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# Association between socioeconomic deprivation and incidence of Infectious Intestinal Disease by pathogen and linked transmission route: An ecological analysis in the UK

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## Summary

Infectious intestinal disease (IID) studies conducted at different levels of the surveillance pyramid have found heterogeneity in association of socioeconomic deprivation with illness. The aim of this study was to analyse the association between socioeconomic deprivation and incidence of IID by certain gastrointestinal pathogens reported to UKHSA. Data were extracted from 2015 to 2018 for *Salmonella, Campylobacter, Shigella, Giardia* species, and norovirus. Rates were calculated per 100,000 person-years by Index of Multiple Deprivation (IMD) quintile and an ecological analysis, using univariate and multivariable regression models for each pathogen, was conducted. Incidence of *Campylobacter, and Giardia* species decreased with increasing deprivation. Conversely, the incidence of norovirus, non-typhoidal *Salmonella*, *Salmonella* typhi/paratyphi*, Shigella* species increased with increasing deprivation. Multivariable analysis results showed that higher deprivation was significantly associated with higher odds of higher number of cases for *Shigella flexneri*, norovirus *and Salmonella* typhi/paratyphi. Infections most associated with deprivation were those transmitted by person-to-person spread, and least strongly are those transmitted by zoonotic contamination of the environment. The reduction of person-to-person transmission by implementing policies targeting over-crowding and poor hygiene, and are likely to be the most effective solution for reduction of IID inequalities.


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**Key findings**

- Incidence of *Campylobacter and Giardia* species decreased with increasing deprivation
- Incidence of norovirus, *Salmonella* and *Shigella* species increased with increasing deprivation.
- Infections most associated with deprivation were transmitted person-to-person
- Infections least associated with deprivation were transmitted by zoonotic transmission
- Policies targeting over-crowding and poor hygiene most effective in reducing inequalities

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## Introduction

Infectious intestinal disease (IID), infection of the gastrointestinal tract that causes gastroenteritis, is estimated to affect 274 people per 1,000 population in the UK per year [1]. While most cases are mild and self-limiting, some pathogens can cause bloody diarrhoea, septicaemia, meningitis, renal failure, or death [1]. Approximately half of people reporting IID have missed work or school due to their symptoms, and for particular pathogens, public health measures require exclusion of individuals in certain risk groups (including children aged five and under, food handlers and healthcare workers) from childcare, school or workplace settings [1, 2]. Consequently, the negative impact of IID extends beyond clinical presentation, potentially affecting the financial and social situations of cases and their carers'. In 2018, the societal cost of foodborne illness in the UK was estimated to be over 9 billion GBP [3].

Additionally, due to the self-limiting nature of most cases of IID, national surveillance captures only a fraction of cases. For every single case reported to national surveillance, there is an estimated 147 cases in the community, with approximately 15 cases presenting to the General Practice [1]. However, the estimates at different levels of the surveillance pyramid [4] differ widely by pathogen, for example, from five cases in the community for every *Salmonella* case reported to national surveillance, to 288 cases in the community for every norovirus case reported to national surveillance [1].

Studies conducted at different levels of the surveillance pyramid have found heterogeneity in association of socioeconomic deprivation with illness [5-8]. In addition, most community or primary care level studies only examine the combined IID/gastroenteritis clinical syndrome, rather than the relationship for individual IID pathogens. As the most common transmission routes (for example, person-person, foodborne, zoonotic, environmental) and sources/vehicles of infection vary by pathogen, it cannot be assumed that the relationship between infection and socio-economic factors are the same for each pathogen. In addition,



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considering the differences in ascertainment at each level of the surveillance pyramid across pathogens, it is likely that of the proportion of each IID pathogen included in each study differs. Analyses of datasets comprising cases linked to a microbiologically confirmed IID would therefore add considerably to the evidence base.

In this paper, we present the analysis of a large national dataset of laboratory diagnosed IID from England. The aim of this study was to analyse the association between socioeconomic deprivation and incidence of IID reported to national surveillance by pathogen. The objectives were to 1) Compare crude incidence for each gastrointestinal (GI) pathogen by Index of Multiple Deprivation (IMD) quintile and 2) Analyse the association between IMD quintile and incidence of each pathogen at neighbourhood level (lower super output area, LSOA).

## Methods

### *Data Sources*

The Second Generation Surveillance System (SGSS) is UK Health Security Agency's (UKHSA) primary method for collecting data on positive cases of infections of clinical significance and antimicrobial resistance from laboratories across England, Northern Ireland and Wales. Introduced in 2014, it replaced the legacy LabBase2, CoSurv and AmSurv applications that had previously supported the reporting of laboratory surveillance data to Public Health England (PHE) and predecessor organisations. The system enables laboratories to meet their statutory obligation under the Health Protection (Notification) Regulations to report laboratory confirmed cases of notifiable causative agents to UKHSA [9].

During the reporting period of this study, one hundred and twenty-seven microbiology and virology NHS and private laboratories across England reported positive test results to SGSS. Guidance on what, when and how they report is documented in the guide for diagnostic laboratories [9].



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Data from the UKHSA SGSS was extracted from 1 January 2015 to 13 December 2018 (inclusive) for *Salmonella, Campylobacter, Shigella, Giardia* species, and norovirus. These data include demographic characteristics for laboratory confirmed cases of infection in England. Transmission pathways for each pathogen are included in the Supplementary Materials [10-15] (Table 1A). A number of other pathogens available in SGSS database (such as STEC) was excluded. It was because those pathogens have the culture samples collected and analysed via their own, separate enhanced surveillance systems. It was not possible to de-duplicate PCR results for the same samples in the reference labs, which is a process ensuring national surveillance's reliability.

Each case was assigned to a LSOA, which are small zones representing neighbourhoods (~1500 people) based on their residential postcode, using data available from the Office for National Statistics (ONS) [16]. There are 32,844 LSOAs in England. Socio-demographic data was obtained from the ONS and included rural/urban classification, region of England, travel abroad (Yes, No, Unsure), population by year by age (Child, if <20 years old and Adults, if >=20 years old) and sex (Male and Female), all at the LSOA level [16]. Area level socioeconomic deprivation was measured through matching individual's LSOA of residence to the 2019 IMD [17]. The IMD is a composite measure based on seven weighted domains: income; employment; health; education; barriers to housing and services; crime and living environment. Mean distance to a general practice (GP) for each LSOA was obtained from the Public Health England Fingertips website [18]. Individuals whose data was missing from age, sex or rural/urban classification were excluded from the multivariable logistic regression analysis.

*Analysis*

For the first objective, rates were calculated per 100,000 person-years by IMD quintile, using the mid-year population estimates by LSOA for 2015, 2016, and 2017, and 2018. *Salmonella* and *Shigella* were disaggregated by species to reflect differing transmission pathway. 95% confidence intervals (CI) were calculated with the 'PHEindicatormethods'



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package which used Byar's method [19]. Rate ratios (RR), with 95% CI comparing the most deprived quintile with the least deprived quintile, were calculated with the 'epitools' package which used the Wald test. All analyses were done in R version 4.2.1.

The second objective involved an ecological analysis using the LSOA as the unit of analysis. Univariate and multivariable ordinal logistic regression models were used, with categorised count of cases as the outcome and person-years as one of the covariates. In the former case, IMD quintile was added as a categorical variable, whereas in the latter case sex (Male and Female), age (Age groups 0-4, 5-9, 10-14, 20-59, 60-69 and >=70), rurality/urbanicity and distance to the GP (0-549 metres, 550-1099 metres, 1100-2199 metres and >=2200 metres) were also added as categorical variables, together with interaction between rurality/urbanicity and distance to the GP. The 1st IMD quintile represented the least deprived areas while the 5th IMD quintile represented the most deprived areas. The p-values were obtained by means of the (composite) Wald test and significance level taken to be 5%. Table 1. shows the case categories chosen for each IID for both univariate and multivariable analysis, based on the distribution of counts for the IID in question. The proportionality of odds assumption was tested in the univariate and multivariable models, using the gologit2 user-written ado program and method described in the article [20] for that program and executed in Stata 17.0, in which all inferential analyses were performed. In those cases where the assumption was not met, a generalised ordinal logistic regression model was fitted using the above program, where the obtained parameter estimates were then exponentiated to obtain overall odds ratios (ORs) for those parameters where the assumption appeared not be violated, and separate ORs for each case category otherwise [14]. In all cases, their 95% confidence intervals (CIs) were obtained and the measure of association, together with these CIs, are presented for the IMD quintile in the results section.

## Results

*Overview of the epidemiology and microbiological data*



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There was a total of 314,381 cases reported to SGSS during the 4-year study period, of which 167,299 (53%) were male and 59,827 (19%) were children (Table 1A.). Distribution of cases across regions ranged from 6% (n=17,831) in the North East of England to 18%, (n=56,331), in the South East of England. Most cases (n=249,802, 79%) lived in urban areas and 4% of cases (n=12,743) reported travelling outside the UK within 7 days of onset of symptoms (Table 1A.). About two-thirds (n=208,016) of cases were infected with *Campylobacter* species, 6% with *Giardia (*n=18,114), 6% were infected with *Cryptosporidium* (n=18,743), 8% with norovirus (n=26,361), 8% with non-typhoidal *Salmonella* (n=26,361), 3% with *Salmonella* typhi/paratyphi (n=8,690), and 3% with *Shigella* (n=8,096). Of the *Shigella* diagnoses that were speciated (76%), 2,135 cases were infected with *Shigella flexneri* and 3,597 were infected with *Shigella sonnei*. *Cryptosporidium* speciation data were incomplete on SGSS and these data were excluded from subsequent analysis. The more deprived quintiles were slightly more represented in the study sample than the two least deprived quintiles with 68,211 (22%) cases representing the most deprived quintile and 51,858 (16%) cases representing the least deprived quintile. IMD quintile classification was not conducted for 134 cases (0.04%) due to lack of valid postcodes (Table 2A.). Six hundred eighty-five individuals had data missing of sex variable, 567 of age variable and 134 of rural/urban classification variable, which represented approximately 0.2% of the total cases.

*Comparison of crude incidence for each GI pathogen by IMD quintile*

There was a clear trend of decreasing likelihood of (a laboratory report with) all IID pathogens with increasing deprivation, with each quintile statistically significantly lower than the preceding quintile. Comparing the lowest and highest quintiles, the rate in the most deprived quintile was 28% lower than that of the least deprived quintile (RR=0.72; 95% CI: 0.71-0.73) (Table 2., Figure 1A.). Incidence of *Campylobacter* species and *Giardia* decreased with increasing deprivation, with both pathogens showing a clear trend of each quintile being lower than the preceding one. The most deprived quintile had a 38% lower rate of *Campylobacter* (RR=0.62; 95% CI: 0.61 – 0.62), and 39% lower rate of *Giardia*



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(RR=0.61; 95% CI: 0.58 – 0.64) as compared to the least deprived quintile (Table 2., Figure 1A.). Conversely, the incidence of norovirus, non-typhoidal *Salmonella*, *Salmonella* typhi/paratyphi*, Shigella flexneri*, *Shigella sonnei*, and other *Shigella* increased with increasing deprivation, with all showing a generic trend across the five quintiles. The most deprived quintile had an 18% higher rate of norovirus (RR=1.18; 95% CI: 1.14 – 1.23), 6% higher rate of non-typhoidal *Salmonella* (RR=1.06; 95% CI: 1.03 – 1.10), 187% higher rate of *Salmonella* typhi/paratyphi (RR=2.87; 95% CI: 2.41 – 3.42), 152% higher rate of *Shigella flexneri* (RR=2.52; 95% CI: 2.16 – 2.95), 20% higher rate of *Shigella sonnei* (RR=1.20; 95% CI: 1.08 – 1.34), and 40% higher rate of other *Shigella* (RR=1.40; 95% CI: 1.23 – 1.60) as compared to the least deprived quintile (Table 2., Figure 1A.).

*Analysis of the association between IMD quintile and incidence rates of each pathogen*

Univariate analysis showed that higher deprivation was significantly associated with higher odds of higher number of cases for *Shigella sonnei*, other *Shigella, Shigella flexneri* and *Salmonella* typhi/paratyphi *(*Table 3.). Similar trend was also seen for norovirus (Table 4.), for which quintile 3 and quintile 5 (most deprived) had the highest odds of higher number of cases. For non-typhoidal *Salmonella*, there was no clear trend with all odds ratios being close to 1 with the exception of two most deprived quintiles which showed a slightly higher odds of higher number of cases (Table 4.). Univariate analysis results showed that higher deprivation was significantly associated with lower odds of higher number of cases for *Giardia* (Table 4.) and *Campylobacter* (Table 5.).

Multivariable analysis results showed that higher deprivation was significantly associated with lower odds of higher number of cases for *Giardia* and *Campylobacter* (Table 6.). There was a similar trend for *Shigella sonnei* but not all quintiles were significant. Multivariable analysis showed that higher deprivation was significantly associated with higher odds of higher number of cases for *Shigella flexneri*, norovirus *and Salmonella* typhi/paratyphi *(*Table

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6.). For other *Shigella* and non-typhoidal *Salmonella*, there was no clear trend with all odds ratios being close to 1 and CI including 1 for all or most quintiles (Table 6.).

## Discussion

In this study, which used national surveillance data, we found a heterogeneous relationship between deprivation and incidence of laboratory confirmed GI infections that varied by pathogen. Previous studies carried out in the UK and elsewhere reported an association between a high incidence of GI infections and high levels of deprivation. For example, nationally representative analysis of 24 million calls to NHS telephone helplines for health advice in England found that there was a greater risk of GI calls from more disadvantaged areas compared to less disadvantaged areas [5]. Retrospective, cross-sectional studies from different countries found a positive link (telephone-based population studies from Australia and the US) [21, 22], no link (telephone-based population study from Canada) [23] or an inverse association (postal questionnaire from Australia) [24] between socioeconomic status and having suffered an episode of GI illness. In contrast, we reported a lower proportion of notifications of GI infection in cases living in deprived areas. However, the analysis suggests that this result reflects the high proportion of *Campylobacter* infections in the dataset.

Overall, pathogens that had common routes of transmission had similar associations with level of deprivation. For waterborne pathogens such, as *Giardia*, the incidence was lower in areas of higher deprivation, even after accounting for rural/urban differences. For pathogens most frequently associated with foodborne transmission, including *Campylobacter* and non-typhoidal *Salmonella*, the incidence was also lower in areas of higher deprivation, especially in the multivariable model. For pathogens transmitted by person-to-person contact, specifically norovirus, *Shigella* species and *Salmonella* typhi/paratyphi, incidence was higher in more deprived neighbourhoods in the crude analysis and univariate model, although results varied in the multivariable models. This indicates that for person-to-person transmission, confounders, such as age and sex, had the biggest impact on the results.



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Additionally, pathogens such as *Shigella* can, less commonly, be water-borne or food-borne, particularly in individuals who travelled to developing countries [11]. *Shigella*, *Campylobacter* and *Giardia* also all share the same transmission pathway: sexual transmission in men who have sex with men (MSM) [11].

Our results support the hypothesis that pathogen transmission routes may impact on the association with IMD. A systematic review on the impact of socioeconomic status on foodborne illness in high-income countries also found an association between infection with *Campylobacter* and *Salmonella* species and higher socioeconomic status [25]. Another systematic review investigating the relationship between socioeconomic status and GI infections in developed countries found that, in univariate analysis, the increased risk comparing low and high socioeconomic status groups was significantly higher for pathogens spread by person-to-person transmission, but lower for environmental pathogens, as compared to foodborne pathogens, which was similar to our results [26]. The study also found that the risk of GI infection for lower socioeconomic status (higher deprivation) was on average significantly higher among studies which analysed hospital cases, compared to studies that analysed laboratory recorded cases [26]. The review also highlighted that the relationship between incidence and deprivation was much stronger in children than in adults. The study by Payment et al., also found that the proportion of GI infections caused by the different routes of exposure varies significantly across communities due to varying behavioural and socioeconomic factors [27].

Previous studies have highlighted overcrowded homes with fewer washing and toilet facilities per person may be associated with a higher incidence of GI infection in more deprived areas [28]. We might therefore expect GI pathogens transmitted primarily by close person-to-person contact to have higher incidence in more deprived areas. Our analyses supported these findings, showing that a higher proportion of cases living in deprived areas reported GI infections caused by *Shigella flexneri* species, *Salmonella* typhi/paratyphi, and



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norovirus. These three pathogen groups do not have significant animal reservoirs, and are often associated with household transmission, institutional outbreaks and outbreaks among people living in close communities [10,11]. Outbreaks of *Shigella sonnei* and *Shigella flexneri* have also been detected among MSM in the UK and other developed countries [11].

Of the zoonotic, foodborne GI pathogens that are rarely associated with person-to-person transmission, *Campylobacter* and non-typhoidal *Salmonella* were reported less frequently among cases living in deprived areas. Our results could be influenced by the fact that individuals who consume fast foods, travellers to low- and middle-income countries as well as those who live in rural areas and have regular contact with livestock have increased risk of *Campylobacter* infection [29]. Adams et al. [6] also suggested that lower risk of GI infection caused by certain foodborne pathogens in individuals living in deprived areas, may be due to reduced opportunities to eat out and less frequent consumption of high-risk foods, such as unpasteurised dairy products.

Zoonotic GI pathogens may be transmitted to humans via multiple routes [12, 14]. Higher use of recreational contaminated water and international travel has been linked to incidence in less deprived individuals [14]; at the same time, individuals living in rural areas are more likely to have contact with animals and the environment, and therefore their risk of infection is increased despite living in less deprived areas [30].

Travel outside the UK, especially to countries where specific GI pathogens are endemic, may increase risk of infection. In the UK, 95% of *Salmonella* typhi/paratyphi cases have a history of travel to an endemic area and the remaining cases are acquired through contact with an infected traveller [2]. Adams et al. [6] suggested that individuals in deprived areas may be less likely to travel abroad, and this risk factor may therefore impact more on individuals from affluent areas. However, as with foodborne exposures, the assumption that

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travellers are from the least deprived areas is confounded by the frequency of travel to high-risk countries to visit family and friends by individuals living in high deprivation areas [2].

The strength of the study was using nationally representative laboratory data which is the most comprehensive source of clinical data on individual GI pathogens for England, which allowed the analysis of specific pathogens and their associated transmission routes. However, the use of national surveillance data results in a dataset that over-represents pathogens such as *Campylobacter* and under-represents the true burden of norovirus infection in the community, which limits generalisability at the level of the community. Data from the Second Study of Infectious Intestinal Disease in the Community (IID2 Study) from 2008-2009 [1] estimated that for every case of *Salmonella* captured by national surveillance, there were 1.4 GP consultations and approximately 5 community cases; and for cases of *campylobacteriosis*, there were 1.3 GP consultations and 9.3 community cases. For every case of norovirus reported to national surveillance, there were 2.3 GP consultations and 288 community cases [1]. Patients reporting IID are otherwise only routinely tested for norovirus if they are children less than 5 years of age, adults over 60 years, food-handlers, or immunocompromised patients [1]. For every national surveillance case of *Giardia*, there were 1.5 GP consultations and approximately 14 community cases [1]. Faecal samples are not routinely tested for *Giardia* as criteria for testing often includes a history of travel [12]. Ethnicity may interact with deprivation in that ethnic groups with ties to countries where *Giardia* is endemic may be more likely to travel, and therefore be tested for *Giardia*, than other ethnic groups.

Testing patterns by geography and deprivation status were not investigated in this study as the dataset contained only positive, infected cases. Consequently, the data may reflect testing bias and differences in access to health services. A systematic review [31] also showed that patients from patients from lower social classes faced less participatory consultations which reduced information sharing. Previous studies in the UK also showed



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lower reporting rates for GI infections among more deprived individuals [32]. Additionally, laboratory cases generally reflect the most clinically severe cases, and while socioeconomic deprivation is associated with more severe illness, pathogens such as norovirus usually causes short-lived symptoms [1]. Consequently, the association of lab-reported incidence of norovirus with socioeconomic deprivation found in this study may be more likely to reflect incidence of outbreak-associated norovirus or those in targeted groups. Other potential confounders, such as ethnicity and travel patterns were not included in the analysis. For example, there are known ethnic differences in the risk of Campylobacter infection in the UK [13, 33]. Finally, as this was an ecological analysis, conclusions cannot be drawn regarding individual risk factors and how they can be targeted to reduce inequalities among deprived groups.

Our study showed that incidence rates can potentially vary across deprivation quintiles, depending on the pathogen and its transmission route, based on laboratory data. Our results were consistent in showing that infections most strongly associated with areas of increasing deprivation were those transmitted by person-person contact, and that those transmitted by zoonotic contamination of the environment were least likely to be associated with areas of deprivation. We therefore suggest that the most effective solution for reduction of IID inequalities is prioritizing reduction of person-to-person infections' spread, especially in children. Development, introduction and mobilisation of safe and effective vaccines against GI pathogens which transmit person-to-person and target risk groups, such as children should be a priority for prevention. As evidenced by the paediatric rotavirus immunisation, GI vaccine introductions can help to reduce socio-economic inequalities in disease burden (both health and socio-economic) [34]. Vaccination against *Salmonella* typhi is recommended for travellers to endemic areas such as parts of Asia (such as India, Pakistan and Bangladesh) to prevent the infection [35]. There are currently no licensed vaccines for noroviruses, *Giardia*, *Campylobacter* and *Shigella* although several candidates are under development [36-40].



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Further research could investigate the relationship between type of symptomatic healthcare presentation and the number of total laboratory samples from primary care/hospitals and deprivation. Primary care and hospitals have access to total faecal samples, including negative samples, which are not reported to SGSS. Self-reporting of GI symptoms and stool sample testing, for example through a website app, could allow us to understand testing patterns for GI by socio-demographic and spatial measures [41]. It would be also interesting to investigate whether ethnicity has an impact on the incidence rates as suggested by other studies [13, 33].

The findings of this study suggest that at the level of national laboratory surveillance, the incidence of pathogens the most strongly associated with increasing deprivation are those transmitted by person-person spread and least strongly associated are those transmitted by zoonotic contamination of the environment. Previous studies have shown increased risk of IID in more deprived regions, particularly in children, at community, primary care and hospital levels [6]. We therefore suggest that the most effective solution for reduction of IID inequalities is prioritizing reduction of person-to-person infections' spread, especially in children.

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## Abbreviations

CI: Confidence Interval

GI: Gastrointestinal

GP: General practice

IID: Infectious Intestinal Disease

IMD: Index of Multiple Deprivation

LSOA: Lower Super Output Area

LRT: Likelihood Ratio Test

MSM: Men who have sex with men

ONS: Office for National Statistics

OR: Odds Ratio

PHE: Public Health England

RR: Rate Ratio

SGSS: Second Generation Surveillance System

UKHSA: United Kingdom Health Security Agency

## Authors' contributions

LB and JH conceptualised and designed the study. LB and CJ were responsible for supervision. MB and SB were responsible for investigation, validation and formal analysis. AOC was responsible for data curation. MB and SB were responsible for writing the original draft. JH was responsible for funding acquisition. NV provided statistical support. MB, SB, CJ, DH, JH and LB edited the manuscript. All authors read and approved the final manuscript.

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## Ethics approval and consent to participate

The UKHSA has approval to handle data obtained through laboratory surveillance under Regulation 3 of the Health Service (Control of Patient Information) Regulations 2002. Informed patient consent was not required as UKHSA has the authority to handle patient data for public health monitoring and infection control under Section 251 of the UK National Health Service Act 2006.

## Consent for publication

Not applicable.

## Availability of data and materials

The data that support the findings of this study are available from UKHSA, but restrictions apply to the availability of these data, which were used under licence for the current study, and so are not publicly available. Aggregated data are, however, available from the authors upon reasonable request and with the permission of UKHSA.

## Competing interests

The authors declare that they have no competing interests.

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## Tables

**Table 1. Categories for the count of cases for each pathogen for univariate and multivariable analysis.**

| Pathogen | Categories for the count of cases | |
|---|---|---|
| | Univariate analysis | Multivariable analysis |
| *Campylobacter* | 0-5, 6-10, >=11 | 0, 1, >=2 |
| *Giardia* | 0, 1, 2, >=3 | 0, 1, >=2 |
| Norovirus | 0, 1, 2, >=3 | 0, 1, >=2 |
| Non-typhoidal *Salmonella* | 0, 1, 2, >=3 | 0, 1, >=2 |
| *Salmonella* typhi/paratyphi | 0, 1, >=2 | 0, 1, >=2 |
| *Shigella flexneri* | 0, 1, >=2 | 0, 1, >=2 |
| *Shigella sonnei* | 0, 1, >=2 | 0, 1, >=2 |
| *Other Shigella* | 0, 1, >=2 | 0, 1, >=2 |

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**Table 2. Incidence rate of each pathogen by IMD quintile and RR by each pathogen comparing the most deprived quintile (5) to the least deprived quintile (1).**

| | Rate per 100,000 person-years (95% CI) | | | | | RR (95% CI) |
|---|---|---|---|---|---|---|
| | IMD quintile | | | | | |
| | 1 (least deprived) | 2 | 3 | 4 | 5 (most deprived) | 5:1 |
| All pathogens | 159.47 (158.28 - 160.68) | 156.40 (155.23 - 157.58) | 150.82 (149.68 - 151.96) | 128.69 (127.65 - 129.74) | 115.10 (114.12 - 116.10) | 0.72 (0.71 – 0.73) |
| *Giardia* | 9.86 (9.57 - 10.17) | 9.18 (8.90 - 9.47) | 9.10 (8.83 - 9.39) | 6.84 (6.60 - 7.08) | 6.00 (5.77 - 6.23) | 0.61 (0.58 – 0.64) |
| *Campylobacter* | 111.98 (110.98 - 112.98) | 107.47 (106.50 - 108.45) | 100.25 (99.32 - 101.18) | 82.04 (81.21 - 82.88) | 68.98 (68.21 - 69.75) | 0.62 (0.61 – 0.62) |
| Non-typhoidal *Salmonella* | 14.51 (14.15 - 14.88) | 14.67 (14.32 - 15.04) | 15.31 (14.95 - 15.68) | 15.39 (15.04 - 15.76) | 15.45 (15.09 - 15.82) | 1.06 (1.03 – 1.10) |
| Norovirus | 10.62 (10.31 - 10.93) | 11.97 (11.65 - 12.30) | 12.41 (12.08 - 12.74) | 11.83 (11.52 - 12.15) | 12.58 (12.26 - 12.91) | 1.18 (1.14 – 1.23) |
| *Shigella sonnei* | 1.37 (1.27 - 1.49) | 1.66 (1.54 - 1.78) | 1.72 (1.60 - 1.84) | 1.70 (1.59 - 1.83) | 1.65 (1.53 - 1.77) | 1.20 (1.08 – 1.34) |
| *Other Shigella* | 0.87 (0.78 - 0.96) | 0.82 (0.74 - 0.91) | 1.16 (1.06 - 1.26) | 1.19 (1.09 - 1.29) | 1.21 (1.11 - 1.32) | 1.40 (1.23 – 1.60) |
| *Shigella flexneri* | 0.51 (0.45 - 0.59) | 0.69 (0.61 - 0.77) | 0.98 (0.89 - 1.07) | 1.30 (1.20 - 1.41) | 1.30 (1.20 - 1.41) | 2.52 (2.16 – 2.95) |
| *Salmonella* typhi/paratyphi | 0.39 (0.34 - 0.46) | 0.37 (0.32 - 0.43) | 0.66 (0.58 - 0.74) | 0.98 (0.89 - 1.08) | 1.13 (1.03 - 1.23) | 2.87 (2.41 – 3.42) |

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**Table 3. Univariate logistic regression for pathogens with case categories 0, 1, >=2.**

| Pathogen | IMD quintile | OR (>=1 cases compared to 0 cases) (95% CI) | OR (>=2 cases compared to =< 1 cases case) (95% CI) | OR (Proportional odds assumption met) (95% CI) | p-value |
|---|---|---|---|---|---|
| *Shigella sonnei* | 1 (least deprived) | 1.00 | 1.00 | | 0.0061 |
| | 2 | 1.09 (0.96-1.24) | 1.50 (1.08-2.09) | | |
| | 3 | 0.99 (0.87-1.13) | 1.47 (1.06-2.05) | | |
| | 4 | 1.05 (0.93-1.19) | 1.84 (1.34-2.52) | | |
| | 5 (most deprived) | 1.06 (0.94-1.21) | 1.85 (1.35-2.54) | | |
| *Other Shigella* | 1 | 1.00 | 1.00 | 1.00 | <0.001 |
| | 2 | | | 0.89 (0.76-1.05) | |
| | 3 | | | 0.97 (0.83-1.14) | |
| | 4 | 1.18 (1.01-1.38) | 1.68 (1.26-2.24) | | |
| | 5 | 1.23 (1.05-1.43) | 1.99 (1.51-2.63) | | |
| *Salmonella* typhi/paratyphi | 1 | | | 1.00 | <0.001 |
| | 2 | | | 0.89 (0.69-1.14) | |
| | 3 | | | 1.47 (1.18-1.83) | |
| | 4 | | | 2.21 (1.80-2.71) | |
| | 5 | | | 2.49 (2.03-3.05) | |
| *Shigella flexneri* | 1 | | | 1.00 | <0.001 |
| | 2 | | | 1.24 (1.02-1.50) | |
| | 3 | | | 1.59 (1.33-1.92) | |
| | 4 | | | 2.34 (1.97-2.78) | |
| | 5 | | | 2.46 (2.08-2.93) | |

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**Table 4. Univariate logistic regression for pathogens with case categories 0, 1, 2, >=3.**

| Pathogen | IMD quintile | OR (>=1 cases compared to 0 cases) (95% CI) | OR (>=2 cases compared to =< 1 cases case) (95% CI) | OR (>=3 cases compared to =< 2 cases case) (95% CI) | OR (Proportional odds assumption met) (95% CI) | p-value |
|---|---|---|---|---|---|---|
| *Giardia* | 1 (least deprived) | 1.00 | 1.00 | 1.00 | 1.00 | <0.001 |
| | 2 | | | | 0.88 (0.82-0.94) | |
| | 3 | | | | 0.83 (0.77-0.89) | |
| | 4 | 0.69 (0.64-0.74) | 0.63 (0.58-0.70) | 0.55 (0.48-0.63) | | |
| | 5 (most deprived) | 0.60 (0.56-0.65) | 0.53 (0.48-0.59) | 0.45 (0.39-0.52) | | |
| Non-typhoidal *Salmonella* | 1 | | | | 1.00 | 0.0042 |
| | 2 | | | | 1.00 (0.93-1.06) | |
| | 3 | | | | 1.00 (0.94-1.07) | |
| | 4 | | | | 1.07 (1.00-1.14) | |
| | 5 | | | | 1.09 (1.03-1.17) | |
| Norovirus | 1 | | | | 1.00 | <0.001 |
| | 2 | | | | 1.18 (1.10-1.27) | |
| | 3 | | | | 1.22 (1.14-1.31) | |
| | 4 | | | | 1.15 (1.07-1.23) | |
| | 5 | | | | 1.29 (1.20-1.38) | |

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**Table 5. Univariate logistic regression for pathogens with case categories 0-5, 6-10, >=11.**

| Pathogen | IMD quintile | OR (>=6 cases compared to =<5 cases) (95% CI) | OR (>=11 cases compared to =<10 cases case) (95% CI) | OR (Proportional odds assumption met) (95% CI) | p-value |
|---|---|---|---|---|---|
| *Campylobacter* | 1 (least deprived) | 1.00 | 1.00 | 1.00 | <0.001 |
| | 2 | | | 0.86 (0.81-0.92) | |
| | 3 | 0.67 (0.62-0.72) | 0.74 (0.68-0.81) | | |
| | 4 | | | 0.40 (0.38-0.43) | |
| | 5 (most deprived) | 0.25 (0.23-0.27) | 0.17 (0.15-0.20) | | |

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**Table 6. Multivariable analysis results for all pathogens.**

| Pathogen | IMD quintile | OR[1] (>=1 cases compared to 0 cases) (95% CI) | OR (>=2 cases compared to =< 1 cases case) (95% CI) | OR (Proportional odds assumption met) (95% CI) | p-value[2] |
|---|---|---|---|---|---|
| *Campylobacter* | 1 (least deprived) | 1.00 | 1.00 | 1.00 | <0.001*** |
| | 2 | | | 0.93 (0.91-0.95) | |
| | 3 | 0.86 (0.84-0.88) | 0.83 (0.81-0.86) | | |
| | 4 | 0.73 (0.71-0.75) | 0.68 (0.66-0.70) | | |
| | 5 (most deprived) | 0.66 (0.64-0.68) | 0.55 (0.53-0.57) | | |
| *Giardia* | 1 | 1.00 | 1.00 | 1.00 | <0.001*** |
| | 2 | | | 0.89 (0.84-0.93) | |
| | 3 | | | 0.82 (0.78-0.87) | |
| | 4 | 0.69 (0.66-0.73) | 0.59 (0.53-0.66) | | |
| | 5 | 0.63 (0.59-0.67) | 0.56 (0.50-0.63) | | |
| *Shigella sonnei* | 1 | | | 1.00 | <0.001*** |
| | 2 | | | 1.07 (0.96-1.21) | |
| | 3 | | | 0.92 (0.82-1.04) | |
| | 4 | | | 0.85 (0.75-0.95) | |
| | 5 | | | 0.84 (0.75-0.95) | |
| *Other Shigella* | 1 | | | 1.00 | 0.2581 |
| | 2 | | | 0.85 (0.73-0.99) | |
| | 3 | | | 0.89 (0.77-1.03) | |
| | 4 | | | 0.93 (0.81-1.08) | |
| | 5 | | | 0.95 (0.82-1.10) | |
| Non-typhoidal *Salmonella* | 1 | 1.00 | 1.00 | 1.00 | 0.008** |
| | 2 | 0.98 (0.94-1.02) | 1.06 (0.98-1.15) | | |
| | 3 | | | 0.99 (0.95-1.03) | |
| | 4 | 1.00 (0.96-1.04) | 1.07 (0.99-1.15) | | |
| | 5 | | | 1.04 (1.00-1.09) | |
| *Shigella flexneri* | 1 | 1.00 | 1.00 | 1.00 | <0.001*** |
| | 2 | | | 1.13 (0.94-1.37) | |
| | 3 | | | 1.38 (1.15-1.65) | |
| | 4 | | | 1.60 (1.35-1.90) | |
| | 5 | 1.67 (1.41-1.98) | 0.94 (0.65-1.38) | | |
| Norovirus | 1 | 1.00 | 1.00 | | <0.001*** |
| | 2 | 1.13 (1.07-1.18) | 1.27 (1.14-1.40) | | |
| | 3 | 1.15 (1.10-1.21) | 1.30 (1.17-1.44) | | |
| | 4 | 1.16 (1.10-1.22) | 1.29 (1.16-1.43) | | |
| | 5 | 1.35 (1.28-1.42) | 1.48 (1.33-1.64) | | |
| *Salmonella* typhi/paratyphi | 1 | | | 1.00 | <0.001*** |
| | 2 | | | 0.87 (0.69-1.11) | |
| | 3 | | | 1.35 (1.09-1.68) | |
| | 4 | | | 1.66 (1.35-2.04) | |
| | 5 | | | 1.79 (1.47-2.20) | |

1.Multivariable analysis adjusted for categorical sex, age, rurality/urbanicity, distance to the GP and interaction between rurality/urbanicity and distance to the GP
2.* p<0.05 **p<0.01 ***p<0.001

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