

To: [REDACTED] [REDACTED]@amsterdamumc.nl]
From: [REDACTED]
Sent: Sun 1/17/2021 9:30:14 AM
Subject: FW: Reminder: Invitation to review a manuscript for Genome Medicine - GMED-D-20-01024R1 - [EMID:fab96e3f5ef94afe]
Received: Sun 1/17/2021 9:30:15 AM

Wil jij deze doen? Dan geef ik dat door als ik decline. Ik heb geen tijd helaas.

-----Original Message-----

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Sent: zondag 17 januari 2021 08:52
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Subject: Reminder: Invitation to review a manuscript for Genome Medicine - GMED-D-20-01024R1 - [EMID:fab96e3f5ef94afe]

GMED-D-20-01024R1

Combined epidemiological and genomic analysis of nosocomial SARS-CoV-2 transmission and associated factors.

[REDACTED]

Genomics UK Consortium (COG-UK) Genome Medicine

Dear [REDACTED]

Recently we contacted you to ask if you could review the above manuscript that was submitted to Genome Medicine.

As we have not yet heard from you but are aiming for a fast review process, I would be grateful if you could let me know whether or not you are able to review this manuscript by accessing the system using the following link and choosing either accept or decline.

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The title, authors and abstract of the manuscript are at the end of this email.

I look forward to hearing from you within the next few days.

Please note that this is an automatic email, so if you have recently contacted us regarding your review then please ignore this reminder.

Best wishes,

[REDACTED]

<https://genomemedicine.biomedcentral.com/>

GMED-D-20-01024R1

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Combined epidemiological and genomic analysis of nosocomial SARS-CoV-2 transmission and associated factors.

[REDACTED]

Genomics UK Consortium (COG-UK) Genome Medicine

Abstract: Background. Many healthcare facilities report nosocomial SARS-CoV-2 infections but analysis to identify clusters and factors impacting on transmission is complicated by the high prevalence of infection.

Methods. Viral genome sequence and epidemiological data were analysed for 574 consecutive SARS-CoV-2 PCR-positive patients during the first 19 days of the pandemic at a large multi-site healthcare institution. Incidence was linked with major infection control interventions and infection in a cohort of 228 HCWs.

Results. 44 epidemiologically-defined transmission clusters were found which included all 90 nosocomial cases. SARS-CoV-2 genome

sequence was obtained from 370/541 (68%) cases, including 89% (80/90) of all probable and definite nosocomial cases and 72% (168/234) of cases placed into epidemiological clusters. Incorporation of genomic sequence data found no support for 31/44 (70%) epidemiologically-defined clusters, and created 14 final clusters involving 80 cases. Haplotypes in these clusters were enriched 1-14 fold compared to the community, included a median of 4 patients (range 2-19), and accounted for 63 of 80 (79%) sequenced nosocomial cases. Applying genomics, we could provide a robust estimate of the incubation period for nosocomial transmission, with a median lower bound and upper bound of 6 and 9 days respectively. Three factors implicated healthcare workers in transmission: i) six (43%) clusters spanned multiple wards with evidence of cryptic transmission. ii) community-onset cases could not be identified in more than half the clusters, particularly on an elective hospital site. iii) the peak of HCW symptom onset overlapped with the increase in incidence of nosocomial cases. Nosocomial cases and healthcare worker symptoms both decreased about 7 days after announcement of progressive community social distancing measures. This decrease occurred whilst admissions of community SARS-CoV-2 cases continued to increase, and before impact of introducing universal face-masks or banning hospital-visitors.

Conclusions. Genomics was necessary to accurately resolve clusters and provided information on direction of transmission and incubation period. Our data supports healthcare workers as important vectors of transmission, and suggests community social-distancing had the dominant impact on reducing initial intensity of nosocomial SARS-CoV-2 transmission potentially by reducing HCW infection in the community.

****Our flexible approach during the COVID-19 pandemic****

If you need more time at any stage of the peer-review process, please do let us know. While our systems will continue to remind you of the original timelines, we aim to be as flexible as possible during the current pandemic.

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