

THE ROLE OF WHOLE GENOME SEQUENCING IN REVEALING AN HCV OUTBREAK IN NORTHERN IRELAND

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Background:

The role of HCV sequencing has mostly been limited to genotyping and resistance testing to inform selection of antiviral therapy. Here we describe how a multi-disciplinary intervention using HCV whole genome sequencing (WGS), undertaken as part of a new national clinical service to supplement routine testing and outreach services, revealed an HCV outbreak and informed public health control measures in real-time.

Methods:

Since mid-2019, HCV genotyping and resistance testing in Northern Ireland (NI) has been performed using UKHSA's accredited WGS assay, giving high-density population coverage. Routine bioinformatic analysis generates phylogenetic trees from multiple recent runs. This process revealed clusters in NI, and a local Incident Management Team was established.

Results:

In mid-2020, a 25-strong cluster containing solely NI sequences was detected. By January 2023, six such clusters had been found involving several hundred individuals across three genotypes (GT1a, 2b, 3a) with the largest (GT1a) containing around 150 individuals. Seven dual infections have been detected, showing "bridging" between clusters.

Although comparison of cluster membership with demographic data revealed predictable strong associations with Belfast city centre postcodes, injecting drug use, homelessness/hostel residency, and a history of prison, clusters also contained significant numbers of non-high-risk individuals. New trends in injecting drug use may partly explain this trend, with cocaine now being the most commonly injected drug instead of heroin, and people injecting multiple times per day.

Conclusion:

Molecular epidemiology can be a very useful adjunct to standard techniques in delivering interventions aimed at HCV harm reduction, including international HCV elimination programs. Targeted testing, awareness of demographic mixing patterns, and improved knowledge of incidence and re-infection rates can be much improved by data analysis of the type presented here. Dense sampling provides the greatest benefit, but even a representative sampling of a local cohort can deliver useful data to support public health programmes.

Disclosure of Interest Statement: *See example below:*

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No conflicts of interest exist outside of the declared affiliations.

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