

## LETTER TO THE EDITOR

### Preliminary estimation of the basic reproduction number of Zika virus infection during Colombia epidemic, 2015–2016



#### KEYWORDS

Zika;  
Transmission;  
Epidemiology;  
Colombia;  
Latin America

#### Dear Editor

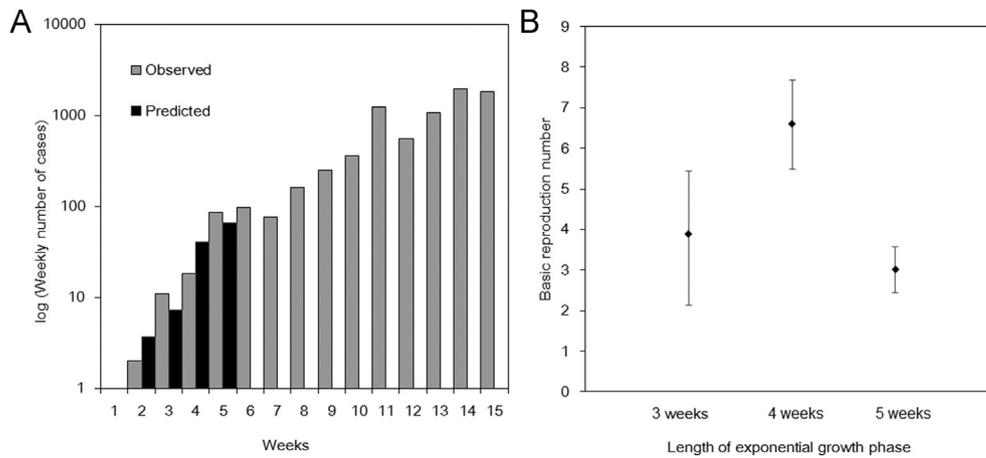
After 2014–2015 chikungunya virus (CHIKV) spread in the Americas [1], as one of consequences of the wide distribution of *Aedes* spp in the region, Zika virus (ZIKV) appeared in Brazil and later in more than 30 territories in the region [2]. Following Brazil, Colombia is the second earliest country that experienced a large-scale ZIKV epidemic in Latin America, 2015. In Colombia, laboratory-based and syndromic surveillance have been underway to capture the epidemic dynamics since its start of the epidemic in 2015 [3]. The transmission potential of ZIKV has been measured by the basic reproduction number,  $R_0$ , interpreted as the average number of secondary human cases generated by a single human case through the mosquito vector [4]. The  $R_0$  has been estimated to range from 2 to 5 in South Pacific countries [4]. Nevertheless, the transmissibility in the South American setting has yet to be reported. Here we present our modeling result from an analysis of Colombian epidemiological data.

Until March 12, 2016, more than 55,000 cases have been reported in Colombia [3]. Index confirmed case in Colombia was diagnosed in week 32, 2015 [3]. Subsequently, an exponential growth of cases has been observed from week 35. Whereas suspected cases and syndromic reports were also counted, their recording started in the midst of the outbreak, and thus, our analysis focused on laboratory confirmed cases from week 35. To estimate  $R_0$ , the exponential growth rate was first estimated assuming that the exponential growth continued for the first 3–5 weeks and

employing the maximum likelihood estimation (MLE) method [4]. Subsequently, using the statistical estimator of  $R_0$  as derived elsewhere [4] and assuming that parameter values that describe the transmission dynamics other than the growth rate are known and fixed, the exponential growth rate was converted to  $R_0$ . Since there were substantial uncertainties with respect to the generation time of ZIKV [5], we performed uncertainty analysis assuming uniformly distributed range of parameters as discussed elsewhere [4,6].

Assuming that the exponential growth continued for 3, 4 and 5 weeks from week 35 (Fig. 1A), the maximum likelihood estimation (MLE) of the growth rate were 0.11 (95% confidence interval (CI): 0.06, 0.16), 0.19 (95% CI: 0.16, 0.21) and 0.09 (95% CI: 0.07, 0.10) per day, respectively. The corresponding estimates of  $R_0$  were 3.9 (95% confidence interval (CI): 2.4, 5.7), 6.6 (95% CI: 5.5, 7.7) and 3.0 (95% CI: 2.5, 3.6), respectively (Fig. 1B). Accounting for parameter uncertainties,  $R_0$  is considered to potentially range from 2.2 to 14.8.

MLE range of  $R_0$  in Colombia (3.0–6.6) is broadly consistent with the estimates from Yap Island, 2007 and French Polynesia, 2013–14 (2–5) as well as those estimated for dengue and chikungunya viruses [4]. The estimated  $R_0$  in Colombia is very insightful into the epidemic dynamics for three reasons. First, our estimate is the first to be reported from South America. Consistency between South Pacific and South America indicates that the transmissibility is comparable given comparable vector ecology and transmission settings. Second, the estimate was derived not only from South America but from week 30s in South America. Olympic Games in Rio de Janeiro, 2016 is expected to take place in an off season of dengue epidemic (5–21 August), but our study has indirectly shown that the ZIKV transmissibility could be substantial during the games season. Indeed, the epidemic of dengue-like illness in Brazil, 2015 that has included a large number of ZIKV infections was in its declining phase during week 30s [7], and the transmissibility of ZIKV during the off season was only addressable by analyzing Colombian data. Our study underscores the need to suspend travel of pregnant women to epidemic areas including off season and thus Olympic Games season. Third, consistent estimate of  $R_0$  would help understand the required coverage of vaccination to achieve herd immunity



**Fig. 1** Transmission dynamics of Zika virus infection in Colombia, 2015–2016. A. Observed and predicted weekly number of new cases during the early period of the ZIKV epidemic (first 15 weeks of the epidemic are shown). Predictions are presented on the assumption that an exponential growth continued for the first 4 weeks. Note that logarithmic scale is adopted for the vertical axis. B. Estimates of the basic reproduction number. Dots represent maximum likelihood estimates, while whiskers extend from lower to upper 95% confidence intervals that were derived from profile likelihood. Case data were collected based on laboratory confirmation (by detecting ZIKV RNA).

in the future, given that the forthcoming vaccine is developed in time.

Finally, as expected, we found a high transmissibility of this emerging virus, comparable to those of dengue and chikungunya, in Colombia, where in fact these arboviruses are maintained to co-circulate, even producing coinfections [8]. These findings would have relevance for vector control programs, as well for the integrated assessment of the ongoing epidemics in this country, including in travel medicine.

## Funding

HN received funding support from the Japanese Society for the Promotion of Science (JSPS) KAKENHI Grant Numbers 26670308 and 26700028, Japan Agency for Medical Research and development, the Japan Science and Technology Agency (JST) CREST program and RISTEX program for Science of Science, Technology and Innovation Policy. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

## Conflict of interest

None of the authors report conflict of interests.

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21 March 2016