Clinic-level variations in contact tracing outcomes: protocol for a cross-sectional study of variation and case-mix adjustment in London, UK

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Abstract

Contact tracing around patients with infectious tuberculosis is used to identify further cases and interrupt transmission. Approaches to contact tracing are thought to vary between different clinical teams, but the extent of this variation and the importance of case mix are unknown. This project will use data from the London Tuberculosis Register to analyse the extent of variation in the number of contacts identified and the proportion that are assessed/screened, and use hierarchical modelling to test whether differences in case-mix explain any variation.

Background

Tuberculosis (TB) is a bacterial infection that can affect almost any part of the body. Pulmonary TB accounts for 55% of cases in the UK. Overall incidence is low in the UK and in long-term decline. Despite this decline, TB is more common in London than other parts of the country at 21.7 per 100,000 in 2017 [1] and in some local neighbourhoods exceeds 100 per 100,000 per year (for comparison, the WHO defines a ‘high incidence’ country as one with at least 150 new cases per 100,000 [2]). London has been called the ‘TB Capital of Europe’, though incidence is now lower than in many Eastern European countries [3].

TB is a legally notifiable disease in the UK, meaning that clinicians have a statutory duty to inform local authorities when they diagnose a patient with an active TB infection. Due to the risk of person-to-person transmission, formalised contact tracing has been recommended since 1983 [4]. Guidance recommends that close contacts of active cases are offered testing for active or latent infection and offered antibiotics if either is detected [5]. Transmission of non-pulmonary TB is rare, therefore current guidance does not explicitly recommend screening contacts of patients with non-pulmonary

TB only. Contact tracing in the UK is managed by community-based teams that treat the index patient and identify close contacts. In London in 2017, 3% of screened contacts had active TB [1].

Anecdotal evidence suggests that the number of contacts identified and assessed varies between clinical teams in different areas, but the extent of this variation is unclear. It is also unclear whether variation in contact tracing is due to differences in practice, or differences in the communities that clinics serve. Patient characteristics are likely to be associated with contact tracing – for example, younger patients and those who live in large households likely to have more close contacts. Clinics that identify and assess more contacts may have more thorough contact tracing practices, or their patients may simply have more close contacts. An improved understanding of variation in contact tracing and the importance of case mix will support further research into differences in practice.

Aim

The aim of the study is to quantify variation in contact tracing between TB clinics in London, using routinely collected data, and quantify how much variation can be explained by case mix.

Study approval

This project is an evaluation of TB services in London, using secondary anonymised data. We used the NHS Health Research Authority decision tool [6] and confirmed that ethical consideration for this analysis not required.

Methods

Data source

The data source will be the London Tuberculosis Register (LTBR), a web-based register of demographic and clinical information on all TB cases notified in London since 2002. Clinical and demographic information is entered directly to the LTBR by TB clinic staff. The data is stored and accessed securely at Public Health England and only anonymised results will be released.

We will restrict analysis to data collected after the introduction of 'cohort review' (1 July 2012), after which the data includes the number of contacts identified, assessed (or screened), found to have latent TB and found to have active TB. We will also restrict the analysis to index cases with pulmonary TB (since guidance no longer explicitly recommends contact tracing for patients with non-pulmonary TB); and those aged 12 years or over (since young children are often less infectious).

Outcome measures

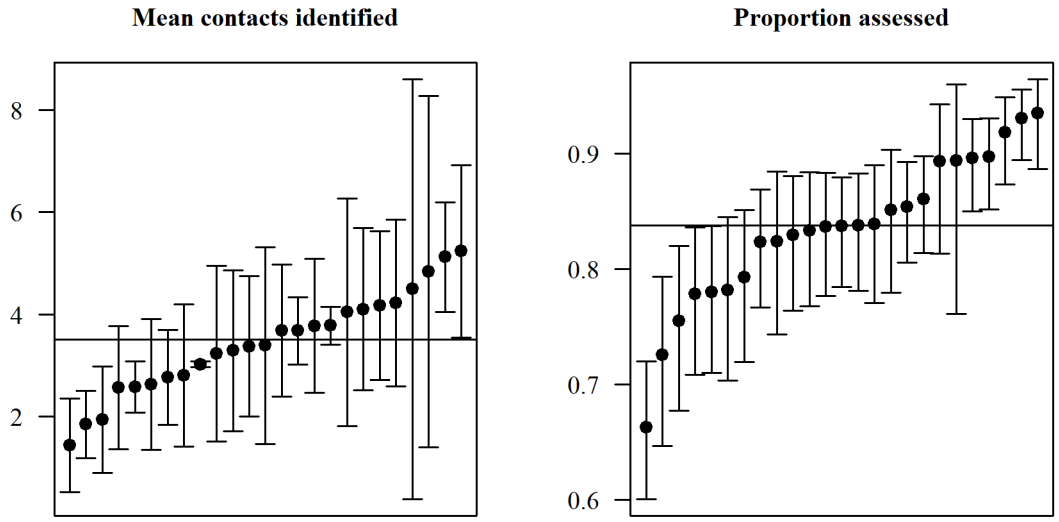
We will include two measures of contact tracing: the number of contacts identified (defined as those deemed eligible for contact tracing locally), and the proportion of identified contacts that are assessed (defined as those that attended an assessment appointment).

Descriptive analysis

We will report the total number of cases, the total number of contacts identified and assessed, and the total number of active and latent TB cases across the whole study population. We will report the 'Number Needed to Screen' for comparison with existing studies.

At clinic level, we will report the crude (unadjusted) means of each outcome, with 95% confidence intervals, and present this data as a caterpillar plot with each clinic compared to the London average. Figure 1 provides an example plot. Clinics will be kept anonymous.

Figure 1: example caterpillar plot showing clinic means for each outcome, with 95% confidence intervals (plots show random data)



Case mix adjustment

We will use hierarchical modelling to estimate differences in contact tracing outcomes between clinics after adjusting for case mix. We will select case-mix variables as those most likely to determine the number of close contacts for a case, or the probability a contact will attend assessment.

In terms of the number of contacts identified, we will use the following characteristics of the index case to define the expected number of contacts:

- **Age**. Age is associated with household composition and economic activity and therefore number of close contacts. It is also associated with infectiousness, with young adults (for example those aged 18-44) having a greater probability of secondary cases [7] than the youngest or oldest patients. This may reflect social as well as disease factors. We will group age into 10-year bins to allow for a non-linear relationship with contact tracing outcomes.
- **Sex.** Associations between sex and contact tracing vary by setting, though most studies in high income settings suggest that male index patients have fewer contacts but present greater risk of transmission [8].
- **Ethnicity and nationality.** Some studies, including studies in the UK, show that ethnicity affects both the number of contacts assessed [8] and the risk of disease in contacts [9]. This may reflect associations between ethnicity and household composition. Patients from white British backgrounds are likely to have fewer contacts but present a greater risk of transmission. This may be partly explained by the higher proportion of patients in other ethnic groups (particularly those from South Asian backgrounds) that present with non-pulmonary TB [6]. We will include a categorical ethnicity variable and a binary variable for born in the UK or elsewhere.
- **Social exclusion**. Homelessness and experience of prison are associated with fewer close contacts [8,10]. The smaller number of contacts may be related to the patients' social circumstances, the difficulty or public health follow-up or the perceptions of healthcare staff.

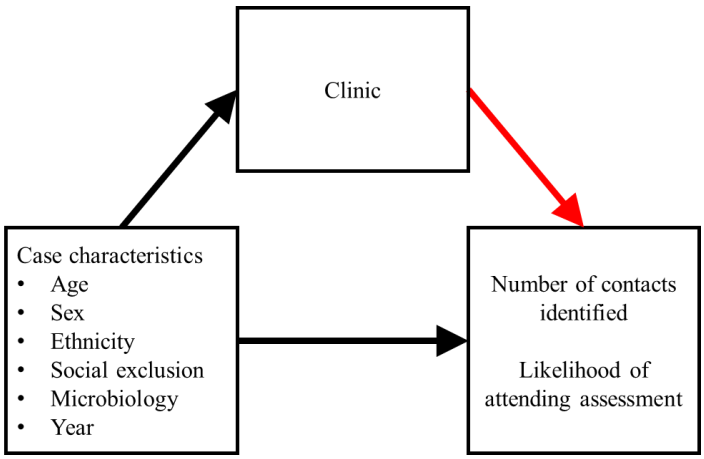
We are not aware of evidence that use of illicit drugs is associated with number of close contacts (though it is an established risk factor for TB infection [11]), so we will exclude this variable.

- **Microbiological status**. The sputum smear or culture status of index patients is unlikely to determine their number of social and work contacts. However, when TB bacteria are found, the first ring of contacts assessed are more likely to have TB [7,8,12–16], which may lead TB teams to consider a wider set of contacts (the 'stone in the pond' principle [8]). We will therefore include a four-way combination positive/negative sputum/culture status.
- **Year when the index case was notified**. Contact tracing practices are likely to change over time.

We will use a similar set of variables to define case mix for the probability that a contact will attend their assessment appointment. We will not include ethnicity, as we do not have a reason to think that ethnicity will change the probability of a contact attending assessment. In terms of social exclusion, we will also include recorded mental health problems and use of illicit drugs.

Diagram

We anticipate that case characteristics ('case mix') is independently associated with contact tracing outcomes and which clinic index patients attend. The main aim of this analysis is to estimate the effect of 'clinic' on contact tracing outcomes (the red arrow in the diagram).



Modelling

For the first outcome (the count of contacts screened), we will:

1) Fit a count model (e.g. a poisson or negative binomial model) with random intercepts for the clinic and no further covariates (model 1). The random intercepts will be similar to the crude clinic means, with 'shrinkage' (which moves values closer to the overall mean, particularly for smaller clinics).
2) Fit a model including fixed effects for the case mix covariates (model 2). A likelihood ratio test between model 1 and model 2 will be used to test whether the covariates explain the variation between clinics. The random intercepts in this model will provide estimates of the clinic-level effect on the number of contacts identified.
3) Report the fixed effects from model 2 to provide insight into the associations between characteristics of index cases and the number of contacts identified.
4) Create a hypothetical scenario for each clinic, where the clinic screens all index patients in London. We will use model 2 to simulate the number of contacts identified for each patient and predict an average for each clinic. We will present these results on caterpillar plots.

We will follow a similar process for second outcome (the proportion of contacts assessed), using a binomial model rather than a count model.

As a secondary analysis, we will consider modelling the effect of 'bringing clinics up to a common standard' on the total number of active and latent cases identified.

Missing data

The LTBR already excludes patients that have missing contact tracing data, and therefore the effect of missing data will be difficult to estimate. We will discuss the potential impact of missing data on our results, based on knowledge of the data generation processes.

Dissemination and publication

We will submit anonymised results to a peer-review journal for publication, following the STROBE guidelines for reporting observational studies [17]. We will also present the results to TB team leads in London. In some cases it may be possible to identify clinics from anonymised plots or tables (for example if there is one particularly large or small clinic that is identifiable from its error range). In these cases we will make a risk assessment of reidentification and if necessary consider alternative approaches to presenting the results.

Next steps

If there is evidence of variation in contact tracing outcomes that is not explained by case mix, we will conduct a confidential qualitative engagement exercise with clinics to explore potential variation in practice.

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