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An insight into the history & epidemiology of Chikungunya fever in India

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Abstract
Chikungunya fever, induced by the Chikungunya virus, is an arboviral disease transmitted by mosquitoes. The vectors, *Aedes aegypti* and *Aedes albopictus*, are widespread across all continents except Antarctica. This arbovirus infection predominantly manifests in tropical, subtropical and temperate biogeographic zones. The primary vectors, female *Aedes* mosquitoes, are diurnal feeders and oviposit in stagnant water environments. The Chikungunya virus was first identified in Tanzania in 1952 and subsequently isolated in Thailand in 1958. Significant outbreaks have been recorded in India, with notable incidences in Calcutta (1963) and Hyderabad (2005), impacting millions in multiple regions. In recent years, the incidence of suspected cases has varied, with the highest prevalence observed in the states of Gujarat, Maharashtra and Karnataka.

Keywords: Chikungunya fever, epidemiology, *Aedes aegypti* and *Aedes albopictus*

Introduction
Chikungunya fever, instigated by the Chikungunya virus and vectored by *Aedes* mosquitoes, has drawn considerable attention due to its extensive distribution and substantial public health ramifications. The primary vectors, *Aedes aegypti* and *Aedes albopictus*, are also known to facilitate the transmission of other arboviruses such as dengue and Zika fever [1]. The term "Chikungunya" originates from the Makonde language of Africa, meaning "bent in pain", a descriptor that aptly captures the severe arthralgia characteristic of the disease [2]. The virus was first identified in Tanzania in 1952, marking the onset of its global dissemination, with subsequent outbreaks documented across various continents.

Review of literature
Aedes aegypti, identifiable by the characteristic markings on its legs, serves as a principal vector for the transmission of Chikungunya [3]. The female mosquitoes, driven by the need for human blood to facilitate egg development, are highly attracted to chemical cues emitted by mammals [4]. These mosquitoes are prevalent across diverse geographical regions, particularly flourishing in tropical and subtropical climates. Research suggests the potential for their range to extend into new territories as a consequence of shifting climatic patterns, which complicates efforts to control the spread of the disease. The virus's genetic structure and transmission mechanisms further contribute to its extensive distribution and persistence in affected areas.

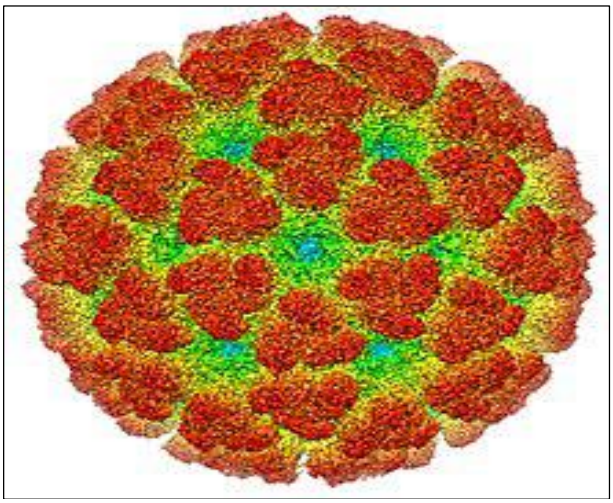
History of chikungunya virus
The Chikungunya virus originates from Africa, with its earliest detections reported in Tanzania, followed by isolations in Thailand. In India, documented occurrences trace back to the 1960s, with substantial outbreaks emerging after 2004. Significant shifts in viral genotypes have been noted, influencing the epidemiology and transmission dynamics of the disease. The virus's capacity to adapt to varied environments and vectors highlights the formidable challenges in curbing its dissemination and mitigating its public health impact [5-7].

Transmission

The transmission of the Chikungunya virus primarily occurs via the bite of infected *Aedes* mosquitoes. Female mosquitoes acquire the virus during hematophagy and subsequently transmit it to humans through successive bites. These mosquitoes display diurnal biting behaviour and preferentially oviposit in stagnant water environments. The efficiency of these transmission cycles facilitates the propagation of the disease within vulnerable populations, underscoring the need for targeted vector control strategies to mitigate transmission [8].

Morphology of Chikv (Chikungunya virus)

The Chikungunya virus is classified within the Alphavirus genus and is distinguished by its single-stranded positive-sense RNA genome. Its structural proteins, notably glycoproteins E1 and E2, play a critical role in mediating viral entry and replication within host cells. The virus exhibits a spherical morphology, characterized by surface spikes and a central nucleocapsid core, which are integral to its infectivity and pathogenic potential. A comprehensive understanding of the virus's structural and functional attributes is crucial for the development of effective diagnostic and therapeutic strategies [9].



Epidemiology

The epidemiology of Chikungunya in India underscores its endemic nature and periodic resurgence across affected regions [10]. Historical outbreaks in Calcutta, followed by the virus's spread to other states, exemplify its capacity to establish persistent transmission cycles [11] Variations in viral genotypes and vector dynamics significantly influence the patterns of disease, with marked shifts observed across different states over time [12-16]. On-going surveillance and molecular epidemiological studies are pivotal in monitoring viral evolution and guiding the development of targeted control strategies [17-19].

Symptoms of chikungunya fever

The clinical spectrum of Chikungunya fever encompasses presentations ranging from acute febrile episodes to incapacitating arthralgia and multisystem involvement. Hallmark symptoms include, high-grade pyrexia, polyarthralgia and a maculopapular exanthem, frequently accompanied by gastrointestinal and neurological manifestations. In severe instances, the disease may advance to neurotropic complications, underscoring the critical importance of prompt diagnosis and appropriate supportive management [21].

Diagnosis of chikungunya fever

The laboratory diagnosis of Chikungunya fever is based on the detection of viral RNA or specific antibodies in patient specimens. Diagnostic methodologies typically include real-time reverse transcription-polymerase chain reaction (RT-PCR) for viral RNA detection and serological assays for identifying antibodies. Prompt detection and confirmation of the infection are crucial for initiating appropriate clinical management and implementing effective public health measures.

Prevention of Chikungunya

Preventive strategies for Chikungunya primarily emphasize vector control and personal protective measures. Reducing mosquito exposure through environmental management and targeted interventions significantly mitigates the risk of transmission. Community engagement and educational campaigns are instrumental in raising awareness about preventive actions and fostering proactive mosquito control practices. Sustained vector control and disease prevention require coordinated efforts between public health authorities and local communities [22, 23].

Discussion

Chikungunya fever continues to pose a significant public health challenge in India, with recurrent outbreaks highlighting the need for comprehensive surveillance and control strategies. The intricate interplay of environmental factors, vector ecology and viral genetics adds to the complexity of disease transmission. On-going research and advancements in diagnostics, therapeutics and vector management are essential for reducing the disease burden and averting future outbreaks.

Conclusion

Chikungunya fever remains a persistent and formidable public health threat, particularly in regions like India where the virus has become endemic. The complex dynamics of its transmission, influenced by environmental conditions, vector behaviour and viral evolution, demand a multifaceted approach to control and prevention. Effective management hinges on the continued integration of advanced diagnostic tools, robust vector control strategies and public education initiatives. Moreover, on-going research into the virus's genetic variability and adaptation mechanisms is crucial for developing innovative therapeutic and preventive measures. Collaborative efforts at the community, national and global levels are imperative to mitigate the impact of Chikungunya and to safeguard public health against future outbreaks.

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