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Bayesian reconstruction of household transmissions to infer the serial interval of COVID-19 by variants of concern: analysis from a prospective community cohort study (Virus Watch)

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Abstract

Background **The serial interval is a key epidemiological measure that quantifies the time between an infector's and an infectee's onset of symptoms. This measure helps investigate epidemiological links between cases, and is an important parameter in transmission models used to estimate transmissibility and inform control strategies. The emergence of multiple variants of concern (VOC) during the SARS-CoV-2 pandemic has led to uncertainties about potential changes in the serial interval of COVID-19. We estimated the household serial interval of multiple VOC using data collected by the Virus Watch study. This online, prospective, community cohort study followed-up entire households in England and Wales since mid-June 2020.**

Methods **This analysis included 5842 symptomatic individuals with confirmed SARS-CoV-2 infection among 2579 households from Sept 1, 2020, to Aug 10, 2022. SARS-CoV-2 variant designation was based upon national surveillance data of variant prevalence by date and geographical region. We used a Bayesian framework to infer who infected whom by exploring all transmission trees compatible with the observed dates of symptoms, given assumptions on the incubation period and generation time distributions using the R package outbreaker2.**

Findings **We characterised the serial interval of COVID-19 by VOC. The mean serial interval was shortest for omicron BA5 (2·02 days; 95% credible interval [CrI] 1·26–2·84) and longest for alpha (3·37 days; 2·52–4·04). The mean serial interval before alpha (wild-type) was 2·29 days (95% CrI 1·39–2·94), 3·11 days (2·28–3·90) for delta, 2·72 days (2·01–3·47) for omicron BA1, and 2·67 days (1·90–3·46) for omicron BA2. We estimated that 17% (95% CrI 5–26) of serial interval values are negative across all variants.**

Interpretation **Most methods estimating the reproduction number from incidence time series do not allow for a negative serial interval by construction. Further research is needed to extend these methods and assess biases introduced by not accounting for negative serial intervals. To our knowledge, this study is the first to use a Bayesian framework to estimate the serial interval of all major SARS-CoV-2 VOC from thousands of confirmed household cases.**

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Contributors

CG, VN, EF, MS, AMDN, SB, TEB, WLEF, AY, JK, IB, RWA, and ACH are part of the Virus Watch Core Team. CG, VN, EF, MS, and AMDN processed the data. CG, AC, TJ, and PW did the data analysis. CG, AC, TJ, and PW wrote the Abstract.

Declaration of interests

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