Geographical Information System (GIS)-based maps for monitoring of entomological risk factors affecting transmission of chikungunya in Sri Lanka

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INTRODUCTION

- **Chikungunya fever is a viral disease transmitted to humans by the bite of infected mosquitoes.**

- **Chikungunya virus is a member of the genus *Alphavirus,* in the family *Togaviridae*.**

- **This virus is spread by *Aedes aegypti* and *Aedes albopictus* mosquitoes.**

- **Chikungunya virus was first isolated from the blood of a febrile patient in Tanzania in 1953, and has since been identified repeatedly in west, central and southern Africa and many areas of Asia.**

- **The disease has been cited as the cause of numerous human epidemics in those areas since that time.**

- **Most recent outbreaks have been reported from India and various Indian Ocean islands including Sri Lanka.**

- **At present, chikungunya is an important disease in Sri Lanka.**

- **Chikungunya remains very much a "neglected disease" and a public health issue, and clearly, there is an urgent need to study on possible risk factors affecting transmission of the disease to bridge the gap of knowledge concerning this pathogen.**

- **Possible risk factors- entomological**
  epidemiological
  environmental
  socio-economic
  knowledge attitude and practices of human

OBJICTIVE

- **To monitor entomological risk factors affecting transmission of chikungunya using GIS mapping.**

RESEARCH DESIGN

- **Entomological risk factors affecting transmission of chikungunya were examined in a selected chikungunya hot-spot in Sri Lanka from April to July in 2008.**

Study area

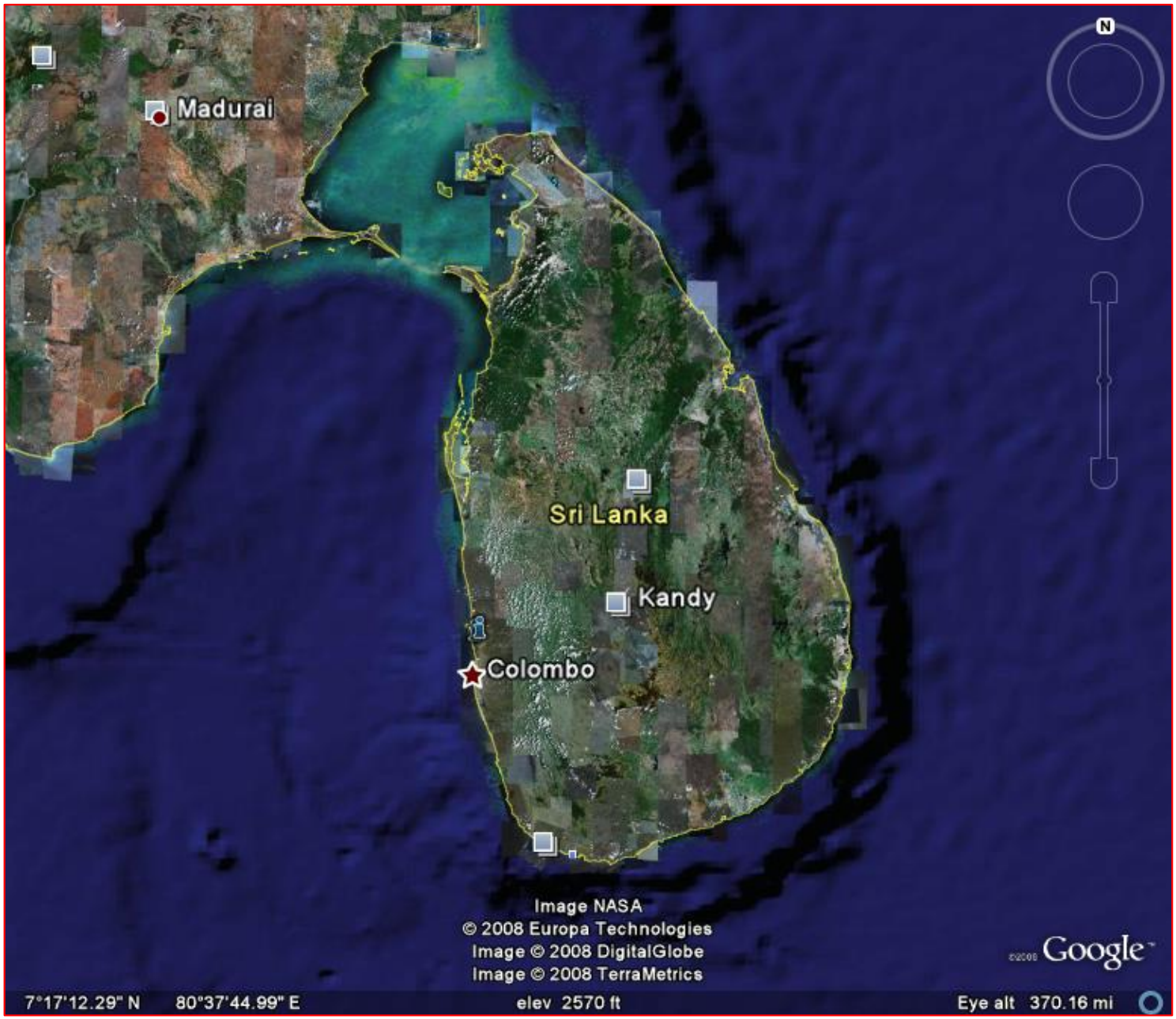
- **Study area was situated in the District of Kandy, in the central part of the island.**

- **Kandy Municipal Council area was selected.**

  the latitude of $7^0$15’53.55” - $7^0$17’16.00” N

  the longitude of $80^0$36’37.55” - $80^0$37’44.75” E

Map1. Sri Lanka showing the study area



Study population

- **Ninety nine house-holds in 33 clusters were recruited. The distant between clusters was at least 200 m which is beyond the maximum flight range of *Aedes* mosquitoes.**

- **3 house-holds/cluster**

- **99 house-holds/33 clusters**

Collection of data

- **Position of each house was recorded using a Global Position System (GPS) receiver.**

- **Monthly surveillance was conducted using standard entomological surveillance methods followed by obtaining information through a pre-tested questionnaire.**

  Adults - Human landing diurnal collection technique

  Larvae - Normal larval surveillance technique

Analysis and presenting data

- **Monthly cluster index for the presence of *Aedes* vectors in each cluster was calculated.**

$$\text{Cluster index} = \frac{\text{No of positive clusters}}{\text{No of clusters examined}} \times 100$$

Cluster index for each species was indicated in each map.

- **66 %**
- **33 %**
- **0 %**

- **Monthly container index for each cluster was calculated.**

$$\text{Container index} = \frac{\text{No of positive containers}}{\text{Total no of containers in a cluster}} \times 100$$

Container index for each species was indicated in each map.

66 %

33 %

0 %

- **GIS was used to display**

1. Spatial distribution of selected house-holds and clusters;

GPS readings of each house-hold were overlaid n digital land used maps using GIS and presented all house-holds and clusters on GIS-based maps.

2. Spatial and temporal distribution of vectors;

Monthly cluster index for each vector species was overlaid on GIS-based maps.

3. Spatial and temporal distribution of key breeding sites;

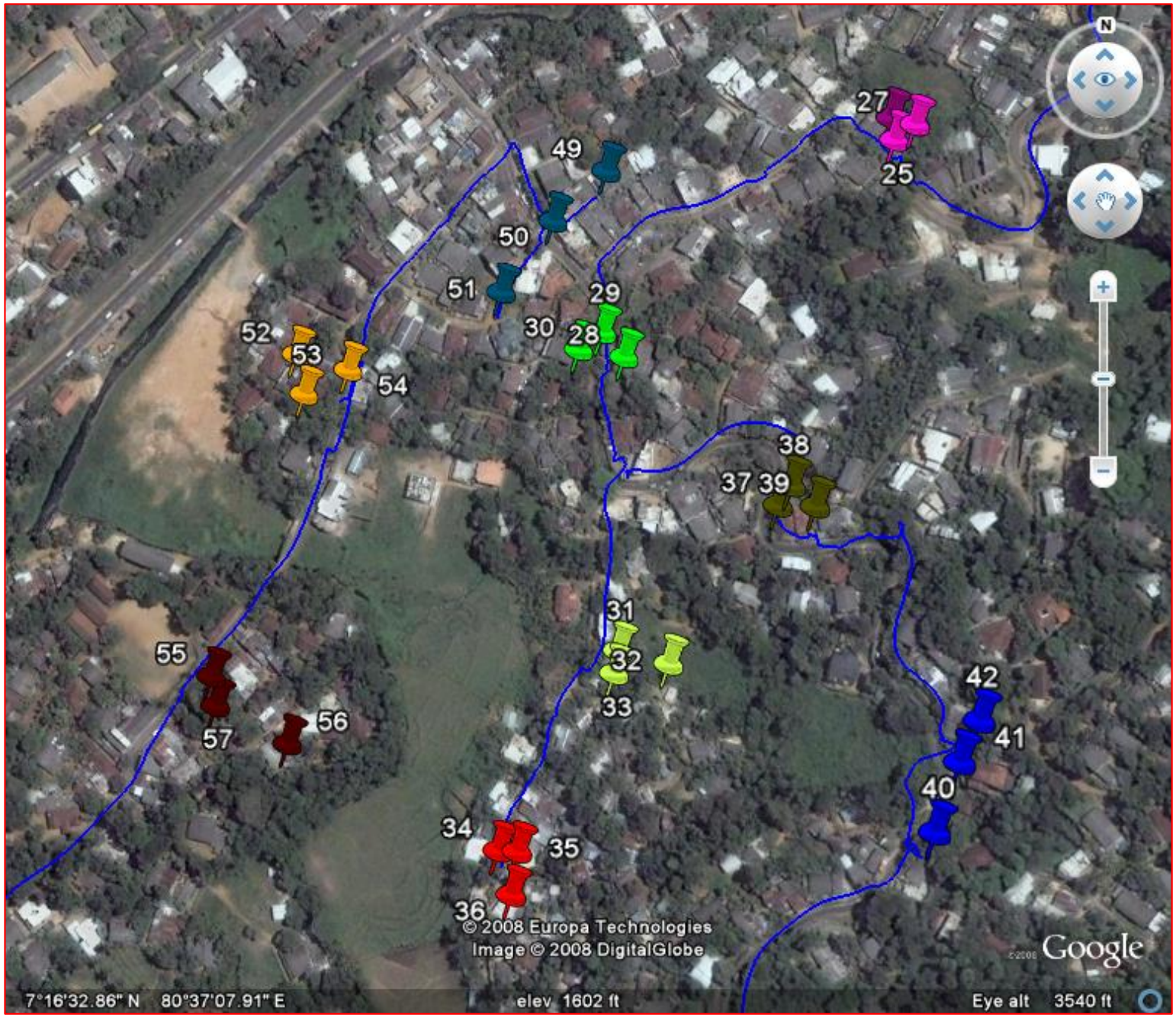
Monthly container index was overlaid on GIS-based maps.

RESULTS

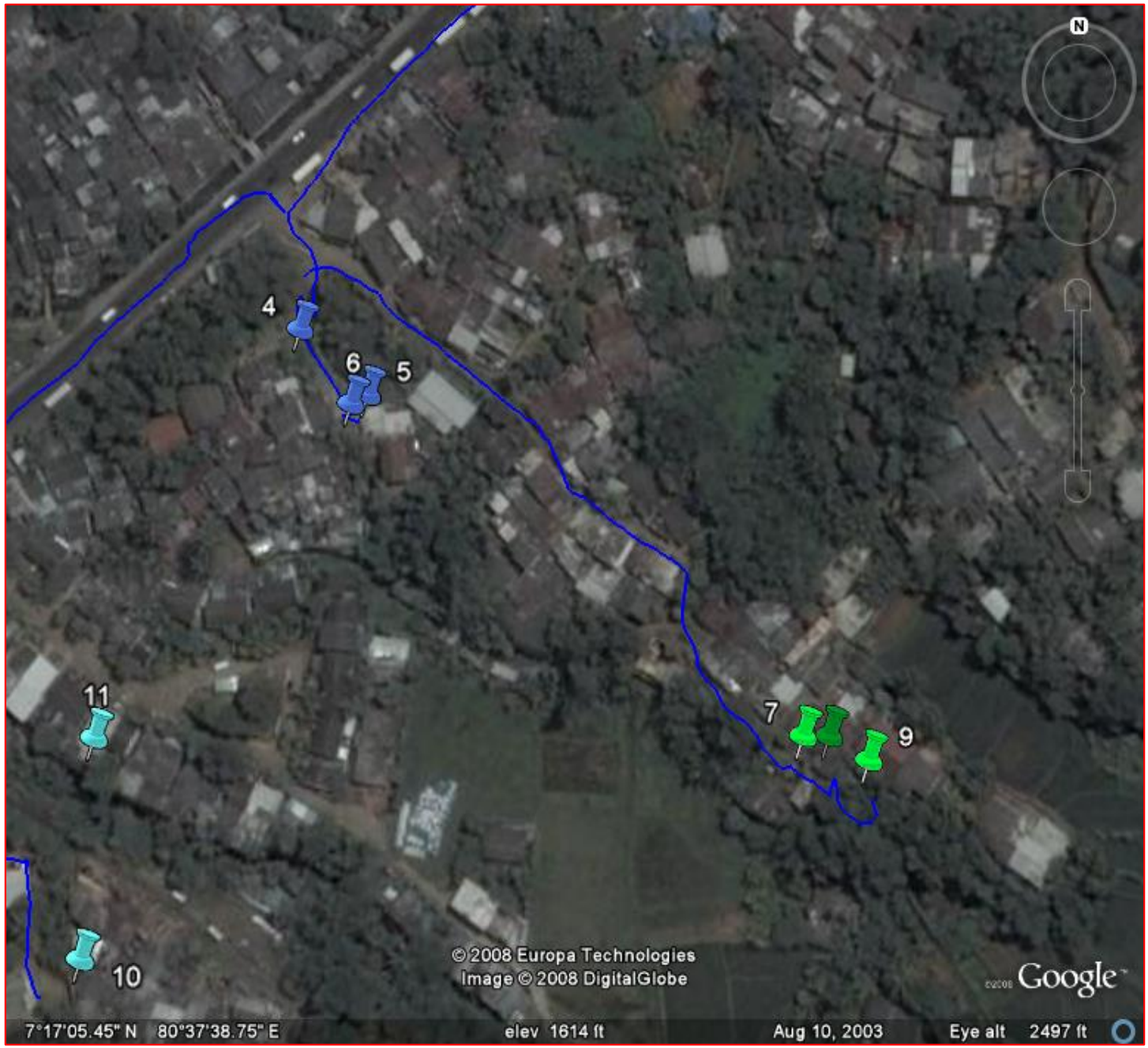
Spatial distribution of selected house-holds and clusters

- **Major land use pattern of the selected area was human dwellings.**

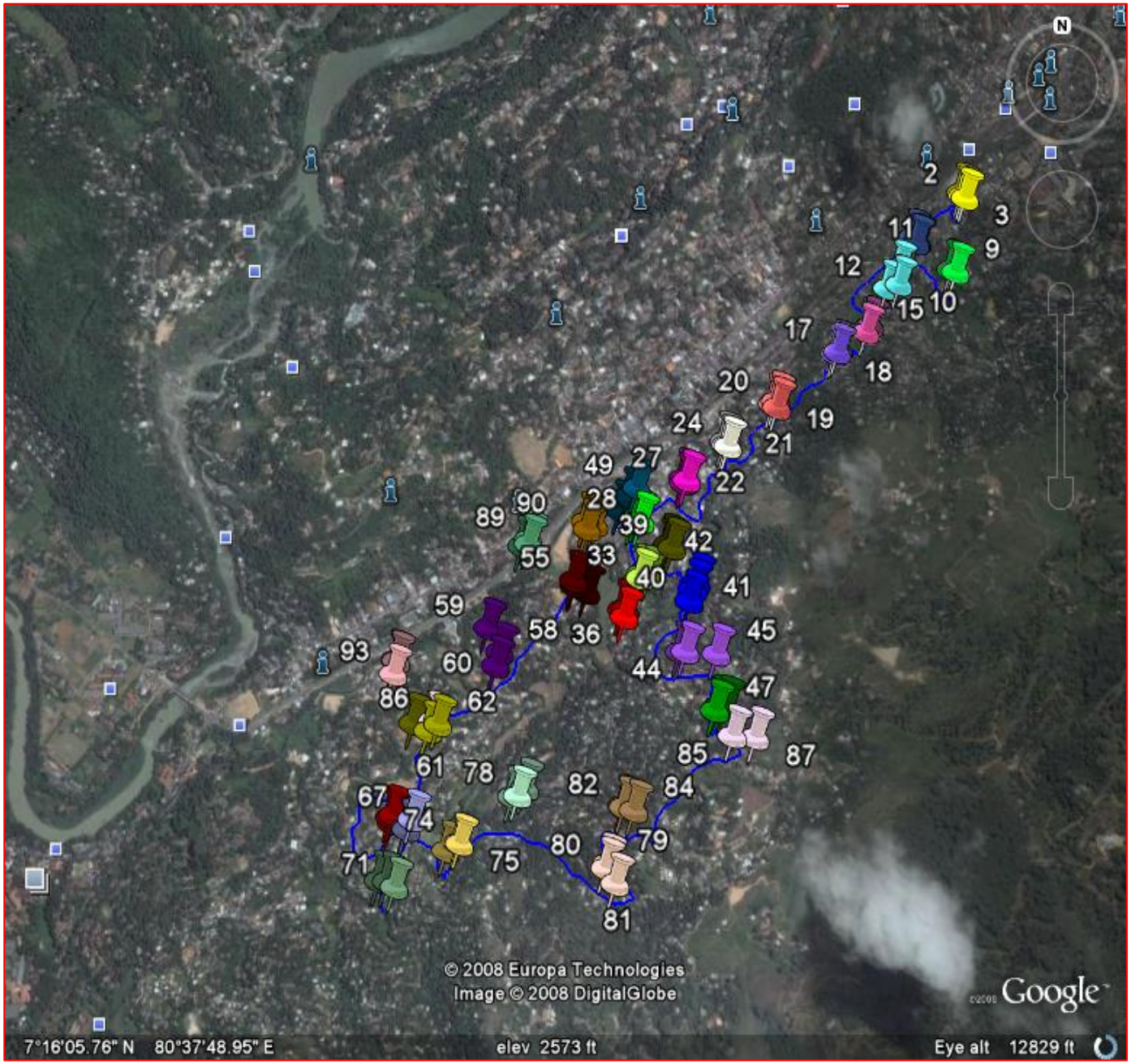
Map 2. Spatial distribution of selected clusters



Map 3. Spatial distribution of selected clusters



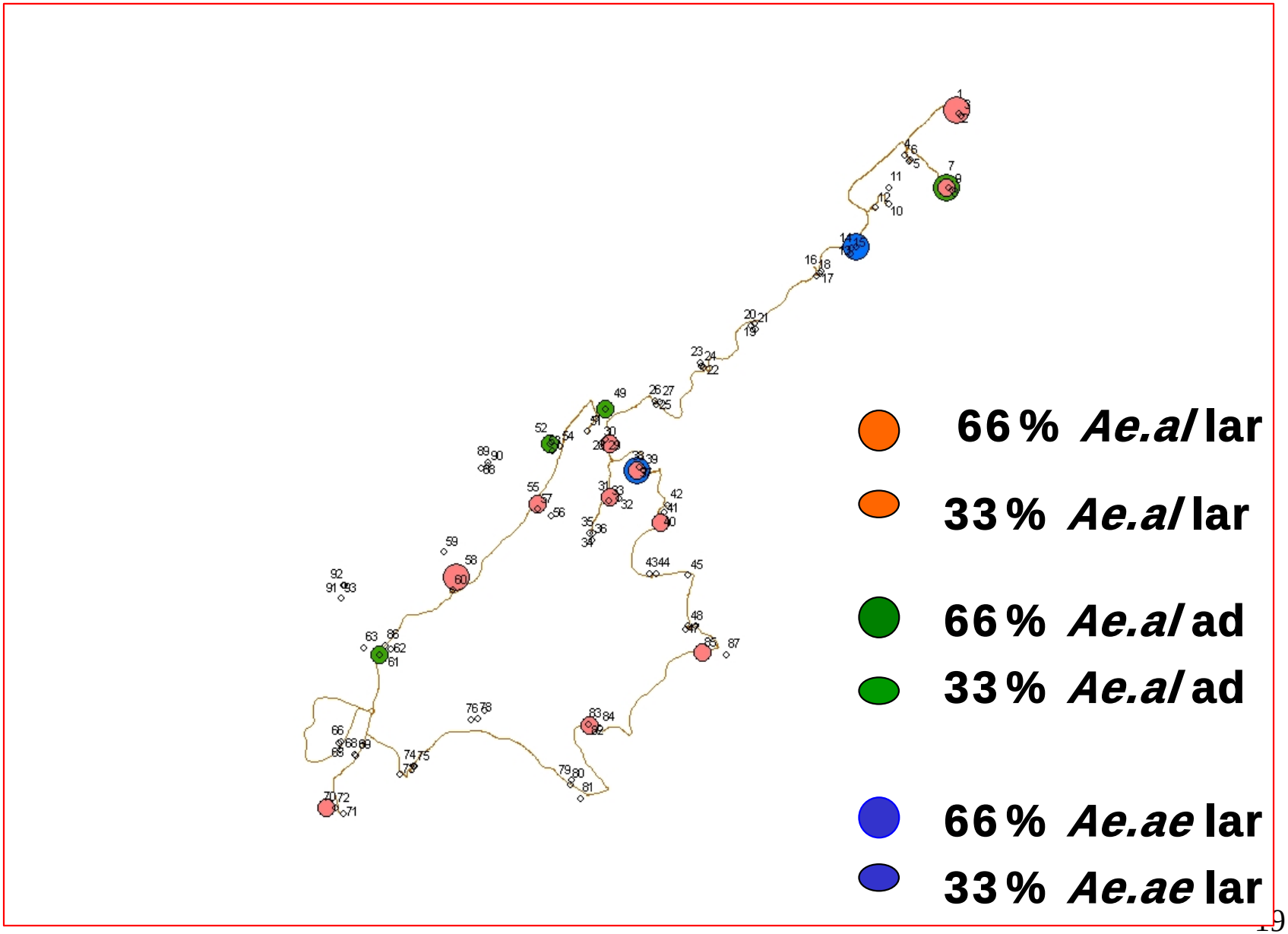
Map 4. Spatial distribution of all 33 clusters



Spatial and temporal distribution of vectors

- **Presence of high density/cluster index of *Ae. albopictus* mosquitoes was observed in all clusters throughout the study period.**

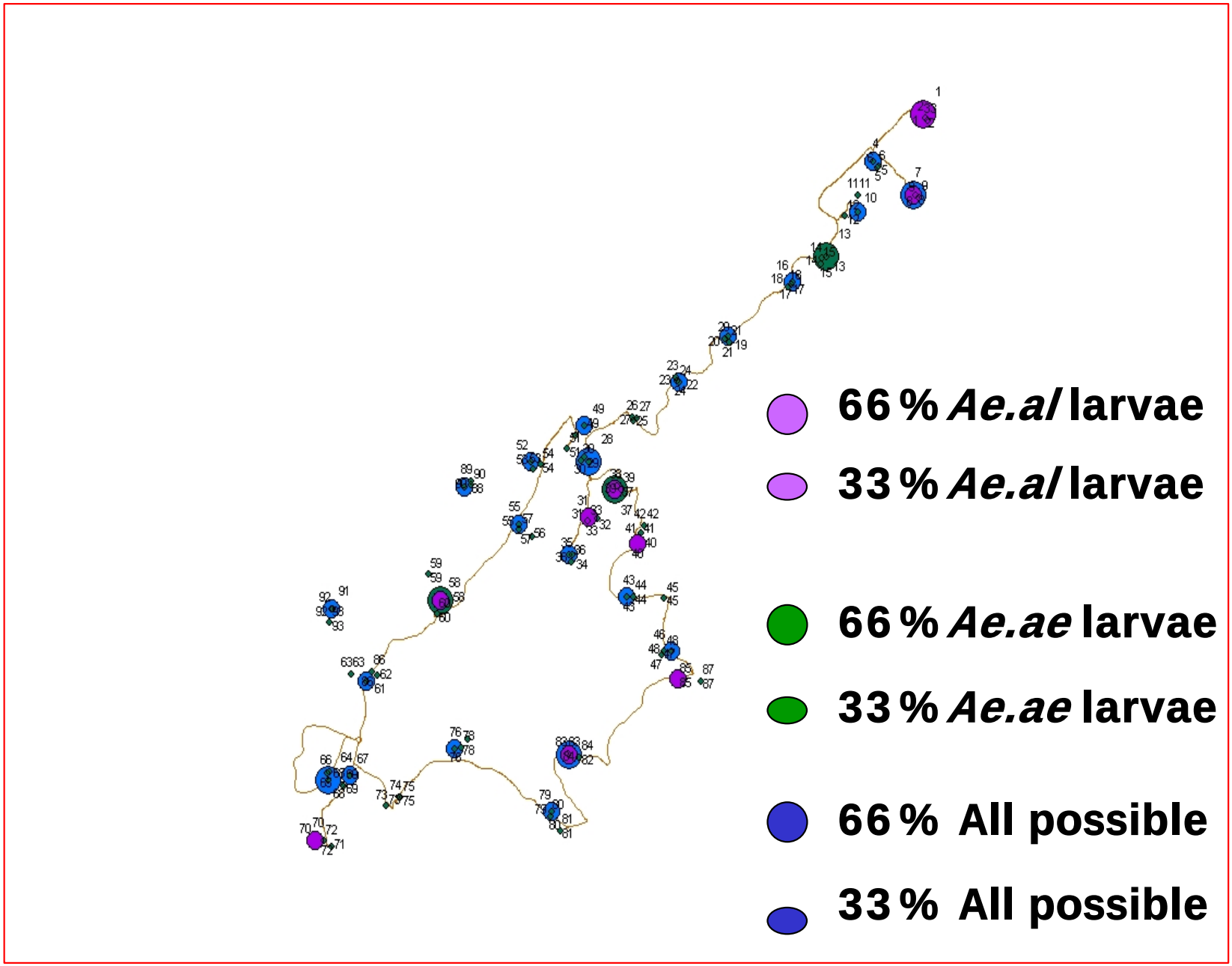
Map 5. Spatial and temporal distribution of vector mosquitoes
Cluster index for *Aedes*, June, 2008



Spatial and temporal distribution of key breeding sites

- **Presence of *Ae. albopictus* mosquitoes in more than 90 % of the key (artificial) breeding habitats was observed in all clusters throughout the study period.**

Map 6. Spatial and temporal distribution of vector breeding sites Container index, June, 2008



CONCLUSIONS

- **Generalized high density of *Ae. albopictus* suggests that this species may play a major role in transmitting chikungunya in the study area.**

- **GIS-based maps may be used as an important tool to find out spatial and temporal distribution of vectors and key breeding sites in a selected hotspot, which would enable cost effective and efficient interventions for vector control in disease endemic areas.**

Discussion cont.

- **Further, information regarding long term surveillance activities conducted in a chikungunya risk area can be manipulated and presented using tools of GIS.**

- **This is important to predict impending epidemics in order to use limited resources in a cost effective and efficient manner to control the epidemics.**

THANK YOU