P1087
Paper Poster Session
Clostridium difficile: epidemiology and risk factors

Genetic relatedness among clinical Clostridium difficile strains within a specific region in Scotland

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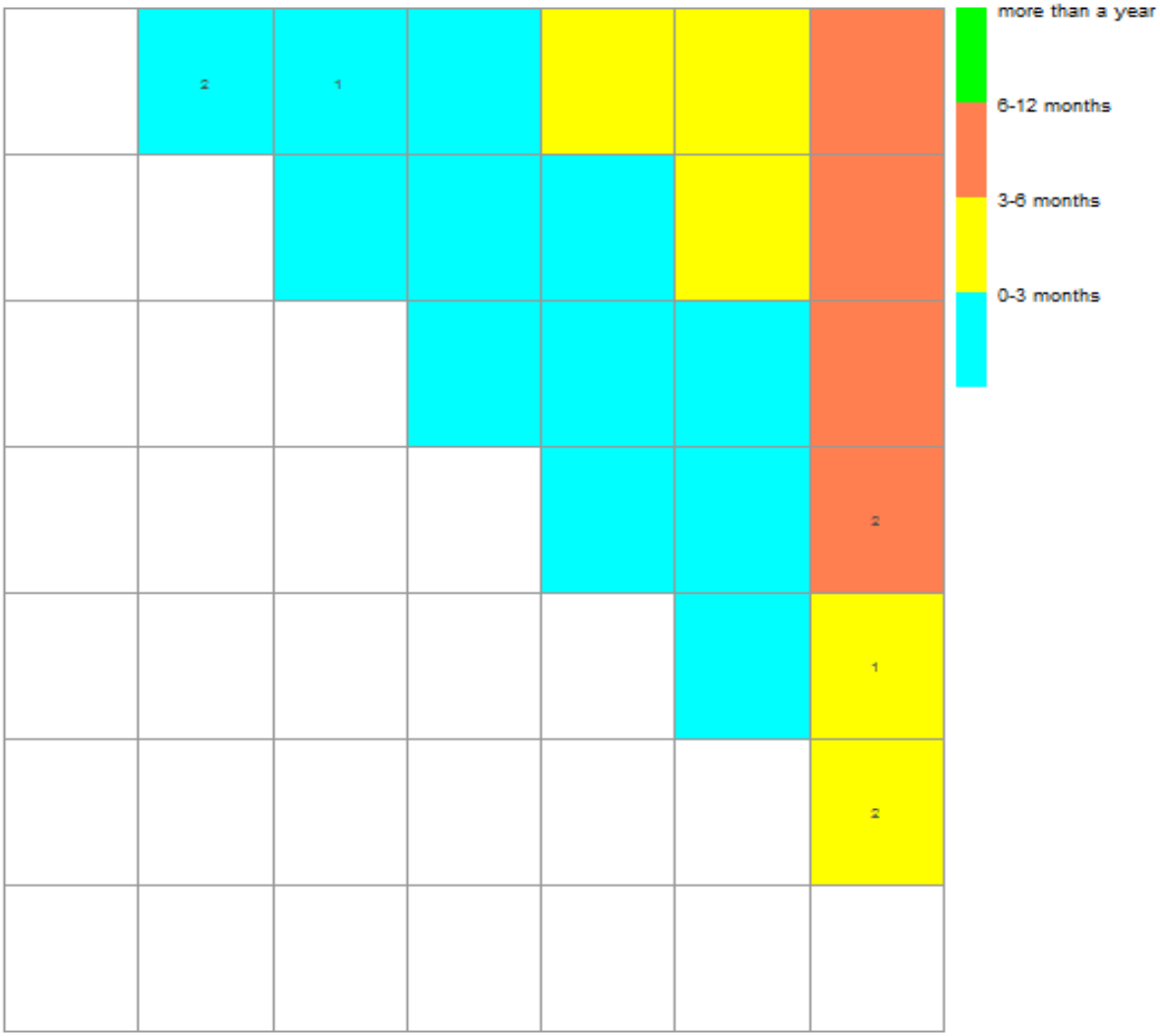
Background: The aim of this project was to investigate the molecular epidemiology of *Clostridium difficile* infection (CDI) by linking patient healthcare data and bacterial whole genome sequence (WGS) data. Combining the genetic relatedness of bacterial strains and information on patients' hospital admissions and region of residence can reveal potential transmissions and reservoirs of infection. We have advanced systems for collation of routine healthcare data and anonymised record linkage in Scotland and have established cross-disciplinary collaborations to incorporate bacterial WGS data.

Material/methods: Strains from specific patients with *C. difficile* infection were identified by the Scottish Microbiology Reference Laboratory for a larger study, with samples genotyped and processed through a bioinformatics pipeline at the University of Glasgow. Epidemiological data were obtained from electronic Data Research and Innovation Service (eDRIS) at NHS National Services Scotland and analysed in the data Safe Haven at the Health Informatics Centre, University of Dundee. For this study, the genotypes of each bacterial isolate within one postcode region were compared to obtain the single nucleotide variants (SNV) difference between any two isolates. Strains from this small geographical region that differed by 0-10 SNVs were considered potentially genetically and epidemiologically related for further investigation. This includes scanning for potential infection transmissions during a hospital stay or in the community by identifying overlaps between patients during incubation and infectious periods.

Results: Of 120 study episodes of CDI from this region there were 36 (30%) strains with 0-10, of which 7 (5.8%) had 0-2, SNVs difference from at least one other strain. A grid plot demonstrating the genetic and temporal relatedness of all strains with 0-10 SNV difference will be presented, where each cell represents comparison between bacterial genotypes from two individuals in the study population. This gives a visual representation of temporal and genomic relatedness of infections in the study population. A plot of strains with 0-2 SNV difference is appended, with the number in the cell representing SNV difference and the colour representing time difference. Analysis identifying potential transmission events, and extension of the grid plot to include all strains with 0-10 SNV difference, are currently underway (results will be available by the time of the meeting).

Figure1: Grid plot of *C. Difficile* that differ by 0-2 SNVs in one postcode region of Scotland



Conclusions: Comparing the genotypes of *C. difficile* strains can identify genetically related isolates but this needs to be linked securely and anonymously to demographic and healthcare data to identify epidemiological links and potential transmission events. More definitive conclusions about transmission and reservoirs of infection will be drawn from our planned next steps of applying these methods in the broader Scottish population and carrying out more extensive and prospective sampling.