Short Reports

Environmental factors of households in five districts of Kerala affected by the epidemic of chikungunya fever in 2007

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ABSTRACT

Background. Two epidemics of chikungunya fever were reported from Kerala in 2006 and 2007. We aimed to investigate the environmental factors of households affected by chikungunya fever and to estimate the proportion of population that suffered from the disease during the epidemic in 2007.

Methods. A cross-sectional survey was conducted in the 5 heavily affected districts of Kerala during October–November 2007. The 2-stage sampling technique was used to collect data from 10 clusters, each having 18 houses from every district, by interviewing the subjects using a structured questionnaire. The sample size was 900.

Results. The proportion of the population affected by chikungunya fever was 57.1% (95% CI: 52.8%–61.4%). There was a significant association between location of houses and disease status. Houses located near a public conveyance facility (within 250 m) were relatively protected from the disease (OR 0.19 [0.06–0.60]). About 69% of the households perceived mosquito infestation as a problem and 46.6% used fumes to avoid mosquitoes. More than 42% of households were not using any anti-mosquito measures at the time of the survey. Stored drinking water was the most common potential breeding source in the houses (23.5%). Households which did not store water inside were protected from the disease (OR 0.22 [0.08–0.65]).

Conclusion. The study indicated the persistence of favourable domestic and environmental factors after the epidemic, reflecting the necessity to strengthen anti-mosquito campaigns.

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INTRODUCTION

A pandemic of chikungunya fever started from the east coast of Africa in 2005.[1] It was estimated that by June 2006, one-third of the total population of Reunion Island was affected. The pandemic then spread to India. The type of chikungunya virus responsible for this outbreak belongs to the East Africa lineage.[2] The vector is thought to be the mosquito *Aedes albopictus*.[2] It is believed that a mutation occurred in the chikungunya virus, shortly after it reached Reunion Island, improving its transmission by *Aedes albopictus*.[2] Historically, the major vector of this disease was *Aedes aegypti*, the African counterpart of *Aedes albopictus*. Investigations regarding the seasonal prevalence, container preferences and geographical distribution of *Aedes albopictus* showed strong ecological adaptability.[3]

India experienced an outbreak in 2006. By the end of 2006, over 1.39 million cases were reported from India.[4] The earlier outbreaks of chikungunya fever in India were thought to be due to the Asian genotype, but the viral strain responsible for the 2006–07 outbreak was of the African genotype as was that in the outbreak in Reunion Island.[5]

Kerala was affected twice by the chikungunya epidemic, first in 2006 and then in 2007. The 2006 outbreak occurred in the 2 coastal districts of Alappuzha and Thiruvananthapuram. The 2007 epidemic was more extensive, involving plantation areas in the east of the state with Kottayam, Pathanamthitta, Kollam, Idukki, Ernakulam and Thiruvananthapuram districts being the most affected. *Aedes albopictus* was the major vector.[6–12]

Kerala is a densely populated state with more than 30 million people residing in about 9.4 million houses. Of these, more than 6.9 million (73.7%) are in rural areas.[13] The state is divided geographically into 3 terrains—high, mid and low land. The climatic conditions are different in these terrains. Plantations and large farmlands are concentrated in the highlands. Environmental factors are thought to be the major determinant for the transition of the epidemic from low land to high land.

The climate and terrain in Kerala are conductive to the breeding of *Aedes albopictus*. Rubber plantations with latex containers, and cocoa and pineapple plantations favour breeding of the vector.[14]

We did a study to estimate the proportion of people affected by chikungunya fever during the 2007 epidemic. We also investigated the environmental factors of the affected households.

METHODS

We did a cross-sectional survey in 5 districts of Kerala (Kollam, Alappuzha, Kottayam, Pathanamthitta and Idukki) during October–November 2007. These 5 districts were the most affected during the 2007 epidemic. Ten *panchayats* were randomly selected from each district. From each *panchayat* a cluster of 18 houses was selected for the study. The study population included families living in the geographical area affected by the epidemic.

The most heavily affected areas were selected with the help of the heads of the *panchayats* and primary health centres. The first house was selected according to convenience. The next 17 houses were selected serially based on the shortest distance from the previous house.

A structured interview schedule was used for data collection. The questionnaire was prepared by a group of epidemiologists, entomologists, sociologists and workers of the Kerala Sasthra Sahithya Parishad. 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 of 2 days before or 2 days after the onset of joint pain.[15] The content and face validity of the questionnaire were assessed.

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Data collection was done by household visits and by interviewing the subjects. The investigators were volunteers of the Kerala Shastra Sahitya Parishad. They were trained in administering the questionnaire, selecting clusters and interviewing subjects. The selection of *panchayats* was done during the training session by the investigators. Selection of clusters was done by the interviewers. The volunteers were asked to collect information from 180 houses under each district (overall sample size of 900). The questionnaires were collected after verifying all entries. Heads of families gave consent for participation in the study. The study protocol was approved by the Human Ethical Committee of the Kerala Shastra Sahithya Parishad. Chi-square test was used to interpret the statistical significance of associations. Odds ratios with 95% confidence intervals were used to estimate the strength of association between dichotomous variables.

RESULTS

Of the 900 households, records for 43 (4.8%) were defective. The remaining 857 households had 3623 people. The average family size was 4.2 persons and 57.1% of the population was affected by chikungunya fever (95% CI: 52.8%–61.4%), an average of 2.4 persons per household. At least 1 member was affected by chikungunya in 843 (98.4%) households.

Around two-third of the houses are located in remote rural areas at least 250 m from a public conveyance facility (Table I). These places are predominantly rubber and pineapple plantations. There was a significant association between location of houses and disease status. Houses located within 250 m of a public conveyance facility were relatively protected from the disease even though the survey was conducted in areas heavily affected by the epidemic. The proportion of houses affected in these localities was 96.4% as compared with 99.3% in the other group (p=0.002). The odds ratio for this comparison was 0.19 (95% CI: 0.06–0.60). The investigators noticed the breeding of mosquitoes in the premises of 15% of houses. Stored drinking water was the main breeding source, being present in 23.5% of households. Water storage in tanks contributed to another 13%. About 50% of households had one or the other potential breeding source.

TABLE I. Environmental and domestic factors including potential breeding sources in the vicinity of houses

Factor	Number of houses (*n*=857)
House in a remote area (≥250 m from a public conveyance facility)	579 (67.6)
Presence of broken plates outside the house*	182 (21.2)
Unused grinding stone with water*	37 (4.3)
Unused tyres in the vicinity*	28 (3.3)
Flower pots outside the house*	118 (13.8)
Shrubs*	205 (23.9)
Tapping rubber trees*	240 (28.0)
Pine trees*	131 (15.3)
Tree holes*	64 (7.5)
Banana plantations*	71 (8.3)
Presence of mosquito larvae*	128 (14.9)
Air cooler	5 (0.6)
Ant trap	8 (0.9)
Flower pots with water	71 (8.3)
Containers for storing water	41 (4.8)
Collected drinking water	201 (23.5)
Fishless water tanks	72 (8.4)

*Variables assessed within a distance of 10 m from the residential unit
Values in parentheses are percentages

Other than environmental factors, the presence of animals attracts mosquitoes. Animal rearing was practised in 371 houses (43.3%). Host preference of mosquitoes varies between species. Though we did not collect mosquitoes, it can be safely assumed that such environments have more mosquitoes. Heavy infestation by mosquitoes was found in 69% of households.

Fumes were often used to avoid mosquitoes (46.6%) in rural areas (Table II). Other mosquito-repellent techniques, which use synthetic pyrethrum, were used by 19.9% of the population. Mosquito nets were not used by the vast majority, possibly due to the heat and humidity.

DISCUSSION

We found that 42.3% of households were not using any anti-mosquito measures. Appropriate measures should be taken to make anti-mosquito measures more widely accepted. Even months after the chikungunya epidemic, domestic and environmental factors favourable to the epidemic persisted in the 5 worst affected districts. The proportion of chikungunya among viral fevers in the state is becoming more comparable to areas where chikungunya is thought to be endemic.[16] Moreover, a potential epidemic of dengue and dengue haemorrhagic fever looms large. Since most people do not prefer mosquito nets owing to the climatic conditions of the state, policy-makers should take into account the feasibility of implementing recommended personal protective measures.

Limitations. It is difficult to comment on the attributable risks of the environmental factors because the sample was taken purposively from an area where more than 98% of houses were affected.

The domestic and environmental features of the houses in the epidemic-affected area indicated a high likelihood of *Aedes albopictus* being the vector.[14] *Aedes albopictus* exploits a wider range of larval habitats, both natural and artificial, than does *Aedes aegypti*, explaining its abundance in rural areas and suburbs.[17]

Aedes aegypti is more closely associated with human habitation, breeding indoors and outdoors in artificial habitats.[17] However, in several locations, *Aedes albopictus* has played a major role in arbovirus transmission (dengue fever and chikungunya).[18] A study in Reunion Island and Vietnam detected the presence of chikungunya virus in the salivary glands of mosquitoes of *Aedes albopictus.*[19] Using infectious clones of the Reunion strain and a West African strain of chikungunya virus, into which either the E1-226 A or V mutation was engineered, it was shown that the mutation was directly responsible for a major increase in chikungunya virus infectivity for *Aedes albopictus.*[20]

An entomological study conducted at Reunion Island also showed that, in the warm wet season, small disposable containers were the principal urban breeding site. In the dry winter season, the species remained abundant throughout the island up to an altitude of 800 m but were seen up to a maximum altitude of 1200 m. The preferred natural breeding sites were bamboo stumps and

TABLE II. Personal protective measures adopted against mosquitoes

Factor	Number of houses (*n*=857)
Fumes (except mosquito coil)	399 (46.6)
Mosquito coils	129 (15.1)
Mosquito mat or liquidator	34 (4.0)
Mosquito nets	22 (2.6)
Repellent application on skin	152 (17.7)
No measures	361 (42.3)

Values in parentheses are percentages

rock holes. Logistic regression models indicated that the optimum breeding sites contained clear water with high organic content and were situated in areas with moderate shade.[3]

Vector density is very high in the case of *Aedes albopictus* compared with any other species in all parts of Kerala. *Aedes aegypti* has not been isolated from high and middle terrains. Latex cups, discarded tyres, plant shoots and roof gutters are the major vector breeding areas in Kerala.[14] The A226V mutation in the glycoprotein envelope 1 (E1) gene[21] of the virus was detected from the 3 worst affected districts of the state during this outbreak. It has been suggested that this mutation is responsible for a major increase in chikungunya virus infectivity in *Aedes albopictus.*[21]

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Obituaries

Many doctors in India practise medicine in difficult areas under trying circumstances and resist the attraction of better prospects in western countries and in the Middle East. They die without their contributions to our country being acknowledged.

The National Medical Journal of India wishes to recognize the efforts of these doctors. We invite short accounts of the life and work of a recently deceased colleague by a friend, student or relative. The account in about 500 to 1000 words should describe his or her education and training and highlight the achievements as well as disappointments. A photograph should accompany the obituary.

—Editor