Rapid communications

An analysis of a short-lived outbreak of dengue fever in Mauritius

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During the month of June 2009, Mauritius experienced a short-lived outbreak of dengue fever localised in its capital city Port Louis. *Aedes albopictus*, a secondary vector of dengue viruses, was the probable vector. We introduce a method which combines Google Earth images, stochastic cellular automata and scale free network ideas to map this outbreak. The method could complement other techniques to forecast the evolution of potential localised mosquito-borne viral outbreaks in Mauritius and in at-risk locations elsewhere for public health planning purposes.

Introduction

Dengue fever is a mosquito-borne viral disease which affects 50-100 million people every year in tropical and sub-tropical regions of the world. Dengue viruses (DENV) appear in four serotypes (DEN-1, DEN-2, DEN-3 and DEN-4) and can cause dengue fever, dengue haemorrhagic fever and dengue shock syndrome among other illnesses [1]. Sporadic cases of dengue fever occurred in Mauritius [2] at the time of a major dengue virus (DEN-2) epidemic in Réunion Island in 1977-1978 [3]. *Aedes aegypti* mosquitoes are the major vectors of DENV but were eradicated in Mauritius and nearly eradicated in Réunion Island during the anti-malaria campaigns in the early 1950s. *A. albopictus*, a secondary vector of DENV, was the probable mosquito vector during the 1977-1978 Réunion Island epidemic [3].

Dengue fever re-emerged in Mauritius in June 2009 as a mild fever localised in the capital city Port Louis (population of 144,000 and size of 45.6 km2) on the north-west coast of the island, with *A. albopictus* as the probable vector. A first suspected case was detected on 3 June 2009. There were 192 serologically confirmed cases from 3 to 18 June 2009. The number of cases decreased over the next five days with 16, 4, 4, 3 and 0 cases, respectively. Most of these 219 cases were from the Port Louis region. Mosquito fogging and larviciding started on 3 June 2009, covered the whole of Port Louis and were repeated every seven days. Mosquito fogging was carried out outdoors early in the morning, early evenings and sometimes late in the evenings, when wind speeds were less than 15 km/h. The insecticide used was Aqua K-Othrine® and thermal foggers were used for the spraying. Public awareness campaigns on the necessity to search and eliminate mosquito breeding sites at home and in the neighbourhood and to protect oneself against mosquito bites were carried out through radio, television and the press through a public private partnership. Detailed information leaflets were also distributed. Target groups included the public, community groups and school children.

We introduce a method which uses Google Earth images, stochastic cellular automata [4] and scale free network [5] ideas to map the evolution of dengue fever in Port Louis in June 2009, and compare a scenario without mosquito control or behavioural change (Scenario 1) with a scenario with mosquito control and human behavioural change (Scenario 2).

Methods

The outbreak was assumed to have been started by the introduction of a human index case into a completely susceptible human and mosquito population. An area of interest of Port Louis where most of the serologically confirmed dengue fever cases occurred was selected from a Google Earth digital image of Port Louis. The area of interest, an area of 2.9 km x 3.6 km, was divided into cells each 0.1 km x 0.1 km in size. The number of houses in each cell was estimated using colour image analysis, and the human population in a cell was estimated by assuming an average number of five inhabitants per house. The mosquito population in a cell depended on the human population as shown in the Table.

Table

Parameters for the evolution of dengue fever in Port Louis for Scenarios 1 and 2

	Scenario 1					Scenario 2			
Intervention	1	2	3	4	5	1	2	3	4
Day of intervention	1	7	14	21	30	1	7	14	21
Human viraemic period [days]	5	5	5	5	5	5	5	5	5
Human infectious period [days]	5	5	5	5	5	5	3	2	2
DENV latent period in humans [days]	5	5	5	5	5	5	5	5	5
DENV latent period in mosquitoes [days]	6	10	12	15	22	6	10	12	15
Mosquito lifetime [days]	30	25	20	20	20	30	20	15	10
Mosquito infectious period [days]	30	25	20	20	20	30	20	15	10
Ratio vector/humans	3	2	2	2	2	3	2	1.5	1
DENV transmission probability	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
Mosquito bite rate [per week]	2	2	2	2	2	2	1	1	1

DENV: Dengue virus

The index case was assumed to reside in an index cell. Individuals in a cell were assumed to interact with mosquitoes in the cell following a SEIR (susceptible-exposed-infected-removed) model for human-mosquito interaction [6]. Individuals in a cell were assumed to be able to move locally with equal probability to each of the eight neighbouring cells and to interact with mosquitoes. They were also assumed to move globally on a scale-free network [5]. Only 40% of the human population of a cell was allowed to move globally (and 50% locally) at any time step (one day) and they returned to their original cell at the end of the time step. Mosquitoes were restricted to their cells.

The scale free network was set up as follows:

1. Four most frequently visited places (hubs) in the area of interest were chosen.
2. Each hub was represented by one cell.
3. The index cell was randomly linked to two of the hubs.
4. Another cell was chosen that was allowed to link itself with the hubs or with the index cell using the Barabási–Albert algorithm [5].
5. Steps 3-4 were repeated for the remaining cells to generate a scale-free network.

The evolution of the outbreak was computed for the two scenarios for the parameter values given in the Table. It was assumed that the mosquito latent period increased with falling temperatures as the month of June passed, accompanied by a decrease in the mosquito lifetime. The decrease in mosquito lifetime was assumed to be greater for Scenario 2 with vector control measures. The human infectious period decreased in Scenario 2 because confinement of affected humans and protection against mosquito bites led to a decrease in the bite rate.

Results

The human population size for the area of interest was computed as 82,580. Figure 1 shows the evolution of the number of infected cases over time for the two scenarios averaged over 100 runs. The average final epidemic size 3,662 cases for Scenario 1 was and 549 cases for Scenario 2.

A histogram of the final epidemic size for 1,000 runs for Scenario 2 is shown in Figure 2.

Figure 3 shows an example of the spread of infected humans over the region of interest in Port Louis 21 days after the first intervention. The outbreak is well-developed and spread over Port Louis with maximum incidence at and around the index cell.

Discussion

We have introduced a method which combines Google Earth images, stochastic cellular automata and scale-free network ideas to yield quantitative estimates for the outcome of a localised dengue fever outbreak. An average of about 550 infected people was computed in Scenario 2 for the period in June 2009 when cases were reported. This number compares well with the actual number about 220 serologically confirmed cases. However, the histogram indicates that larger epidemics can occur, although

Figure 1

Temporal evolution of the number of infected humans (averaged over 100 runs) for Scenarios 1 and 2

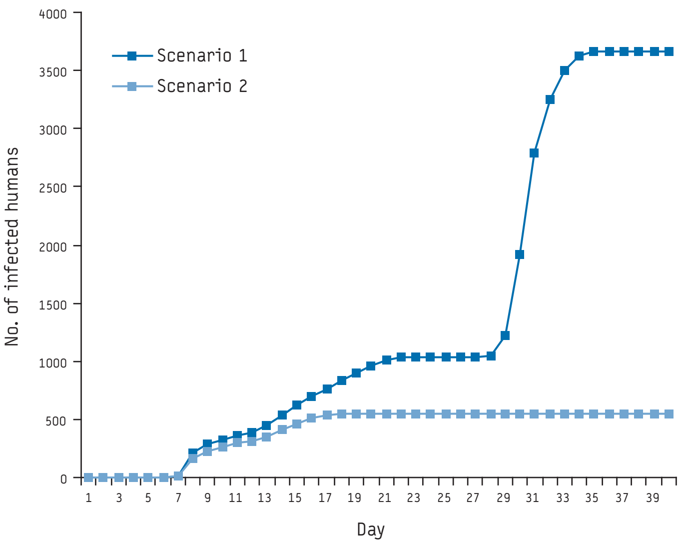


Figure 2

Histogram for the final epidemic size for 1,000 runs for Scenario 2

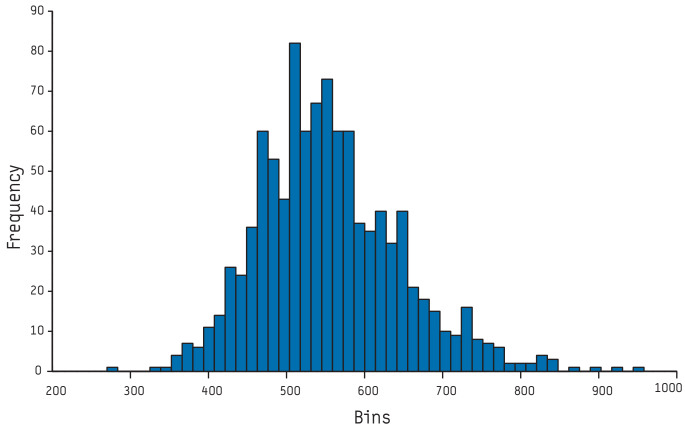
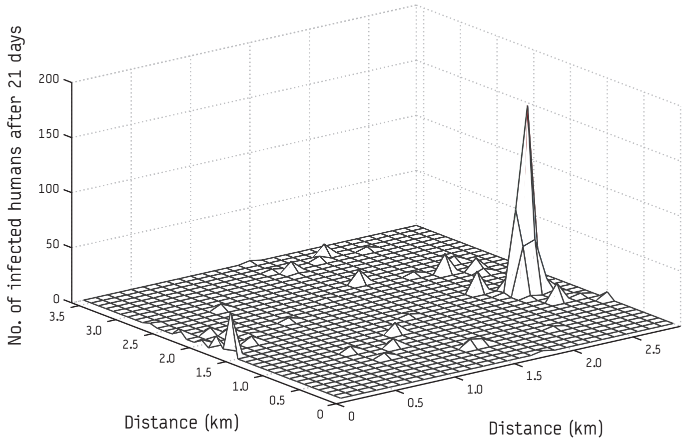


Figure 3

Example of the spread of infected humans over the region of interest in Port Louis 21 days after the first intervention for Scenario 2



with lower probability. Computations for Scenario 1 indicate that, without the intense mosquito fogging campaign and – to a lesser extent – the public awareness campaign carried out by Mauritius authorities in June 2009, the number of cases could have been in the thousands. Larviciding is unlikely to have played a major role in controlling the outbreak, given the very short duration of the outbreak.

The localised nature of the dengue virus outbreak in Mauritius in June 2009 suggests an isolated event limited by by falling temperatures, by the fact that only one secondary vector (*A. albopictus*) for DENV was present, and by the fact that infected mosquitoes outside of the outbreak area did not generate additional cases. The occurrence of the outbreak is not surprising considering the recent resurgence of dengue fever in many countries [7] and global air travel. However, the timing of the outbreak at the beginning of winter in Mauritius is surprising and highlights the risk of an emergence of dengue fever in those countries in the north temperate zone which have established populations of *A. albopictus* and where climatic conditions favourable for the propagation of dengue viruses may prevail in the summer [7]. The modelling technique described here could complement other techniques to forecast the evolution of potential localised mosquito-borne viral outbreaks in Mauritius and in at-risk locations elsewhere for public health planning purposes.

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References

1. World Health Organization. Dengue and dengue haemorrhagic fever. Fact sheet No.117. March 2009. Available from: http://www.who.int/mediacentre/factsheets/fs117/en
2. Schwarz TF, Dobler G, Gilch S, Jäger G. Hepatitis C and arboviral antibodies in the island populations of Mauritius and Rodrigues. J Med Virol. 1994;44(4):379-83.
3. Paupy C, Girod R, Salvan M, Rodhain F, Failloux AB. Population structure of Aedes albopictus from La Réunion Island (Indian Ocean) with respect to susceptibility to a dengue virus. Heredity. 2001;87(Pt 3):273-83.
4. Mikler AR, Venkatachalam S, Abbas K. Modelling infectious diseases using global stochastic cellular automata. J Biol Syst. 2005;13(4):421–39.
5. Barabási AL, Albert R, Jeong H. Mean-field theory scale-free random networks. Physica A. 1999;272(1-2):173-87.
6. Derouich M, Boutayeb A, Twizell EH. A model of dengue fever. Biomed Eng Online. 2003;19;2:4.
7. Jelinek T. Trends in the epidemiology of dengue fever and their relevance for importation to Europe. Euro Surveill 2009;14(25):pii=19250. Available from: http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=19250