Modelling and estimating person-to person spread of human gastrointestinal infections.

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Gastrointestinal infections of humans mainly come from animal reservoirs via food but some can also spread from person to person. Mostly this is not sustained and so produces amplification via these secondary cases without a human reservoir of infection developing. However the extent of this varies substantially across different infections.

Some well characterised transmission chains have been identified and linked to particular societal groups, For example an overall increase in *Shigella* infection (causing dysentery) was seen to be driven by a substantial expansion of infection among men who have sex with men.

We think models based on parameters for each infection may clarify why this varies across pathogens. Parameters for models include duration of carriage, infectious dose and estimated contact patterns.

We propose to model person to person spread of gastrointestinal pathogens based on their parameters to (1) understand the mechanism for different age and gender patterns across GI pathogens generated by to person to person spread and (2) optimise any surveillance approach to pick up evidence for spread by this route against the larger background of mainly foodborne infection, including comparing model predictions to national surveillance data to optimise analysis and interpretation of that surveillance data.

Where genetic data is available this will also be reviewed to identify evidence for sustained transmission. For example, using the example given above of *Shigella* spreading among men having sex with men – whole genome sequencing identified particular strains responsible for this. This allows the use of the contrasting demographic pattern (gender, age, geography) of those infected by this strain to act as a probe to monitor surveillance data for a recurrence of infection in this group. A similar approach using other more typically sexually transmitted diseases among MSM, could further map out the expectation of the patterns that might fit with this mode of spread. The same approach could be applied to other demographic groups.

The mathematical aspects will include (i) dynamic infection modelling, (ii) analysis of large scale surveillance datasets and interpretation in formed by modelling results, and (iii) analysis of genomic surveillance at a population level. The first of these three might best fit to a masters project with a PhD adding in the additional strands of work. These later stages would be in collaboration with Public Health England and the NIHR Health Protection Research Unit in Gastrointestinal Infections. Students would therefore have access to the NIHR academy and professional training offered by that and to placements in Public Health England.