Epidemiol. Infect. (2010), **138**, 1744–1747. © Cambridge University Press 2010
doi:10.1017/S0950268810001457

SHORT REPORT
Putative household outbreaks of campylobacteriosis typically comprise single MLST genotypes

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(*Accepted 26 May 2010; first published online 29 June 2010*)

SUMMARY

During a 15-month period in Scotland a small but important number of human *Campylobacter* cases (3·2%) arose from 91 putative household outbreaks. Of the 26 outbreaks with known strain composition, 89% were composed of the same MLST which supports the potential use of MLST in public health epidemiology. The number of cases associated with household outbreaks is much larger than general outbreaks and there is some evidence to indicate that there may be secondary transmission, although this is relatively rare.

Key words: *Campylobacter*, epidemiology, genotyping, infectious diseases, multi-locus sequence typing, outbreaks.

Campylobacter is the leading cause of bacterial intestinal infection in the developed and developing world [1], and infections appear predominantly sporadic. The most common exceptions are household outbreaks, which comprise 3–5% of infections as reported in Denmark [2] and in Wales [3].

Two-thirds of family-associated outbreaks in a region of South Wales (1996–1999) [3] each contained a single strain, as defined by serotyping and phage-typing. But the identification of *Campylobacter* outbreaks is hindered by the co-occurrence of different *Campylobacter* strains in individual outbreaks [4] and the lack of agreed portable typing methodologies [2].

Multi-locus sequence typing (MLST) is a genotypic strain-typing method based on DNA sequences from seven housekeeping genes [5] that has been applied to many bacterial species. The sequence types (STs) generated can then be used to compare strains and provide molecular evidence for identifying outbreaks. The aims of this study were to (i) identify putative household outbreaks in cases reported to national surveillance in Scotland, (ii) characterize their further epidemiological attributes, and (iii) evaluate genotypic strain composition as a means of confirming these outbreaks.

During July 2005 to September 2006, 5831 cases of human campylobacteriosis were reported to national surveillance in Scotland. *Campylobacter* isolates, from

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Table 1. *Epidemiological data for putative household outbreaks genotyped by MLST sequence type*

Putative household outbreak	Age (yr)	Sex	MLST type	Reported time difference between cases
1	8	F	583	<1 week
	6	M	583	
2	57	F	5	<1 week
	60	M	5	
3	7	F	464	3–4 weeks
	4	M	464	
4	5	M	21	2–3 weeks
	2	F	21	
5	45	M	21	2–3 weeks
	16	F	21	
6	77	M	206	<1 week
	74	F	206	
7	7	M	53	2–3 weeks
	5	M	53	
8	42	F	1365	<1 week
	1	M	2131	
9	3	F	273	3–4 weeks
	1	M	273	
10	16	F	21	<1 week
	15	F	21	
11	2	F	2030	<1 week
	4	M	2030	
12	12	M	2030	<1 week
	10	M	2030	
13	36	F	400	1–2 weeks
	7	M	42	
14	39	M	75	<1 week
	14	F	75	
15	42	M	267	<1 week
	41	F	962	
16	44	F	51	<1 week
	46	M	51	
17	5	M	53	<1 week
	3	M	53	
18	21	M	61	1–2 weeks
	50	M	61	
19	3	M	262	<1 week
	38	F	262	
	0	M	262	
20	72	F	257	<1 week
	72	M	257	
21	41	M	257	<1 week
	40	F	257	
22	33	F	45	<1 week
	6	M	45	
23	31	M	262	<1 week
	28	F	262	
24	82	F	52	<1 week
	88	M	52	
25	8	F	19	<1 week
	4	F	19	
26	7	M	475	1–2 weeks
	4	F	475	

https://doi.org/10.1017/S0950268810001457 Published online by Cambridge University Press

reported human cases, were submitted from public health bacteriology laboratories and typed by MLST as previously described [6]. Linkage between epidemiological data (address, age, sex and date of report) and MLST type was achieved for 3713 cases. Putative household outbreaks were defined as $\geqslant 2$ cases with the same residential address and family surname, and reporting dates within 28 days. Ninety-one such outbreaks were identified (86 with 2 cases, three with 3 cases and two with 4 cases), and these comprised 3·2% of all reported *Campylobacter* cases. According to a randomization test [7], these groups were significantly more frequent ($P<0{\cdot}00001$) than the 6·4 groups expected to occur by chance in the 2·29 million households in Scotland during the study period [8]. During this period >30-fold household outbreaks were reported than general outbreaks ($n=3$). This is of the same order of magnitude to that found in Denmark where >21-fold household outbreaks were reported than general outbreaks [2]. Further, it is worth noting that in Scotland the three general outbreaks comprised a total of 40 cases which suggests that there are about five times as many cases associated with household outbreaks. However, a larger study is required to confirm the robustness of this difference.

Twenty-six of these putative household outbreaks had complete MLST genotyping information (Table 1). In 23 (89%) of these putative household outbreaks the cases within each group shared the same ST, and this was significantly more often ($P<0{\cdot}00001$) than expected by chance (13%). The high frequency of strain matching within the putative household outbreaks resembled the strain composition of family-associated outbreaks in Wales [3]. From these results it can be hypothesized that the other five putative household outbreaks which contained different STs were caused by co-infection with different strains from the same source, e.g. food vehicle, as is known to have occurred in an outbreak attributed to chicken liver pâté [4].

The cases in each putative household outbreak showed the following differences in reporting dates: 62% were up to 1 week apart, 20% were 1–2 weeks apart and 18% were 2–4 weeks apart. The group at 2–4 weeks apart is suggestive of secondary infections, which are believed to be very rare in *Campylobacter* [1]. Further analyses based on date of onset rather than reporting date are needed to quantify the incidence of secondary infections more precisely. It would also be important to ensure that this was not due to differential exposure to a foodstuff prior and post freezing.

Campylobacteriosis is more common in males than females up to about age 20 years [9], but the male/female incidence ratio is about unity in older patients. This age-stratified change in the gender incidence ratio has been attributed to child-to-mother transmission [10]. In the dataset there were 11 groups which involved both an adult and a child aged <16 years with reporting dates more than 1 week apart. In seven of these, the child's infection was reported first, and six of the seven the adults were female. These trends are not statistically significant (binomial distribution $P=0{\cdot}06$) and the one outbreak (outbreak no. 13) where MLST typing data are available shows different sequence types. Therefore further analyses based on larger datasets are needed for evaluating the contribution of child-to-mother transmission to the higher infection rates in adult females.

This study demonstrates that putative household outbreaks of *Campylobacter* in Scotland occurred at a similar incidence as previously found in Wales and Denmark, that household cases are much more common than general outbreaks and that ST strain composition can provide evidence that cases from such outbreaks are epidemiologically related.

ACKNOWLEDGEMENTS

The Food Standards Agency, Scotland funded this work. This publication made use of the *Campylobacter jejuni* multi-locus sequence typing website (http://pubmlst.org/campylobacter/) developed by Keith Jolley and Man-Suen Chan and sited at the University of Oxford.

DECLARATION OF INTEREST

None.

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https://doi.org/10.1017/S0950268810001457 Published online by Cambridge University Press