Reviewer's report

Title: A Local Outbreak Of Dengue Caused By An Imported Case in Dongguan China

Version: 2 Date: 31 July 2011

Reviewer: Nikos Vasilakis

Reviewer's report:

This manuscript is an improved version of the previous submission by Peng et al. describing a local outbreak of dengue fever in Dongguan, China, that was caused likely by an imported case from Malaysia. Although several improvements have been made there are remaining issues that require the authors' attention.

Although there is some improvement in the English language there are several structural deficits remaining. I would strongly suggest the authors employ the services of a professional English-speaking editorial service to eliminate use of several colloquialisms that reduce clarity of the manuscript.

Major compulsory revisions:

1. The authors have failed to include any information about the method(s) used to derive the phylogenetic tree. The statement in page 7, line 7-8, is unacceptable and does not meet the minimum required standards. I would strongly suggest, that the authors at a minimum should perform phylogenetic analyses preferably based on 2 robust methods such as Maximum Likelihood (with robust bootstrap values) and Bayesian analysis (with at least 5 million reiterations). In addition, the empirical parameter values used for the substitution type, optimal base composition, proportion of invariable sites, as well as the shape parameter of the # distribution of rate variation among sites estimated from the data should be included or be available upon request.

2. Page 10, line 12-14. The low bootstrap values do not support the inferences described here. A 99% nucleotide homology should result in higher bootstrap values. This may be an indication that inappropriate and not robust phylogenetic analyses were utilized. Furthermore, the authors may consider adding additional strains belonging to genotype I, available from the GenBank, as to obtain better resolution in the strain relationships.

3. The presentation of the tree is outdated. The authors should consider employing the mid-root as to present a more informative tree. Additionally, bootstrap values below 75 are not reliable and should not be included in the figure.

Minor Essential revisions.

Page 2, line 4. The authors misrepresent the term prevalence. The correct term
here would be ‘occurrence’ or ‘introduction’ (if it was not an autochthonous case).

Page 2, line 6. Aedes Albopictus is a preridomestic mosquito. The words ‘which is a kind of’ should be removed.

Page 2, line 7. In this case ‘Rapid and uncontrolled urbanization’ is a more appropriate term to describe the realities in developing countries.

Page 3, line 17. The prevalence of dengue has currently been documented in ~100 countries.

Page 3, line 20-21. This statement about description of course of dengue illness is inaccurate and misleading. The authors may opt to rewrite it for greater clarity and accuracy.

Page 5, line 20. Replace ‘staffs’ with ‘representatives’

Page 6, line 10-12. This sentence lacks clarity and should be rephrased.

Page 7, line 1. It is puzzling as to why the authors opted to inoculate the virus in suckling mice. This method is outdated and replication in brain results in rapid accumulation of mutations. Primary amplification in C6/36 cells is currently the golden standard and does not result in the accumulation of tissue-specific mutations.

Page 8, line 16. Remove ‘totally’.

Page 8, line 17. Best to say: ‘Some of the reported cases exhibited clustering …’

Page 9, line 15-17. Capitalization should be avoided. For example, myalgia, hemorrhage etc

Page 10, line 5. Replace ‘B6/36’ with ‘C6/36’

Page 10, line 5. The authors should adhere to consistency. Earlier (page 6, line 21), it was described as ‘suckling mice’, a more accurate definition, and here as infant mice.

Page 10, line 9. Replace with “BlastN search showed that all these isolates were strains sharing strong nucleotide identity with strains of serotype 1, genotype I.”

Page 11, line 5. Do the authors mean September 16?

Page 12, line 6. Although this inference may seem valid at first sight, it is not fully supported by the low bootstrap values. As indicated above the authors should: (a) include additional genotype I sequences available in the GenBank, and (b) employ at least 2 different methods of phylogenetic analysis with robust models.

Page 12, line 11-12. This statement is inaccurate and misleading. I believe the authors want to imply that the vectorial capacity of these 2 species is different with Ae. albopictus playing a minor role in human dengue transmission. However, this issue may be controversial and there is wealth of evidence in the
literature supporting both sides. Therefore, citing only “Lambrechts etal” may be biased and misleading.

Page 13, line 3. Replace ‘Firstly’ with ‘First’

Page 13, line 10. Replace ‘Secondly’ with ‘Second’

Page 15. There are several misspellings in the “Authors’ contribution” section. Additionally, capitalization should be avoided in mid-sentence.

Page 17, line 15. There is nowhere in the manuscript an indication that the authors employed PAUP. As it is indicated in page 7, line 8, the phylogenetic analysis was performed by employing MEGA 3.1.

Figure 2. The authors have not adopted the standard identifiers appearing in their trees as suggested earlier. The inclusion of the genotype does not belong in the text of the tree. The authors could opt to indicate the genotype by drawing lines or brackets that encompass all strains belonging to a said genotype. Furthermore I would suggest that the authors adopt the standard identifiers as for example: DENV-2/AU/TSV01/1993.

Level of interest: An article whose findings are important to those with closely related research interests

Quality of written English: Needs some language corrections before being published

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:

I declare that I have no competing interests