Campylobacter epidemiology: a descriptive study reviewing 1 million cases in England and Wales between 1989 and 2011

Gordon L Nichols,[1,2,3] Judith F Richardson,[1] Samuel K Sheppard,[4,5] Chris Lane,[1] Christophe Sarran[6]

[1]HPA Colindale, Health Protection Agency, London, UK
[2]University of Thessaly, Larissa, Greece
[3]University of East Anglia, Norwich, UK
[4]Department of Zoology, University of Oxford, Oxford, UK
[5]Institute of Life Science, College of Medicine, Swansea University, Swansea, UK
[6]Met Office, Exeter, Devon, UK

Correspondence to
Professor Gordon L Nichols; gordon.nichols@hpa.org.uk

ABSTRACT

Objectives: To review *Campylobacter* cases in England and Wales over 2 decades and examine the main factors/mechanisms driving the changing epidemiology.

Design: A descriptive study of *Campylobacter* patients between 1989 and 2011. Cases over 3 years were linked anonymously to postcode, population density, deprivation indices and census data. Cases over 5 years were anonymously linked to local weather exposure estimates.

Setting: Patients were from general practice, hospital and environmental health investigations through primary diagnostic laboratories across England and Wales.

Participants: There were 1 109 406 cases.

Outcome measures: Description of changes in *Campylobacter* epidemiology over 23 years and how the main drivers may influence these.

Results: There was an increase in *Campylobacter* cases over the past 23 years, with the largest increase in people over 50 years. Changes in the underlying population have contributed to this, including the impacts of population increases after World War I, World War II and the 'baby boom' of the 1960s. A recent increase in risk or ascertainment within this population has caused an increase in cases in all age groups from 2004 to 2011. The seasonal increase in cases between weeks 18 (Early May) and 22 (Early June) was consistent across ages, years and regions and was most marked in children and in more rural regions. *Campylobacter* prevalence by week in each region correlated with temperature 2 weeks before. There were higher prevalences in areas with a low population density, low deprivation and lower percentage of people of ethnic origin. Data from sero—phage and multilocus sequence typing show a few common types and many uncommon types.

Conclusions: The drivers/mechanisms influencing seasonality, age distribution, population density, socioeconomic and long-term differences are diverse and their relative contributions remain to be established. Surveillance and typing provide insights into *Campylobacter* epidemiology and sources of infection, providing a sound basis for targeted interventions.

ARTICLE SUMMARY

Article focus
- *Campylobacter* is the most common bacterial cause of diarrhoea, affecting about half a million people annually.
- Chicken is thought to be the most common source of infection and the most common vehicle for transmission while environmental sources are suspected to play an important role the seasonality.
- A few types are common and many types are rare.

Key messages
- *Campylobacter* is increasing in older people, particularly men, and population structure is partly driving this increase.
- Antibiotic resistance has increased over recent years.
- There are lower rates of reporting in more densely populated areas and more deprived areas.
- The distribution of types suggests that immunity may be important.

Strengths and limitations of this study
- The study is large and captures patients from across the country, pulling together a good picture of the epidemiology of *Campylobacter*.
- The disease burden may be underestimated due to low reporting in deprived areas that may reflect poor access to healthcare or prior infection.

INTRODUCTION

Campylobacter is the most common bacterial cause of gastroenteritis in many developed countries and has been the subject of extensive research, with over 7500 peer-reviewed articles with *Campylobacter* in the title. It has been estimated that in the UK there were

over half a million cases in the community in 2008−2009 and around 80 000 general practice (GP) consultations.[1] Chicken has been implicated as the source of infection in up to 80% of infections[2] and as the risk factor associated with transmission in 41%.[3] Actions to reduce the contamination of chickens in New Zealand have shown dramatic reductions in human cases.[4 5] Despite this, the epidemiology of *Campylobacter* remains complicated and some of the features seem difficult to explain. These include the strong seasonal increase in cases,[6] the higher rates of infection in men,[6] the changing age distribution,[7] the higher rates of infection and different risk factors in rural than in urban environments and the greater seasonality in rural than in urban environments.[4 8−14] The study was set up to review the data reported to national surveillance on human *Campylobacter* infections in England and Wales over the past 22 years to provide an overview of trends and possible drivers, mechanisms and transmission routes.

METHODS

Campylobacter surveillance data reported from diagnostic laboratories in England and Wales from 1989 to 2011 were extracted from the Oracle (LabBase) database and analysed. Most of the analyses were for the period 1989 to 2009, but annual cases were extended to 2011 (2011 data provisional). All were laboratory-confirmed cases, most were symptomatic and included patients with extraintestinal infections. Standard antimicrobial testing methods, used in primary diagnostic laboratories, were predominantly disc diffusion methods. Where speciation was reported, it was conducted in diagnostic laboratories using conventional phenotypic methods. Cases were linked by postcode to lower-level super output area and medium-level super output area (MSOA), deprivation index, ethnic origin, population density and census data using data held on the Office for National Statistics website (http://www.statistics.gov.uk/cci/nugget.asp?id=6). Postcodes of the diagnostic laboratories involved in primary isolation were used to link cases to local weather parameters held by the Met Office for 2005 to 2009. Temporal data were adjusted from day of year using a 7-day rolling mean, systematic adjustments for the reduced reporting over bank holidays and for long-term trend.

Phenotypic typing results were on human isolates, predominantly from samples taken in defined studies rather than during routine sampling. Data for the period of 1989 to 2009 included patients in a *Campylobacter* sentinel surveillance project,[15] a case−control study[3] and miscellaneous other sources. The majority of isolates were collected in a systematic way from all age groups, although the case−control study was confined to adults older than 18 years. Serotyping and phage typing were conducted at HPA Colindale using standard protocols,[16 17] and multilocus sequence typing (MLST) used recognised methods.[18] Data from clinical samples are archived on the PubMLST database along with isolates from other sources, and figures are those entered in the database to September 2011.

RESULTS

Clinical presentation

Routine surveillance of 994 791 *Campylobacter* patients between 1989 and 2009 showed that they were predominantly from gastrointestinal sites (99.65%) and were associated with diarrhoea. There were 82 *Campylobacter*-related deaths (0.008%). Overall, 242 (0.25%) of isolates were from infections involving a sterile body site, including blood (1665), brain or cerebrospinal fluid (67), wounds (45), cardiac prostheses (15), peritoneum (6) and joints (3). A majority of *Campylobacter fetus* cases (61 of 72; 85%) were invasive and 75% of *C fetus* patients were older than 50 years compared with 44% of all *Campylobacter* isolates. Invasive infections were below 0.13% of all infections in people younger than 60 years (1013/793 874), but represented 0.37% of those between 60 and 79 years (539/145 533) and 0.78% of infections in people older than 80 years (190/24 252). Central nervous system cases were spread across the age groups in a broadly similar distribution to non-CNS cases when examined as a percentage of all cases (figure 1A), whereas fatal cases were more common in people older than 60 years than in other ages (figure 1B). There were 48 *Campylobacter* patients with Guillain−Barré or Miller-Fisher syndromes. Published studies indicate that the rate of Guillain−Barré syndrome in *Campylobacter* infections, when examined using a general practice research database,[19 20] was higher by a factor of 10−40 times in England, with an estimated 1.17 cases per 1000 per year.[21] Three patients with *Campylobacter* had haemolytic uraemic syndrome, but without evidence that *Campylobacter* was the cause. Because reporting is passive and reliant on clinical details being recorded, there is likely to be under-reporting in both Guillain−Barré or Miller-Fisher syndromes and mortality data and differences in ascertainment of these between regions.

Long-term changes

There were 1 109 406 laboratory-confirmed cases reported to national surveillance between 1989 and 2011. Cases in 2011 were 45% above 2004 figures and 3% above 2010 figures (figure 1C). The cases rose from 33 280 in 1989 to a peak of 58 235 in 2000 before dropping to 44 544 in 2004 and rising to a maximum 64 582 in 2011 (2011 data provisional). There was a marked long-term increase in the percentage of cases in people older than 50 years (figure 1D), with a decline in the incidence in babies and children younger than 10 years from 2000 and a subsequent increase from 2006 to 2010. Figure 1C shows an increase in cases within all three age groups between 2004 and 2011 (<10, 36%; 10−49, 25%; 50+, 81%), but for the period 1994 to 2000, a 17% decrease in babies and children younger than 10 years, an increase in ages 10−49 years of 28% and an increase in people older than 50 years by 75%.
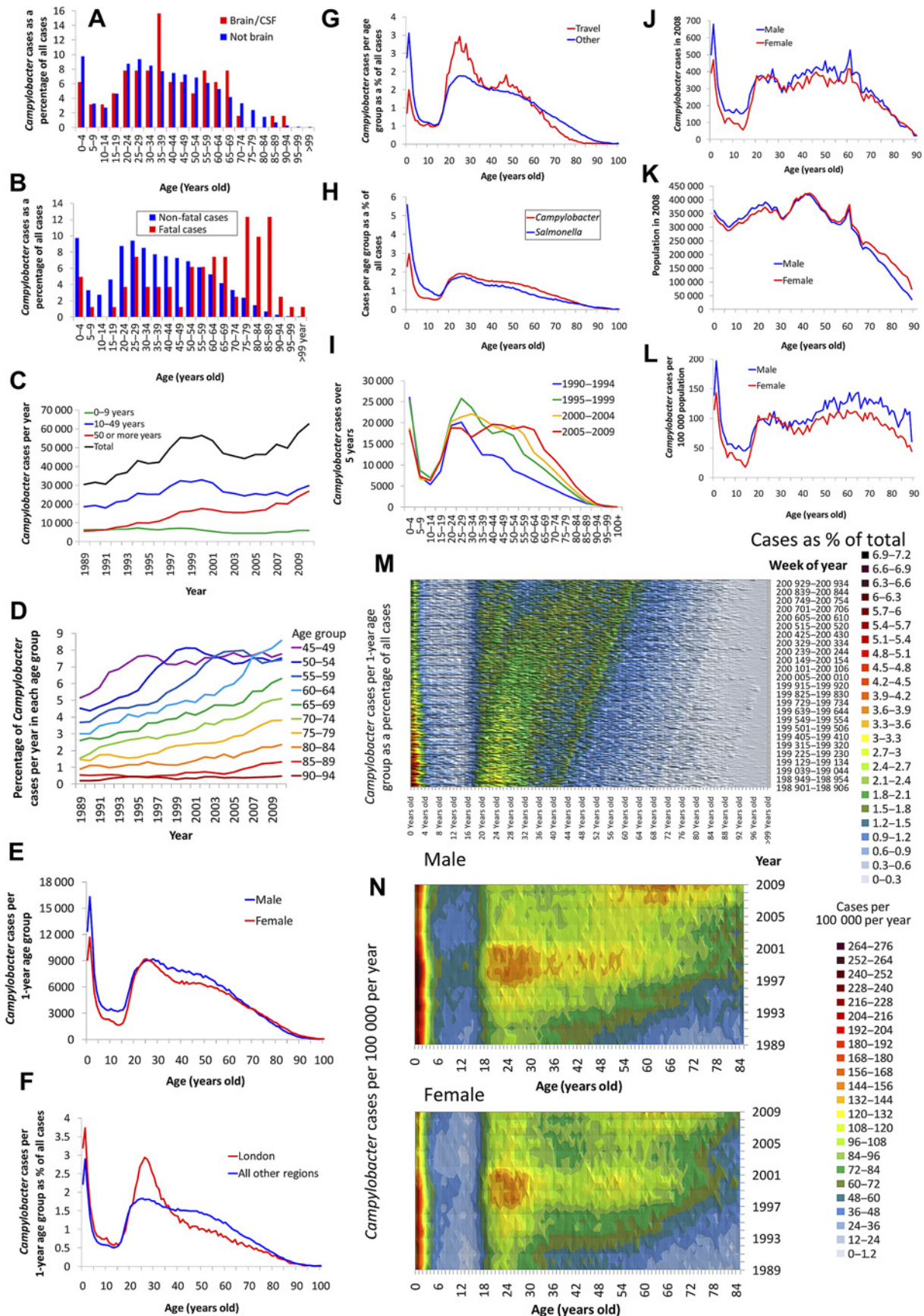
Figure 1 Age distribution. Data from 1 109 406 laboratory-confirmed cases reported in England and Wales to national surveillance between 1989 and 2011. (A) *Campylobacter* isolates from patients with and without meningitis in different age groups as a percentage of all cases, 1989−2009. (B) *Campylobacter* isolates from fatal and non-fatal cases in different age groups as

Age distribution

There were 14% more reported *Campylobacter* cases in men than in women and a 1.14 M/F ratio across most ages (figure 1E). This was mirrored by the age-specific prevalence, which showed a 30% higher prevalence in men compared with women across most age groups (figure 1L). The age distribution varied geographically, with London having more infections in young adults and less in people older than 40 years (figure 1F). The age distribution of travel-related cases showed lower rates in children and people over 60 years and more cases in people between 20 and 35 years (figure 1G). The age distribution of cases between 1989 and 2010 differed significantly between *Salmonella* and *Campylobacter*, with a higher proportion of *Salmonella* cases in children and a higher proportion of *Campylobacter* cases in adults (figure 1H). The age structure of cases has shifted over 20 years with more infection in older people in recent years (figure 1I). For example, comparison of *Campylobacter* data from 2008 (figure 1J) with 2008 population estimates (figure 1K) shows the impact of the age structure of the population on the prevalence in 2008 (figure 1L). The steady increase in the percentage of people older than 50 years (figure 1M) partly reflects ageing of the underlying population. When examined as an age-specific prevalence, there has been a recent increase in infections in older people, particularly in men (figure 1N). There was also an increase in 20−32-year-olds of both sexes around 2000 that was linked to the general increase in cases at this time. There was also a decline in the prevalence in children younger than 4 years from 2000 onwards. The seasonality of *Campylobacter* was much more marked in young children than in other ages (figure 2).

Typing

Campylobacter isolates from human cases between 1989 and 2009 (29 081/994 791; 2.9%) could be differentiated into 64 serotypes (HS), 86 phage types (PT) and 949 combined HS/PT types. Isolates of *Campylobacter jejuni* contained 57 serotypes, 80 phage types and 866 HS/PT types and two thirds of serotypes of *C jejuni* were represented in seven serotypes (table 1). *Campylobacter coli* contained 25 serotypes, 30 phage types and 102 HS/PT types, with five serotypes making up 84% of isolates (table 1). When the combined ST/PT of typable isolates were examined, then no type exceeded 9% of the total typed *C jejuni* and 18% of typed *C coli* strains. Among the combined HS/PT types, most isolates had few repre-

sentatives (figure 3A), although the distribution differed when HS and PT were examined separately (figure 3B). Only 18 013 of 26 688 (67%) *C jejuni* isolates and 1936 of 2393 (81%) *C coli* isolates were typable. When combined as HS/PT type, this decreased to 16 362 of 26 688 (61%) for *C. jejuni*, making phenotyping a poor tool for use in epidemiological investigation. Most of the HS/PT typing was undertaken between 2000 and 2004.

For the MLST data, all human cases reported on the PubMLST database were grouped by the seven sequenced genes (figure 3C−J), the ST and CC (figure 3K; table 1). Up to September 2011, there were 33 CCs and 757 STs among isolates from people with *Campylobacter* submitted to the PubMLST website (http://pubmlst.org/campylobacter/). 94.8% of *C coli* were of one type (ST-828 complex) and 34.2% of *C jejuni* of two types (ST-21 complex and ST-257 complex). While most isolates clustered into one of the predominant CCs, the STs showed a distribution with a few common types and many types with low numbers of isolates (figure 3C−J). This may partly reflect the submission patterns for the PubMLST database, with 'rare' STs over-represented as a proportion of all isolates, although a similar distribution was found for the combined HS and PT types (figure 3A) where this was not an issue. The distribution of individual serotypes and phage types (figure 3B) mirrored that of the CCs (figure 3I).

Antimicrobial resistance

Over the period from 1989 to 2009, there was an increase in the percentage of *Campylobacter* isolates that were fully or intermediately resistant to ampicillin, ciprofloxacin, nalidixic acid, tetracycline and erythromycin (figure 4A). The percentage of strains that were resistant to ciprofloxacin was higher in people who had recently travelled abroad (1042/1601; 65%) compared with those who had not (2005/6530; 31%) and where travel status was not recorded (28 646/90 095; 32%). Isolates with high rates of resistance to ciprofloxacin were found in people who had travelled to India (79%), Egypt (79%), Spain (78%) and Thailand (80%).

Weekends, bank holidays and other holidays

The onset date was not reported for most *Campylobacter* infections; the specimen date was recorded in surveillance. Specimens with any single weekday ranged from 16.8% to 22.3% (average 19.0) of all cases, whereas cases were less common on Saturday (2.5%−4.1%; average

[Continued]
a percentage of all cases, 1989−2009. (C) Campylobacter cases per year from 1989 to 2011 by age (2011 data provisional). (D) *Campylobacter* cases per year 1989−2010 as a percentage of cases in different age groups over 45 years. (E) *Campylobacter* cases by age and sex, 1989−2009. (F) *Campylobacter* cases by age as a percentage of all cases for London and all other areas, 1898−2009. (G) *Campylobacter* cases in people who had recently returned from abroad and all other cases, 1989−2009. (H) Age distribution of *Salmonella* and *Campylobacter*. (I) Change in age distribution over four 5-year time periods. (J) *Campylobacter* age and sex distribution in 2008. (K) Population age and sex distribution in 2008. (L) *Campylobacter* cases per 100 000 in 2008 by age and sex. (M) *Campylobacter* cases per 1-year age group as a percentage of all cases per year, 1989−2009. (N) *Campylobacter* prevalence per 100 000 per year between 1989 and 2009 by age and sex. CSF, cerebrospinal fluid.
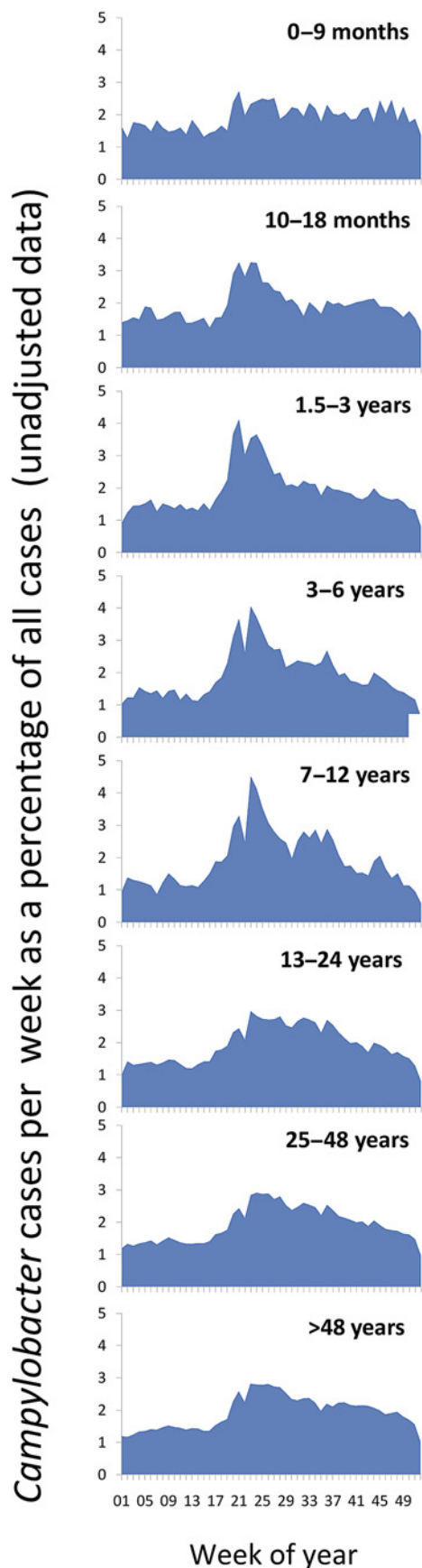
Figure 2 The weekly distribution of *Campylobacter* cases as a percentage of all cases over different age groups (unadjusted data).

3.2) and Sunday (1.4−2.1; average 1.7%), presumably reflecting problems accessing medical services on weekends. This would include access to GP, hospital or diagnostic laboratory. The reporting of infections was on average 28% lower in the 7 days of bank holiday weeks, presumably reflecting difficulties in accessing medical services. There was extra reporting in the week following some bank holiday weeks, suggesting that some cases are merely delayed by the holiday (figure 4B). Other school holidays (eg, half term) may have some effect on case reporting but are more difficult to determine as they are arranged locally rather than nationally. There was no long-term trend in the bank holiday effect. August bank holidays are during a period when there is no school attendance, and school holidays are therefore less likely to contribute.

Seasonality

Cases were normalised to take account of day of week, bank holidays and long-term trend. This was applied to daily infection rates to create a well-defined time series that shows a regular seasonal increase in the late spring with some of the features of an annual epidemic (figure 4C), as previously observed,[22] and is followed by a gradual decline over the rest of the year. The timing of the increase varies slightly between regions and between years. The increased rate of infection between weeks 18 (Early May) and 22 (Early June) is consistently seen every year in all regions but is more pronounced in young children (figure 4D,E), in some regions than others, and was less marked in London (figure 4F). Cases in this period represent 8%−12% of all annual cases and show a dramatic change over a few weeks in the exposure of people to infection, as short-term changes in ascertainment or susceptibility are unlikely. There was a relationship between *Campylobacter* prevalence and temperature that was partly a reflection of the higher seasonality in summer months when it is warmer (figure 4K) but could also represent a temperature-sensitive driver.

Postcode prevalence

The patient postcode is required to determine the local prevalence of *Campylobacter* and to produce maps of the MSOAs (figure 4G). However, in 2009, only 76% of patient surveillance records had an associated postcode, so the actual prevalence for some MSOAs was higher than this. The prevalence was higher in young children than in other ages (figure 1L). Overall prevalence in England and Wales for 2009 was 105 per 100 000 per year. *Campylobacter* prevalence in some MSOAs was artificially lowered due to low postcode reporting. These maps show some areas with much higher rates of infection locally (320−1290 cases per 100 000) that were not all in areas of low population density. When MSOAs were examined, 76.5% of the areas had between 10 and 150 *Campylobacter* cases per 100 000 per year, with 10.9% showing <10 per 100 000 per year and 12.6% having between 150 and 560 per 100 000 per year.

Table 1 Serotypes (HS)*, phage types (PT)†, MLST sequence types (ST) and MLST clonal complexes (CC) of *Campylobacter jejuni* and *Campylobacter coli* in England and Wales, 2000−2009‡

Serotype HS	C. jejuni	C. coli	Total
HS1	397		397
HS2	778	2	780
HS3	155		155
HS4	691		691
HS5	592		592
HS6	466		466
HS7	22		22
HS8	398		398
HS9	357	33	390
HS10	22		22
HS11	203		203
HS12	347	1	348
HS13	4008		4008
HS14	13	263	276
HS15	19	1	20
HS16	161		161
HS17	2		2
HS18	889	1	890
HS19	386		386
HS21	295		295
HS22	31		31
HS23	280		280
HS24		32	32
HS25		4	4
HS26		9	9
HS27	239		239
HS28	3	259	262
HS29	1		1
HS30	33	17	50
HS31	1315	2	1317
HS32	11		11
HS33	28		28
HS34	3	10	13
HS35	69		69
HS36	9		9
HS37	892		892
HS39		9	9
HS40	20		20
HS41	9		9
HS42	57		57
HS43	33		33
HS44	127		127
HS45	10		10
HS48	1	23	24
HS49	1	200	201
HS50	3528		3528
HS51	2	41	43
HS52	50		50
HS53	2		2
HS55	70		70
HS56	7	699	706
HS57	42		42
HS58	2		2
HS59	4	32	36
HS60	413		413
HS61	1	82	83
HS62	10		10
HS63	217	1	218
HS66		215	215
HS67	117		117
HS68	101		101
HS69	74		74
UT	8675	457	9132
Total	26688	2393	29081

Phage type PT	C. jejuni	C. coli	Total
PT1	8647	201	8848
PT2	2681	758	3439
PT3	4		4
PT4	7		7
PT5	1636	5	1641
PT6	538	7	545
PT7	8	139	147
PT8	545	11	556
PT9	15		15
PT10	63	2	65
PT11	13		13
PT13	12		12
PT14	557	3	560
PT15	34	1	35
PT16	1		1
PT17	63	5	68
PT18	63		63
PT19	473	1	474
PT20	336		336
PT21	138		138
PT22	4		4
PT23	23		23
PT24	14		14
PT25	100	2	102
PT27	1		1
PT28	14		14
PT29	9	3	12
PT30	3		3
PT31	7		7
PT32	9	9	18
PT33	1726	4	1730
PT34	1499		1499
PT35	630	1	631
PT36	573	2	575
PT37	4		4
PT38	150	1	151
PT39	968	27	995
PT40	117	1	118
PT41	20		20
PT42	6		6
PT43	32		32
PT44	922	927	1849
PT45	34		34
PT46	4		4
PT47	2		2
PT48	64		64
PT49	5		5
PT50	15		15
PT51	3		3
PT52	10		10
PT53	75		75
PT54	127		127
PT55	4		4
PT56	18		18
PT57	7		7
PT58	19		19
PT59	18		18
PT60	13		13
PT61	11		11
PT62	170		170
PT63	139	2	141
PT64	87	2	89
PT65	102	1	103
PT66	16	3	19
PT67	201	1	202
PT68	6		6
PT69	11	1	12
PT70	8		8
PT71	20		20
PT72	7		7
PT73	66		66
PT74	18		18
PT75	61		61
PT76	12		12
PT77	43		43
PT78	20	1	21
PT79	9	3	12
PT80	147		147
PT81	1		1
PT82	47	2	49
PT83	5		5
PT84	7		7
PT85	4		4
PT86	1		1
PTRDNC	1052	53	1105
PTUT	1334	214	1548
Total	26688	2393	29081

Clonal complex CC	C. jejuni (From PubMLST dataset)	C. coli	Total
CC 21	268	1	269
CC 22	22	0	22
CC 42	19	0	19
CC 45	92	0	92
CC 48	79	0	79
CC 49	16	0	16
CC 52	24	0	24
CC 61	51	0	51
CC 206	51	0	51
CC 257	117	1	118
CC 283	16	0	16
CC 353	80	0	80
CC 354	40	0	40
CC 362	2	0	2
CC 403	19	0	19
CC 433	3	0	3
CC 443	58	0	58
CC 460	14	0	14
CC 464	9	0	9
CC 508	3	0	3
CC 573	12	0	12
CC 574	40	2	42
CC 607	22	0	22
CC 658	30	0	30
CC 661	12	0	12
CC 677	1	0	1
CC 692	2	0	2
CC 702	2	0	2
CC 828	1	73	74
CC 1034	9	0	9
CC 1287	1	0	1
CC 1332	1	0	1
No CC	166	24	190
Total	1293	101	1394

Sequence type ST	C. jejuni (From PubMLST dataset)	C. coli	Total
ST 5	17	0	17
ST 17	4	0	4
ST 19	25	0	25
ST 21	44	0	44
ST 22	9	0	9
ST 42	6	0	6
ST 44	3	0	3
ST 45	31	0	31
ST 47	7	0	7
ST 48	32	0	32
ST 49	7	0	7
ST 50	27	0	27
ST 51	35	0	35
ST 52	6	0	6
ST 53	22	1	23
ST 61	26	0	26
ST 93	7	0	7
ST 104	15	0	15
ST 137	7	0	7
ST 205	4	0	4
ST 206	11	0	11
ST 227	6	0	6
ST 233	3	0	3
ST 257	59	0	59
ST 262	7	0	7
ST 267	7	0	7
ST 311	3	0	3
ST 353	6	0	6
ST 354	14	0	14
ST 356	5	0	5
ST 367	5	0	5
ST 397	3	0	3
ST 400	9	0	9
ST 436	3	0	3
ST 447	3	0	3
ST 464	3	0	3
ST 475	7	0	7
ST 572	8	0	8
ST 573	4	0	4
ST 574	29	0	29
ST 583	7	0	7
ST 607	5	0	5
ST 658	9	0	9
ST 814	3	0	3
ST 824	3	1	4
ST 825	0	6	6
ST 827	0	11	11
ST 828	0	3	3
ST 829	0	4	4
ST 843	3	0	3
ST 872	0	3	3
ST 877	3	0	3
ST 883	5	0	5
ST 904	3	0	3
ST 977	3	0	3
ST 1009	0	3	3
ST 1079	3	0	3
ST 1371	3	0	3
ST 1374	3	0	3
ST 2496	3	0	3
ST 3466	3	0	3
ST 2 cases	126	14	140
ST 1 case	572	54	626
ST unknown	7	1	8
Total	1293	101	1394

While isolates from some HS/PT types were confined to *C jejuni* or *C coli*, 17 types occurred in both, although in most there was a predominance of one species. The exception was HS9 PT44, which was roughly equal in numbers. Other types included HS12 PT44, HS14 PT1, HS14 PT44, HS18 PT2, HS2 PT44, HS30 PT1, HS31 PT39, HS34 PT1, HS49 PT2, HS51 PT2, HS56 PT1, HS56 PT2, HS56 PT44, HS61 PT1, HS9 PT1, HS9 PT2. It is notable that in isolates showing the same phage and serotype pattern between *C jejuni* and *C coli*, the HS56, HS9, PT1, PT2 and PT44 phenotypes were prominent.

*Two thirds of serotypes of *C jejuni* were represented in seven serotypes (HS13, 22%; HS50, 20%; HS31, 7%; HS37, 5%; HS18, 5%; HS2 and HS4, 4%).

†84% of *C coli* were in five serotypes (HS56, 36%; HS14, 14%; HS28, 13%; HS66, 11%, HS49, 10%).

‡Campylobacter typing results are from *C jejuni* and *C coli*, but other species identified at HPA Colindale were: *Arcobacter butzleri* (50), *A cryaerophilus* (4), *A species* (1), *Campylobacter fetus* (123), *C hyointestinalis* (2), *C lari* (8), *C upsaliensis* (50), *Helicobacter canadensis* (2), *H cinerea* (1), *H pullorum* (2).
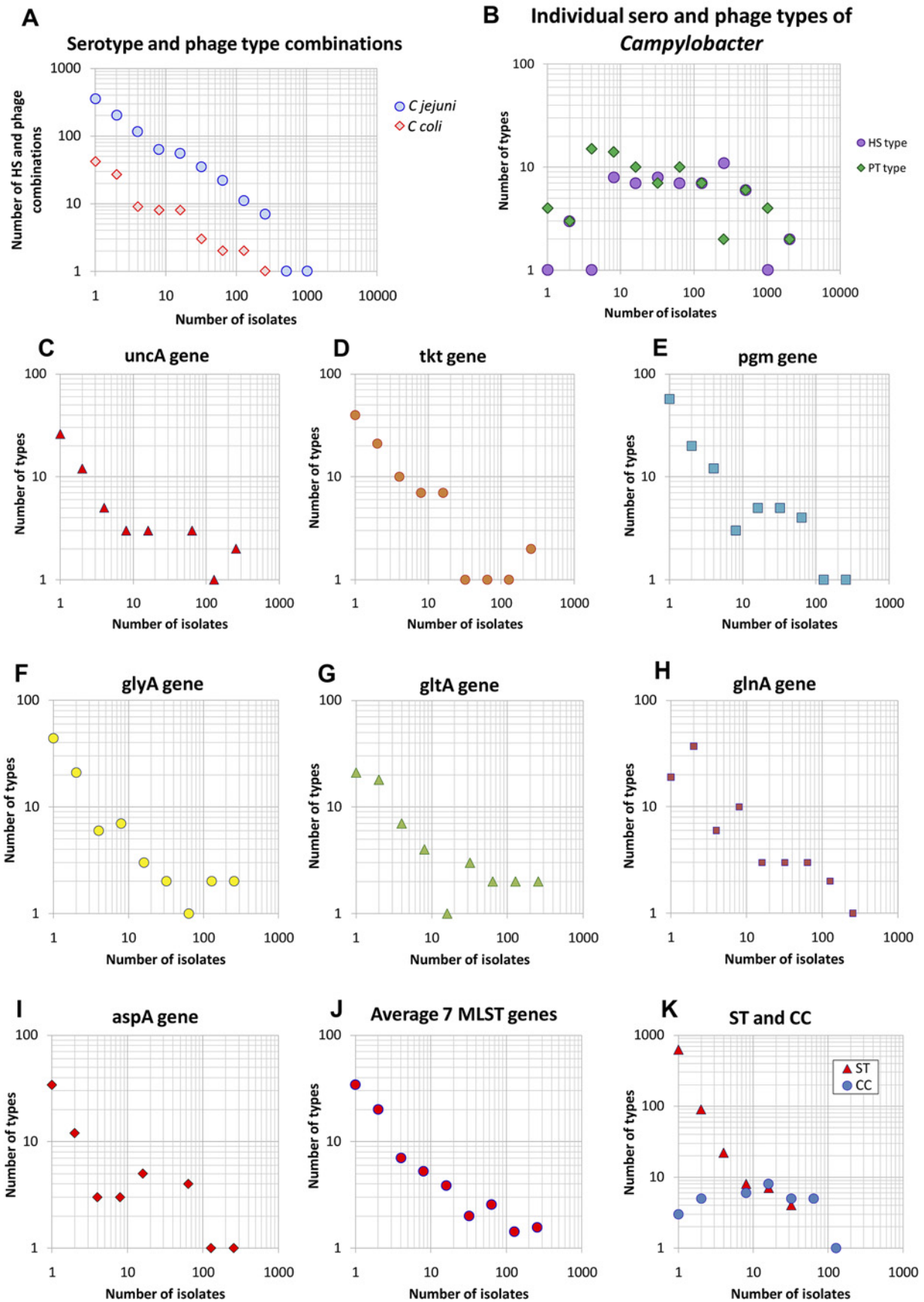
Figure 3 Typing. Typing data on cases of *Campylobacter* from England and Wales, 1989–2009. Data in the HPA data set (29 081 isolates) includes the number of *Campylobacter jejuni* and *Campylobacter coli* combined serotype (HS) and phage type (PT) combinations (HS/PT) against the number of isolates in each type (A) the separate HS and PT types for *C jejuni* and *C coli* (B).

Population density, urban/rural distribution, ethnicity and deprivation

For years 2007 to 2009 data, population density and deprivation were derived from the postcode data. Cases of *Campylobacter* per 100 000 population were higher in areas of low population density (rural) compared with areas of high population density (urban settings) (figure 4I). Less postcode reporting in areas of high population density or deprivation could introduce some bias; however, subset analysis of areas with over 90% postcode reporting still showed higher prevalence in areas of lower population density. The reason for the urban/rural difference remains unclear but could reflect proximity to ruminants and other farmed animals or differences in access to healthcare. There was an inverse relationship between *Campylobacter* prevalence and the Oxford Index of Multiple Deprivation. People with *Campylobacter* from deprived areas were less frequently reported to surveillance than in less deprived areas (figure 4J). The reason could reflect different diets, prior exposure conferring some resistance or reduced access to healthcare. The prevalence of *Campylobacter* in communities where more than 95% of the population was 'white British' was greater than those where the percentage was <50%, possibly due to poorer access to healthcare, greater susceptibility or increased exposure.

Overseas travel

Overseas travel to both EU and non-EU countries was associated with almost a fifth of all *Campylobacter* infections in data from enhanced surveillance. Spain, the country most visited, remains the country with the largest source of travel-related cases. Routine surveillance of travel-related cases shows poor and inconsistent ascertainment. Less is known about the risk factors responsible for travel-related *Campylobacter* than from indigenous infections and the risks may vary between countries visited.

Chicken production

The long-term change in *Campylobacter* cases in England and Wales was compared with poultry produced in the UK after removing exports and including imports (figure 4H). Data were from the Defra website (http://www.defra.gov.uk/statistics/foodfarm/food/slaughter/). Chicken production was used as a surrogate for chicken consumption and showed that over the 23-year period the relationship was not linear, implying that *Campylobacter* prevalence is not directly related to the amount of chicken consumed.

DISCUSSION

The reasons for large long-term changes in *Campylobacter* cases, the spring increase, the increase in older people,

the higher cases in rural communities and more cases in less deprived people could be related to features of diagnosis and reporting (commonly referred to as ascertainment) or of disease within the population as a result of increased exposure or susceptibility (here referred to as risk). The increase in cases in all three age groups between 2004 and 2009 can be compared with the period 1994 to 2000 where there was a decrease in cases in babies and children younger than 10 years, the increase in cases in people aged 10−49 years and the large increase in people older than 50 (figure 1C). This suggests that the drivers are complex and may include changes in attribution and risk. It has been suggested that some of the cases in children may be less likely to attend a physician and have a specimen taken as a result of the triaging associated with NHS Direct,[7] although the people responding to NHS Direct are a small proportion of those with diarrhoea.[1]

In order to examine the impacts of various factors on the long-term change, seasonal increase, increase in people more than 50 years old, the urban/rural split and the socioeconomic factors, a table was drawn up (table 2). The increase in *Campylobacter* in patients older than 50 years between 2004 and 2010 is dramatic and may be linked to proton pump inhibitor use. These drugs may increase people's susceptibility to *Campylobacter*;[3 8 23−25] and the older population group are more likely to be taking these drugs than the younger ones. The underlying demographic drive in figure 1M, where the increased birth rate after World War I and World War II and the 1960s baby boom is represented by diagonal lines, shows the impact of population size on *Campylobacter* cases over the years. This demographic drive is likely to contribute to the age distribution of cases, as the number of older people in the population is increasing but may also influence year-on-year changes. The economic downturn, which began in 2008, may have changed people's eating habits and exposed people to foods that are more commonly contaminated with *Campylobacter*. Alternatively, the chicken products within retail shops may have become more contaminated or there could be increased consumption of more contaminated products like chicken liver. There may also be effects resulting from a reduction in GP consultations for infectious intestinal disease.[26] The increase in cases since 2004 seems to be across all ages. People may be eating outside the home more than they were 20 years ago and travel abroad is more common. Some of the discontinuities in laboratory reporting may have an impact on long-term trends as the data show particular periods where reporting was incomplete. However, there is also evidence from laboratories that have consistently reported over the 20-year surveillance period that the

[Continued]

The PubMLST database (1394 isolates) shows the number of types from human cases against the number of patient isolates. The figures represent individual sequenced genes for uncA (C), tkt (D), pgm (E), glyA (F), gltA (G), glnA (H) and aspA (I), with an average of the seven genes (J) and the individual ST and CC (K).
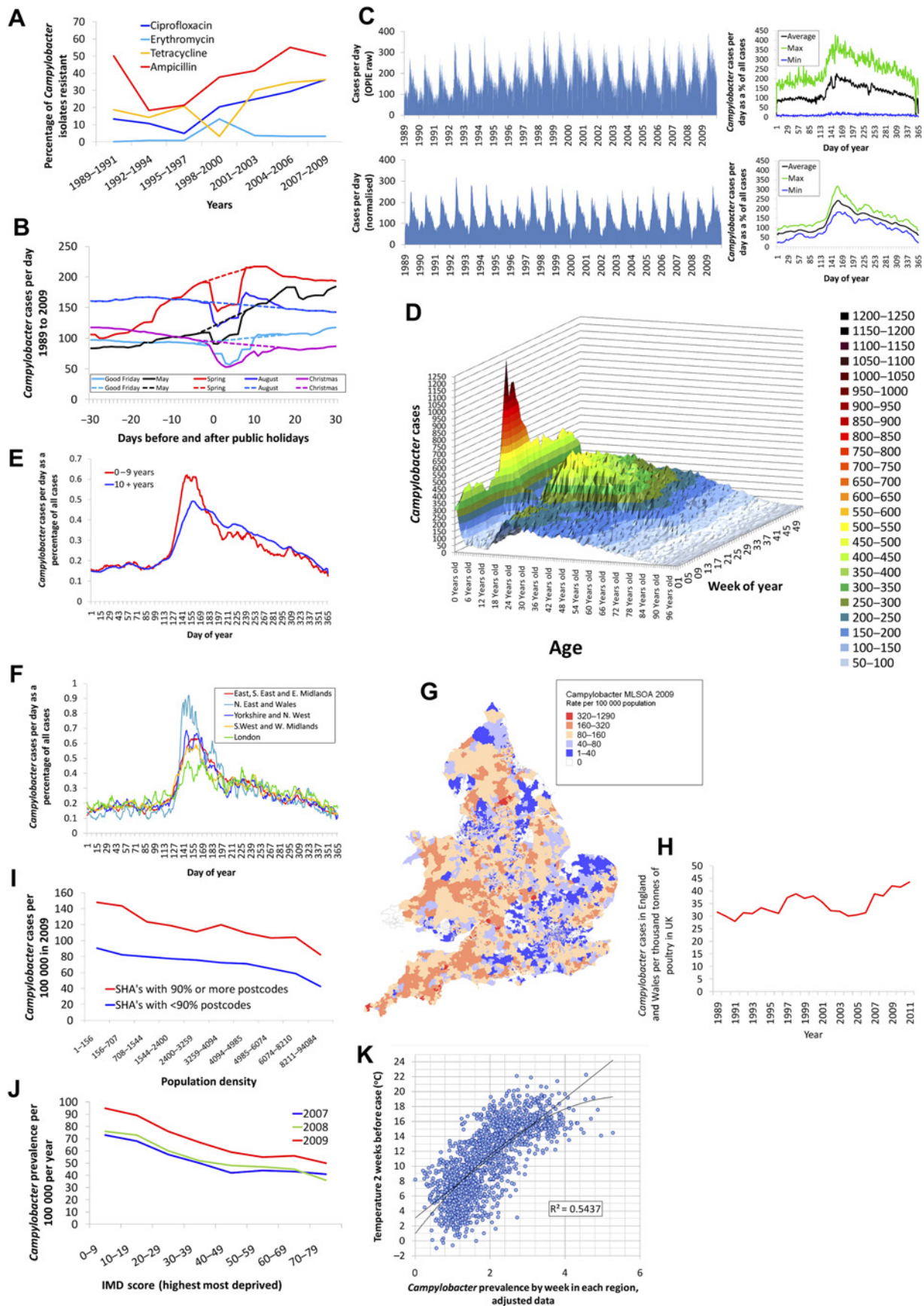
Figure 4 Resistance, spatial, social and temporal distribution. (A) Resistance of *Campylobacter* isolates to antibiotics between 1989 and 2009. (B) *Campylobacter* cases per day before and after bank holidays in England and Wales, 1989–2009. The dotted line represents an estimate of the cases that would have occurred if there had not been a bank holiday. (C) Time series of

rates of long-term change were similar to those for all laboratories. There could have been systematic change in recent years in the efficiency of isolation, either through reduced specimen delay or improved culture media or culture conditions (eg, atmosphere). In a longitudinal study of infectious intestinal disease, detection of *Campylobacter* was better with culture and/or PCR than with culture alone.[1] In addition, there was better isolation by culture alone in community cases than in those presenting to GPs when compared with culture and PCR, possibly reflecting greater delay in GP samples being sent for culture compared with community cases (Tam, personal communication).

Seasonality

The late spring increase in cases, particularly in children where the increase over a few weeks can be fourfold in some regions, has remained an enigma for many years[6 27 28] and implies a seasonal driver that is probably indirect and related to environmental and climatic conditions.[6] The seasonality differs by region, by year and by latitude and longitude, suggesting that weather combined with the farming environment is important. Possible drivers include increased contamination of chicken[29−32] and transmission by flies[22 33] (table 2). Published evidence indicates that children in rural areas are more likely to be infected with ruminant strains,[10] presumably from direct or indirect contamination from the environment. Data on seasonal distribution (figure 4C), and from typing data (table 1), make it unlikely that a single common source is the driver and imply contamination from multiple sources. There remains a need to tease out the contributions from possible drivers. There is a similar seasonality in *Campylobacter* contamination of chicken flocks[34] and human disease[35] where environmental drivers may be important.[6 28 36] While the seasonality of human infections correlates with climatic variables[28 36] and chicken contamination,[37 38] the rise in human cases can precede that in chickens,[39] consistent with a common factor causing the increase in both. It has been suggested that flies might be the route by which *Campylobacter* enter chicken flocks,[40−42] and some modelling of chicken data supports this hypothesis.[43] In addition, transmission of *Campylobacter* to humans by flies has been hypothesised as a way of explaining the characteristic seasonality of human *Campylobacter* infections,[22 33 44] although testing this may prove difficult.[45] The seasonal distribution of

Campylobacter in different countries may be related to their differing weather patterns.[28] While water-based hypotheses are attractive because *Campylobacter* is common in natural waters, the general absence of geographically located point-source outbreaks would be inconsistent with this transmission route contributing to seasonality. Travel-related infections are seasonal but do not coincide with the spring increase.

Typing

The typing of *Campylobacter* isolates has proved useful in outbreak investigation using HS/PT typing and MLST typing and also in attributing strains to particular host sources using MLST typing.[46 47] The distribution of different HS/PT types, with a few common types and a long tail of rare ones, is similar to that previously reported for *Campylobacter* using MLST typing, but the ability to group into clonal complexes makes MLST a more practical scheme for attribution. These data provide some indication of the potential diversity of phenotypes that reflect the labile genetic structure of this organism.

Data on the individual seven MLST alleles and on the HS/PT typing provide a way of looking at the genetic diversity of *Campylobacter* isolates from human infections. The frequency of different types from PubMLST may be influenced by inconsistencies in data submission and by bias towards rarer types so more unusual types appear than they would in a natural population. For the Sentinel Surveillance data, the isolates were collected in a more systematic way and are therefore more representative. The observed distribution for individual MLST alleles, for ST types and for combined HS/PT types might suggest that the most common types are perhaps those most easily able to propagate themselves within human or animal hosts. However, there is little evidence supporting this conjecture. The CCs have a clear utility in gathering up the organisms that are genetically similar, with the result that there is a different distribution with many CCs having more isolates within them, making source attribution more straightforward. The CCs shows a rough similarity, in comparing the number of isolates of different type, to the individual HS types and to the individual PT types.

Antibiotics

The increasing resistance of isolates to antibiotics is partly due to an increase in quinolone resistance in

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[Continued]
Campylobacter by day of year 1989−2009 showing unmodified data (OPIE raw), data adjusted for day of week (OPIE), for bank holidays (adjusted) and also adjusted for long-term trend (normalised). (D) *Campylobacter* cases by age and week of year. (E) Seasonal distribution of cases over and under 10 years of age (normalised data). (F) Regional differences in seasonal distribution (normalised data). (G and H) *Campylobacter* prevalence per 100 000 for 2009 based on the medium-level lower super output areas (MLSOA) (H) *Campylobacter* cases in England and Wales per thousand tonnes of poultry in the UK. (I) *Campylobacter* cases per 100 000 in 2009 by population density and completeness of postcode reporting. (J) *Campylobacter* prevalence per 100 000 per year and the Index of Multiple Deprivation (IMD) score. Differences between 2007 and 2009 reflect improving postcode reporting as cases cannot be included in the figures without a postcode. (K) *Campylobacter* prevalence by week in each region against the local temperature 2 weeks before the case specimen date (2005−2009).

Table 2 The main hypothesised drivers/mechanisms/transmission routes for changes in *Campylobacter*

Hypothesised contributing factor	Estimated likelihood of causing				
	Long-term change	Seasonal spring increase	Increase in adults older than 50 years	More rural than urban cases	More cases in the more affluent
Surveillance ascertainment					
Impacts of NHS Direct	Medium	Low	Low	Low	Low
National reporting	Medium	Low	Low	Low	Low
Changes in the surveillance system	Low	Low	Low	Low	Medium
Changes in *Campylobacter* culture media	Medium	Low	Low	Low	Low
Laboratory testing policy	Medium	Low	Low	Low	Low
New laws requiring laboratory notification of *Campylobacter**	Low	Low	Low	Low	Low
Susceptibility					
Increased proton pump inhibitor use	**High**	Low	**High**	Low	Low
Immunity through prior exposure or infection	Low	Low	Low	Low	Medium
Physiological differences between gender	Low	Low	Low	Low	Low
Exposure					
Increased contamination of chicken	**High**	Medium	Low	Low	Low
Increased consumption of chicken	Medium	Low	Low	Low	Medium
Increased systemic *Campylobacter* infection in chicken	**High**	Medium	Low	Low	Low
Sourcing chicken from different areas	Medium	Low	Low	Low	Medium
Increase in non-chicken-related sources	Low	Low	Low	Medium	Low
Transmission from cattle to chickens by flies	Low	**High**	Low	Low	Low
Transmission from faeces or raw meat to ready-to-eat food by flies	Low	**High**	Low	**High**	Low
Biosecurity interventions for *Salmonella* control	Medium	Low	Low	Low	Low
Country walks	Medium	Medium	Medium	**High**	Medium
Contamination from agricultural animals	Medium	Medium	Low	**High**	Medium
Contamination from pets	Low	Medium	Low	Medium	Low
Contamination from wild birds	Low	Medium	Low	Low	Low
Food preparation involving raw meats	Medium	Low	Low	Medium	Low
Educational farm visits	Medium	Medium	Low	Medium	Medium
Barbecued or grilled meat	Medium	**High**	Medium	Low	Low
Private or untreated water supplies	Low	Medium	Low	Medium	Medium
Mains drinking water	Low	Low	Low	Low	Low
Surface water/sewage exposure	Medium	Medium	Low	Medium	Low
Social factors					
Population ageing/demographic change	**High**	Low	**High**	Medium	Low
The economic situation	Medium	Low	Low	Low	Medium
Socioeconomic status	Medium	Low	Low	Medium	**High**
Changes in *Campylobacter* in other countries	Medium	Medium	Low	Low	Low
Kitchen behaviour	Low	Low	Low	Low	Low
GP access	**High**	Low	Low	**High**	**High**
Two weekly waste bin collections	Low	Low	Low	Low	Low
Travel abroad	Medium	Low	**High**	Low	**High**
Eating out	Medium	Low	Medium	Low	Medium
Environmental factors					
Temperature	Low	Medium	Low	Low	Low
Rainfall	Low	Low	Low	Low	Low
Latitude/longitude	Low	Medium	Low	Medium	Low

The evidence for the above scoring is included as a supplementary file with this paper.
*Human disease notification.

people returning from travel abroad and partly increased resistance to other antibiotics in isolates from all areas. The rise in resistance to erythromycin has been less dramatic and does not show an association with foreign travel. It is therefore probably related to domestic human use of this drug.

Poultry

This study suggests that long-term changes in *Campylobacter* infection in humans do not correlate well with poultry production. This suggests that the degree of contamination may be more important than the total poultry weight produced. Most human infections are

caused by *C jejuni* and *C coli*. Large studies have indicated that the *Campylobacter* isolates causing human infection contain a large diversity of types. Attribution studies indicate that strains that are commonly found in chickens are found in a majority of human infections.[2 48] This implies that the source of the *Campylobacter* is chicken. Epidemiological studies of *Campylobacter* patient's risk factors suggest that contact with or consumption of chicken is important as the transmission route of infection. In published studies, the chicken attribution to source of *Campylobacter*[2] is higher than the risk factor data representing the transmission route.[3] This may result from transmission from chicken being indirect and not through the usual eating or handling routes. Chickens can carry multiple strains[49] and co-infection with more than one isolate occurs in about 8% of patients.[50]

Disease burden

The disease burden from *Campylobacter* has been estimated to be 500 000 cases per year with 80 000 GP consultations, based on cohort and GP studies conducted over 16 months.[1] However, there could be substantial underascertainment in areas with greater deprivation and/or a larger ethnic population. It remains unclear why there are more cases in men than in women, and why infection is more common in rural than in urban environments.

Implications

Research needs to be focused on intervention, which in turn requires a better understanding of the epidemiology. Typing data has been useful for attribution to sources and may also be useful in measuring the impact of interventions targeted at reducing the contamination of chickens. This work suggests that there could be advantages in using the archive of strains that have been typed by serotype and phage type as a resource for examining longer term changes by linking the phenotypic and MLST typing and applying source attribution. There is a need for whole genome MLST typing on a percentage of strains obtained through surveillance over a longer time period. However, there is also a need to better understand the drivers for change other than source (eg, transmission route, climate, impacts of immunity). The work suggests that the underlying population contributes significantly to the disease epidemiology and this is an area where further examination may be productive. The five elements of difference and the factors that are driving these are examined in table 2. It would be attractive to better understand whether the numerous rare types are a reflection of recent emergence as a result of immunological pressure or are just rare, with a longer pedigree. There is also scope for additional work on transmission vectors, such as flies, which seem to play a role in biosecurity problems and may also directly contribute to human disease.

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