Antibiotic resistance: estimating the population level distribution of Extended-Spectrum Beta-Lactamases (ESBLs) in West Yorkshire, UK

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Summary

Antibiotic resistance is of concern and GPs are encouraged to reduce prescribing levels. An important type of antimicrobial resistance is caused by Extended-Spectrum Beta-Lactamases. This study aims to establish whether obtaining faecal samples is an acceptable form of 'screening' and to use GIS methods to analyse diagnoses. There are observable differences in levels of resistance within Bradford and Leeds and inverse distance weighting provides an estimated surface of resistance. A spatial cluster of unusually high antibiotic resistance is found within Bradford. This deserves further study as does the use of data with improved geographic resolution and wider geographical coverage.

KEYWORDS: Antibiotic resistance; Health geography; GIS; Inverse distance weighting; Spatial Clustering

1. Introduction

One of the most important types of antimicrobial resistance is caused by Extended-Spectrum Beta-Lactamases (ESBLs) that can be produced by enterobacteriaceae. ESBLs confer resistance to a wide variety of antibiotics and are associated with worse clinical outcomes. ESBLs have been reported as causing outbreaks in hospitals, and there is now increasing evidence for the transmission of ESBL in the community, (Rodríguez-Baño et al., 2008) however, the mechanism(s) for this are unclear.

The on-going study based in Leeds Teaching Hospitals (LTH) and Bradford Teaching Hospitals (BTH), "Are stool samples an effective and acceptable method of looking for antibiotic resistance in the community?" aims to establish whether obtaining faecal samples is an acceptable form of 'screening' for faecal carriage of ESBL. The screening log for the study was generated by the LTH Microbiology database, (Telepath, IBM Corporation) and contains details of individuals who have had a clinical sample that has tested positive for ESBL. Patients can be included in the study if they have had an ESBL producing organism isolated from a sample obtained during their inpatient stay at LTH and BTH, or from a sample obtained in the community (e.g. A culture was requested by a General Practitioner) within 7 days prior to their admission to hospital.

When the screening log was reviewed, it appeared that a relatively high proportion of individuals diagnosed with ESBL reside in relatively few postal sectors within West Yorkshire, which may reflect areas of ongoing transmission in the community.

We are seeking to explore whether these apparent 'hot spots' were genuine areas of high ESBL incidence using a Geographical Information System (GIS) to examine disease distribution and how this

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can be influenced by other variables such as socio-geographic factors. The use of GIS in investigating disease processes is well-established, but very few studies have utilised the tool with respect to antimicrobial resistance (Galvin et al., 2013).

2. Methods

All ESBL positive clinical samples obtained from BTH, LTH, and from the community during the period 13.5.2014 to 13.5.2015 were identified using the screening log. The postcode for the patient's home address was identified during this process. Only individuals living within the Leeds and Bradford Metropolitan areas were included in the GIS analysis. Data was collated so that the number of individuals diagnosed with ESBL in each postal sector (e.g. LS1 1) was calculated. These data were then processed using commercial GIS software, ArcGIS, at the University of Leeds.

Maps were generated to display the distribution of individuals diagnosed with ESBL, a 'surface' of an estimated distribution and the identification of spatial clusters. The distribution was evaluated against population density and the Index of Deprivation. A number of postal sectors were discounted from this analysis owing to possibility of an 'edge effect' caused by samples from certain GP practices being sent to neighbouring pathology laboratories.

3. Results

2,272 clinical samples from 1,559 individuals were found to have a positive culture for ESBL during the study period. The requesting locations for these samples are shown in |Figure 1; 13% were obtained from acute assessment locations (such as Emergency Departments or Acute Assessment units) and 33% were obtained in General Practice. Types of sample that were positive for ESBL are shown in Figure 2; 173 patients had at least one positive sterile site ESBL culture. 1,399 individual patients living in Leeds and Bradford Metropolitan areas were diagnosed with ESBL infection.

Figure 1. Requesting location of ESBL positive samples

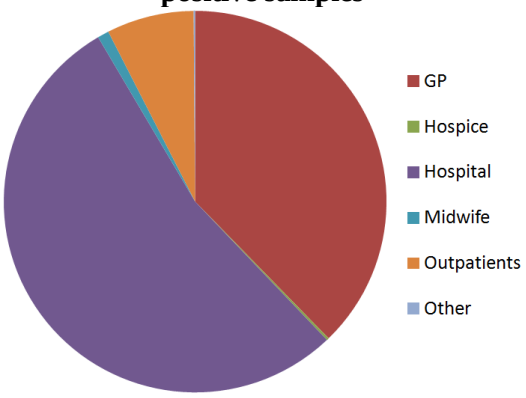


Figure 2. Types of ESBL-positive sample

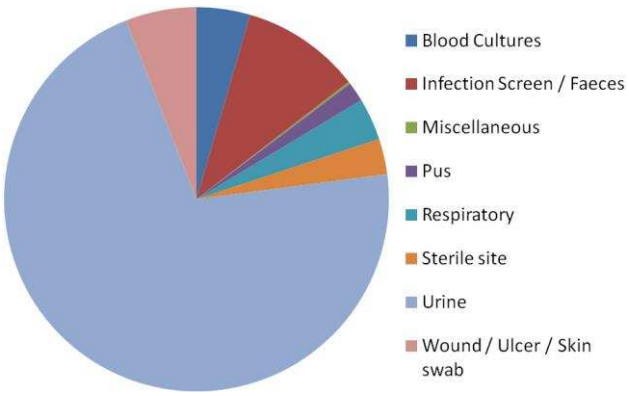


Figure 3 shows the percentage of persons in each postal sector who are antibiotic resistant (larger dots represent higher rates). Bradford seems to have a concentration in SE which is the city centre and surrounds. Leeds is slightly different with the locations more evenly spread out.

Figure 4 is an interpolation of the point data using 'Inverse Distance Weighting'. This is the same method as Galvin et al 2013 in their study of Galway). The class intervals of the map as the same as used in Figure 3. In effect IDW calculates a 'weighted average' between adjacent points. The 'surface' which is mapped is an estimate across space of what the antibiotic resistance would be. The processing is sensitive to a distance decay choice. Further work can use a range of IDW estimates to give values within which the % resistance might lie. (Not strictly a confidence interval, more a plausibility range.) Given that the estimate is based on postal sector centroids, a better resolution of the point data would lead to better estimates so individual postcode location would improve this work (currently, patient confidentiality considerations have restricted the spatial detail released).

So are there any spatial clusters of high values? Using Openshaw's Geographical Analysis Machine (GAM) (developed originally to look at Sellafield's possible leukaemia clusters) Figure 5 shows that there is an excess over what would be expected in SE Bradford. This controls for background population density so more is going on here than just because it is high density. The wards which have clusters are City, Manningham, Great Horton, Bolton & Undercliffe and Bradford Moor.

There are correlations between % ESBLs and Persons per hectare of 0.19 ($p = 0.03$) and between % ESBLS and Index of Deprivation of 0.33 ($p = 0.000$).

Figure 3. Distribution of cases of ESBL per head of population located by postal sector (centroid)

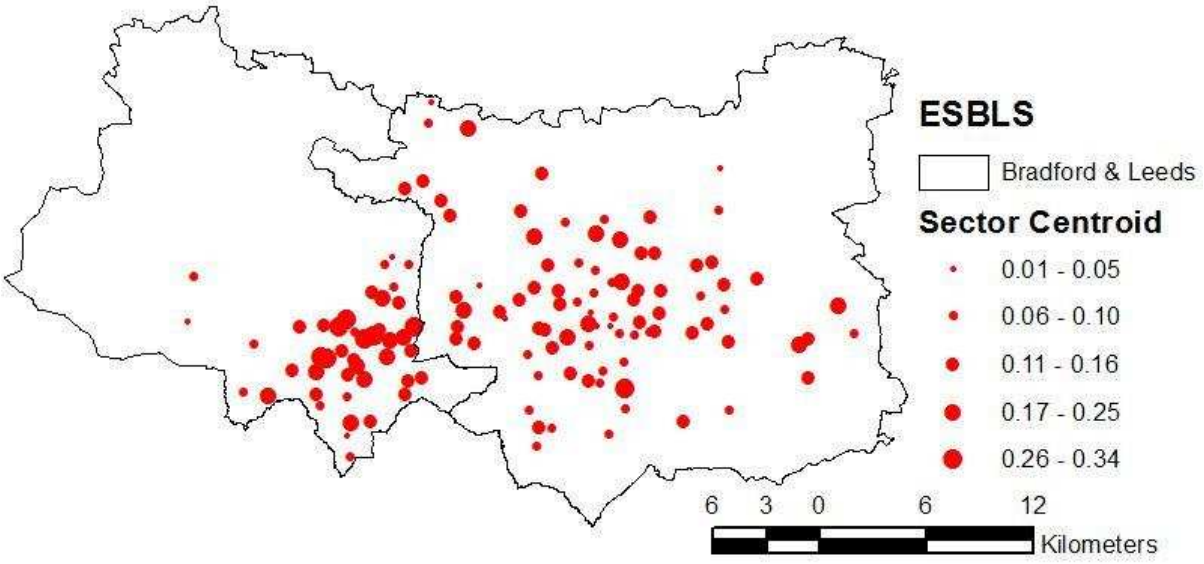


Figure 4. Distribution of ESBL per head of population per year estimated using inverse distance weighting (IDW) which displays the average number of cases over space

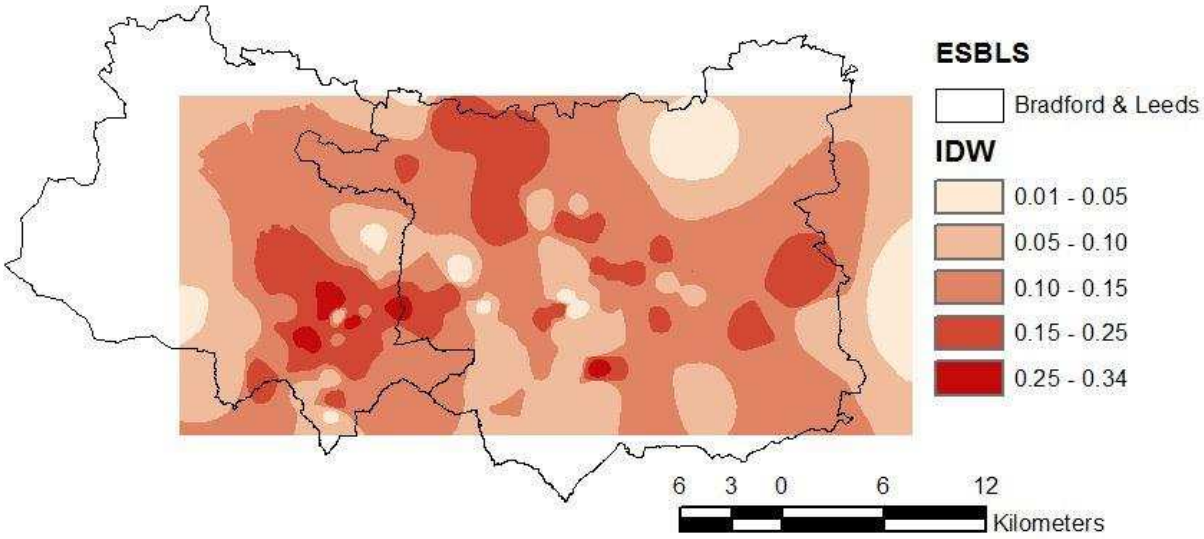
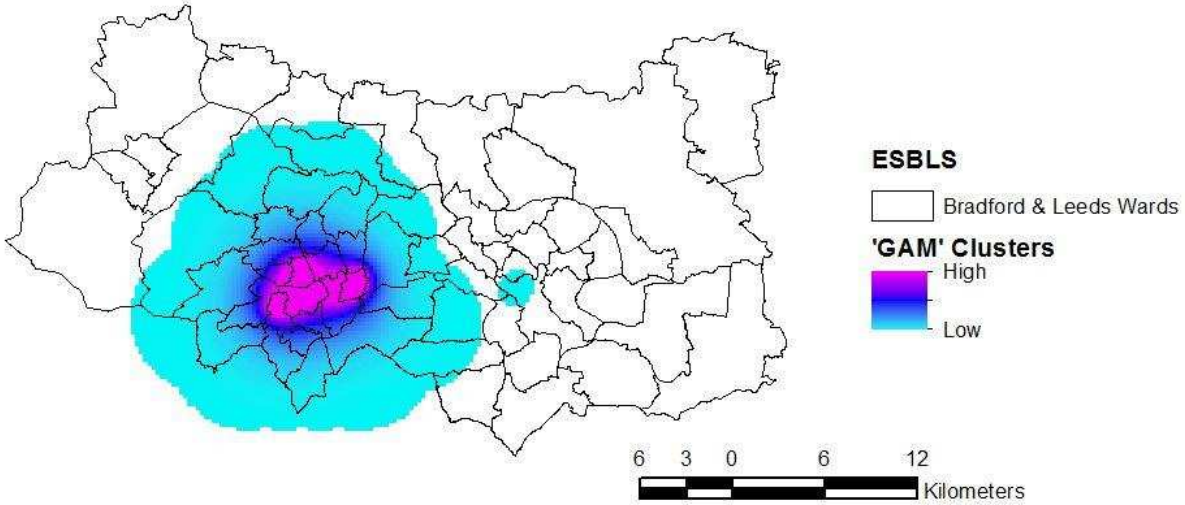


Figure 5. Spatial clusters identified using Openshaw's Geographical Analysis Machine which controls for background population density

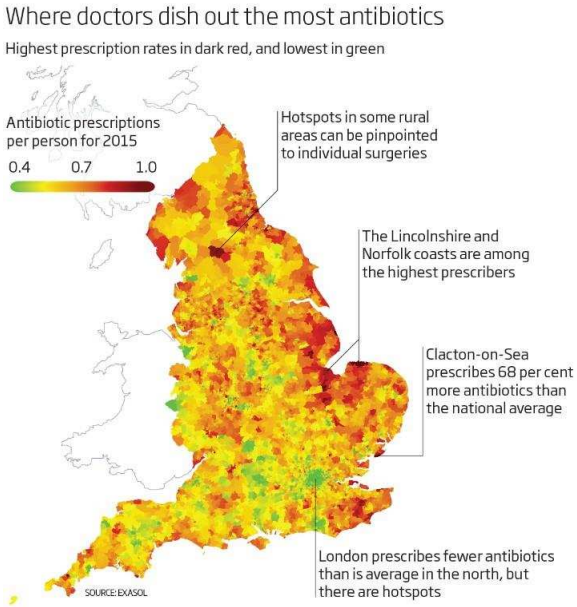


4. Discussion

There appears to be a significant cluster of cases of ESBL in certain areas within Bradford, which is as yet unexplained. There is some evidence of the transmission of ESBL in the community; although reasons for this are unclear. There are a number of relationships that could potentially be explored including antimicrobial prescribing patterns, ethnicity, foreign travel, and food consumption. A comparison with prescribing data from GPs can reveal whether there is a relationship between antibiotic prescriptions per person (New Scientist, 2015) and community resistance (Figure 6).

Further work to explore trends over time and over a larger geographical area with improved geographical resolution using unit postcode locations may go a long way to explaining the current high numbers of cases of ESBL that are seen in clinical samples in West Yorkshire.

Figure 6: Variations in antibiotic prescribing levels by GP (New Scientist, 2015)



5. Acknowledgements

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6. Biography

Paul Norman is a Lecturer in Human Geography researching: small area sociodemographic, morbidity and mortality data in time-series analysis of demographic and health change; area typologies to understand migration patterns and resulting health outcomes; individual microdata to understand differences in population health over time.

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7. References

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