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MORNING BRIEF

Scientific Review

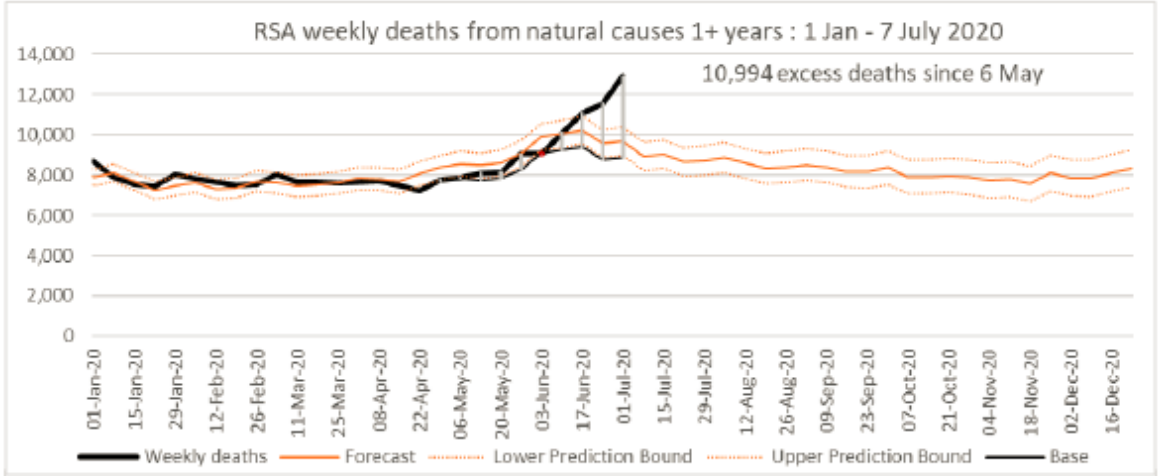
20 July 2020

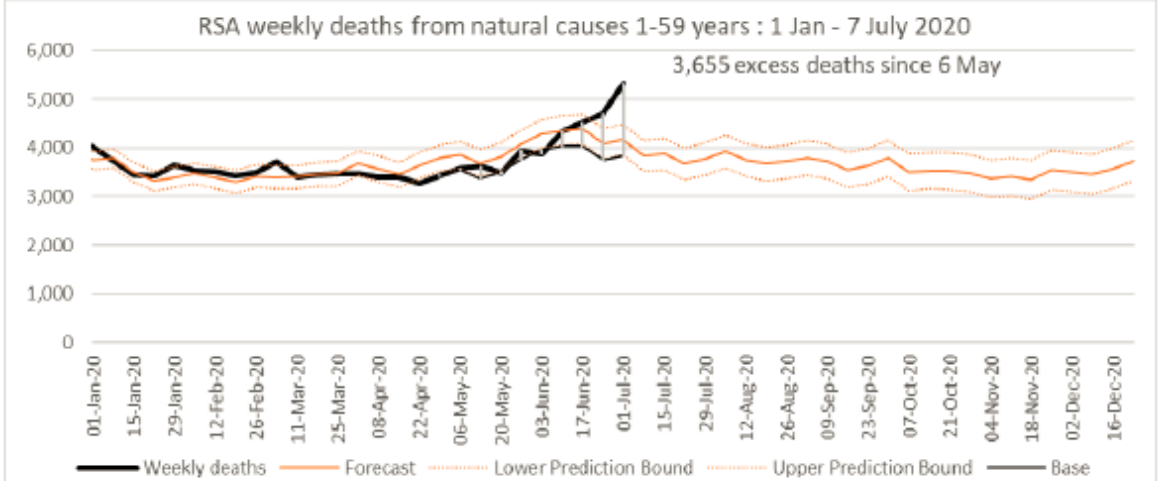
The purpose of the Morning Brief is to summarize and present key information, research articles and other relevant publications pertaining to critical care and COVID-19.

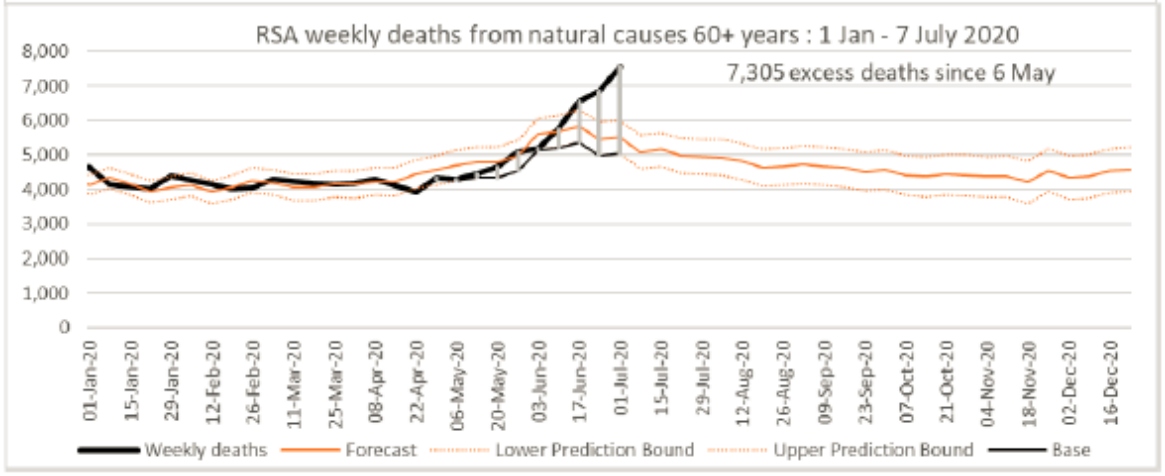
Stellenbosch University Research Response Team

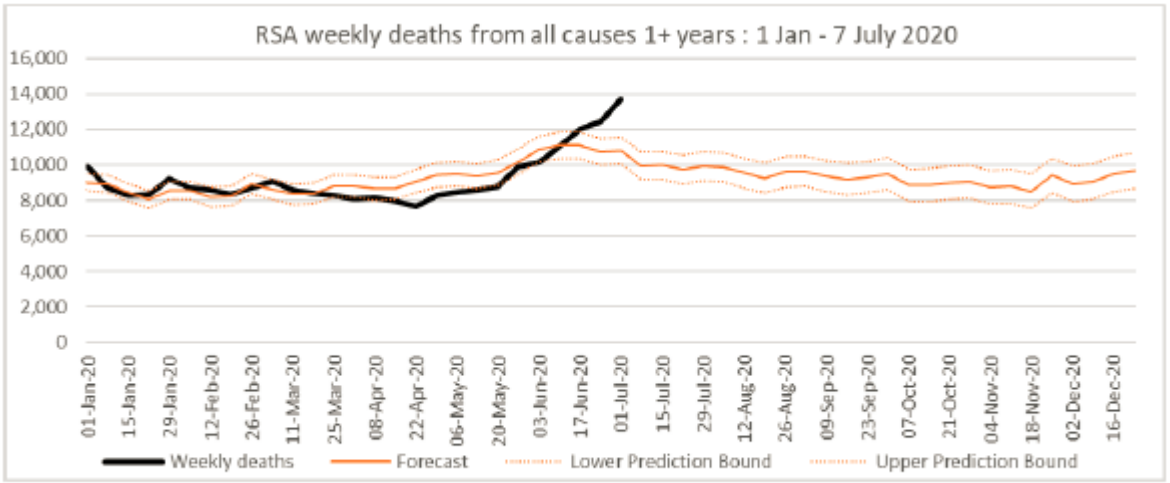
Content

Statistics
Whole genome sequencing surveillance



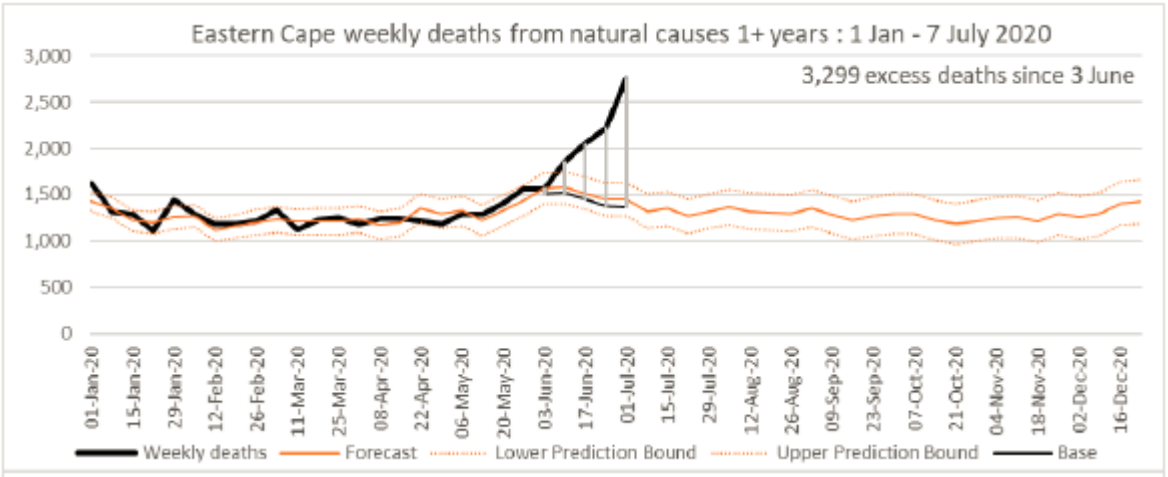


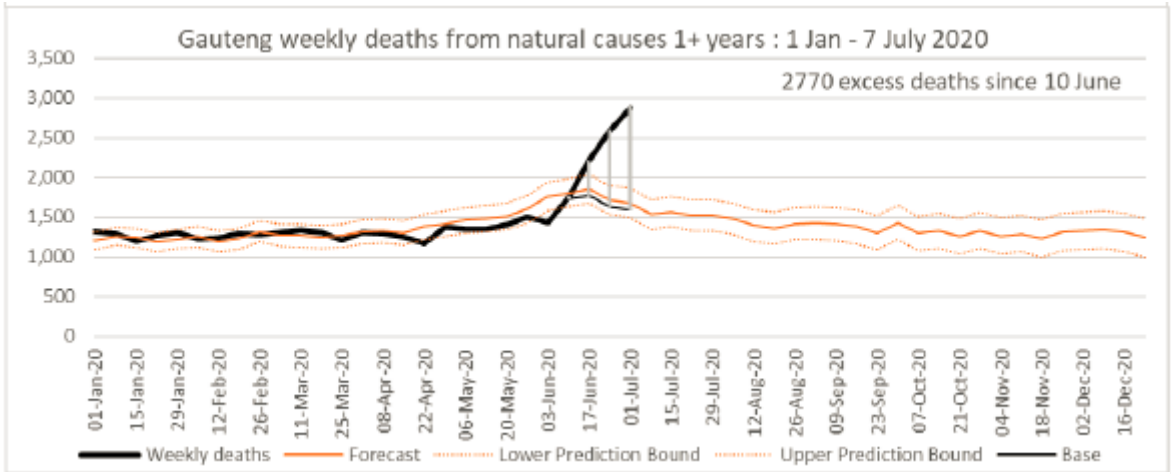


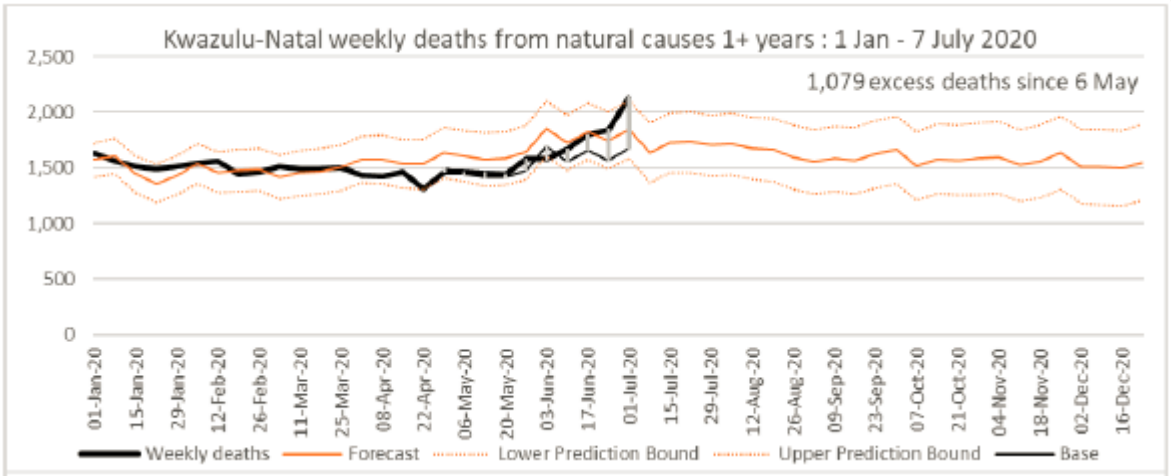


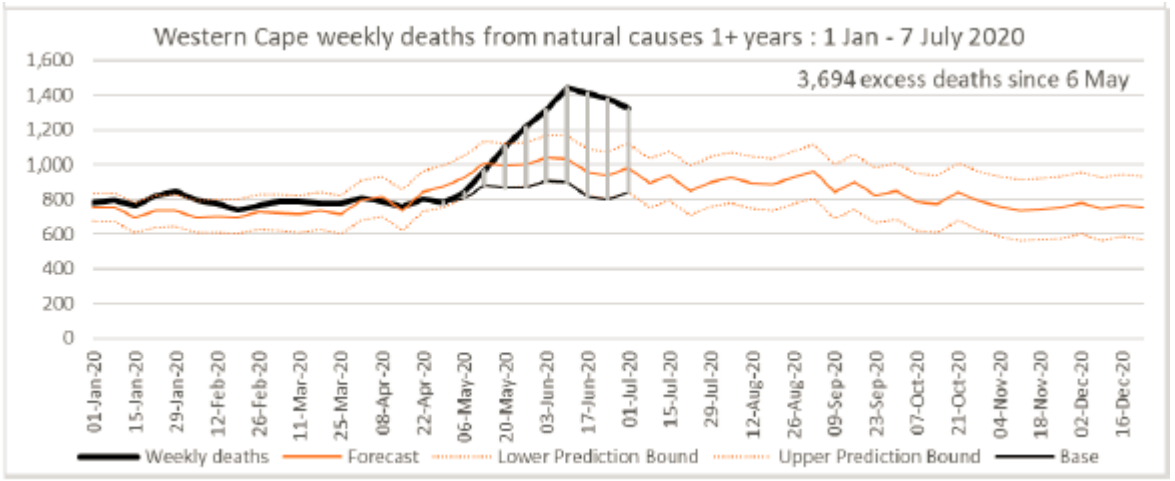
Numbers have been scaled to the estimated actual number of death and for the last week has been adjusted for delayed registrations

https://www.samrc.ac.za/reports/report-weekly-deaths-south-africa









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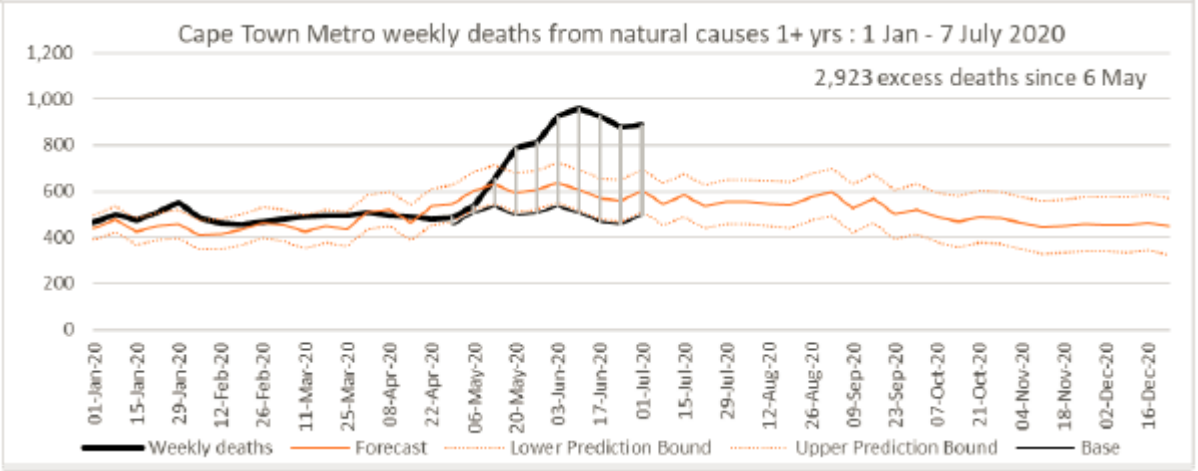

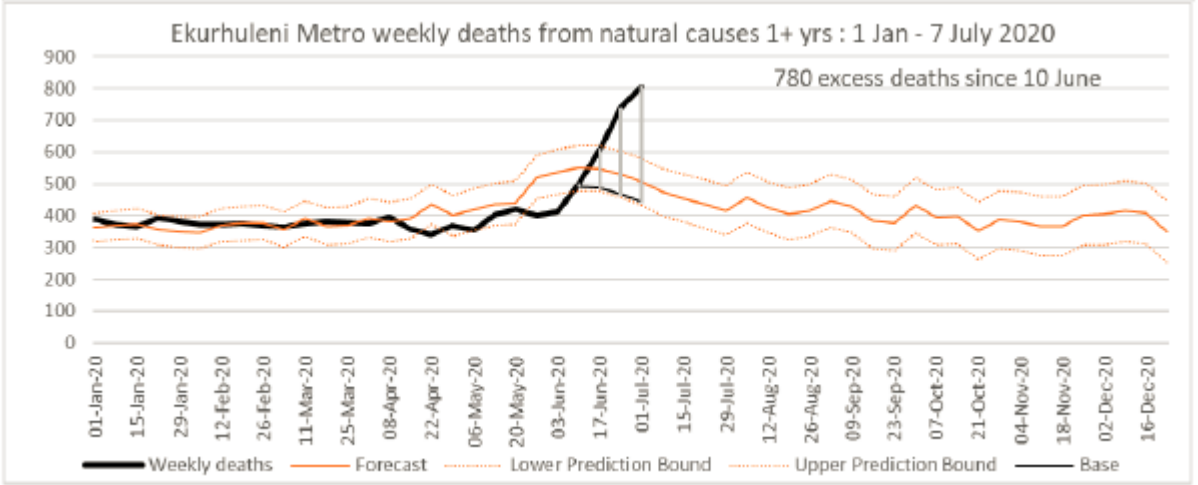

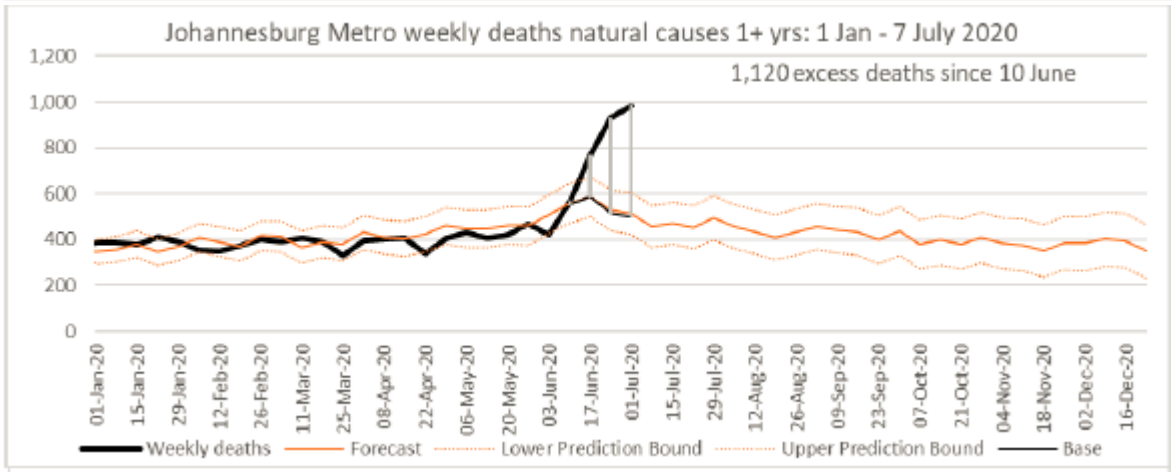

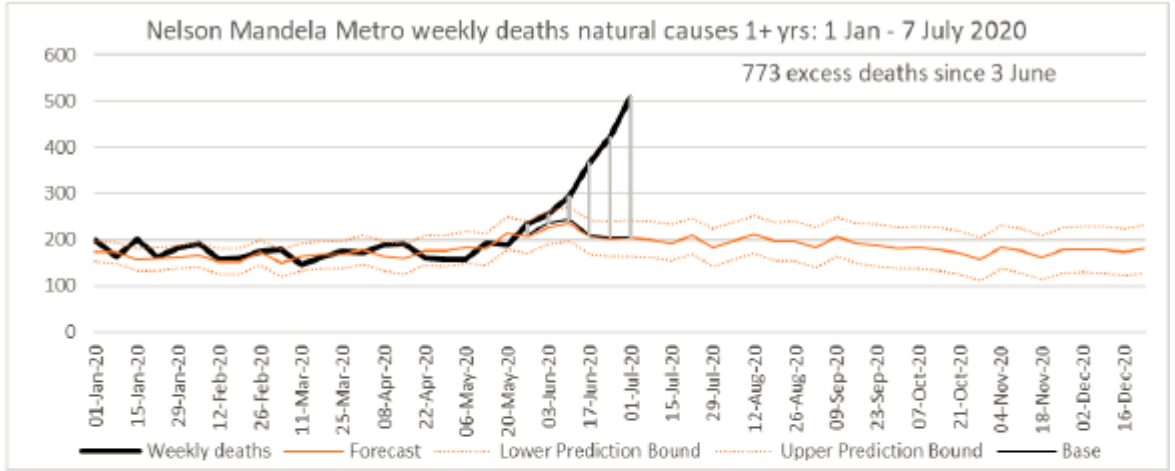

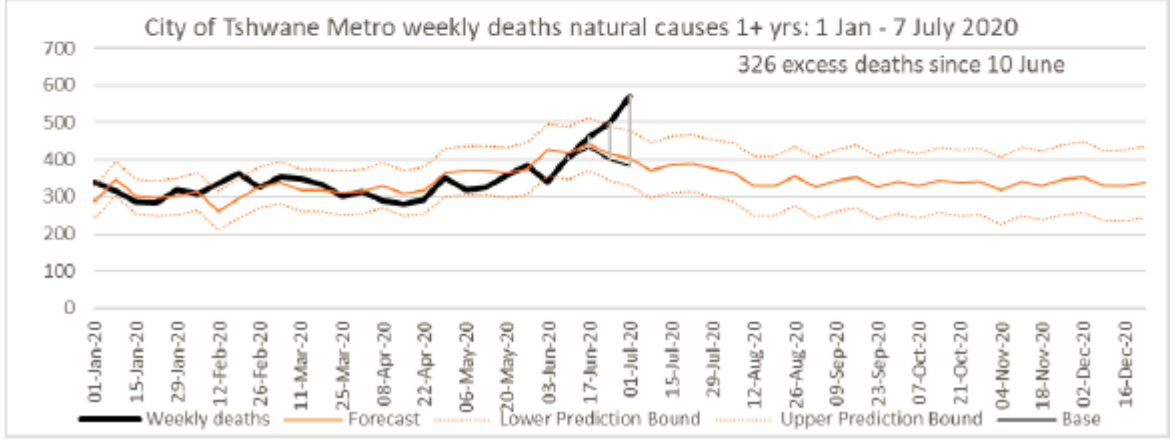

https://www.samrc.ac.za/reports/report-weekly-deaths-south-africa

Recommended read:
Recovery trial

The NEW ENGLAND JOURNAL of MEDICINE

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...IEW
...s — Toward
...ship in Medicine

NEJM Catalyst eBook:
The Clinician Role in Health Care Delivery and Innovation

EDITORIAL
Diagnosing and Treating Systemic Racism

IMAGE CHALLENGE
What is the diagnosis?

PERSPECTIVE
Racial Health Disparities and Covid-19 — Caution and Contex

ORIGINAL ARTICLE

Dexamethasone in Hospitalized Patients with Covid-19 — Preliminary Report

The RECOVERY Collaborative Group*

Article | Figures/Media | Metrics

July 17, 2020
DOI: 10.1056/NEJMoa2021436

Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study

Luke W Meredith*†, William L Hamilton*†, Ben Warne, Charlotte J Houldcroft, Myra Hosmillo, Aminu S Jahun, Martin D Curran, Surendra Parmar, Laura G Caller, Sarah L Caddy, Fahad A Khokhar, Anna Yakovleva, Grant Hall, Theresa Feltwell, Sally Forrest, Sushmita Sridhar, Michael P Weekes, Stephen Baker, Nicholas Brown, Elinor Moore, Ashley Popay, Iain Roddick, Mark Reacher, Theodore Gouliouris, Sharon J Peacock, Gordon Dougan, M Estée Török*‡, Ian Goodfellow*‡

Summary

Background The burden and influence of health-care associated severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infections is unknown. We aimed to examine the use of rapid SARS-CoV-2 sequencing combined with detailed epidemiological analysis to investigate health-care associated SARS-CoV-2 infections and inform infection control measures.

Lancet Infect Dis 2020
Published Online
July 14, 2020
https://doi.org/10.1016/S1473-3099(20)30562-4

Focused on transmission events in healthcare settings
Used rapid sequencing and epidemiological information to identify transmission events and inform interventions
Prospective surveillance study
Samples from their tertiary centre and 18 hospitals in East England
Sequenced
- all positive samples from tertiary centre – symptomatic patients
- about 2 randomly selected samples from other hospitals per day – symptomatic patients
- 37 samples from healthcare worker screening at tertiary centre

Included both low and high Ct value samples

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Platform MinION, Oxford Nanopore

Weekly discussions of results and decisions on interventions

Between 13 March and 24 April
This analysis on 374 tertiary centre patients – some samples failed sequencing quality control
262 available genomes from 299 sequenced from tertiary centre
Median age 64 years (range 0–98)
233 (62%) of 374 male
74 (20%) of 374 admitted to critical care units 75 (20%) died

SARS-CoV-2 has low genetic diversity due to recent introduction – sequences may be identical by chance

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159 of 262 genomes in 35 clusters shared at least one identical sequence
Largest cluster = 18 identical genomes
92/159 (58%) had strong epidemiological evidence for transmission within a few days or weeks
20% intermediate evidence
22% no evidence
Transmission events with genomic and epidemiological evidence were identified in 12 wards and an outpatients dialysis unit
9 were no COVID-19 wards
3 healthcare workers in transplant ward with identical genomes to 4 patients
Transmission events in 3 care homes
1 cluster in paramedics

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6 patients in dialysis unit – shared transport and neighbouring dialysis chairs
Cluster in the care home involved residents, workers in the care home, paramedics and family members of the paramedics

Hospital onset, healthcare associated

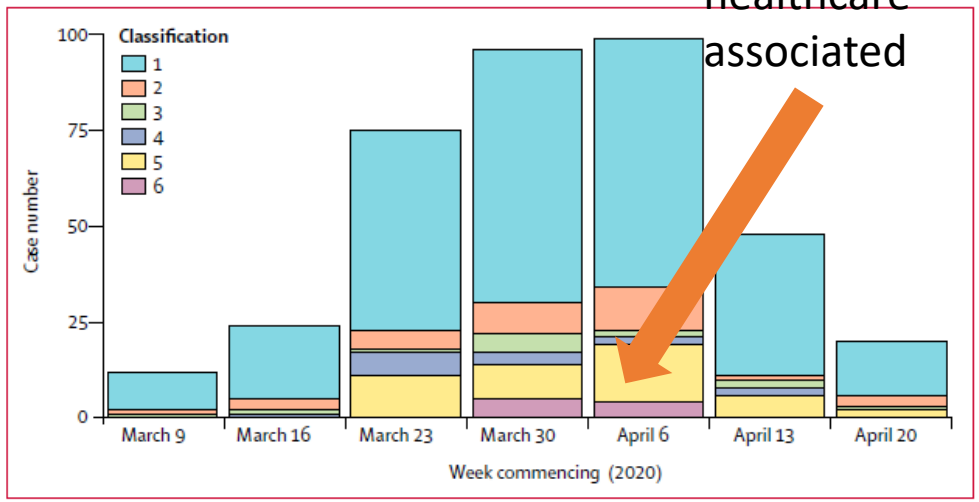

Figure 2: **Epidemic curve of COVID-19 at CUH**
Data for 374 patients tested at CUH. Classification of infection: (1) community onset, community associated; (2) community onset, suspected health-care associated; (3) hospital onset, indeterminate health-care associated; (4) hospital onset, suspected health-care associated; (5) hospital onset, health-care associated; (6) health-care worker. These data do not include 37 health-care workers identified through the CUH screening programme, but do include nine health-care workers that self-presented for testing. Note that data for week commencing April 20, 2020, stops at 8 AM on April 24, 2020, so does not include the weekend. CUH=Cambridge University Hospitals National Health Service Foundation Trust.

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Lancet Infect Dis 2020
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Discussion

1000 genomes sequenced in 5 weeks

Successfully incorporated genomic sequencing into infection control process of tertiary hospital

Genomic variation was low, majority of samples from the B1 lineage

Median 8 (range 0 – 24) SNP differences between genomes

4.5% no or 1 SNP difference

Linked transmission within days to few weeks based on 2 or fewer SNP differences

No identifiable epidemiological connection for 22% of samples in clusters – likely due to low genetic diversity in circulating SARS-CoV-2

Genomic information alone useful for ruling out transmission links, e.g different lineages from renal care ward and outpatient dialysis unit

The genomic data informed reviews of patient placement and
isolation procedures, assessment of PPE use, and staff
break arrangements

Could not unravel mechanism and direction of transmission in clusters

Limitations

All samples not sequenced

Missing epidemiological data

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This summary was prepared by Dr E Maasdorp as part of the daily brief to the TBH ICU team.