Peer Community In Infections

Epidemiological modeling to optimize the detection of zoonotic viruses in wild (reservoir) species

Aurelien Tellier *based on peer reviews by* ***Hetsron Legrace NYANDJO BAMEN*** *and 1 anonymous reviewer*

David R.J. Pleydell, Innocent Ndong Bass, Flaubert Auguste Mba Djondzo, Dowbiss Meta Djomsi, Charles Kouanfack, Martine Peeters, Julien Cappelle (2024) A Bayesian analysis of birth pulse effects on the probability of detecting Ebola virus in fruit bats. bioRxiv, ver. 3, peer-reviewed and recommended by Peer Community in Infections.
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Various species of Ebolavirus have caused, and are still causing, zoonotic outbreaks and public health crises in Africa. Bats have long been hypothesized to be important reservoir populations for a series of viruses such as Hendra or Marburg viruses, the severe acute respiratory syndrome coronavirus (SARS-CoV, SARS-CoV-2) as well as Ebolaviruses [2, 3]. However the ecology of disease dynamics, disease transmission, and coevolution with their natural hosts of these viruses is still poorly understood, despite their importance for predicting novel outbreaks in human or livestock populations. The evidence that bats function as sylvatic reservoirs for Ebola viruses is yet only partial. Indeed, only few serological studies demonstrated the presence of Ebolavirus antibodies in young bats [4], albeit without providing positive controls of viral detection or identifying the viral species (via PCR). There is thus an unexplained discrepancy between serological data and viral detection [2, 4].

In this article, Pleydell et al. [1] use a modeling approach as well as published serological and age-structure (of the bat population) data to calibrate the model simulations. The study starts with the development of an age-structured epidemiological model which includes seasonal birth pulses and waning immunity, both generating pulses of Ebolavirus transmission within a colony of African straw-coloured fruit bats (*Eidolon helvum*). The epidemiological dynamics of such system of ordinary differential equations can generate annual outbreaks, skipped years or multi-annual cycles up to chaotic dynamics. Therefore, the calibration of the parameters, and the definition of biologically relevant priors, are key. To this aim, the serological data are obtained from a previous study in Cameroon [5], and the age structured of the bat population (birth and

mortality) from a population study in Ghana [6]. These data are integrated into the Bayesian analysis and statistical framework to fit the model and generate predictions. In a nutshell, the authors show an overlap between the data and credibility intervals generated by the calibrated model, which thus explains well the seasonality of age-structure, namely changes in pup presence, number of lactating females, or proportion of juveniles in May. The authors can estimate that 76% of adults and 39% of young bats do survive each year, and infections are expected to last one and a half weeks. The epidemiological model predicts that annual birth pulses likely generate annual disease outbreaks, so that weeks 30 to 31 of each year, are predicted to be the best period to isolate the circulating Ebolavirus in this bat population. From the model predictions, the authors estimate the probability to have missed an infectious bat among all the samples tested by PCR being approximately of one per two thousands. The disease dynamics pattern observed in the serology data, and replicated by the model, is likely driven by seasonal pulses of young susceptible bats entering the population. This seasonal birth event increases the viral transmission, resulting in the observed peak of viral prevalence. With the inclusion of immunity waning and antibody persistence, the model results illuminate therefore why previous studies have detected only few positive cases by PCR tests, in contrast to the evidence from serological data.

This study provides a first proof of principle that epidemiological modeling, despite its many simplifying assumptions, can be applied to wild species reservoirs of zoonotic diseases in order to optimize the design of field studies to detect viruses. Furthermore, such models can contribute to assess the probability and timing of zoonotic outbreaks in human or livestock populations. This article illustrates one of the manifold applications of mathematical theory of disease epidemiology to optimize sampling of pathogens/parasites or vaccine development and release [7, 8]. The further coupling of such models with population genetics theory and statistical inference methods (using parasite genome data) increasingly provide insights into the adaptation and evolution of parasites to human, crops and livestock populations [9, 10].

References:

[1] Pleydell D.R.J., Ndong Bass I., Mba Djondzo F.A., Djomsi D.M., Kouanfack C., Peeters M., and J. Cappelle. 2023. A Bayesian analysis of birth pulse effects on the probability of detecting Ebola virus in fruit bats. bioRxiv, ver. 3 peer reviewed and recommended by Peer Community In Infections. https://doi.org/10.1101/2023.08.10.552777

[2] Caron A., Bourgarel M., Cappelle J., Liégeois F., De Nys H.M., and F. Roger. 2018. Ebola virus maintenance: if not (only) bats, what else? Viruses 10, 549. https://doi.org/10.3390/v10100549

[3] Letko M., Seifert S.N., Olival K.J., Plowright R.K., and V.J. Munster. 2020. Bat-borne virus diversity, spillover and emergence. Nature Reviews Microbiology 18, 461–471. https://doi.org/10.1038/s41579-020-0394-z

[4] Leroy E.M., Kumulungui B., Pourrut X., Rouquet P., Hassanin A., Yaba P., Délicat A., Paweska J.T., Gonzalez J.P., and R. Swanepoel. 2005. Fruit bats as reservoirs of Ebola virus. Nature 438, 575–576. https://doi.org/10.1038/438575a

[5] Djomsi D.M. et al. 2022. Dynamics of antibodies to Ebolaviruses in an *Eidolon helvum* bat colony in Cameroon. Viruses 14, 560. https://doi.org/10.3390/v14030560

[6] Peel A.J. et al. 2016. Bat trait, genetic and pathogen data from large-scale investigations of African fruit bats *Eidolon helvum*. Scientific data 3, 1–11. https://doi.org/10.1038/sdata.2016.49

[7] Nyandjo Bamen H.L., Ntaganda J.M., Tellier A. and O. Menoukeu Pamen. 2023. Impact of imperfect vaccine, vaccine trade-off and population turnover on infectious disease dynamics. Mathematics, 11(5), p.1240. https://doi.org/10.3390/math11051240

[8] Saadi N., Chi Y.L., Ghosh S., Eggo R.M., McCarthy C.V., Quaife M., Dawa J., Jit M. and A. Vassall. 2021. Models of COVID-19 vaccine prioritisation: a systematic literature search and narrative review. BMC medicine, 19, pp.1-11. https://doi.org/10.1186/s12916-021-02190-3

[9] Maerkle, H., John S., Metzger, L., STOP-HCV Consortium, Ansari, M.A., Pedergnana, V. and Tellier, A., 2023. Inference of host-pathogen interaction matrices from genome-wide polymorphism data. bioRxiv, https://doi.org/10.1101/2023.07.06.547816.

[10] Gandon S., Day T., Metcalf C.J.E. and B.T. Grenfell. 2016. Forecasting epidemiological and evolutionary dynamics of infectious diseases. Trends in ecology & evolution, 31(10), pp.776-788. https://doi.org/10.1016/j.tree.2016.07.010

Reviews

Evaluation round #1

DOI or URL of the preprint: https://doi.org/10.1101/2023.08.10.552777
Version of the preprint: 1

Authors' reply, 12 February 2024

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Decision by Aurelien Tellier, posted 18 October 2023, validated 19 October 2023

Minor revisions needed

Dear authors,

The reviewers and myself concur that your study is very interesting and fits squarely in what we would like to recommend at PCI Infections. I am therefore very thankful that you submitted a nice well thought through and well conducted study and analyses. The model is interesting and well described, and the statistical analyses are adequate to support the robust conclusions. I have read the paper myself and very much liked the inference analysis based on a Bayesian framework with Likelihood functions build to represent some sampling distributions. The reviewers have some minor comments regarding the presentation (notations) of the model, few typos or lack of clarity here and there.

These can be easily and quickly addressed in a revised version.

Best regards,

Aurelien Tellier

Reviewed by Hetsron Legrace NYANDJO BAMEN, 16 October 2023

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Reviewed by anonymous reviewer 1, 18 October 2023

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