Forecasting mosquito abundance to prevent Japanese encephalitis

Japanese encephalitis (JE), commonly known as 'brain fever', is a mosquito-borne viral disease. JE outbreaks occur frequently in 14 Asian countries and a total of about 3060 million people live at risk of infection. The latest annual incidence data[1] from these countries show that there were about 45,000 cases and 10,000 deaths during 1997. The lack of reporting system and poor diagnostic tools available for JE limit the appropriate estimation of cases as on date. Further, there is no specific treatment on hand for JE. The use of vaccine is restricted to certain situations only, and no standard formulation is available yet.

The JE mosquito vector (disease-transmitting insect) species, *Culex vishnui* gr breed in the rice fields, and human cases occur scattered over extended rural areas. The incidence, however, varied in different countries; the highest occurrence is found in the rice-growing areas of the country. From this, one may surmise an ecological connection with the irrigation facilities and paddy cultivation. Further, the increased water availability during a particular stage of the paddy cultivation is reported to be a premonitory sign that can lead to markedly increased population of the vector mosquitoes[2]. The basic requirement is to determine the site-specific critical value for the vector density in the epidemic-prone areas, above which control measures should be initiated. Appropriate preventive action could be taken in time if the indications for the spurt in vector density is known in advance.

Once the prevalence and density of the JE vector mosquitoes from different areas are obtained through seasons by manual methods, it would be easy to monitor any sharp increase in the vector density by using such modern tools as Remote Sensing (RS) and Geographical Information Systems (GIS), which would provide reliable information on a desired spatial and temporal scale. The possibility of using remote sensing in identification of the habitats of vectors has already been described elsewhere for many other diseases[3–5].

The basic products that are commonly extracted from RS data are vegetation index (VI), surface temperature and cloud temperature. The VI can contribute not only to knowledge on the vegetation status, but also factors such as land use changes and surface moisture. There are several types of VI, but the most important one is the normalized difference vegetation index (NDVI). It is determi-

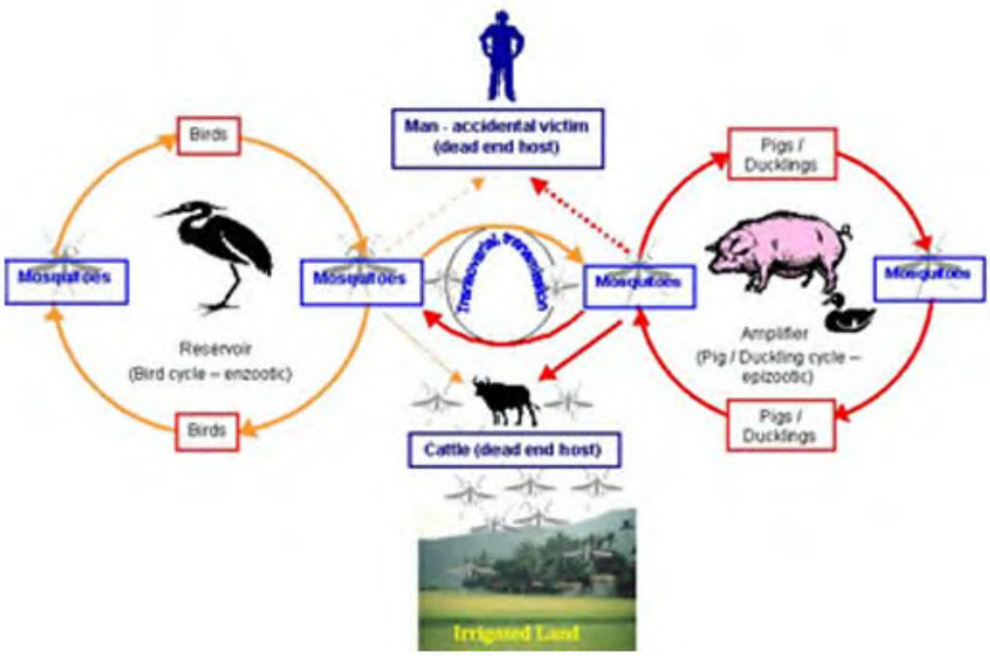

Figure 1. Transmission cycle of Japanese encephalitis. The vectors of JE are zoophilic/ornithophilic, preferring animal/bird to human blood[7]. When their density increases enormously, a few of them spill over to humans. Man is an incidental and dead-end host. Man-to-man transmission does not occur in nature. Cattle also act as dead-end host in the transmission cycle. As the cattle circulate only a low level of virus, they do not develop disease. From Ardeid birds, JE infection is transmitted by mosquitoes to pigs/ducklings. The pigs/ducklings serve as amplifying hosts since the virus multiplies in them. Man or cattle get infected either from birds or pigs/ducklings through mosquitoes. Ardeid bird–mosquito–Ardeid bird and pig/duckling–mosquito–pig/duckling cycle exist in nature. The bird cycle is more stable, persistent and enzootic. The pig cycle appears to be temporary and epizootic. The epidemic in man appears to follow pig epizootics, and this coincides especially when the vector density shoots up. Though the JE virus transmission from mosquito to mosquito via reproductive route ('transovarial' transmission) has been reported[8], it has not been considered seriously on account of a very low virus titre. Still, it bears epidemiological significance, as the mosquitoes themselves maintain the virus during the non-transmission (lean) period[9].

ned by the formula: NDVI = (near infrared – red)/(near infrared + red), where red and near infrared are the bi-directional reflectance factors in red and near infrared channels respectively[6]. Depending on the time of year (season), the values derived from the remote sensing data can be used to identify the vegetation type and growth stage of plants and predict the possible vector-breeding sites.

The cloud temperature is known to be related to the rainfall. Cold cloud duration (CCD) values obtained from cloud temperature represent the length of time during which a cloud top is below a particular, cold threshold temperature. This product has been shown to be very good in providing rainfall estimates[6]. The CCD is valid for monitoring a particular type of rain, that from convective clouds. Incidentally, this method of rainfall estimation will work well in the present JE-prone areas, as most of the cloud in this region (tropics/subtropics) are convective. A linear discriminant analysis, using the NDVI, rainfall and temperature can identify periods with and without mosquito immatures. The satellite imagery could thus be used in the estimation of larval abundance and consequently adult abundance. A GIS will facilitate acceptance of satellite information, fit it to a vector mosquito model and produce imagery, indicating best estimates of where the vector population can breed and survive. A combination of both CCD and NDVI may be the best way to indicate a probable sharp increase in vector abundance, which is critical in JE outbreaks, when the host transmission parameters are conducive.

There is, at present, neither long-term strategy for disease vector control nor any emergency preparedness to prevent the epidemics in any of the JE problem countries. Rapid response and prevention are the immediate requirements. When there is a precise probability on the key element – 'vector abundance', predictability will be stronger, and the decision makers could use this information for taking precautionary action to avert the possible disease outbreaks.

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ACKNOWLEDGEMENTS. I thank Dr P. K. Das, Director of Vector Control Research Centre, Pondicherry for his critical comments on this manuscript.

S. SABESAN

Vector Control Research Centre,
Medical Complex,
Indira Nagar,
Pondicherry 605 006, India
e-mail: sabesan1@yahoo.com

Microbes strike again

Ingenuity, knowledge, and organization alter but cannot cancel humanity's vulnerability to invasion by parasite forms of life. Infectious disease which antedated the emergence of humankind will last as long as humanity itself, and will surely remain, as it has been hitherto, one of the fundamental parameters and determinants of human history.

William H. Mc Neill,
Plague and Peoples (1976)

Killer flue grips the world, a news item in *Times of India* dated 4 April 2003 reminds us of yet another epidemic of a killer infection. Until quite recently there was a growing feeling in the developed world that the struggle against infectious diseases was almost won. Global eradication of small pox predicted eradication of polio in the near future, near-total control of plague, diphtheria and tetanus from most developed regions of the world led to a certain degree of complacency. Research on infectious diseases was relegated to non-priority status. Thus in 1969, the US surgeon General William H. Stewart declared that it was 'time to close the book on infectious disease'. Today, less than 10% of global research and development budget is used to address the largest disease burden, which is found among poorer populations of the world. It came to be believed that most of the infectious diseases, predominantly restricted to the developing countries, specially the sub-saharan Africa and Asia, can be traced to malnutrition, poor sanitation, and lack of both clean drinking water and basic preventive health care. While this is no doubt true to a great extent, it is far from the whole truth. The first wake-up call was provided by the unsuspected appearance of HIV/AIDS which has rapidly acquired pandemic proportions. Already approximately 4 million persons are estimated to be infected with HIV in India. World Bank warns that India could have 37 million people infected with HIV by the year 2005 unless preventive measures are accelerated. With the advent of HIV/AIDS, tuberculosis once again raised its head even in the developed countries. WHO has already declared tuberculosis to be a global emergency. The number of TB cases worldwide is currently reported to be rising at 2% per year.

More than 30 new, previously unknown highly infectious diseases have been identified since 1973. In addition to HIV/AIDS, these include Ebola-type haemorrhagic fever, Henta virus, hepatitis C, *Helicobacter pylori*, *Legionella pneumophila*, *Vibrio cholerae 0139*, New variant of Creutzfelt–Jacob (mad-cow) disease, etc. According to Cohen[1], hepatitis C (HCV) discovered in 1989 has infected an estimated 170 million people worldwide – more than four times as many as HIV, and it is predicted that during the next few years, the number of annual US deaths from HCV-caused liver damage and cancer may overtake deaths caused by AIDS.

Major outbreaks of infectious diseases through food-chain are now well recognized in spite of the highly regulated and