



# The potential for the establishment of new arbovirus transmission cycles in Europe

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Mosquito-borne viruses are an increasing health threat to humans, and potentially other vertebrates, in areas where they have not previously existed or from which they had been eradicated. Chikungunya virus emergence exemplifies how multiple factors can act synergistically resulting in rapid, large-scale redistribution and establishment. Despite our increased capacity to collect and analyze large amounts of data, we still lack epidemiological models to facilitate accurate predictions of when and where new diseases may occur. Models focusing on climate changes may have long-term value; however, there is an urgent need for mathematical modeling of viral epidemiology to enable forecasting immediate or near-term threats.

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During the past 10 years, chikungunya virus (CHIKV) has demonstrated an extraordinary capacity to spread from its original tropical niche in Africa and Asia into more temperate areas. This geographic redistribution has been fueled by multiple factors, including increased commercial transportation, viral genetic changes and the expansion of the geographical distribution of the highly invasive Asian tiger mosquito, *Aedes albopictus*. Between 2005 and 2014, introductions of CHIKV into Europe were predominantly of the East Central South African (ECSA) genotype. The virus briefly established itself in Italy during 2007 and France in 2010, causing autochthonous (i.e., locally transmitted) cases of the ECSA genotype.<sup>1,2</sup> In both instances, the transmission cycle involved *Ae. albopictus*, but while the Italy/2007 CHIKV had the well-characterized A226 V mutation that significantly increases the infectivity of CHIKV for this mosquito species, the France/2010 CHIKV did not.<sup>3</sup> Since the beginning of 2014, many humans infected with the Asian genotype of CHIKV have traveled to Europe, especially in France, from islands in the Caribbean where an ongoing epidemic involving the vector *Ae. aegypti* has resulted in over 1.3 million cases.<sup>4,5</sup> The Caribbean epidemic has resulted in the Asian genotype being introduced into multiple countries in South and Central America. In November, the ECSA genotype was detected in Brazil. The likely impact of having two genotypes co-circulating in the Americas, one of which has the known capacity to adapt to increased transmission efficiency by *Ae. albopictus*, gives cause for concern.

With the continued spread of *Ae. albopictus* into regions of Europe that have a climate conducive to year-round mosquito activity, the possibility that CHIKV could become established is

being taken seriously and risk assessments and contingency plans have been developed (see for example <http://ecdc.europa.eu/search/Pages/results.aspx?k=chikungunya> and <https://www.gov.uk/chikungunya>). It seems inevitable that CHIKV cases will continue to be introduced into continental Europe and the UK, but the important questions are: will further autochthonous cases occur and could CHIKV become established in Europe, especially in southern regions with conditions that favor sustained mosquito activity? With the establishment of five invasive mosquitoes in Europe during the past 40 years, including *Ae. aegypti* on the Portuguese Island of Madeira that enabled local transmission of dengue virus during 2012, there is legitimate concern that other introduced viruses could become established.<sup>6-8</sup>

There are two factors that could enable rapid implementation of responses to control an outbreak of CHIKV in Europe; these are the high symptomatic rate and the general lack of non-human vertebrate hosts. Since most people that become infected develop symptoms, with a suitable surveillance system based, for example, on physician reporting, health authorities should quickly become aware of cases and could initiate mosquito-control efforts. This was effective in limiting the spread of CHIKV in Italy and controlling the outbreak. Since the principle vertebrates involved in transmission are humans and specific non-human primate species, a sylvatic cycle in much of Europe seems highly unlikely. However, as demonstrated by the recent autochthonous transmission of CHIKV throughout the Caribbean and much of South and Central America, the potential for CHIKV to become established in some parts of Europe should not be ignored.

Any discussion on mosquito-borne pathogens in Europe inevitably involves concerns regarding climate change. Mosquito distribution is in part determined by species-specific tolerance to environmental conditions. Maximum and minimum temperatures, the periods of time related to these temperatures and humidity can all influence where a species of mosquito can occur and for how long the adult stage is active. Much time, effort and funding has been directed towards the development of models to predict future distribution of, for example, *Ae. albopictus* in Europe. As recently suggested by Proestos et al., policy decisions to control vector-borne diseases may utilize these models.<sup>9</sup> However, models are only as good as the data upon which they are based, and when it comes to the potential impact of climate change there is much speculation and many unknowns. The biology of *Ae. albopictus* has been a subject of interest for many years, with Mitchell discussing concerns related to its spread in Europe.<sup>10,11</sup> It would be irresponsible not to model climate change driven spread, but we should probably model multiple scenarios and have response options that can be implemented according to what actually happens. Only having a response based on an alarmist worst-case scenario may not be optimal. One recent model, which utilized climate predictions for 2050, estimated that approximately 2.4 billion individuals in a land area of nearly 20 million km<sup>2</sup> will potentially be exposed to *Ae. albopictus*.<sup>9</sup> They suggest that these new insights into vector-borne disease spread will support disease control and policy making.

Despite the enormous technological advances in virological analysis in recent decades, we are still unable to predict future epidemiological scenarios. Although the general sentiment may have been that things will get worse, nobody predicted that West Nile virus would become established throughout North America and CHIKV would begin an intercontinental redistribution. On the positive side, novel mosquito control approaches and vaccine technologies that were unimagined 35 years ago have been developed and are already being applied in the fight against vector-borne diseases.

In their recent publication on climate change effects on vector-borne diseases in the UK, Medlock and Leach review several governmental and other reports related to predicted climate change.<sup>12</sup> Conclusions that 'it is generally inappropriate to make assessments of the effect of changing temperature alone on vector-borne diseases', and that direct effects on these diseases cannot be predicted with any real confidence, are important and support a statement that a primary focus for decision makers must be to ensure that adaptive strategies for climate change must not actually exacerbate the risks. A balance between rushing to conclusions and implementing poor and potentially counterproductive policies, and on the other hand being complacent and not taking advantage of the available data, must be struck. On the whole, Europe's proactive approach towards the goal of preparing for introductions of new vector-borne diseases and increased incidence is to be applauded. The development of models that take into account the complexities of vector-borne diseases is very challenging but is critical in order to prepare for the surprises that nature has in store for us. Models must, however, evolve to accommodate real-world changes of the many factors that influence vector-borne disease transmission cycles. To

accomplish this, surveillance programs, supported by experts in many areas, must be implemented and sustained. In many respects, the European Centre for Disease Prevention and Control's VectorNet initiative was established in 2014 for this very purpose.<sup>13</sup>

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## References

- 1 Rezza G, Nicoletti L, Angelini R et al. Infection with chikungunya virus in Italy: an outbreak in a temperate region. *Lancet* 2007;370:1840–6.
- 2 Grandadam M, Caro V, Plumet S et al. Chikungunya virus, southeastern France. *Emerg Infect Dis* 2011;17:910–3.
- 3 Tsetsarkin KA, Vanlandingham DL, McGee CE, Higgs S. A single mutation in chikungunya virus affects vector specificity and epidemic potential. *PLoS Pathog* 2007;3:e201.
- 4 Mansuy JM, Grouteau E, Mengelle C et al. Chikungunya in the Caribbean—threat for Europe. *Emerg Infect Dis* 2014;20:1423–5.
- 5 Paty MC, Six C, Charlet F et al. Large number of imported chikungunya cases in mainland France, 2014: a challenge for surveillance and response. *Euro Surveill* 2014;19:20856.
- 6 Medlock JM, Hansford KM, Versteir V et al. An entomological review of invasive mosquitoes in Europe. *Bull Entomol Res* 2015;1–27.
- 7 Sousa CA, Clairouin M, Seixas G et al. Ongoing outbreak of dengue type 1 in the Autonomous Region of Madeira, Portugal: preliminary report. *Euro Surveill* 2012;17:pii:20333.
- 8 Reiter P. Yellow fever and dengue: a threat to Europe? *Euro Surveill* 2010;15:19509.
- 9 Proestos Y, Christophides GK, Erguler K et al. Present and future projections of habitat suitability of the Asian tiger mosquito, a vector of viral pathogens, from global climate simulation. *Philos Trans R Soc Lond B Biol Sci* 2015;370: pii:20130554.
- 10 Hawley WA. The biology of *Aedes albopictus*. *J Am Mosq Control Assoc Suppl* 1988;1:1–39.
- 11 Mitchell C. Geographic spread of *Aedes albopictus* and potential for involvement in arbovirus cycles in the Mediterranean basin. *J Vector Ecol* 1995;20:44–58.
- 12 Medlock JM, Leach SA. Effect of climate change on vector-borne disease risk in the UK. *Lancet Infect Dis* 2015;15:721–30.
- 13 VectorNet: A European network for sharing data on the geographic distribution of arthropod vectors, transmitting human and animal disease agents. [http://ecdc.europa.eu/en/activities/diseaseprogrammes/emerging\\_and\\_vector\\_borne\\_diseases/Pages/VBORNENET.aspx](http://ecdc.europa.eu/en/activities/diseaseprogrammes/emerging_and_vector_borne_diseases/Pages/VBORNENET.aspx) [accessed 13 July 2015].