

Practical Strategies for Emerging Incidences of Chikungunya Fever in Kenya

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Abstract

Chikungunya fever is an alphavirus transmitted through mosquito bites causing serious musculoskeletal pain and acute fever. There are several previous cases across the globe especially in the coastal areas of the Indian Ocean, Asia, Europe, and other African countries. In 2004 and 2005, Kenya reported serious incidences of chikungunya virus in Lamu and Mombasa. The chikungunya fever re-occurred in 2016 together with cholera in the northern parts of Kenya and caused hospitalisation to more than 500 people. This calls for the need to put in place studies that identify novel molecules with therapeutic potentials and uncovers the virulent genes. Such outbreaks will keep repeating unless we find alternative approaches of tackling these viral conditions to complement the existing measures that control the mosquitoes transmitting the virus. Research that identifies potential hosts and elucidates new virulent molecules could guide the identification of molecules that inhibit viral replication. Besides, documenting epidemiological, environmental factors and the development of alternative diagnostic kits is vital for early detection and institution of corrective measures. The previous and recent trends should inform the directions of the future studies. Such studies will add value to the one health approach toward controlling the recent and future incidence of chikungunya virus and other emerging diseases that cause serious health and economic challenges to the underprivileged communities.

Keywords: Chikungunya Fever; Kenya; Disease outbreaks; Incidence

Introduction

Arthropods play a critical role in the transmission of viral pathogens to humans and animals [1]. The Diptera: Culicidae, which encompass mosquitoes, poses the main challenge in the tropics and other parts of the world because they act as the main vectors for the transmission of parasitic and viral pathogens [2,3]. Examples of these diseases include West Nile, Yellow Fever, Chikungunya, Malaria, Rift Valley Fever, and forms of Equine encephalitis among others [3]. The three main families of arboviruses or arthropod borne viruses include the Bunyaviridae (that includes Rift Valley Fever virus), Flaviviridae (consists of Dengue virus), and Togaviridae that comprise of chikungunya virus [4]. These arboviruses are transmitted through bites from infected mosquitoes *Aedes aegypti* and recently *Aedes albopictus* [4,5]. The clinical manifestation range from severe joint pain, muscular pain, fatigues, to fever [3,5,6]. However, the clinical manifestations are shared within the arbovirus families and other conditions like bacterial infections, dysentery, fever and malaria thereby making it difficult to control [3,6]. Other challenges include poor approaches toward diagnosis because the laboratory tests are limited. The disease was first reported in Africa in 1950s and since then several cases emerging from African nations and Asia has been on the rise as previously reported [5]. Kenya experienced a re-emergence of Chikungunya virus in 2004 in Lamu, which is an island in the Indian Ocean coast [4-6]. According to previous reports, there were 13500 confirmed cases of the virus in Lamu, which showed that more than 70% of the island population experienced the outbreak [4]. A few months later, the virus infected population in the adjacent towns of Mombasa within the Indian Ocean coast before spreading to other regions along the Indian Ocean like the Comoros [7].

Outbreak of Chikungunya fever

Several reports show that Chikungunya infection has spread to various parts of Africa, Europe, and Asia since it was first reported in 1950s (6). Early studies grouped the virus into three genotypes to correspond with the location and endemic regions; these include the Asian genotype, East/Central African genotype, and the West African type [7]. Although most outbreaks were reported along the coastline of the Indian Ocean the first outbreak in Kenya occurred in 1982 [4]. Regions that have experienced it include India [7] Comoros Island [7,8], La Reunion [9], Italy [10], parts of Asia [11], France [12,13] and Africa [14] including Kenyan coast towns of Mombasa and Lamu [15,16]. Besides, cases of Dengue virus were reported in 1982 and 2011 in the Kenyan coast and the North Eastern parts Kenya respectively [4]. Reports attribute these outbreaks to three serotypes namely DEN-1, DEN-2, and DEN-3 [4].

On May 27th 2016, there were reports of confirmed cases of chikungunya fever incidences. Reports from the health professionals working for the Kenyan government confirmed a double outbreak of Chikungunya virus and cholera disease in the northern parts of Kenya [17]. These resulted in hospitalisation of more than half of the 540 people with confirmed tests attributed to the viral infection [17]. Samples collected from the new cases could play a role in unravelling if there are any genetic variations from the last outbreak that occurred in 2004-2005 [4,5,16]. Besides, undertaking research to assess, identify, and compare circulating growth factors, chemokines and cytokines between patients with positive cases and healthy individuals will assist with the strategies of developing modulators that could halt severity and progression of the disease. The identification of neutralising antibodies could also act as an alternative therapeutic for the disease. Other interesting studies in this area include the assessment of molecular mechanisms controlling the chikungunya

virus. For example, the expression profiles will elucidate molecules that facilitate development of the condition and this could assist with the efforts of targeting replication activities. Undertaking these researches and sharing information with the relevant parties will complement existing vector control strategies to attain a one-health approach toward control of chikungunya virus and improve control strategies.

In 2013, the World Health Organization reported cases of chikungunya transmission in the Caribbean and the United States with most transmission associated with returning travelers from areas with known transmissions [18-20]. These reports termed the occurrence as local transmission of the virus in the Western Hemisphere with estimated 795,000 cases in 37 countries [18,19]. The CDC estimates that most of the cases with infections returned from Asia [18,19], Indonesia, the Pacific and the Caribbean [20].

Emerging Risk factors and status in Kenya

The transmission of chikungunya virus happens through the bite of mosquito *Aedes aegypti*, which thrives in environments with certain climatic variables [20]. For instance, the low land and other environments with optimum relative humidity, temperature, and rainfall determine the abundance of the vector thereby increasing their transmission. The recent outbreak in the Northern Kenya signifies extension in their distribution. Conventionally, high altitude areas provided ample environment for the multiplication and vector transmission, however, the changing patterns of weather associated with warming could accelerate the adaptability and fitness of the vector thereby increasing transmission [21]. These development means that new studies to assess the altitudinal distribution of Chikungunya and other vector-borne diseases as well as the genetic differences may shed light toward its management in Kenya. Such studies need to focus on vegetation, elevation, and climatic factors, perhaps studies would assess the vector fitness in different regions and provide leads into their management approaches.

Symptoms and complications of Chikungunya fever

The name Chikungunya originates from a tribe in Tanzania, who were first to experience the fever [21,22]. The condition is self-limiting, non-fatal, and presents itself into acute and chronic phases [6]. The patients in the acute phases present clinical signs like pains in the joint, malaise, muscle pains, fever, and rashes on the skin [23], which may last for a week after infection. During the chronic phases, one third of the infected patients may experience prolonged symptoms like tenosynovitis, myositis, chronic arthritis, and fatigue for several years [6,24,25]. The diagnosis of the condition is challenging because it manifests itself with clinical signs similar to malaria and other conditions like dengue and zika [3,5]. The recent case of outbreak in Kenya was a double infection with cholera. Perhaps, such development presents an interesting area of research to uncover the association between the fever and bacterial infection.

Control and preventive measures

Arboviruses like dengue, west Nile and chikungunya fevers pose the main health concern because there are no vaccines developed for these diseases. The main control strategy and preventive measure involves controlling the mosquito vectors that transmit these conditions [3]. The main challenge associated with the *Aedes* mosquito is that it bites during the day [4]. Strategies like using repellants, clearing grasses and eradicating potential breeding sites are the main strategies for controlling the condition [3]. Other strategies include using chemicals with mosquitocidal activities to kill the nascent stages of the vector development. However, reports emerge that other species of *Aedes* transmit the fever. For instance, ecological pressure and climate changes have recently resulted in *Aedes albopictus* (Tiger mosquito) acting as a vector for the virus [4-6]. For instance, previous studies demonstrate

that when E1 glycoprotein undergoes single point mutations through the replacement of alanine with valine, it results in increased infectivity of the new mosquito vector. The paradigm shift is associated with increased infectivity because the *A. albopictus* is considered as the most lethal vector for the virus compared to *A. aegypti*. The enhancement of transmission strategies means that the risks for future outbreaks could have significant impact on social and health welfare [5,6].

Conclusions and Future strategies

The impacts of climate change and other environmental factors like drought could worsen future outbreaks. It is important to undertake studies that uncover the possibilities of mutations on both the vector and the virus genome. Genetic studies on both the vector and the virus transmitting chikungunya fever from different regions with outbreaks will provide leading information such as new virulent molecules. For instance, such studies will assess any changes in the genetic makeup that could affect the virulence. It also provides essential information on the signature molecules as well as immunological factors produced during infection to provide leads for future drug design. Designing diagnostic kits, which discriminates the chikungunya fever from other arbovirus is pivotal in early detection. Interestingly, studies could also assess potential hosts that could harbour the virus and identify molecules that enable such hosts to avoid infectivity.

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Conflict of Interest: None

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