Supporting Information for Potential for Zika virus to establish a sylvatic transmission cycle in the Americas
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Model description

The model is based on a previously published model of sylvatic dengue transmission [1, 2]. Briefly, primates are born susceptible to Zika virus (ZIKAV) at various rates, \( \mu_{pi} \) (proportional to the lifespan of the primate) and are infected by infectious mosquitoes at rate \( r_{mjpi} \beta_{mjp}(t) \) for mosquito species \( 1, \ldots, j \). Primates recover at rate \( \gamma_{pi} \) and mosquitoes are infectious for their entire lifespan. Parameters are given in Table S1.

The transition rates for our stochastic model are below:

\[
\begin{align*}
S_{mj} \rightarrow S_{mj} + 1 & = \mu_{mj}(S_{mj}(t) + (1 - \rho)I_{mj}(t)) \quad (1) \\
S_{mj} \rightarrow S_{mj} - 1 & = \nu_{mj}S_{mj} \quad (2) \\
S_{mj} \rightarrow S_{mj} - 1 & = \sum_i r_{mjpi} \beta_{mjp}(t)I_{pi}S_{mj}/N_j \quad (3) \\
I_{mj} \rightarrow I_{mj} + 1 & = \rho I_{mj} \quad (4) \\
I_{mj} \rightarrow I_{mj} - 1 & = \nu_{mj}I_{mj} \quad (5) \\
S_{pi} \rightarrow S_{pi} + 1 & = \mu_{pi}N_{pi} \quad (6) \\
S_{pi} \rightarrow S_{pi} - 1 & = \nu_{pi}S_{pi} \quad (7) \\
I_{pi} \rightarrow I_{pi} + 1 & = \iota N_{pi} \quad (8) \\
S_{pi} \rightarrow S_{pi} - 1 & = \sum_j r_{mjpi} \beta_{mjp}(t)I_{mj}S_{pi}/N_j \quad (9) \\
I_{pi} \rightarrow I_{pi} + 1 & = \rho_{pi}I_{pi} \quad (10) \\
R_{pi} \rightarrow R_{pi} + 1 & = \gamma_{pi}I_{pi} \quad (11) \\
I_{pi} \rightarrow I_{pi} - 1 & = \nu_{pi}R_{pi} \quad (12) \\
R_{pi} \rightarrow R_{pi} - 1 & = \nu_{pi}R_{pi} \quad (13)
\end{align*}
\]

with
\[
\begin{align*}
\beta_{p,m_j}(t) & = b_{p,m_j}[1 + c_j \cdot \cos(t \ast 2\pi/365)] \quad (14) \\
\beta_{m_j,p_i}(t) & = b_{m_j,p_i}[1 + c_j \cdot \cos(t \ast 2\pi/365)] \quad (15) \\
N_{m_j} & = S_{m_j} + I_{m_j} \quad (16) \\
N_{p_i} & = S_{p_i} + I_{p_i} + R_{p_i} \quad (17) \\
N_j & = \sum_i \left( \frac{r_{m_j,p_i}}{\sum_i r_{m_j,p_i}} \right) N_{p_i} \quad (18)
\end{align*}
\]

We run simulations with 1 infectious primate introduced into an entirely susceptible population. We examine the effects of primate and mosquito population size, primate birthrate (population turnover), and force of infection on the probability of ZIKV establishment. Simulations were run and we calculated the proportion of simulations not becoming extinct after introduction of a ZIKV infected host (ie, establishing a sylvatic cycle).

**Population turnover**

Key to calculating the probability of establishing Zika is the rate at which the host population produces susceptible individuals to maintain endemic infection levels. Using data from Ernest et al. [3] we examine the number of litters per primate per year by the birthrate, as well as the rate of population turnover (defined as the reciprocal of litters per year). Figure S1 shows relatively fast population turnover at birthrates explored in the model. Additionally we highlight primate species found in Brazil (green triangles).
References

