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Bunyaviruses and climate change

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Abstract

It is generally accepted that the planet is undergoing climatic changes, and 'climate change' has become the scapegoat for many catastrophes, including infectious disease outbreaks, as acknowledged by Randolph and Ergonul, who state 'Climate change is the current ubiquitous explanation for increased incidence of infections of many sorts' (*Future Virology* 2008; **3**: 303–306). However, as these authors argue, this is a highly simplistic view and, indeed, there is a complex network of factors that are responsible for disease emergence and re-emergence. In this short review, the role that climate change could play in the emergence of bunyavirus disease is considered, using a few selected examples.

Keywords: Arbovirus, bunyavirus, climate change, emerging disease, mosquito, vector competence

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Introduction

The Wildlife Conservation Society published a report in October 2008 entitled 'The Deadly Dozen: Wildlife Diseases in the Age of Climate Change' (http://www.wcs.org/deadly-dozen/wcs_deadly_dozen), which lists 12 pathogens that could spread to virgin territory as the result of climatic alterations. To quote S. Sanderson, President of the Wildlife Conservation Society, *'The term 'climate change' conjures up images of melting ice caps and rising sea-levels that threaten coastal cities and nations. But just as important is how increasing temperatures and fluctuating precipitation levels will change the distribution of dangerous pathogens'.* In this review, the validity of that statement will be considered with regard to bunyaviruses, a family of viruses that includes Rift Valley fever virus, a member of 'The Deadly Dozen'. Epidemics of Rift Valley fever are closely associated with climatic conditions; outbreaks frequently occur after periods of heavy rain, such as those driven by El Nino/Southern Oscillation events [1–3], when mosquitoes hatch from dormant eggs infected with the virus. Indeed, transovarial transmission [4,5] appears to play a significant role in maintenance of the virus in inter-epidemic periods (see below). The take-home message will be that the effects of climate change on vector-borne infectious disease are numerous, complex, not necessarily bad and not entirely predictable.

Bunyaviruses

The family *Bunyaviridae*, whose members are collectively known as bunyaviruses, is the largest family of RNA viruses and contains more than 350 named isolates. Membership of the family is based on common properties including an enveloped, spherical virion approximately 100 nm in diameter; possession of a tripartite single-stranded RNA genome having a negative- or ambi-sense coding strategy; cytoplasmic site of replication; and virion maturation in the Golgi complex [6]. All bunyavirus particles comprise just four structural proteins: two external virion surface glycoproteins (Gn and Gc) that are encoded by the M (medium-sized) genome RNA segment, and two internal proteins, N, the nucleocapsid protein encoded by the S (small) segment that encapsidates the genomic RNA, and L, the viral RNA-dependent RNA polymerase, which is encoded by the L (large) genome segment. Viruses in the family are divided into five genera (i.e. *Orthobunyavirus*, *Hantavirus*, *Nairovirus*, *Phlebovirus* and *Tospovirus*) on the basis of serological relationships and biochemical characteristics such as the patterns of genome RNA segment sizes and structural protein sizes that are conserved in a genus-specific manner [6–8].

Orthobunyaviruses, nairoviruses and phleboviruses are arboviruses (i.e. arthropod borne viruses) whose natural lifecycle involves replication in haematophagous arthropods

TABLE 1. Selected important pathogens in the family *Bunyaviridae*

Genus/virus	Disease	Principal vector	Distribution
Orthobunyavirus			
Akabane	Cattle: abortion and congenital defects	Midge	Africa, Asia, Australia
Cache Valley	Sheep, cattle: congenital defects	Mosquito	North America
La Crosse	Human: encephalitis	Mosquito	North America
Ngari	Human: haemorrhagic fever	Mosquito	Africa
Oropouche	Human: fever	Midge	South America
Tahyna	Human: fever	Mosquito	Europe
Hantavirus			
Hantaan	Human: severe haemorrhagic fever with renal syndrome (HFRS), fatality 5–15%	Field mouse	Eastern Europe, Asia
Seoul	Human: moderate HFRS, fatality 1%	Rat	Worldwide
Puumala	Human: mild HFRS, fatality 0.1%	Bank vole	Western Europe
Sin Nombre	Human: hantavirus cardiopulmonary syndrome, fatality 50%	Deer mouse	N. America
Nairovirus			
Crimean-Congo haemorrhagic fever	Human: haemorrhagic fever, fatality 20–80%	Tick	Eastern Europe, Africa, Asia
Nairobi sheep disease	Sheep, goat: fever, haemorrhagic gastroenteritis, abortion	Tick, mosquito	Africa, Asia
Phlebovirus			
Rift Valley fever	Human: encephalitis, haemorrhagic fever, retinitis, fatality 1–10%. Domestic ruminants: necrotic hepatitis, haemorrhage, abortion	Mosquito	Africa
Naples sandfly fever	Human: fever	Sandfly	Europe, Africa
Sicilian sandfly fever	Human: fever	Sandfly	Europe, Africa
Tospovirus			
Tomato spotted wilt	Plants: over 650 species, various symptoms	Thrips	Worldwide

and warm-blooded vertebrate species. Tospoviruses are plant pathogens and are also transmitted by arthropods; in their case, by different thrips species. Hantaviruses are not vectored by arthropods but are maintained in nature as persistent infections of rodents and insectivores, and are transmitted to humans in infected secretions and excretions [9]. Viruses in all five genera impinge on human health and well-being, either directly in causing disease or indirectly in causing disease to livestock or crop plants (Table 1).

Emerging/Re-Emerging Disease

The definition of an emerging disease, according to the National Institute of Allergy and Infectious Diseases, is 'an outbreak of previously unknown diseases or known diseases whose incidence in humans has significantly increased in the past two decades' (http://www3.niaid.nih.gov/topics/emerging/introduction.htm); certainly, many bunyavirus-mediated diseases fall within this definition (e.g. Rift Valley fever virus, Crimean-Congo haemorrhagic fever virus, Sin Nombre hantavirus). In this article, consideration of the effects of climate changes in relation to disease emergence is restricted to the arthropod-transmitted members of the bunyavirus family, whereas the hantaviruses are dealt with separately by B. Klempa.

The factors associated with emergence/re-emergence of viral disease are numerous [10], and among the most important are the following.

Virus evolution: for example, by mutation, genome segment reassortment or recombination.

Modification of host behaviour: as a result of advances in medical procedures requiring prolonged immunosuppression, or blood and blood-product transfusions; failure of vaccination policies; recreational drug abuse, particularly with needle sharing; international air travel; breakdown in healthcare systems because of political upheaval and wars; mass migration of refugees and refugee camps; increased urbanization.

Changes in agricultural practice: land use, deforestation, irrigation projects, etc., leading to increased contact with vectors; increased worldwide transportation of livestock, birds, plants and invertebrates; animal feed production.

Improved virus recognition and detection: for example, as a result of PCR-based methods.

Increased contact with vectors is usually cited as the major factor in the emergence of arthropod-borne disease and, although land use changes as described above or human activities such as more adventurous holidays may play a role, changes in vector distribution and density as a result of climate change would currently appear to be of greater concern. However, the emergence of a particular disease can rarely be attributed to a single factor. Certainly, there are specific examples for which recognized changes can be highlighted (e.g. dam building or forest clearance) [11] but other factors always contribute to the development of disease outbreaks, at least to a detectable level. Furthermore, climate change impacts directly on many of the factors cited above, indicating that, in the case of arboviruses, climate change