseases of pandemic potential.

In the context of vector borne diseases, the mechanical translocation and subsequent adaptation of vectors between endemic and non-endemic areas is a common phenomenon that can lead to the introduction of infection; for example, it is well documented that the mosquito *Aedes aegypti*, vector of Yellow fever, Dengue, Chikungunya and Zika viruses was shipped by steamers along the Magdalena River from Cartagena in the 1880s (1). A century after the Yellow Fever epidemic in New Orleans and Alabama, the first outbreak of urban yellow fever arose in the state of Santander between 1906 and 1930; by the 1950's the mosquito had reached the south of the country.

In 2010 *Aedes aegypti*, had already been reported throughout the Colombian territory. This vector not only adapted and colonized rural environments where it originally emerged but also spread to sprawling urban landscapes; this is likely to contribute to the increase of urban transmission of diseases such as dengue hemorrhagic fever (2). In the past, infected mosquitoes traveled along rivers and canals but today their movement can be facilitated by road and airway networks. For this reason, the risk of vector borne diseases such as malaria, leishmaniasis or urban trypanosomiasis is becoming more of a concern in tropical countries like Colombia.

Recent evidence has demonstrated the presence of Zika and Chikungunya viruses in species of *Culex* mosquitoes (3). However, the detection of these viruses in *Culex* mosquitoes is not conclusive evidence of transmission in that their detection could be the result of recent bite of a transient viremic vertebrate. Whether Zika virus can effectively replicate in *Culex* requires further investigation. It is therefore important to conduct studies in Colombia and other Latin American countries to determine the role of wild and peridomestic vertebrates in the dynamics of viral transmission. While there is a greater frequency of *Culex* captures in peridomestic and rural areas of the Colombian Caribbean, preliminary entomological studies at our laboratory have shown the detection of dengue virus by PCR in *Culex*. However, neither Zika nor Chikungunya viruses were found in these investigations.

Not only arboviruses are changing their modes of transmission in association with vectors. The cat flea *Ctenocephalides felis* has traditionally been considered the only confirmed vector of *Rickettsia felis*; however, recent evidence has demonstrated that mosquitoes *Anopheles gambiae* –the main vector of malaria in sub-Saharan Africa– can be a competent vector for *R. felis*. *Anopheles gambiae* and *Aedes albopictus* mosquitoes are also a competent vector of *R. felis* (4). In addition, *R. felis* has been detected in febrile patients in tropical areas where *Aedes albopictus* or *Aedes aegypti* readily bite humans. Therefore, it is very likely that *Aedes* spp mosquitoes might be able to transmit *Rickettsia felis*.

Recent evidence has also identified changing patterns of transmission of rodent borne diseases such as *Leptospira*, Hantavirus and Arenaviruses (including lymphocytic choriomeningitis virus). For example, while *Leptospira* and Lymphocytic choriomeningitis arenavirus are transmitted by urban rodents such as *Rattus rattus* and *Mus musculus*, recent evidence suggests that wild rodents such as the *New World Sigmodontins* are chronic carriers of these zoonotic viruses. Other mammals such as bats can act as reservoirs to groups of zoonotic bacteria, protozoa, viruses and fungi and are able to spread these pathogens over large distances, including the Nipha, Hendra and *Bat Lissa* viruses, which are important zoonotic pathogens of bats in other parts of the world, especially in Australia and its neighboring countries. Little is known about the epidemiology of bat borne diseases in Colombia and other countries in Latin America and their role in the zoonotic transmission of viruses such as Ebola, coronavirus, influenza virus, dengue, and influenza among others (5).

The epidemiology and transmission dynamics of diseases transmitted by vectors, bats and rodents are currently a significant gap in knowledge in Latin America compared to other countries where diseases are endemic. The study of synanthropic and wild vectors is crucial in Latin America to better understand the adaptation and transmission of vector borne diseases, geographical boundaries, as well as the risk factors for their occurrence.

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