Domestic and Environmental Factors of Chikungunya-affected Families in Thiruvananthapuram (Rural) District of Kerala, India

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ABSTRACT

Background: The world is experiencing a pandemic of chikungunya which has swept across Indian Ocean and the Indian subcontinent. Kerala the southernmost state of India was affected by the chikungunya epidemic twice, first in 2006 and then in 2007. Kerala has got geography and climate which are highly favorable for the breeding of *Aedes albopictus*, the suspected vector. **Aim:** The aim of the study was to highlight the various domestic and environmental factors of the families affected by chikungunya in 2007 in Thiruvananthapuram district (rural) of Kerala. Settings and design: This is a cross-sectional survey conducted in Thiruvananthapuram (rural) district during November 2007. **Materials and Methods**: Samples were selected from field area under three Primary Health Centers. These areas represent the three terrains of the district namely the highland, midland, and lowland. The sample size was estimated to be 134 houses from each study area. The field area of health workers was selected as clusters and six subcenters from each primary health center were randomly selected (lot method). **Results and Conclusions:** The proportion of population affected by chikungunya fever is 39.9% (38.9–40.9%). The investigators observed water holding containers in the peri-domestic area of 95.6% of the houses. According to regression (binary logistic) analysis, the area of residence [adjusted odds ratio (OR) = 8.01 (6.06–14.60)], residing in a non-remote area [adjusted OR=0.25 (0.16–0.38)], perceived mosquito menace [adjusted OR=3.07 (2.31–4.64)], and containers/tires outside the house [adjusted OR=5.61 (2.74–27.58)] were the independent predictors of the occurrence of chikungunya in households.

Key words: Chikungunya, Domestic factors, Environmental factors, Kerala

INTRODUCTION

The world is experiencing a pandemic of chikungunya, which started from the eastern coast of Africa during early 2005. Historically chikungunya circulates throughout sub-Saharan Africa in a sylvatic cycle involving primates and, typically, forest-dwelling species of Aedes.^[1] A major outbreak commenced in the islands of the western Indian Ocean in February 2005. By June 2006 there had been an estimated 266 000 cases in La Réunion, roughly one third of its population. The virus belongs to the East African lineage, and *Aedes albopictus* appears to have been the sole vector. Shortly after chikungunya virus reached La Réunion, it is believed that a mutation occurred that is thought to have increased its transmission through *Aedes albopictus*.^[2] Investigations regarding the seasonal prevalence, container

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preferences, and geographic distribution of the species (*Ae. albopictus*) showed strong ecological adaptability.^[3]

Subsequently in 2006, an outbreak developed in India affecting at least 213 districts in 15 states of the country.^[4] The viral strain responsible for this outbreak was of the same lineage (African genotype) as that in the Reunion island outbreak whereas previous outbreaks in India had involved an Asian genotype.^[5] The primary vector in the 2006 outbreak is thought to *be Ae. albopictus*. The previous focal outbreaks were generally associated with high densities of *Ae. aegypti*.

Kerala was affected twice by the chikungunya epidemic, first in 2006 and then in 2007. Alappuzha and Thiruvananthapuram were the two districts extensively affected by the first epidemic in Kerala. The outbreak was confined to the coastal region. The second attack in 2007 was more extensive and the geographical location shifted to the plantation areas on the eastern side.^[6] Kottayam, Pathanamthitta, Kollam, and Thiruvananthapuram (east) were the heavily hit districts. Many studies from the pandemic affected areas all over the world including Kerala suggested the *Ae. albopictus* species as the major villain.^[6] Kerala has got geography and climate which highly favor breeding of *Ae. albopictus*, which is thought to breed in natural water collections. Rubber plantations with its latex containers, cocoa plantations, and pineapple plantations in the high land add to the burden. ^[7] The geographical and ecological factors of the state is such that the eastern high ranges have high humidity and rainfall^[8] which will in turn support the breeding of mosquitoes. At the same time, the urban type of dwellings, plastics, and water scarcity provide favorable indoor breeding sites for the endophilic, *Ae. aegypti*^[9] in the coastal belt.

The aim of the study is to find out the domestic and environmental factors of chikungunya-affected households in Thiruvananthapuram (rural) district of Kerala during the 2007 epidemic.

MATERIALS AND METHODS

Thiruvananthapuram, the southernmost district of Kerala, was one of the grossly affected districts in the epidemic of 2007. The district was struck by the 2006 chikungunya epidemic as well. There was a difference in the geographical location of the two outbreaks [Figure 1]. The coastal belt was hit in 2006 and the high ranges in 2007 [Figure 2]. Thiruvananthapuram is a densely populated district (1476 persons/square kilometer) with more than 3.2 million people residing in about 7.6 lakh households. Out of the total population more than 2.1 million (65.6%) belong to the rural area.^[10]

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Figure 1: Chikungunya-affected areas of Thiruvananthapuram district 2006–7 (Source: Directorate of Health Services, Government of Kerala)

Chikungya affected areas 2007

This cross-sectional survey was conducted in Thiruvananthapuram (rural) district during November 2007. Samples were selected from areas under three Primary Health Centers: Vithura, Aryanad, and Vakkom. These areas were selected to represent the different terrains of the district [Figure 2]. Study population included families in the geographical area affected by chikungunya epidemic. The report by an inter-disciplinary team of Government of Kerala about the prevalence of chikungunya in Pathanamthitta, Kollam, and Thiruvananthapuram districts during the 2007 viral fever outbreak was used to estimate the sample size. According to the report 60% of the houses were affected by chikungunya fever.^[11] The sample size of the present study was estimated to be 134 by giving a design effect of 2. It was decided to collect 134 samples from each Health Center area for meaningful cross-tabulations.

The cluster sampling technique was used to collect the information. It was decided to include 6 clusters each having 23 houses. Field areas of health workers were selected as clusters. Six sub-centers from each primary health center were randomly selected (lot method). Twenty-three houses from each sub-center area were arbitrarily included in the study.

A structured questionnaire was used for data collection. The questionnaire was prepared under the guidance of the epidemiologists, entomologists, and sociologists in the Department Of Community Medicine, Medical College, Thiruvananthapuram. We had to resort to the syndromic approach for case detection because of resource constraints. The content validity of the questionnaire was assessed with the help of the faculty in the department.

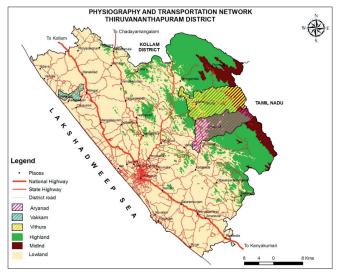


Figure 2: The topography and conveyance facilities of Thiruvananthapuram district (Source: Resource Analysis Division (RAD), Centre for Earth Science Studies (CESS), Thiruvananthapuram

The major domains of the questionnaire were housingrelated parameters (e.g.: location, walls, roof, etc), mosquito breeding-related information (e.g. presence and nature of containers, breeding, perceived mosquito menace, etc) and practice of mosquito control.

The case definition of chikungunya used was an attack of joint pain affecting more than one joint with the appearance of fever within a period 2 days prior to and 2 days after the onset of joint pain. The case definition was developed based on the investigation of chikungunya epidemic carried out by the faculty during the early phase. This case definition has a sensitivity of 88% and a specificity of 50.4% compared to IgM ELISA test for chikungunya.[11] The Junior Health Inspectors and Junior Public Health Nurses in selected sub-centers were briefed regarding the correct usage of the questionnaire. The health workers were asked to collect information from 138 houses under each health center (over all sample size of 414). They collected information from 528 houses altogether. The questionnaires were collected back after verifying all the entries. The data regarding all the 528 houses were entered and included in the study. As the study dealt with the domestic and environmental factors related to the outbreak, houses were considered as sampling units.

Ethics

Informed consent from each of the heads of families and ethical clearance from the institutional human ethical committee was obtained. Around 114 interview schedules were collected in addition to the estimated sample size. After collection of data authors felt that it is unethical on our part not to use it. Therefore we have included these data also in the analysis.

Statistical analysis

Frequencies and proportions with 95% confidence interval were used to interpret the data. Chi-square tests were used to interpret the statistical significance of associations and odds ratio with 95% CI was used to estimate the strength of association between the dichotomous variables. Binary logistic regression was used to identify the independent predictors of chikungunya occurrence in a family.

RESULTS

A total of 528 households were studied covering 2241 people with an average of 4.24 persons per house. The proportion of population affected by chikungunya fever was 39.9% (38.9–40.9%) which comes to an average of 1.7 persons per household. But 377 households that

is 71.4% (67.5–74.3%) of the houses have at least one member affected by chikungunya. The major domestic and environmental factors of houses in the epidemic-affected area are described in Table 1. The proportion of houses that had water holding containers in the peri-domestic area (within 50 m from the outer walls of the house) was 95.6% [Table 1]. The type of containers is given in Table 2. Water containing plant shoots (65.5%) and coconut shells with water (60%) were present within 50 m of majority of the houses.

Potential mosquito breeding places in the intra-domestic area were noted in 29.2% of houses [Table 1]. Households not using any anti-adult mosquito measures were 74.4% at the time of the survey conducted just after the peak of the epidemic [Table 3]. Anti-adult mosquito measures adopted by the families in the epidemic struck area are described in Table 3.

The chikungunya-affected households were compared with those unaffected by the disease to find out the predictors of disease occurrence. The factors described in Table 4 were found significantly associated with the occurrence of chikungunya in families. Binary logistic regression analysis was used to eliminate the potential confounders in this analysis. According to regression (binary logistic) analysis, area of residence [adjusted OR=8.01 (6.06–14.60)], perceived mosquito menace [adjusted OR=3.07 (2.31–4.64)] and containers/tires outside the house [adjusted OR=5.61 (2.74–27.58)] are the independent predictors of the outcome. Residing far from a remote area is a protective factor with adjusted OR=0.25 (0.16–0.38). Cox–Snell R² value of the regression analysis is 0.26.

DISCUSSION

A study conducted by Kerala Sastra Sahitya Parishad and Department of Community Medicine, Medical College, Thiruvananthapuram, estimated the prevalence of chikungunya in the southern districts of Kerala during 2007 as high as 56.6%.^[12] The high prevalence observed could be due to selection of sample population from areas which were heavily affected by chikungunya epidemic. But in the present study, one of the study areas (Vakkom, the coastal region) was not heavily affected by chikungunya and this may be the reason for an overall decreased prevalence.

The domestic and environmental features of the houses in the epidemic struck area indicate the high likelihood of *Ae. albopictus* as the vector. *Ae. albopictus* exploits a wider range of larval habitats, both natural and artificial, than does *Ae. aegypti*, explaining its abundance in rural areas as well as

Table 1: Domestic and environmental factors					
Feature of the house	Number of houses	Percentage			
Remote or hilly area ^a	420	79.5			
Mosquito menace present	385	72.9			
Not a pukka home	373	70.7			
Domestic animals present	182	34-5			
Water holding containers inside the home	154	29.2			
Peri-domestic containers ^b	505	95.6			
Presence of large waterbodies ^c	155	29.4			
Presence of tapping rubber trees ^d	392	74.2			

^aAt least 250 m away from a public conveyance facility. ^bWithin 10 m from the outer wall of the home. ^cRivers, backwaters, or lakes at least 250 m from the house. ^dTapping rubber trees within 250 m from the house not protected using a shade or plastic sheet

Table 2: Types of peri-domestic containers

Containers	Frequency	Percentage
Coconut shells	317	60.0
Flowerpots	123	23.3
Egg shells	42	8.0
Tires	36	6.8
Plantain/pineapple/other plant shoots	346	65.5
Tree holes	34	6.4
Nil	23	4.4

Table 3: Anti adult-mosquito measures adopted by the family

Antimosquito measures adopted	Frequency	Percentage
Fuming	89	16.9
Liquidator or mat	30	5.7
Others (mosquito nets, repellents to be applied on skin, etc)	16	3.0
No measures	393	74-4
Total	528	100.0

Table 4: Environmental factors significantlyassociated to the occurrence of chikungunya asper logistic regression analysis

Variable	Adjusted odds ratio (95%CI)	P value
Area of residence (highland or midland vs lowland)	8.01 (6.06-14.60)	0.000
Residing in a non-remote area	0.25 (0.16-0.38)	0.000
Perceived mosquito menace	3.07 (2.31-4.64)	0.000
Containers/tires outside the house	5.61 (2.74-27.58)	0.000

parks and suburbs. *Ae. aegypti* is more closely associated with human habitation, breeding indoors, and outdoors in artificial habitats.^[13] Over the last 50 years the Asian tiger mosquito *Ae. albopictus* has spread to all continents in the old and the new world. This anthropophilic species is able to adapt to most climates. Although long considered as a secondary disease vector, it has been shown to be competent enough for arbovirus transmission under laboratory conditions. In several locations that it has invaded, the tiger mosquito has played a major role in arbovirus transmission.^[14] Chikungunya virus has been isolated from the salivary glands of mosquitoes of the species, *Ae. albopictus*.^[15] Using viral

infectious clones of the Reunion strain and a West African strain of CHIKV, into which either the E1-226 A or V mutation was engineered, it has been demonstrated that the mutation was directly responsible for a significant increase in CHIKV infectivity for *Ae. albopictus*.^[16]

An entomological study conducted in the Reunion Island showed that, in the warm wet season, small disposable containers were the principal urban breeding site, with 1939 positive containers in 750 houses. In the dry winter season, the species remained abundant throughout the island up to 800 m altitude and their presence was seen up to a maximum altitude of 1200 m. The preferred natural breeding sites were bamboo stumps and rock holes. Logistic regression models indicated that the optimum breeding sites contained clear water with high organic content and were situated in those areas with moderate shade.^[3] The eco-climatic conditions associated with the emergence of chikungunya fever along coastal Kenya were assessed using epidemiologic investigations and satellite data. The major finding was that unusually dry, warm conditions preceded the outbreaks in the coastal regions.^[17] This finding is consistent with the observation that water stored in the houses during summer season is a major breeding source of mosquitoes in the coastal regions of Kerala.^[9] But this is not a usual practice in the non-coastal areas (midland and highland) and there water collected in the latex cups kept in rubber plantations is the potential breeding source.^[9] This kind of a difference in the breeding preference of the mosquitoes was noted in the Reunion islands also. Small disposable containers were the principal breeding sites in the urban areas but the preferred developmental sites were bamboo stumps and rock holes in peri-urban and gully areas of the island.^[18] The natural flora is associated with chikungunya infection in other parts of the globe also. It has been reported that the presence of gardens are associated with chikungunya infection in the Reunion islands.^[19] It is to be noted that in our study three fourth of the houses are located in plantation areas.

The vector density of *Ae. albopictus* is very high when compared to any other species in all geographical planes in Kerala. *Ae. aegypti* has literally not been isolated from the high and middle terrains. Latex cups, discarded tires, plant shoots, and roof gutters are the major vector breeding areas in Kerala.^[9]

CONCLUSION

The presence of water holding containers in the premises is the most significant modifiable predictor of the occurrence of chikungunya in a house. So source reduction must be initiated and continued to limit the epidemic progression. A majority of the population is not adopting any personal protective measures. Not using any personal protective measure is a risk factor according to the bi-variate analysis. So the use of personal protective measures should be encouraged. Even after the occurrence of such a large vector borne epidemic and in spite of the large scale information–education–communication (IEC) activities the extent of breeding continues to be in dangerous levels. It will be quite interesting to observe the reasons for the paucity of anti mosquito activity in the present social scenario.

The bionomics of mosquitoes prevalent in an area is highly dependent on the geographical, environmental, and living conditions in that area. Recently, Kerala has seen reemergence of mosquito-borne diseases like malaria, Japanese encephalitis, dengue, and chikungunya. Also a change has been noted in the vector species prevalent in Kerala. However, no scientific studies on the influence of the environmental factors on the pattern of vector species has been done till date. The entomological surveillance system should be strengthened in order to facilitate the timely recognition of transition in the vector bionomics. Virological studies in Aedes mosquitoes are to be done to establish the cause–effect relationship.

Limitations of the study

Chikungunya is a communicable disease which may tend to cluster. The sampling technique used is cluster sampling. This can affect the estimation of prevalence. The intracluster correlation in co-variates can also give a false impression of the determinants. These effects have been minimized by increasing the sample size. The cases have been included in the study based on a purely clinical definition and confirmation using IgM ELISA was not done.

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