



# Editorial: Chikungunya-A Reemerging Disease: Challenges and Coping Up During 1952-2020

Mishra S\*

IFTM University, India

\*Corresponding author: Sanjay Mishra, School of Biotechnology, IFTM University, Delhi Road (NH 24), Moradabad-244102, Uttar Pradesh, India, Email: sanjaymishra@iftmuniversity.ac.in

Editorial

Volume 2 Issue 1

Received Date: August 17, 2020

Published Date: August 31, 2020

## Editorial

Chikungunya is a mosquito-borne disease caused by the CHIKV virus of the family *togaviridae* belongs to the genus alpha virus. The first sought of the disease made in the year of 1952 when the very first case was registered in the Tanganyika (now known as Tanzania) then in the subsequent year i.e. 1953 first outbreak of chikungunya took place in the region affected the large population. Most of the population got affected from the outbreak and the disease made a remarkable entry in the society [1]. The chikungunya disease has resemblance with Dengue but the severe joints pain is the contrasting features of chikungunya make it different from dengue. Common symptoms like high grade fever, rigors, headache, and rashes on skin [1]. Africa is the first continent to face the first ever case of chikungunya in the year 1952 in Tanzania and after that several countries of African continent faces the effect of chikungunya and in the year of 1956 south Africa faces another outbreak of chikungunya and still bearing the burden of disease [2]. Central African Republic, Uganda, Nigeria and Democratic Republic of Congo had exercised series of outbreaks during the year of 1960's to 1990's. Lamu island of Kenya struggled with the drastic outbreak in the year 2004; more than 70% of the population got affected with chikungunya [3].

The observed pattern of the infection was almost similar in all the society of the plateau region, which is situated around 2000 feet from the sea level. Once the infection occurred in the family all the member of the family got affected by this. Primarily the affected member belongs to the group of adult (>45 age group) or from infant. After the first outbreak in Tanzania, the second outbreak took place in the regions of Africa in the year of 1956. From then several incidences had occurred. During 1960-1990 several regions such as Angola, Burundi, Central African Republic, Democratic Republic of Congo, Guinea, Malawi, Nigeria, South Africa and Uganda of African continent got affected and the number of patients increasing day by day. In the beginning of 2004 the

disease reemerges on Lamu Atoll, Kenya and spreads in the surrounding regions like La Reunion, Comoros etc. resulting approximately half million of cases [4]. The CHIK virus was detected first time in the year of 2005 with limited number of cases, while in 2006 the number of registered cases increased exponentially. When the epidemic was at their peak that time approximately 40,000 cases [5] was getting registered per week.

Total of 266,000 cases [5] were anticipated to get occurred during the time of outbreak. The special features of infection were also come into the knowledge. Neurological manifestations, fetal infections and mortality [5] were also observed during the outbreak occurred in 2006 [5]. In 2009 France encountered the case of CHIKV in the traveller of France, who returned from the Maldives. After that in the year of 2010, autochthonous transmission of CHIKV caused the chikungunya infection and 2 cases were identified for the CHIKV positive [6]. Again in the year of 2014 the environmental conditions were found favourable for the autochthonous transmission of CHIKV and this result in the total of 126 laboratory confirmed cases of chikungunya on the land of France. The traveller who returned from the Caribbean islands faces the outbreak at the island and they were the cause of the infection in the France [7]. Apart from this several such events had taken place in Europe, where travellers from the different part of world were the main cause for the CHIKV infection. Spain and Portugal also have met with such events that 10 and 4 cases of CHIKV were found respectively [8]. United States were remain untouched with this severe infection for a long, only 3 cases were registered in between the 1995 to 2005 and these 3 registered patients were traveller returning from the places where outbreak took placed [9].

During the time from 2006 to 2013 the number of chikungunya cases were increased slightly i.e. 26 cases

per year but this number increased to 29 per year later on [9]. All the registered cases were viremic on returning to US from the region where the risk of the disease was high. In Asia, Bangkok was the first place where chikungunya was identified in the year of 1958, the disease was kept expanding till 1964 and again re-emerged in the year of 1970 and got declined in the year of 1976. The main cause of the disease was the Asian genotype of CHIKV and vector was *Aedes aegypti* [10]. The disease re-emerged in the Southern Thailand in the year of 2008-2009, in which approximately 45000 [10] cases were registered. The cause of the disease was the ECSA genotype (East Central South African) of CHIKV and the vector was *Aedes aegypti* [11]. China faced a major chikungunya outbreak in the year of 2010. In the Guangdong Province of China, people were reporting the dengue like symptoms, in the laboratory testing it was observed that the high grade fever with the joint pain was not caused by the dengue fever while CHIKV is responsible for that. The first chikungunya case was reported on 1st of September and the number of cases increased rapidly, that indicates a severe outbreak in the city. The 174 cases were reported and none of the patient had a travel history, which confirms the outbreak in the province [12]. Malaysia had experienced various chikungunya outbreaks and the region of this was the same as Thailand that is high traveller index. The first chikungunya was observed in Klang in 1998, followed by an outbreak in the year 2006 in the rural area of Perak and further in 2008 urban area of Johor experienced another chikungunya outbreak. The outbreak in 1998 was caused by the Asian genotype while the further outbreak was caused by the ECSA genotype [13].

Bangladesh had experienced the major outbreak in the capital of country Dhaka in the year of 2017. The disease prolonged in the region from January to September. This outbreak affects most of the surrounding area. Environmental conditions were suitable for the vector to cause the infection. The special symptoms are characterized in the outbreak of Bangladesh. The joint pain are the main characterization of CHIKV infection which occurs on the onset of infection, but in the outbreak of Bangladesh joint pain was observed in the patient before the fever [14]. Chikungunya is well known in India since 1963. The very first outbreak of chikungunya had taken place in the Eastern part of country and affected large number of the population. The disease had no previous history so it got confused with the dengue fever but the laboratory test confirms that it was different from the dengue and characterized by the joint pain and high grade fever [15]. In the subsequent year 1964 CHIKV caused infection in the region of South India (Vellore, Pondicherry, Chennai), 306 cases were identified positive for the CHIKV infection [15]. In 1965 the CHIKV infection enters the state of India that is Andhra Pradesh (Now divided into two parts Andhra Pradesh and Telangana). The intensity of the infection was very high

and reaches to various districts of the states (Vijayawada, Vishakapattanam, Rajahmundry etc.). In 1973 the infection reached to North India and first found in the Barsi (Bhiwani, Haryana). The infection was caused by the Asian genotype around the country [16].

The disease disappears after the 1973 and again re-emerged after 32 years with the more virulent form and caused a major outbreak in the various states of India including Tamilnadu, Karnataka, Andhra Pradesh, Maharashtra, West Bengal, Uttar Pradesh, & Madhya Pradesh. The genotype of the virus had changed this time, the African genotype was the cause of the infection [16].

## Conclusion

Chikungunya is reemerging disease worldwide. The burden of this infectious disease is increasing day by day throughout the globe. At present there is no vaccine or medicine available to treat this disease. The expansion of disease is increase to the regions which are favorable for the growth of vector. So this review study summaries the available outbreak and the genomic mutation of the genome. The aim of this compilation was to bring out the focus of researchers and scientists towards this re-emerging disease to overcome the burden of this disease from the human society, and, therefore, work along these notions and objectives have been in active state evident by research outputs as a continuous efforts through in silico studies [17,18], and further work to validate these outcomes through physiological and biochemical experimental laboratories is in progress.

## References

1. Hertz JT, Munishi OM, Ooi EE, Howe S, Lim WY, et al. (2012) Chikungunya and dengue fever among hospitalized febrile patients in northern Tanzania. *Am J Trop Med Hyg* 86(1): 171-177.
2. Johansson MA, Powers AM, Pesik N, Cohen NJ, Staples JE (2014) Nowcasting the Spread of Chikungunya Virus in the Americas. *PLoS ONE* 9(8): e104915.
3. Robinson MC (1955) An epidemic of virus disease in Southern Province, Tanganyika Territory, 1952-53. *Trans R Soc Trop Med Hyg* 49(1): 28-32.
4. Pistone T, Ezzedine K, Boisvert M, Receveur MC, Schuffenecker I, et al. (2009) Cluster of chikungunya virus infection in travelers returning from Senegal, 2006. *J Travel Med* 16(4): 286-288.
5. Ansumana R, Jacobsen KH, Leski TA, Covington AL, Bangura U, et al. (2013) Reemergence of Chikungunya Virus in Bo, Sierra Leone. *Emerg Infect Dis* 19(7): 1108-

- 1110.
6. Kumarasamy V, Prathapa S, Zuridah H, Chem YK, Norizah I, et al. (2006) Re-Emergence of Chikungunya Virus in Malaysia. *Med J Malaysia* 61(2): 221-225.
  7. Noridah O, Paranthaman V, Nayar SK, Masliza M, Ranjit K, et al. (2007) Outbreak of Chikungunya Due to Virus of Central/East African Genotype in Malaysia. *Med J Malaysia* 62(4): 323-328.
  8. Chua KB (2010) Epidemiology of chikungunya in Malaysia: 2006-2009. *Med J Malaysia* 65(4): 277-282.
  9. Hossain MS, Hasan MM, Islam MS, Islam S, Mozaffor M, et al. (2018) Chikungunya outbreak (2017) in Bangladesh: Clinical profile, economic impact and quality of life during the acute phase of the disease. *PLoS Negl Trop Dis* 12(6): e0006561.
  10. Rashid MDHO, Patwary MH, Imtiaz A, Abdullah SA, Zahedur R, et al. (2018) Seroprevalence of Chikungunya during Outbreak in Dhaka, Bangladesh in 2017. *J Virol Antivir Res* 7: 2.
  11. Shah KV, Gibbs CJ Jr, Banerjee G (1964) Virological investigation of the epidemic of haemorrhagic fever in Calcutta: isolation of three strains of Chikungunya virus. *Indian J Med Res* 52: 676-683.
  12. Kumar NP, Suresh A, Vanamail P, Sabesan S, Krishnamoorthy KG, et al. (2011) Chikungunya virus outbreak in Kerala, India, 2007: a seroprevalence study. *Memórias Do Instituto Oswaldo Cruz* 106(8): 912-916.
  13. Kaur N, Jain J, Kumar A, Narang M, Zakaria MK, et al. (2017) Chikungunya outbreak in Delhi, India, 2016: report on coinfection status and comorbid conditions in patients. *New Microbes New Infect* 20: 39-42.
  14. Singh RK, Tiwari S, Mishra VK, Tiwari R, Dhole TN (2012) Molecular epidemiology of Chikungunya virus: Mutation in E1 gene region. *J Virol Methods* 185(2): 213-220.
  15. Hawman DW, Carpentier KS, Fox JM, May NA, Sanders W, et al. (2017) Mutations in the E2 Glycoprotein and the 3' Untranslated Region Enhance Chikungunya Virus Virulence in Mice. *Journal of Virology* 91(20): 816-817.
  16. Gao Y, Goonawardane N, Ward J, Tuplin A, Harris M (2019) Multiple roles of the non-structural protein 3 (nsP3) alphavirus unique domain (AUD) during Chikungunya virus genome replication and transcription. *PLOS Pathogens* 15 (1): e1007239.
  17. Saxena P, Mishra S (2020) Study of the binding pattern of HLA Class I alleles of Indian frequency and cTAP binding peptide for Chikungunya vaccine development. *International Journal of Peptide Research and Therapeutics*.
  18. Mishra S, Saxena P, Saxena M (2020) In silico study on the binding pattern of cTap binding epitopes of S-27 strain with the common HLA alleles for the Chikungunya vaccine development. *J Biochem Mol Med* 2(1): 91-96.

