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# Life Sciences Reporting Summary

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Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study.

For final submission: please carefully check your responses for accuracy; you will not be able to make changes later.

## Experimental design

1. Sample size

   Describe how sample size was determined.

   The paper represents an analysis of data coming out of a school based cohort that ran in Thailand 1998-2002. There were 3,451 participants. A rolling recruitment approach was used to keep an average sample size of around 2,000 as children aged out of the cohort. The model used in this paper are based on antibody titers to all four serotypes from blood draws taken on average every 91 days from these participants (143,548 titer readings). As the paper represents a reanalysis of existing data, there were no sample size calculations in determining the cohort size. We used all available data in the analysis.

2. Data exclusions

   Describe any data exclusions.

   No data were excluded

3. Replication

   Describe the measures taken to verify the reproducibility of the experimental findings.

   Model parameter estimates were calculated using an MCMC approach that incorporates uncertainty estimates. We used a bootstrap approach for the relationship between titer and risk of infection/disease to incorporate sampling uncertainty. In order to ensure that our framework could reliably estimate the parameters, we built a simulated dataset with known parameters and then re-estimated them with our model. We were able to obtain the correct parameter values. This analysis is presented in the paper.

4. Randomization

   Describe how samples/organisms/participants were allocated into experimental groups.

   Not an experimental design so there were no groups

5. Blinding

   Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

   Not an experimental design so no blinding

Note: all in vivo studies must report how sample size was determined and whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

| n/a | Confirmed |
|---|---|
| ☐ | ☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.) |
| ☐ | ☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| ☐ | ☒ A statement indicating how many times each experiment was replicated |
| ☐ | ☒ The statistical test(s) used and whether they are one- or two-sided<br>*Only common tests should be described solely by name; describe more complex techniques in the Methods section.* |
| ☐ | ☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons |
| ☐ | ☒ Test values indicating whether an effect is present<br>*Provide confidence intervals or give results of significance tests (e.g. P values) as exact values whenever appropriate and with effect sizes noted.* |
| ☐ | ☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range) |
| ☐ | ☒ Clearly defined error bars in all relevant figure captions (with explicit mention of central tendency and variation) |

*See the web collection on statistics for biologists for further resources and guidance.*

## Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.

Analysis was conducted using c++ and R

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

## Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a third party.

No unique materials were used

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

No antibodies were used

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

No eukaryotic cell lines were used

b. Describe the method of cell line authentication used.

No eukaryotic cell lines were used

c. Report whether the cell lines were tested for mycoplasma contamination.

No eukaryotic cell lines were used

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.

No eukaryotic cell lines were used

## Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide all relevant details on animals and/or animal-derived materials used in the study.

No animals were used

Policy information about studies involving human research participants

## 12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

The data comes from a school based cohort where children of both genders were 7-13 in age. Diagnoses of symptomatic dengue disease were made during windows of active surveillance (June to mid-November of each year).