

BACKGROUND AND METHODS

Nosocomial outbreaks of COVID-19 cause significant burdens on healthcare systems and lead to inpatient morbidity and mortality. We investigated an outbreak which occurred on “ward 1” in Our Lady of Lourdes Hospital Drogheda in November 2020 using contact tracing and viral whole-genome sequencing (WGS).

- We postulated the index case was “patient A”, who had a background of hearing impairment, who was electively admitted to ward 1 from a residential care facility (RCF) for surgery on 2/11/20, and discharged on 3/11/20.
- SARS-CoV-2 was not detected on pre-admission swab on 30/10/20.
- SARS-CoV-2 was detected on pre-discharge swab on 3/11/20.
- On review it was found that patient A’s residential care facility had an active COVID-19 outbreak. Patient A was asymptomatic.

RESULTS

Contact tracing:

- No inpatient close contacts of patient A were identified.
- Three staff close contacts from theatre were identified; for all 3 SARS-CoV-2 was not detected on day 7 swabs.
- Only one staff close contact from ward 1 was identified who tested positive on day 7. Of 17 casual staff contacts from ward 1, nine tested positive on day 7.
- Following mass testing of inpatients, staff and contacts linked to ward 1, a total of 14 positive patients and 25 staff were identified.
- Of these positive cases, one patient had been transferred from ward 1 to a step-down hospital (“hospital 2”), where two other patients and one staff member then acquired infection.

WGS:

- 41 hospital associated SARS-CoV-2 samples from November-December 2020 were referred to the National Virus Reference Laboratory (NVRL), of which 33 were genetically linked to patient A; belonging to the same PANGOLIN lineage B.1.177 with less than two mutations distinguishing them (see Fig. 1)
- From cases epidemiologically related to ward 1, 26 of 39 samples were available for viral whole-genome sequencing.
 - Of these 9/9 patient samples (patient A, 5 patients from ward 1 and 3 patients from hospital 2) and 16/17 staff samples (13 staff from ward 1, 2 household contacts of ward 1 staff and 1 staff from hospital 2) were linked.
- Unexpectedly, 4/4 samples from a later outbreak on another ward (“ward 2”) and 3/3 samples from an outbreak involving security staff were also linked to patient A, as well as two staff members from other ward areas. (See Fig 2).

Fig 1: Phylogenetic tree (data from viral whole-genome sequencing)

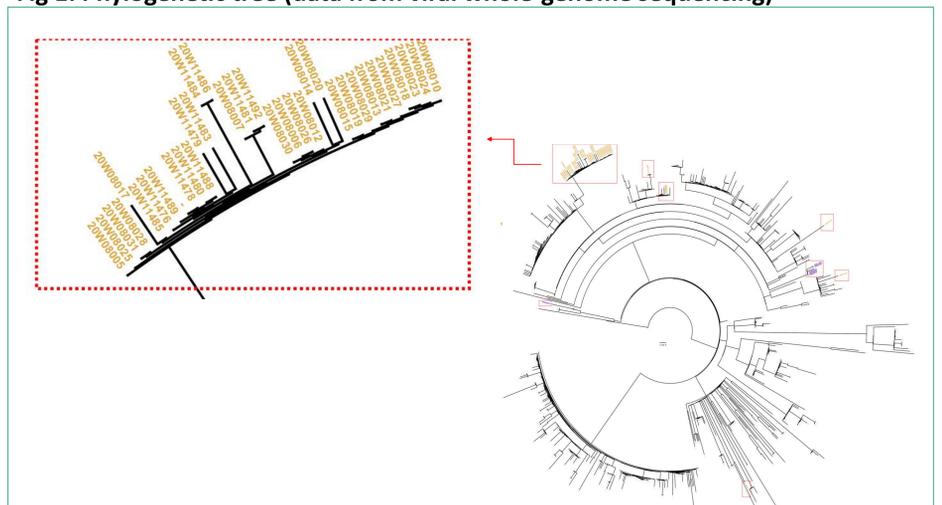
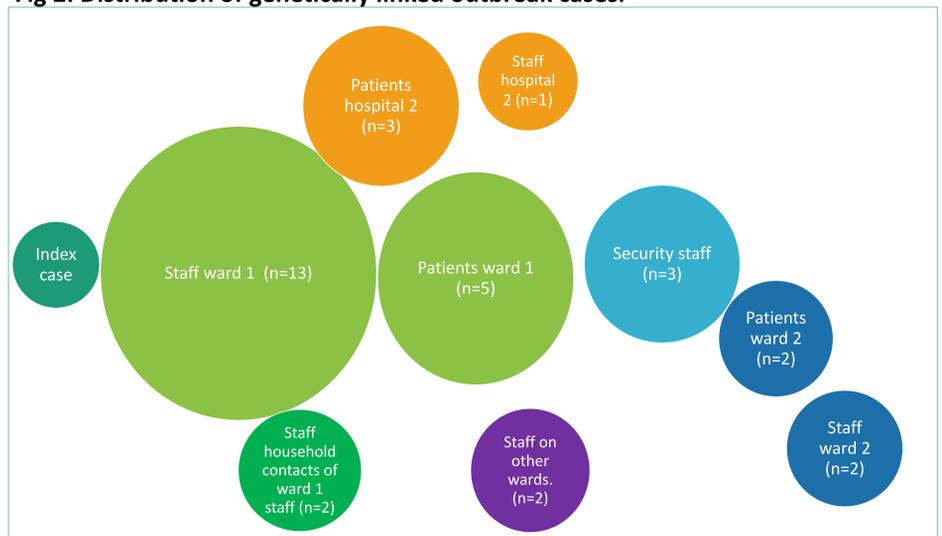


Fig 2: Distribution of genetically linked outbreak cases.



CONCLUSIONS

- This was a large, potentially preventable, outbreak of COVID-19 which affected staff and inpatients.
- Viral whole-genome sequencing confirmed that patient A was the index case as postulated.
- Difficulties in communication due to patient A’s hearing loss led to breaches in personal protective equipment (PPE) as the patient lip-read; this may have caused staff acquisition.
- Security staff who had contact with agitated patients on ward 1 may have propagated onward spread to ward 2.
- Transfer of a patient from ward 1 to hospital 2 led to further nosocomial transmission.

LEARNING POINTS

- **Risk assessment:** A thorough risk assessment on admission would have identified patient A’s risk of COVID-19 given the RCF outbreak.
- **Communication:** Availability of masks with transparent mouth pieces could have prevented PPE breaches (see image below).
- **Ventilation:** Although casual contacts from ward 1 acquired COVID-19, close contacts from theatre did not, perhaps due to superior ventilation in theatre compared to on ward 1.
- **Isolation precautions:** Isolation of patients for 14 days on transfer to other hospitals in periods of high incidence of SARS-CoV-2 transmission may be advisable to prevent inter-hospital outbreaks.

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