Epidemiology and Infection

www.cambridge.org/hyg

Association between socioeconomic deprivation and incidence of infectious intestinal disease by pathogen and linked transmission route: An ecological analysis in the UK

Matylda Buczkowska[1,2], Saira Butt[1,2], Claire Jenkins[1,2], Dan Hungerford[2,3,4], Jeremy Hawker[2,5], Neville Q. Verlander[6], Anne-Marie O'Connell[6] and Lisa Byrne[1,2]

[1]Gastro and Food Safety (One Health) Division, UK Health Security Agency, London, UK; [2]National Institute for Health Research Health Protection Research Unit in Gastrointestinal Infections, University of Liverpool, Liverpool, UK; [3]Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Liverpool, UK; [4]Field Epidemiology Northwest, Field Service, Health Protection Operations, UK Health Security Agency, Liverpool, UK; [5]UK Field Epidemiology Service, UK Health Security Agency, Birmingham, UK and [6]Data & Analytics, UK Health Security Agency, London, UK

Original Paper

Cite this article: Buczkowska M, Butt S, Jenkins C, Hungerford D, Hawker J, Verlander NQ, O'Connell A-M, Byrne L (2023). Association between socioeconomic deprivation and incidence of infectious intestinal disease by pathogen and linked transmission route: An ecological analysis in the UK. *Epidemiology and Infection*, **151**, e109, 1–9
https://doi.org/10.1017/S0950268823000869

Received: 06 January 2023
Revised: 09 March 2023
Accepted: 22 May 2023

Keywords:
deprivation; ecological analysis; gastrointestinal disease; incidence; inequalities; infectious intestinal disease; laboratory data; surveillance; transmission route

Corresponding author:
Claire Jenkins;
Email: claire.jenkins1@ukhsa.gov.uk

Abstract

Infectious intestinal disease (IID) studies conducted at different levels of the surveillance pyramid have found heterogeneity in the 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 the index of multiple deprivation quintile, and an ecological analysis was conducted using univariant and multvariable regression models for each pathogen. 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 S. typhi*/paratyphi. Infections most associated with deprivation were those transmitted by person-to-person spread, and least associated were those transmitted by zoonotic contamination of the environment. Person-to-person transmission can be contained by implementing policies targeting over-crowding and poor hygiene. This approach is likely to be the most effective solution for the reduction of IID.

Introduction

Infectious intestinal disease (IID), an infection of the gastrointestinal (GI) 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 the people reporting IID have missed work or school due to their symptoms, and for particular pathogens, public health measures require the 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 (GP) [1]. However, the estimates at different levels of the surveillance pyramid [4] differ widely by pathogen, for example, from 5 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 the 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 socioeconomic factors is the same for each pathogen. In addition, considering the differences in ascertainment at each level of the surveillance pyramid across

pathogens, it is likely that 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 is to analyse the association between socioeconomic deprivation and the incidence of IID reported to national surveillance by pathogen. The objectives were to (1) compare crude incidence for each GI pathogen by index of multiple deprivation (IMD) quintile and (2) analyse the association between IMD quintile and incidence of each pathogen at the 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 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 infection to UKHSA [9].

During the reporting period of this study, 127 microbiology and virology NHS and private laboratories across England reported results to SGSS. Guidance on what, when, and how they report is documented in the guide for diagnostic laboratories [9].

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] (Supplementary Table 1A). Certain pathogens were excluded because the SGSS data was not complete. A number of other pathogens available in the SGSS database (such as STEC) was.

Each case was assigned to a lower super output area (LSOA), which are 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 were 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 the 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 GP for each LSOA was obtained from the PHE Fingertips website [18]. Individuals who had missing age, sex, or rural/urban classification data 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, 2017, and 2018. *Salmonella* and *Shigella* were disaggregated by species to reflect differing transmission pathways. 95% confidence intervals (CI) were calculated with the 'PHEindicatormethods' 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 m, 550–1099 m, 1100–2199 m, and ≥2200 m) 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 the significance level was 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 to be violated, and separate ORs for each case category otherwise [14]. In all cases, their 95% CIs were obtained and the measure of association, together with these CIs, is presented for the IMD quintile in the results section.

Results

Overview of the epidemiology and microbiological data

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 (Supplementary 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

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

https://doi.org/10.1017/S0950268823000869 Published online by Cambridge University Press

(*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 (Supplementary Table 1A). About two-thirds (*n* = 208,016) of cases were infected with *Campylobacter* species, 6% with *Giardia* (*n* = 18,114), 6% 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 thus 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 a lack of valid postcodes (Supplementary Table 2A). Six hundred and 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 and Supplementary Figure 1A). The 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* (RR = 0.61; 95% CI: 0.58–0.64) as compared to the least deprived quintile (Table 2 and Supplementary Figure 1A). Conversely, the incidence of norovirus, non-typhoidal *Salmonella*, *S. typhi*/paratyphi, *S. flexneri*, *S. 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 *S. typhi*/paratyphi (RR = 2.87; 95% CI: 2.41–3.42), 152% higher rate of *S. flexneri* (RR = 2.52; 95% CI: 2.16–2.95), 20% higher rate of *S. 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 and Supplementary 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 a higher number of cases for *S. sonnei*, other *Shigella, S. flexneri*, and *S. typhi*/paratyphi (Table 3). A similar trend was seen for norovirus (Table 4), for which quintile 3 and quintile 5 (most deprived) had the highest odds of a higher number of cases. For non-typhoidal *Salmonella*, there was no clear trend with all ORs being close to 1, with the exception of the two most deprived quintiles which showed slightly higher odds of a higher number of cases (Table 4). Univariate analysis results showed that higher deprivation was significantly associated with lower odds of a 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 a higher number of cases for *Giardia* and *Campylobacter* (Table 6). There was a similar

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)

https://doi.org/10.1017/S0950268823000869 Published online by Cambridge University Press

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)	

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)	

https://doi.org/10.1017/S0950268823000869 Published online by Cambridge University Press

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)		

trend for *S. sonnei*, but not all quintiles were significant. Multivariable analysis showed that higher deprivation was significantly associated with higher odds of a higher number of cases for *S. flexneri*, norovirus, and *S. typhi*/paratyphi (Table 6). For other *Shigella* and non-typhoidal *Salmonella*, there was no clear trend with all ORs 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, a 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 the 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 *S. 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. Less commonly, human host-adapted pathogens such as *Shigella*, may be waterborne or foodborne, particularly in individuals who travelled to developing countries [11]. *Shigella*, *Campylobacter*, and *Giardia* are also associated with sexual transmission in men who have sex with men (MSM) [11].

Our results support the hypothesis that pathogen transmission routes may have an 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 among lower socioeconomic groups, the risk of infection was significantly higher from pathogens spread by person-to-person transmission, compared to foodborne pathogens [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 (2001) also found that the proportion of GI infections caused by the different routes of exposure varied 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 to 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 a 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 *S. flexneri* species, *S. typhi*/paratyphi, and 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 *S. sonnei* and *S. 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 a 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]. Factors such as exposure to contaminated

https://doi.org/10.1017/S0950268823000869 Published online by Cambridge University Press

Table 6. Multivariable analysis results for all pathogens

Pathogen	IMD quintile	OR[a] (≥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[b]
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)	

[a]Multivariable analysis adjusted for categorical sex, age, rurality/urbanicity, distance to the GP, and interaction between rurality/urbanicity and distance to the GP.
[b]*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$.

https://doi.org/10.1017/S0950268823000869 Published online by Cambridge University Press

recreational water, and international travel have been linked to a higher incidence of GI infection in less deprived individuals [14]. Moreover, individuals living in affluent rural areas are more likely to have contact with animals and the environment, and therefore their risk of infection is increased despite their higher economic status [30].

Travel outside the UK, especially to countries where specific GI pathogens are endemic, may increase the risk of infection. In the UK, 95% of *S. 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 travellers are from the least deprived areas is confounded by the frequency of travel by individuals living in high-deprivation areas to high-risk countries to visit family and friends [2].

The strength of the study was the use of 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. The data from the second study of infectious intestinal disease in the community (IID2 Study) from 2008 to 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 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 include 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 lower social classes faced less participatory consultations, which reduced information sharing. Previous studies in the UK also showed 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 cause 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 the 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. The development, introduction, and mobilisation of safe and effective vaccines against GI pathogens which transmit from 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 socioeconomic inequalities in disease burden (both health and socioeconomic) [34]. Vaccination against *S. 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].

Further research could investigate the relationship between the 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 also be 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 that are 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 an 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 the reduction of IID inequalities is prioritising the reduction of person-to-person infections' spread, especially in children.

Abbreviations

CI	confidence interval
GI	gastrointestinal
GP	general practice
IID	infectious intestinal disease
IMD	index of multiple deprivation
LRT	likelihood ratio test
LSOA	lower super output area
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

Supplementary material. The supplementary material for this article can be found at https://doi.org/10.1017/S0950268823000869.

https://doi.org/10.1017/S0950268823000869 Published online by Cambridge University Press

Data availability statement. 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.

Acknowledgements. The authors acknowledge the contributions of Theme 1 (People and Places) NIHR Health Protection Research Unit in Gastrointestinal Infections members.

Author contribution. L.B. and J.H. conceptualised and designed the study. L.B. and C.J. were responsible for supervision. M.B. and S.B. were responsible for investigation, validation, and formal analysis. A.-M.O. was responsible for data curation. M.B. and S.B. were responsible for writing the original draft. J.H. was responsible for funding acquisition. N.Q.V. provided statistical support. M.B., S.B., C.J., D.H., J.H., and L.B. edited the manuscript. All authors read and approved the final manuscript.

Funding statement. This study is funded by the National Institute for Health and Care Research (NIHR) Health Protection Research Unit in Gastrointestinal Infections, a partnership between the UK Health Security Agency, the University of Liverpool, and the University of Warwick. The views expressed are those of the author(s) and not necessarily those of the NIHR, the UK Health Security Agency, or the Department of Health and Social Care.

Competing interest. The authors declare that they have no competing interests.

Ethical standard. 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.

References

[1] **Tam CV, Viviani L, Adak B, Bolton E, Dodds J, Cowden J, Evans M, Gray J, Hunter P, Jackson K and Letley L** (2012) *The Second Study of Infectious Intestinal Disease in the Community (IID2 Study): Final Report*. London: UK Food Standards Agency.

[2] **Ejidokun TH, Hawker J, Lighton L, Paranthaman K, Stiff R and Ward G** (2019) Recommendations for the Public Health Management of Gastrointestinal Infections 2019: Principles and Practice. PHE Publications Number: GW-1020.

[3] **Daniel NC, Casadevall N, Sun P, Sugden D and Aldin V** (2020) *The Burden of Foodborne Disease in the UK 2018*. London: Food Standards Agency.

[4] **Lake IR, Nichols G, Harrison FC, Bentham G, Sari Kovats R, Grundy C and Hunter PR** (2009) Using infectious intestinal disease surveillance data to explore illness aetiology; A cryptosporidiosis case study. *Health Place* **15**, 333–339. http://doi.org/10.1016/j.healthplace.2008.06.005

[5] **Adams NL, Rose TC, Elliot AJ, Smith G, Morbey R, Loveridge P, Lewis J, Studdard G, Violato M, O'Brien SJ, Whitehead M, Taylor-Robinson DC, Hawker JI and Barr B** (2019) Social patterning of telephone health-advice for diarrhoea and vomiting: Analysis of 24 million telehealth calls in England. *Journal of Infection* **78**, 95–100. http://doi.org/10.1016/j.jinf.2018.09.008

[6] **Adams NL, Rose TC, Hawker J, Violato M, O'Brien SJ, Whitehead M, Barr B and Taylor-Robinson DC** (2018) Socioeconomic status and infectious intestinal disease in the community: A longitudinal study (IID2 study). *European Journal of Public Health* **28**, 134–138. http://doi.org/10.1093/eurpub/ckx091

[7] **Rose TC, Adams NL, Barr B, Hawker J, O'Brien SJ, Violato M, Whitehead M and Taylor-Robinson DC** (2017) Socioeconomic status is associated with symptom severity and sickness absence in people with infectious intestinal disease in the UK. *BMC Infectious Diseases* **17**, 447. http://doi.org/10.1186/s12879-017-2551-1

[8] **Tam CC, Rodrigues LC, Viviani L, Dodds JP, Evans MR, Hunter PR, Gray JJ, Letley LH, Rait G, Tompkins DS, O'Brien SJ** and **IID2 Study Executive Committee** (2012) Longitudinal study of infectious intestinal disease in the UK (IID2 study): Incidence in the community and presenting to general practice. *Gut* **61**, 69–77. http://doi.org/10.1136/gut.2011.238386

[9] **Public Health England** (2020) Laboratory Reporting to Public Health England: A Guide for Diagnostic Laboratories.

[10] **de Wit MA, Koopmans MP and van Duynhoven YT** (2003) Risk factors for norovirus, Sapporo-like virus, and group A rotavirus gastroenteritis. *Emerging Infectious Disease* **9**, 1563–1570. http://doi.org/10.3201/eid0912.020076

[11] **Serafino Wani RL, Filson SA, Chattaway MA and Godbole G** (2015) Invasive Shigellosis in MSM. *International journal of STD & AIDS* **27**(10), 917–919. https://doi.org/10.1177/0956462415610275

[12] **Dunn N and Juergens AL** (2022) Giardiasis. In: *StatPearls* [Internet]. Treasure Island, FL: StatPearls Publishing [Updated 2022 May 8; cited 2022 June 8]. Available at https://www.ncbi.nlm.nih.gov/books/NBK513239/ (accessed May 2023).

[13] **Gillespie IA, O'Brien SJ, Penman C, Tompkins D, Cowden J and Humphrey TJ** (2008) Demographic determinants for Campylobacter infection in England and Wales: Implications for future epidemiological studies. *Epidemiology & Infection* **136**, 1717–1725. http://doi.org/10.1017/S0950268808000319

[14] **Janssen B and Snowden J** (2022) Cryptosporidiosis. In: *StatPearls* [Internet]. Treasure Island, FL: StatPearls Publishing [Updated 2021 Nov 30; cited 2022 June 8]. Available at https://www.ncbi.nlm.nih.gov/books/NBK448085/ (accessed May 2023).

[15] **Ajmera A and Shabbir N** (2022) Salmonella. In: *StatPearls* [Internet]. Treasure Island, FL: StatPearls Publishing; [Updated 2022 Aug 8]. Available at https://www.ncbi.nlm.nih.gov/books/NBK555892/ (accessed May 2023).

[16] **Office of National Statistics** [Internet]. [Cited 2022 Jun 08]. Available at https://www.ons.gov.uk/ (accessed May 2023).

[17] **English Indices of Deprivation - Postcode Lookup** (2019) [Internet]. [Cited 2022 Jun 08]. Available at https://imd-by-postcode.opendatacommunities.org/imd/2019 (accessed May 2023).

[18] **Wider Determinants of Health - Built and Natural Environment Resources Page** [Internet]. [Cited 2022 Jun 08]. Available at https://fingertips.phe.org.uk/profile/wider-determinants/supporting-information/built-and-natural-environment (accessed May 2023).

[19] **Breslow NE and Day NE** (1987) Statistical methods in cancer research. Volume II. The design and analysis of cohort studies. *International Agency for Research on Cancer Scientific Publications* **82**, 1–406.

[20] **Williams R** (2006) Generalized ordered logit/partial proportional odds models for ordinal dependent variables. *The Stata Journal* **6**, 58–82.

[21] **Hall GV, Kirk MD, Ashbolt R, Stafford R and Lalor K** (2006) Frequency of infectious gastrointestinal illness in Australia, 2002: Regional, seasonal and demographic variation. *Epidemiology & Infection* **134**, 111–118. http://doi.org/10.1017/S0950268805004656

[22] **Herikstad H, Yang S, Van Gilder TJ, Vugia D, Hadler J, Blake P, Deneen V, Shiferaw B and Angulo FJ** (2002) A population-based estimate of the burden of diarrhoeal illness in the United States: FoodNet, 1996–7. *Epidemiology & Infection* **129**, 9–17. http://doi.org/10.1017/s0950268801006628

[23] **Majowicz SE, Doré K, Flint JA, Edge VL, Read S, Buffett MC, McEwen S, McNab WB, Stacey D, Sockett P and Wilson JB** (2004) Magnitude and distribution of acute, self-reported gastrointestinal illness in a Canadian community. *Epidemiology & Infection* **132**, 607–617. http://doi.org/10.1017/s0950268804002353

[24] **Bytzer P, Howell S, Leemon M, Young LJ, Jones MP and Talley NJ** (2001) Low socioeconomic class is a risk factor for upper and lower gastrointestinal symptoms: A population-based study in 15 000 Australian adults. *Gut* **200149**, 66–72. http://doi.org/10.1136/gut.49.1.66

[25] **Newman KL, Leon JS, Rebolledo PA and Scallan E** (2015) The impact of socioeconomic status on foodborne illness in high-income countries: A systematic review. *Epidemiology & Infection* **143**, 2473–2485. http://doi.org/10.1017/S0950268814003847

[26] **Adams NL, Rose TC, Hawker J, Violato M, O'Brien SJ, Barr B, Howard VJK, Whitehead M, Harris R and Taylor-Robinson DC** (2018) Relationship between socioeconomic status and gastrointestinal infections in developed countries: A systematic review and meta-analysis. *PLoS One* **13**, e0191633. http://doi.org/10.1371/journal.pone.0191633

[27] **Payment P** (2001) Transmission of gastrointestinal diseases: Hygiene as the final barrier. *American Journal of Infection Control* **29**, 218–221. http://doi.org/10.1067/mic.2001.115683

[28] **WHO Housing and Health Guidelines**. Geneva: World Health Organization [Internet]. 2018 March, Household Crowding [Cited 2022 June 8]. Available at https://www.ncbi.nlm.nih.gov/books/NBK535289/ (accessed May 2023).

[29] **Bessell PR**, **Matthews L**, **Smith-Palmer A**, **Rotariu O**, **Strachan NJ**, **Forbes KJ**, **Cowden JM**, **Reid SW and Innocent GT** (2010) Geographic determinants of reported human Campylobacter infections in Scotland. *BMC Public Health* **10**, 423. http://doi.org/10.1186/1471-2458-10-423

[30] **Leitch GJ and He Q** (2012) Cryptosporidiosis - An overview. *Journal Biomedical Research* **25**, 1–16. http://doi.org/10.1016/S1674-8301(11)60001-8

[31] **Willems S**, **De Maesschalck S**, **Deveugele M**, **Derese A and De Maeseneer J** (2005) Socio-economic status of the patient and doctor–patient communication: Does it make a difference? *Patient Education Council* **56**,139–146. http://doi.org/10.1016/j.pec.2004.02.011

[32] **Olowokure B**, **Hawker J**, **Weinberg J**, **Gill N and Sufi F** (1999) Deprivation and hospital admission for infectious intestinal diseases. *Lancet* **353**, 807–808. http://doi.org/10.0.3.248/S0140-6736(99)00611-X

[33] **Manaseki S**, **Hawker J and Ali S** (2004) Ethnic inequalities in campylobacter infection in Birmingham, UK: Descriptive study of notified cases. *Journal of Epidemiology & Community Health* **58**, 278–279. http://doi.org/10.1136/jech.2003.012294

[34] **Hungerford D**, **Vivancos R**, **Read JM**, **Iturriza-Gómara M**, **French N and Cunliffe NA** (2018) Rotavirus vaccine impact and socioeconomic deprivation: An interrupted time-series analysis of gastrointestinal disease outcomes across primary and secondary care in the UK. *BMC Medicine* **16**, 10. http://doi.org/10.1186/s12916-017-0989-z

[35] **Sulieman S** (2022) Travel vaccination update. *Delaware Journal Public Health* **8**, 40–41. http://doi.org/10.32481/djph.2022.03.007

[36] **Debbink K**, **Lindesmith LC and Baric RS** (2014) The state of norovirus vaccines. *Clinical Infectious Disease* **58**, 1746–1752. http://doi.org/10.1093/cid/ciu120

[37] **Haserick JR**, **Klein JA**, **Costello CE and Samuelson J** (2017) Cryptosporidium parvum vaccine candidates are incompletely modified with O-linked-*N*-acetylgalactosamine or contain N-terminal N-myristate and S-palmitate. *PLoS One* **12**, e0182395. http://doi.org/10.1371/journal.pone.0182395

[38] **Davids BJ**, **Liu CM**, **Hanson EM**, **Le CHY**, **Ang J**, **Hanevik K**, **Fischer M**, **Radunovic M**, **Langeland N**, **Ferella M**, **Svärd SG**, **Ghassemian M**, **Miyamoto Y and Eckmann L** (2019) Identification of conserved candidate vaccine antigens in the surface proteome of giardia lamblia. *Infection & Immunity* **87**, e00219–19. http://doi.org/10.1128/IAI.00219-19

[39] **Poly F**, **Noll AJ**, **Riddle MS and Porter CK** (2019) Update on Campylobacter vaccine development. *Human Vaccines & Immunotherapeutics* **15**, 1389–1400. http://doi.org/10.1080/21645515.2018.1528410

[40] **Böhles N**, **Böhles N**, **Busch K**, **Busch K**, **Hensel M and Hensel M** (2014) Vaccines against human diarrheal pathogens: Current status and perspectives. *Human Vaccines & Immunotherapeutics* **10**, 1522–1535. http://doi.org/10.4161/hv.29241

[41] **Davies R**, **Iturriza-Gómara M**, **Glennon-Alty R**, **Elliot AJ**, **Vivancos R**, **Alvarez Nishio A**, **Cunliffe NA and Hungerford D** (2022) Public acceptability of a technology-mediated stool sample collection platform to inform community-based surveillance of infectious intestinal disease: A pilot study. *BMC Public Health* **22**, 958. http://doi.org/10.1186/s12889-022-13307-5

https://doi.org/10.1017/S0950268823000869 Published online by Cambridge University Press