

CORRECTION

Correction: The epidemiology of Mayaro virus in the Americas: A systematic review and key parameter estimates for outbreak modelling

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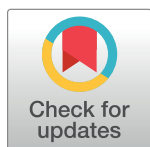
There is an error in [Table 3](#). The mean for the intrinsic incubation period should be 3.0 (95% CrI: 2.4–4.1) days not 3.0 (95% CrI: 2.2–3.8) days. The standard deviation for the intrinsic incubation period should be 0.3 (95% CrI: 0.0–2.1) days not 1.2 (95% CrI: 1.0–1.7) days. Please see the correct [Table 3](#) below.

Table 3. Estimates of the mean and standard deviation of the generation time distribution and its components.

	Mean (95% CrI)	Standard deviation (95% CrI)	Source
Intrinsic incubation period (days)	3.0 (2.4–4.1)	0.3 (0.0–2.1)	estimated
Time to viral clearance (days)	3.9 (3.5–4.4)	1.0 (0.8–1.2)	estimated
Human-to-mosquito generation time (days)	3.4 (2.0–4.8)	0.7 (0.5–1.1)	estimated
Extrinsic incubation period (days)	9.4 (8.4–10.7)	4.6 (3.3–6.7)	estimated
Mosquito life time (days) (as for <i>Aedes aegypti</i>)	5.3 (fixed)	1.4 (fixed)	[32]
Mosquito-to-human generation time (days)	11.9 (8.6–16.3)	6.2 (4.2–9.5)	estimated
Mayaro virus generation time (days)	15.2 (11.7–19.8)	6.2 (4.2–9.5)	estimated

<https://doi.org/10.1371/journal.pntd.0011034.t001>

There is an error on page 6 of [S1 Text](#). The text says, “We estimated a mean incubation period μ_{IP} of 3.0 (95% CrI: 2.2–3.8) days and a standard deviation σ_{IP} of 1.2 (95% CrI: 1.0–1.7) days.” It should say, “We estimated a mean incubation period μ_{IP} of 3.0 (95% CrI: 2.4–4.1) days and a standard deviation σ_{IP} of 0.3 (95% CrI: 0.0–2.1) days.” Please view the correct [S1 Text](#) below.



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Citation: Caicedo E-Y, Charniga K, Rueda A, Dorigatti I, Mendez Y, Hamlet A, et al. (2023) Correction: The epidemiology of Mayaro virus in the Americas: A systematic review and key parameter estimates for outbreak modelling. PLoS Negl Trop Dis 17(1): e0011034. <https://doi.org/10.1371/journal.pntd.0011034>

Published: January 4, 2023

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Supporting information

S1 Text. Fig A. Flowchart showing the selection of studies. Fig B. Viral load detected in plasma in Mayaro infected cases per day post symptoms onset. Mean and range for 21 patients are shown. **Fig C. Maximum likelihood EIP probability density function (left) and cumulative distribution function (right).** The aggregated proportion of mosquitoes that tested positive at the relative days post-infection are shown as bars. **Table A. Boolean algorithms for literature search. Table B. Data classification of MAYV studies in humans. Table C. Values used in estimate_R() function in EpiEstim package. Table D. Characteristics of Mayaro fever case reports. Table E. Characteristics of Mayaro fever cases included in the intrinsic incubation period analysis (N = 15). Table F. Characteristics of hospital-based surveillance studies included in the analysis. Table G. Characteristics of MAYV cross-sectional seroprevalence studies. Table H. Studies with possible evidence of MAYV**

transmission. These studies were not classified in other categories but strongly indicate presence of MAYV. **Table I. Studies that detected MAYV in animals. Table J. Full genomes of MAYV included in the phylogenetic analysis. Table K. Nucleotide substitution models.** The best-fitting model is in bold.
(DOCX)

Reference

1. Caicedo E-Y, Charniga K, Rueda A, Dorigatti I, Mendez Y, Hamlet A, et al. (2021) The epidemiology of Mayaro virus in the Americas: A systematic review and key parameter estimates for outbreak modelling. PLoS Negl Trop Dis 15(6): e0009418. <https://doi.org/10.1371/journal.pntd.0009418> PMID: [34081717](https://pubmed.ncbi.nlm.nih.gov/34081717/)