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COG-UK Project Hospital-Onset COVID-19 Infections (HOCI) Study: How effective are infection prevention and control measures that are informed by genetic analysis of coronavirus (rapid and standard) at preventing COVID-19 in NHS hospitals?

Submission date
12/05/2020

Recruitment status
No longer recruiting

Registration date
20/05/2020

Overall study status
Completed

Last Edited
23/04/2025

Condition category
Infections and Infestations

[X] Prospectively registered
[X] Protocol
[X] Statistical analysis plan
[X] Results
[X] Individual participant data

Plain English summary of protocol

Background and study aims
COVID-19 is a condition caused by the coronavirus (called SARS-CoV-2) that was first identified in late 2019. This virus can infect the respiratory (breathing) system. Some people do not have symptoms but can carry the virus and pass it on to others. People who have developed the condition may develop a fever and/or a continuous cough among other symptoms. This can develop into pneumonia. Pneumonia is a chest infection where the small air pockets of the lungs, called alveoli, fill with liquid and make it more difficult to breathe.
In 2020, the virus has spread to many countries around the world and neither a vaccine against the virus or specific treatment for COVID-19 has yet been developed. As of April 2020, it is advised that people minimize travel and social contact, and regularly wash their hands to reduce the spread of the virus.
Groups who are at a higher risk from infection with the virus, and therefore of developing COVID-19, include people aged over 70 years, people who have long-term health conditions (such as asthma or diabetes), people who have a weakened immune system and people who are pregnant. People in these groups, and people who might come into contact with them, can reduce this risk by following the up-to-date advice to reduce the spread of the virus.
Hospitals are recognised to be a major risk for the spread of infections despite the availability of protective measures. Under normal circumstances, staff may acquire and transmit infections, but the health impact of within hospital infection is greatest in vulnerable patients. For the novel coronavirus that causes COVID-19, like recent outbreaks such as the SARS and Ebola virus, the risk of within hospital spread of infection presents an additional, significant health risk to healthcare workers. Infection Prevention and Control (IPC) teams within hospitals engage in practices that minimise the number of infections acquired within hospital. This includes surveillance of infection spread, and proactively leading on training to clinical and other hospital

teams. There is now good evidence that genome sequencing of epidemic viruses such as that which causes COVID-19, together with standard IPC, more effectively reduces within hospital infection rates and may help identify the routes of transmission, than just existing IPC practice. The aims of the study are to evaluate the benefit of genome sequencing in this context, and whether rapid (24-48 hour) turnaround on the data to IPC teams has an impact on that level of benefit.

Who can participate?
Inpatients who are COVID-19 positive and suspected of having been transmitted the virus from the hospital setting (where positive over 48 hours after admission)

What does the study involve?
The study involves the use of genomic sequencing of COVID-19-positive patients in hospitals to inform Infection Prevention Control (IPC) measures undertaken within the hospital in the hopes of reducing hospital transmission of the virus. The study team will ask participating NHS hospitals to collect IPC information as per usual practice for a short time to establish data for comparison. Where patients are confirmed to have a COVID-19 infection thought to have been transmitted within hospital, their samples will be sequenced with data fed back to hospital teams during the intervention phase. A final phase without the intervention may take place for additional information on standard IPC practice when the COVID-19 outbreak is at a low level nationwide.

What are the possible benefits and risks of participating?
Any participants in this study will already have confirmed COVID-19 infection. Therefore any benefits to these patients of the intervention will be indirect. The potential benefit to the participants will be dependent on the effectiveness of the intervention and their location within the hospital. In the event the intervention results in a lower level of nosocomial transmissions, it is likely that participants will benefit from lower numbers than otherwise of COVID-19 cases at the NHS site, and therefore more staffing resource on a per participant basis being available. The substantive overarching benefit of proven effectiveness for this study would be for patients generally within the hospital setting, and potentially the wider public. There are no anticipated risks to participation beyond having confirmed COVID-19 infection.

Where is the study run from?
University College London (UCL)

When is the study starting and how long is it expected to run for?
March 2020 to July 2021

Who is funding the study?
1. COG-UK Consortium (UK)
2. UKRI - MRC (UK)

Who is the main contact?
Unfortunately, this study is not recruiting public volunteers at this time. Please do not contact the research team as they will not be able to respond. For more information about COVID-19 research, visit the Be Part of Research homepage.

Contact information

Type(s)

Public

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Type(s)
Scientific

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Additional identifiers

Clinical Trials Information System (CTIS)
Nil known

Integrated Research Application System (IRAS)
283014

ClinicalTrials.gov (NCT)
NCT04405934

Protocol serial number
CTU/2020/353, IRAS 283014

Study information

Scientific Title

A Phase III prospective, interventional, cohort, superiority study to evaluate the benefit of rapid COVID-19 genomic sequencing (the COVID-19 GENOMICS UK Project) on infection control in preventing the spread of the virus in UK NHS hospitals

Acronym
COG-UK HOCI

Study objectives
Hospitals are recognised to be a major risk for the spread of infections despite the availability of protective measures. Under normal circumstances, staff may acquire and transmit infections, but the health impact of within hospital infection is greatest in vulnerable patients. For the novel coronavirus that causes COVID-19, like recent outbreaks such as the SARS and Ebola virus infections, the risk of within-hospital spread of infection presents an additional, significant health risk to healthcare workers.

Infection Prevention and Control (IPC) teams within hospitals engage in practices that minimise the number of infections acquired within hospital. This includes surveillance of infection spread, and proactively leading on training to clinical and other hospital teams.

There is now good evidence that genome sequencing of epidemic viruses such as that which causes COVID-19, together with standard IPC, more effectively reduces within-hospital infection rates and may help identify the routes of transmission, than just existing IPC practice. It is proposed to evaluate the benefit of genome sequencing in this context, and whether rapid (24-48 h) turnaround on the data to IPC teams has an impact on that level of benefit.

The study team will ask participating NHS hospitals to collect IPC information as per usual practice for a short time to establish data for comparison. Where patients are confirmed to have a COVID-19 infection thought to have been transmitted within the hospital, their samples will be sequenced with data fed back to hospital teams during the intervention phase. A final phase without the intervention may take place for additional information on standard IPC practice when the COVID-19 outbreak is at a low level nationwide.

Ethics approval required
Old ethics approval format

Ethics approval(s)
Approved 23/04/2020, East of England - Cambridge South Research Ethics Committee (The Old Chapel, Royal Standard Place, Nottingham, NG1 6FS, UK; +44 (0)207 104 8065; cambridgesouth.rec@hra.nhs.uk), ref: 20/EE/0118

Study design
Phase III prospective interventional cohort superiority study

Primary study design
Interventional

Study type(s)
Prevention

Health condition(s) or problem(s) studied

Hospital-onset COVID-19 (SARS-CoV-2 infection)

Interventions

Current interventions as of 14/04/2021:
Allocation to either rapid local sequencing (c. 24-48 h) or lack of rapid local sequencing (i.e. via Wellcome Sanger Institute at >96 h) will be dependent on the time of the study (see below). All sites will perform both rapid and standard sequencing in sequentially.

Proposed study duration: 12 months; comprising 6 months of set-up, baseline data collection, interventional data collection) and up to 6 months of data cleaning, data analysis and reporting.

Study intervention: Genomic-sequence informed IPC measures: Use of virus (COVID-19) genome sequence report to inform infection prevention control procedures. Rapid or standard (time to return to sites) receipt of virus (COVID-19) genomic sequencing reports.

1. Baseline/control phase 1
Sample collection and genomic sequencing from COVID-19 positive participants suspected of acquiring infection in hospital (suspected nosocomial COVID-19 infection where tested positive >48 h after hospital admission) where sequencing reports are not received by Infection Prevention Control (IPC) site teams.

2. Site intervention phase
Sample collection and genomic sequencing from COVID-19 positive participants suspected of acquiring infection in hospital where sequencing reports generated both rapid or standard and received by site IPC teams for interpretation and action.

3. Control phase 2 (only upon approval from the data monitoring committee)
Sample collection and genomic sequencing from COVID-19 positive participants suspected of acquiring infection in hospital where sequencing reports not interpreted/actioned by IPC site teams - where deemed ethical and approved by oversight committee.

Cohort follow baseline (no report receipt), then rapid vs standard sequencing report receipt phase, then return to baseline phase (no report receipt).

Proposed study duration: 15 months total; comprising set-up, 7 months baseline data collection, interventional data collection) and up to 5 months of data cleaning, data analysis and reporting.

Previous interventions:
Allocation to either rapid local sequencing (c. 24-48 h) or lack of rapid local sequencing (i.e. via Wellcome Sanger Institute at >96 h) will be dependent on the time of the study (see below). All sites will perform both rapid and standard sequencing in sequentially.

Proposed study duration: 12 months; comprising 6 months of set-up, baseline data collection, interventional data collection) and up to 6 months of data cleaning, data analysis and reporting.

Study intervention: Genomic-sequence informed IPC measures: Use of virus (COVID-19) genome sequence report to inform infection prevention control procedures. Rapid or standard (time to return to sites) receipt of virus (COVID-19) genomic sequencing reports.

1. Baseline/control phase 1
Sample collection and genomic sequencing from COVID-19 positive participants suspected of acquiring infection in hospital (suspected nosocomial COVID-19 infection where tested positive

>48 h after hospital admission) where sequencing reports are not received by Infection Prevention Control (IPC) site teams.

2. Site intervention phase
Sample collection and genomic sequencing from COVID-19 positive participants suspected of acquiring infection in hospital where sequencing reports generated both rapid or standard and received by site IPC teams for interpretation and action.

3. Control phase 2
Sample collection and genomic sequencing from COVID-19 positive participants suspected of acquiring infection in hospital where sequencing reports not interpreted/actioned by IPC site teams - where deemed ethical and approved by oversight committee.

Cohort follow baseline (no report receipt), then rapid vs standard sequencing report receipt phase, then return to baseline phase (no report receipt).

Proposed study duration: 12 months total; comprising 6 months of set-up, baseline data collection, interventional data collection) and up to 6 months of data cleaning, data analysis and reporting.

Intervention Type
Other

Primary outcome(s)
Current primary outcome measures as of 14/04/2021:
1. Incidence rate of PHE/IPC-defined SARS-CoV-2 HAIs (defined as SARS-CoV-2 cases with an interval of >8 days from admission to symptom onset, if known, or sample date), measured as incidence rate of recorded cases per week per 100 inpatients, during each phase of the study.
2. Identification of linkage to individuals within an outbreak of SARS-CoV-2 nosocomial transmission using sequence report data for HOCIs in whom this was not identified by pre-sequencing IPC evaluation, for each patient during study phases in which the sequence reporting tool is in use.

Previous primary outcome measures:
1. Incidence rate of IPC-defined HOCIs, measured as incidence rate of recorded cases per week per 100 inpatients based on case report forms during each phase of the study
2. Identification of nosocomial transmission using sequencing data in potential HOCIs in whom this was not identified by pre-sequencing IPC evaluation, measured using pre- and post-sequencing case report forms for each enrolled patient during study phases in which the sequence reporting tool is in use

Key secondary outcome(s))
Current secondary outcome measures as of 14/04/2021:
1. Incidence rate of IPC-defined SARS-CoV-2 hospital outbreaks, defined as cases of hospital transmission linked by location and with intervals between diagnoses no greater than 28 days, measured as incidence rate of outbreak events per week per 100 inpatients during each phase of the study
2. Incidence rate of IPC+sequencing-defined SARS-CoV-2 hospital outbreaks involving HOCI cases, defined as IPC-defined SARS-CoV-2 hospital outbreaks with the additional condition of clustering of viral sequences and measured as outbreak events per week per 100 inpatients during study phases in which the sequence reporting tool is in use. Genetic clusters are defined

as having maximal viral sequence pairwise SNP distance of 2 between each individual included and their nearest neighbour within the cluster.
3. Changes to IPC actions implemented and following receipt of SARS-CoV-2 sequence report, for each enrolled patient during study phases in which the sequence reporting tool is in use.
4. Changes to IPC actions that would ideally have been implemented but may not have been following receipt of SARS-CoV-2 sequence report, for each enrolled patient during study phases in which the sequence reporting tool is in use.
5. Health economic benefit of both slow and rapid sequencing reports to IPC against baseline
6. The number of HCW periods of sickness/self-isolation, assessed as a proportion of the number of staff usually on those wards impacted by HOCI cases, for all phases of the study

Previous secondary outcome measures:
1. Incidence rate of IPC-defined hospital outbreaks, defined as cases of hospital transmission linked by location and with intervals between diagnoses of no greater than 2 weeks (relevant data extracted from case report forms), measured as incidence rate of outbreak events per week per 100 inpatients during each phase of the study
2. Incidence rate of IPC+sequencing-defined hospital outbreaks, defined by retrospective review of all available sequencing and epidemiological data for identification of transmission clusters and measured as outbreak events per week per 100 inpatients during each phase of the study
3. Changes to IPC actions implemented following receipt of viral sequence report, measured using pre- and post-sequencing case report forms for each enrolled patient during study phases in which the sequence reporting tool is in use
4. Changes to IPC actions that would ideally have been implemented (given unlimited resources) following receipt of viral sequence report, measured using pre- and post-sequencing case report forms for each enrolled patient during study phases in which the sequence reporting tool is in use
5. Health economic benefit of standard and rapid sequencing reports to IPC measured using bespoke health economic case report data comparison between baseline, standard and rapid sequencing phases
6. Number of HCW days off work measured from sampling these data points on case report forms at all study phases

Completion date
31/07/2021

Eligibility

Key inclusion criteria
Current inclusion criteria as of 14/04/2021:
1. Participants must have confirmed COVID-19 infection and be a hospital-onset COVID-19 infection (HOCI)
2. Participants must have provided nasal swab/pharyngeal swab/combined nasal and pharyngeal swab/nasopharyngeal aspirate or bronchoalveolar lavage sample for evaluation in the COG-UK project.
3. Participants may be of any age or gender to be included in the study. For clarity, in the above criterion a potential HOCI is an admitted patient at site with first confirmed test for COVID-19 >48 h after admission, where they were not suspected to have COVID-19 at time of admission

Previous inclusion criteria:
1. Participants must have confirmed COVID-19 infection and either:
1.1. Be a potential hospital-onset COVID-19 infection (HOCI), or

1.2. Potential workplace infection with SARS CoV-2 for site-based healthcare workers
2. Participants must have provided nasal swab/pharyngeal swab/combined nasal and pharyngeal swab/nasopharyngeal aspirate or bronchoalveolar lavage sample for evaluation in the COG-UK project.
3. Participants may be of any age or gender to be included in the study. For clarity, in the above criterion a potential HOCI is an admitted patient at site with first confirmed test for COVID-19 >48 h after admission, where they were not suspected to have COVID-19 at time of admission

Participant type(s)
Patient

Healthy volunteers allowed
No

Age group
All

Sex
All

Total final enrolment
2170

Key exclusion criteria
Does not meet inclusion criteria

Date of first enrolment
01/06/2020

Date of final enrolment
31/05/2021

Locations

Countries of recruitment
United Kingdom

England

Scotland

Study participating centre
Imperial College Healthcare NHS Trust
The Bays, St Mary's Hospital
South Wharf Road
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Study participating centre
NHS Greater Glasgow and Clyde
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Sponsor information

Organisation
University College London

ROR
https://ror.org/02jx3x895

Funder(s)

Funder type
Research organisation

Funder Name
COG-UK Consortium

Funder Name
UK Research and Innovation

Alternative Name(s)
UKRI

Funding Body Type
Government organisation

Funding Body Subtype
National government

Location
United Kingdom

Funder Name
Medical Research Council

Alternative Name(s)
Medical Research Council (United Kingdom), UK Medical Research Council, MRC

Funding Body Type
Government organisation

Funding Body Subtype
National government

Location
United Kingdom

Results and Publications

Individual participant data (IPD) sharing plan
Current IPD sharing statement as of 15/02/2022:
The terms of the project's funding require the fully anonymised dataset from the COG-UK HOCI study to be stored in a publicly available repository. The UCL Data Repository will be used for this purpose so that the dataset may be evaluated and/or used for future work by other researchers. The study protocol will also be made available. Access will be on a fully open policy. This will be done within 6 months of public reporting of results. The data will be available for 5 years.

Previous IPD sharing statement as of 26/04/2021:
The datasets generated during and/or analysed during the current study will be stored in a publicly available repository. The terms of the funding requires the COG-UK HOCI study dataset to be shared on CSDR (https://clinicalstudydatarequest.com/) or an equivalent data-sharing platform so that the data may be reused by other researchers. This will be done within 6 months of public reporting of results.

Previous IPD sharing statement:
The data-sharing plans for the current study are unknown and will be made available at a later date (due to the requirement for further legal clarity in relation to the upcoming expiry of the COPI notice with regards to the trial team's obligations under the United Kingdom data protection regulation).

IPD sharing plan summary

Stored in publicly available repository

Study outputs

Output type	Details	Date created	Date added	Peer reviewed?	Patient-facing?
Results article		13/09/2022	27/09/2022	Yes	No
Protocol article		19/04/2022	12/08/2022	Yes	No
Basic results	version 1.0	12/08/2022	15/08/2022	No	No
Dataset			05/09/2022	No	No
HRA research summary			28/06/2023	No	No
Other publications	Qualitative process evaluation	17/04/2025	23/04/2025	Yes	No
Participant information sheet	Participant information sheet	11/11/2025	11/11/2025	No	Yes
Statistical Analysis Plan	version 1.0	21/04/2021	05/09/2022	No	No
Study website	Study website	11/11/2025	11/11/2025	No	Yes