

Moving Arbovirology in a Changing World

Jean-Paul Gonzalez^{1,2}, Tom Vincent³

¹Centaurus Biotech., Chantilly, Virginia, USA

²Georgetown University, School of Medicine, Washington D.C, USA

³CRDF Global, Arlington, Virginia, USA

*Correspondence should be addressed to Jean Paul Gonzalez; jpgonzalez2808@gmail.com

Received date: December 17, 2019, **Accepted date:** December 20, 2019

Copyright: © 2019 Gonzalez JP, et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Arbovirology, Arbovirus, Arthropod-borne virus –, these are scientific terms that refer to viruses that infect via “blood sucker” arthropod vectors and are capable of multiplying and transmitting the virus to vertebrates through their bite. These vectors are essentially mosquitoes (male only), ticks, and sandflies that feed mainly on mammals, but sometimes on other vertebrates (e.g. birds, reptiles). However, some arboviruses can exclusively infect arthropods and do not replicate in vertebrates; they are known as “host-restricted insect-specific viruses”. Some of them are genetically similar to well-known virus families (Flaviviridae, Togaviridae, Phenuiviridae) that include highly pathogenic arboviruses for vertebrates (e.g. dengue virus, western equine encephalitis virus). Do these viruses have the potential to jump into vertebrates as a new potential host and generate another emerging disease? Also, can we use these viruses as a tool to eventually aid the prevention of arbovirus transmission and protect the populations against arbovirus threats? [1]. Only the continuous efforts of scientific research will allow us to answer.

Once upon a time, Zika was just a forest in Uganda. Today, it is known to most as a disease-causing virus, but many do not truly understand that it has made a journey from an anonymous, undiscovered, yet widely circulating virus with zero to minimal pathogenic characteristics within mammals, to one of the most notorious viruses in the world. And though this has been an unlikely journey, any virus has the potential to undergo such a similar transformation. To understand Zika’s journey is to understand the nature of arboviruses, their frequently neglected status with respect to disease surveillance, and

their potential to emerge as severe public health risks.

Many people understand that there are mosquito-borne illnesses that are spread by viruses, but it may come as a surprise that there are thousands of viruses that are spread by mosquitos that can infect humans. The overwhelming majority of these infections do not cause disease, either because they are not capable of proliferating within the human ecosystem, or they are easily overcome by our immune systems, or in some rare cases, the disease they produce is undetectable or inconsequentially mild. The sheer number of these viruses make it difficult to justify funding for research or surveillance for every virus, much less a virus that does not cause disease in humans. This was precisely the case for Zika prior to 2015 when it emerged in the Americas as one of several viruses known to circulate among mosquitos and non-human primates, which posed no significant risk of illness among humans.

From the recent article on “Exploiting the Legacy of the Arbovirus Hunters” [2], it is clear that “a generational gap has developed in the community of arbovirus research.” This has several origins, with the well-recognized one starting in the early 1980s, when the HIV pandemic suddenly moved the resources and the scientists away from arbovirology to a neglected field of retroviruses, also, with a positive impact by funding the emerging biotechnologies successfully accompanying the domain (Pathogen Molecular detection). Since that period, the historical richness of field-oriented virus discovery has reduced. Moreover, since the 1990s, new technologies (i.e. next generation sequencing) have resulted in an increase of virus discovery - more

new virus sequences of novel virus isolates - that are changing our understanding of the virus world and dramatically impairing the field of arbovirology toward eco-epidemiology - viruses and natural hosts suspected or unknown - and the fundamentals of the immune response. Nevertheless, the oxymora of the relentless tide of “big” data generated by sequencing, too often partially described or understood, has had a negative impact for public health, as the goal has been to promptly detect and characterize emerging arbovirus pathogenic for human or animal. As an example, within a five year study of mosquito and tick collection in China, 28 non-dengue and non-Japanese encephalitis viral strains were isolated from different places and confirmed to be part of the classical Togaviridae arbovirus family [3]. All these new isolates belong to a family known to harbor highly pathogenic viruses for human and animals and need to be distinctly characterized for their potential threat for human and animals. New arboviruses should continue to be identified and isolated in China and their extension more accurately known [4].

Nevertheless, Arbovirus are spreading and will spread with their vectors [5], while arbovirology is shrinking. As an example, taken by these authors “The global population at risk from mosquito-borne diseases including dengue, yellow fever, chikungunya and Zika is expanding in concert with changes in the distribution of two key vectors: *Aedes aegypti* and *Aedes albopictus*. The distribution of these species is largely driven by both human movement and the presence of suitable climate.” Indeed, human exponential population growth and subsequently increasing numbers of exchanges and interactions and intensity (trade, travel, migration, etc.), as well as climate change and virus-mosquito transportation in permissive previously naïve environments (e.g. the classical model of infected mosquitos’ eggs transported by sea cargo), all are concurring as main drivers of arbovirus spread and outspreading endemicity.

Nonetheless, it is difficult to forecast which arboviruses will become public health threats when there so many to choose from, and so many that are innocuous to humans. But this is precisely the paradox that many public health decision-makers face: how do you determine which of the multitude of arboviruses to surveil or research, when any of them can emerge as threats to humans? Most would agree that we would benefit from some advanced warning on what could be “the next Zika”. This advanced warning, though, comes from proper arbovirus surveillance, which can be costly. This is the conundrum we face with respect to finding “the next Zika”: adequate arbovirus surveillance is costly, and the results of the surveillance may be as innocuous as the viruses being surveilled.

Against the inexorable circulation and spread of arboviruses, and the discovery and emergence of new arboviruses among naïve populations and previously unscathed territories, we ultimately need to be prepared, and arbovirology must persist in the concert of medical sciences.

References

1. Öhlund P, Lundén H, Blomström AL. Insect-specific virus evolution and potential effects on vector competence. *Virus genes*. 2019 Apr 1;55(2):127-37.
2. Vasilakis N, Tesh RB, Popov VL, Widen SG, Wood TG, Forrester NL, Gonzalez JP, Saluzzo JF, Alkhovsky S, Lam SK, Mackenzie JS. Exploiting the Legacy of the Arbovirus Hunters. *Viruses*. 2019 May;11(5):471.
3. Chen W, Qiu F, Calisher CH, Liu J, Chen H, Li X, Zhao Z, Chen Y, Kuang J, Wang M. Twenty-eight alphavirus strains isolated from mosquitoes and ticks captured from Hainan Island, China. *Zhonghua shi yan he lin chuang bing du xue za zhi= Zhonghua shiyan he linchuang bingduxue zazhi= Chinese journal of experimental and clinical virology*. 1997 Jun;11(2):144-6.
4. Meng WS, Zhang JB, Sun XH, Liu QN, Chen Z, Zhai YG, Fu SH, Cao YX, Wang HY, Ding J, Chu FJ. Isolation and identification of arboviruses from mosquito pools in some regions of Liaoning province, China. *Zhonghua liu xing bing xue za zhi=Zhonghua liuxingbingxue zazhi*. 2009 Jan;30(1):50-4.
5. Kraemer MU, Reiner RC, Brady OJ, Messina JP, Gilbert M, Pigott DM, Yi D, Johnson K, Earl L, Marczak LB, Shirude S. Past and future spread of the arbovirus vectors *Aedes aegypti* and *Aedes albopictus*. *Nature microbiology*. 2019 May;4(5):854.