Phenotypic diversity of *Campylobacter* isolates from sporadic cases of acute human gastroenteritis in Northern Ireland

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Thermophilic campylobacters, particularly C*ampylobacter jejuni*, *C. coli* and *C. lari*, remain the most common cause of acute bacterial enteritis in Northern Ireland (Fig. 1). Most recent confirmed data for 2006 recorded 937 laboratory reports for Northern Ireland,[1] approximating to 53.8 cases per 100,000 individuals, compared to an attack rate of 86.7 and 42.8 cases per 100,000 individuals for England and Wales and the Republic of Ireland,[2] respectively. However, in a previous epidemiological study,[3] it was estimated that the true prevalence of this infection was approximately 10.3-fold higher, due to patient under-reporting.

Campylobacter spp. have a natural reservoir in the intestines of a wide range of feral and domesticated animals and birds, and enter the human food chain on raw animal products such as poultry, red meat and offal. Untreated milk has been the vehicle for several large outbreaks.[4] Campylobacters can be found in inland and coastal waters as a result of faecal contamination by animals and sewage discharge. Human infection with *Campylobacter* spp. arises from direct contact with animals or through contact with naturally contaminated raw or undercooked food products. Fortunately, large outbreaks of disease are rare and the majority of infections are considered sporadic. However, the vehicle of infection in most cases remains unidentified.

Investigation of the epidemiology of *C. jejuni* enteritis is hampered by the lack of a standardised identification and typing scheme. Few laboratories in the UK identify their isolates to species level and fewer still utilise any of the recognised typing schemes. The consequence is that there is scanty information about the frequency and distribution of strain types that cause human infection and where they are to be found in the food chain.

Differences in the attack rate between England and Wales and Northern Ireland merit further examination, in that there are approximately 38% less laboratory reported cases per 100,000 population of campylobacteriosis in Northern Ireland compared to England and Wales. Elucidation of the reasons for these differences may permit the introduction of effective intervention controls to help reduce the incidence of the disease within the British Isles. Hence, it may be

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Table 1. Distribution of phagetypes among 219 isolates of campylobacters isolated in 2002 from human faecal material at the Northern Ireland Public Health Laboratory, Belfast City Hospital. There were 14 untypable isolates (6%) in this collection.

Phagetype	Number of isolates	Percentage of total population
1	48	21.9
2	34	15.5
5	32	14.6
33	18	8.2
44	15	6.8
6	8	3.7
14	6	2.7
25	6	2.7
8	5	2.3
34	4	1.8
80	4	1.8
35	3	1.4
39	3	1.4
62	2	0.9
67	2	0.9
82	2	0.9
4	1	0.5
10	1	0.5
15	1	0.5
19	1	0.5
21	1	0.5
37	1	0.5
40	1	0.5
63	1	0.5
64	1	0.5
65	1	0.5
68	1	0.5
73	1	0.5
74	1	0.5

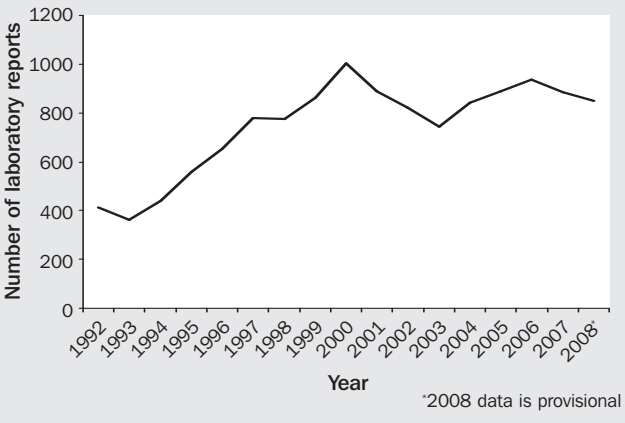

Fig. 1. Laboratory reports of faecal isolates of campylobacters in Northern Ireland 1993–2008. (Source: Communicable Disease Surveillance Centre [NI], accessible at www.cdscni.org.uk/surveillance/Gastro/Campylobacter_sp.htm).

postulated that such differences may be attributed to social behaviour and food hygiene practices in the two populations and/or the occurrence of less virulent *Campylobacter* strains and subspecies types in the Northern Ireland (NI) populations than in Britain.

The most recent and unpublished phagetyping data available in Northern Ireland is from 2002, which demonstrated the presence of 29 phagetypes among 219 faecal *Campylobacter* isolates, with 14/219 (6.4%) isolates being non-typable (Table 1). When compared with phagetypes from Wales,[5] Northern Ireland isolates shared similarities with the Welsh isolates. The most common phagetype in both regions was phagetype 1, with the second most common being phagetype 2 in both regions. The third and fourth most common phagetypes in Northern Ireland were 5 and 33, respectively, which were inverted in Wales. The four most common phagetypes in Northern Ireland accounted for 60.2% of total isolates examined, whereas in Wales this value was lower at 42.3% of total isolates examined. However, it must be borne in mind that these two data sets were not matched contemporaneously, as there were no data available to match over a similar period of time.

Overall, this comparison of a limited number of Northern Ireland isolates with a larger proportion of isolates from Wales demonstrates that there are no marked differences in the frequency of phagetypes of clinically significant campylobacters found in Northern Ireland and Wales, when employing the Colindale phagetyping scheme as an epidemiological marker. This would suggest that phenotypic differences in isolates do not account for the differences in attack rates between England and Wales and Northern Ireland and that the latter shares a similar pool of phenotypes with England and Wales.

Previously, LaFong and Bamford[6] suggested that differences in attack rates between Britain and Northern Ireland may be due to (a) relatively low consumption of unpasteurised milk in Northern Ireland compared to Britain, (b) a higher ratio of red meat to white meat consumption in Northern Ireland, (c) climatic factors and (d) a social likeness for food to be 'well done' in Northern Ireland.

The data presented here would support the hypothesis that such differences are probably due to social aspects of human behaviour (e.g., food preparation), as well as the four points suggested by LaFong and Bamford,[6] rather than to any differences in isolate type.

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Do equine strains of *Pseudomonas aeruginosa* carry the Liverpool epidemic strain markers relevant to patients with cystic fibrosis?

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Recently, in the UK, there have been several reports describing the emergence of the Liverpool epidemic strain (LES) of *Pseudomonas aeruginosa*, isolated from the sputum of cystic fibrosis (CF) patients.[1,2] What remains unclear is whether or not strains of *P. aeruginosa* carrying the LES genetic markers[3] are important in terms of their virulence and/or transmissibility, or are these markers purely of epidemiological interest?

Thus, it is important to have a full understanding of the epidemiology of where such epidemic strains originate, their persistence and transmissibility, particularly in relation to their risk to patients with CF. In order to address this and help to determine whether LES strains exist in *P. aeruginosa* solely within the CF community and not outside CF, we examined the presence of LES in a population of clinically significant *P. aeruginosa* isolates originating in infections from a comprehensive population of *P. aeruginosa*-infected horses.

P. aeruginosa isolates (n=86) were obtained from the bacteriological culture archive of the Irish Equine Centre, Johnstown, Naas, Co. Kildare, Ireland, over a five-year period (2003–2007). These strains were originally isolated from sites in infected and symptomatic equines, including abscess, ear, eye, faeces, genitourinary, guttural pouch, lung, nose, pharynx, semen, skin scrapings, throat, tissue, urine

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