Domestication of *Campylobacter jejuni* NCTC 11168

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Repositories

Short read data are archived on the NCBI SRA repository, associated with BioProject accession PRJNA517467 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA517467; **Table S1**).

Abstract

Reference and type strains of well-known bacteria have been a cornerstone of microbiology research for decades. The sharing of well-characterised isolates among laboratories has parallelised research efforts and enhanced the reproducibility of experiments, leading to a wealth of knowledge about trait variation in different species and the underlying genetics. *Campylobacter jejuni* strain NCTC 11168, deposited at the National Collection of Type Cultures in 1977, has been adopted widely as a reference strain by researchers worldwide and was the first *Campylobacter* for which the complete genome was published (in 2000). In this study, we collected 23 *C. jejuni* NCTC 11168 reference isolates from laboratories across the UK and compared variation in simple laboratory phenotypes with genetic variation in sequenced genomes. Putatively identical isolates identified previously to have aberrant phenotypes varied by up to 281 SNPs (in 15 genes) compared to the most recent reference strain. Isolates also display considerable phenotype variation in motility, morphology, growth at 37^{o}C, invasion of chicken and human cell lines and susceptibility to ampicillin. This study provides evidence of ongoing evolutionary change among *C. jejuni* isolates as they are cultured in different laboratories and highlights the need for careful consideration of genetic variation within laboratory reference strains.

Impact statement

In this paper, we comment on the changing role of laboratory reference strains. While the model organism allows basic comparison within and among laboratories, it is important to remember the effect even small differences in isolate genomes can have on the validity and reproducibility of experimental work. We quantify differences in 23 reference *Campylobacter* genomes and compare them with observable differences in common laboratory phenotypes.

Data summary

Short read data are archived on the NCBI SRA associated with BioProject accession PRJNA517467 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA517467).

All assembled genomes are also available on FigShare (doi: 10.6084/m9.figshare.7849268).

Phylogeny visualised on microreact: https://microreact.org/project/NCTC11168.

The authors confirm all supporting data, code and protocols have been provided within the article or through supplementary data files.

Introduction

The sharing of bacterial reference or type strains among laboratories is a fundamental part of microbiology. This often informal, usually uncelebrated, enterprise has supported academic, health, food and veterinary research worldwide underpinning microbiology innovation. The history of the exchange and classification of bacterial type strains has incorporated the work of some of the most influential microbiologists [1]. One such strain belongs to the important food-borne pathogen species *Campylobacter jejuni*.

For *C. jejuni*, the publication of a simplified culturing technique and deposition of a reference isolate at the National Collection of Type Cultures (NCTC 11168) in 1977 (by Martin Skirrow), marked the end of the first century of research into this organism [2]. The first description of an organism likely to be *Campylobacter* was made in Naples in 1884. Theodor Escherich observed spiral bacteria in stool specimens from patients with diarrhoeal disease but he was unable to culture them [3, 4]. Successful isolation of *Bacterium coli commune* (now *Escherichia coli*) from his young dysenteric patients helped pioneer bacterial genetics and lay the foundations of modern microbiology [1, 5]. However, throughout his career, Escherich continued to identify '*spirilla*' in cases of cholera-like and dysenteric disease. It is likely that the microorganisms he described were *Campylobacter* with their typical spiral morphology and association with enteritis [4, 6].

Early in the 20th century researchers investigating veterinary cases of foetal abortion and winter dysentery in cattle [7] described several species that would later become part of the *Campylobacter* genus, including *Vibrio jejuni* [8], *V. fetus* [9], *V. fetus venerealis and V. fetus intestinalis* [10]. Isolation techniques that permitted the growth of *Campylobacter* from human faeces drew attention to its importance as a human pathogen [11–13]. The genus name *Campylobacter* (meaning curved rod) was proposed by Sebald and Véron in 1963 and subsequently verified in 1973 with the broader acceptance of *Campylobacter* spp. as human pathogens [14, 15]. Skirrow's more convenient culturing technique and the availability of a model reference strain sparked renewed interest in *Campylobacter* research later in the 20th century [16, 17]. Model strains allowed for comparison of experiments within laboratories and isolates were passed among laboratories across the world [18–23]. When the *C. jejuni* NCTC 11168 genome was sequenced in 2000 [24] this type strain was cemented as an

important reference strain for *Campylobacter* research. Additional detail was added to the *C. jejuni* genome following its re-annotation (accession: AL11168.1), including revised coding sequence (CDS) identification incorporating potential for phase variation [25–29].

Today, many aspects of the biology of this organism are well characterised. Identification of genomic regions primed for posttranslational modification, in particular decoration of surface proteins with glycans [30], pseudaminic acid [31–33] and legionaminic acid [34] have improved understanding of the mechanisms of ganglioside mimicry [35], epithelial cell invasion, host immune-evasion, colonisation [36, 37] and development of neurological sequelae such as Guillain-Barré syndrome [38]. Furthermore, insights into virulence traits including strategies to sequester the iron required for infection were detailed using NCTC 11168 [39–41]. Vaccine targets have been identified [42–44] and the mechanisms of core metabolic processes [45, 46], biofilm production [47–51], capsule production [52] and resistance to oxidative stress have been elucidated [53, 54]. Accidental passage through a laboratory worker also identified putative human host adaptations *in vivo* [55].

Since 1977 the NCTC 11168 strain has been an important part of efforts to better understand this pervasive pathogen. However, there are limitations to the use of type strains, the most obvious being that bacteria display considerable variation within species. For example, in *C. jejuni*, some strains cause a significant amount of disease in humans while others do not – owing, in part, to their inability to survive the passage from reservoir host through the food production chain to contaminate human food [56]. This kind of phenotypic variation among strains is well-documented in many species and is a central reason for the growing emphasis on population genomics when trying to understand the ecology and evolution of bacteria [57]. A second, more inconspicuous limitation on the use of type strains shared among laboratories is that they might not all be the same. Strains are not *sensu stricto* clones and may display low levels of genetic variation. Clearly, when frozen there is little opportunity for genome evolution to occur [58]. However, whenever there is growth, for example in the process of sub-culturing isolates, there is an opportunity for genetic variability to be generated within the population. This may be important for interpreting research findings in different groups as even single SNPs can potentially have an impact on phenotype, for example in antimicrobial resistance [59] or host tropism [60]. The aim of our study was to investigate if, over time,

138 multiple passages under potentially different growth conditions in different laboratories have
139 introduced genotypic and phenotypic variation into a collection of NCTC 11168 *C. jejuni*.
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Methods

Isolates and genome sequencing

Twenty-three laboratory reference *C. jejuni* NCTC 11168 isolates from around the United Kingdom were collected and (re)sequenced. The year in which the laboratory received the isolate is noted along with its known heritage (**Table 1**). DNA was extracted using the QIAamp DNA Mini Kit (QIAGEN, Crawley, UK), according to manufacturer's instructions and quantified using a Nanodrop spectrophotometer. Genome sequencing was performed on an Illumina MiSeq sequencer using the Nextera XT Library Preparation Kit. Libraries were sequenced using 2 × 300 bp paired end v3 reagent kit (Illumina). Short read paired-end data was trimmed using TRIMMOMATIC (version 0.35; paired-end mode) and assembled using the *de novo* assembly software, SPAdes (version 3.8.0; using the *careful* command). The average number of contigs in the resulting assemblies was 19.7 (range: 13-36) for an average total assembled sequence size of 1,629,408 bp (range: 1,612,402 - 1,694,909 bp). The average N50 contig length was 173,674 bp (range: 100,444 - 271,714 bp) (**Table S1**).

Population structure and phylogenies

Sequence alignments and genome content comparison analyses using BLAST were performed gene-by-gene, as implemented in the BIGSdb platform [61, 62] as described in previous *Campylobacter* studies [63–66]. A gene was considered present in a given genome when its sequence aligned to a NCTC 11168 locus with more than 70% sequence identity over at least 50% of sequence length using BLAST [67]. Genomes were aligned by concatenating single-gene alignments using MAFFT [68]. For context, collected NCTC 11168 isolates were augmented with 83 previously published genomes representing the known genetic diversity in *C. jejuni* (**Table S2**). Genes present in 90% or more of the isolate genomes were aligned (1,359,883 bp; **Supplementary File 1**) and a maximum-likelihood phylogeny constructed in FastTree (version 2.1.10; with the generalized time reversible substitution model)[69]. A second alignment of just the collected NCTC 11168 strains was made (1,555,326 bp; **Supplementary File 2**) to build an additional maximum-likelihood tree, which was used as input for ClonalFrame-ML to mask putative recombination sites (version 1.11-3)[70] and visualised in microreact: https://microreact.org/project/NCTC11168 [71].

Estimating genome variation

Sequence reads were compared to the completed NCTC 11168 reference genome (AL11168.1) using SNIPPY (version 3.2dev)[72] to estimate nucleotide differences between our laboratory reference isolates and the originally sequenced genome. Assembled genomes were annotated with PROKKA (version 1.13)[73] and recombination was inferred using Gubbins (version 2.3.1)[71]. All high performance computation was performed on MRC CLIMB in a CONDA environment [74, 75].

Phenotype testing

Isolates were recovered from frozen storage on Columbia blood agar (E&O Labs, BonnyBridge, UK) and incubated in microaerobic conditions at 37°C and sub-cultured in Mueller Hinton broth (Oxoid Ltd, Basingstoke, UK) and grown microaerobically overnight at 37^{o}C.

Bacterial growth assays

Broth cultures were standardised to an OD_{600} nm of 0.05. For growth curves at 37 ^{o}C and 42^{o}C, 20 µl of the standardised broth culture was added to 180 µl of Mueller Hinton broth in a microtitre plate. Optical densities were measured at hourly intervals over a period of 48 hours using an OMEGA FLUOstar (BMG LabTech, Aylesbury, UK) plate reader with an atmospheric environment of 10% CO_2 and 3% O_2. Growth curve assays were performed in triplicate, with three technical replicates for each biological replicate. Multiple comparisons among isolates at 37°C and 42°C were compared using a one-way ANOVA with a Tukey post-test [76].

Swarming assays and motility

For each isolate, a 1 ml aliquot of the standardised pre-culture (OD_{600}=0.05) was transferred to 5 ml of fresh Mueller Hinton broth and 2 µl pipetted onto the centre of semi-solid Mueller Hinton agar (11.5 g of Muller Hinton Broth, 2.5 g of Agar 3 (Oxoid) in 500 ml of deionised water) and incubated at 42°C for 24 hours. Variation in isolate swarming was observed on Mueller-Hinton motility plates. Motile isolates spread across the plates and halo diameters were measured after 1 day of incubation. Isolates were grouped into three categories: non-motile isolates did not spread across the plate; isolates with halo diameters up to 1.5 cm were

categorised as motile; and those with halos of a diameter above 1.5 cm were designated as hyper-motile [36].

Invasion assays

A chicken gut epithelial cell line (MM-CHiC clone, 8E11; Micromol, Germany) and a human colon epithelial adenocarcinoma cell line (HT29) were used to assay invasion of *Campylobacter in vivo*. A 24-well plate was seeded with 8E11 cells in assay medium (modified McCoy's 5A/DMEM/F-12 with L-glutamine (5 mM) and supplemented with 5% FBS) and incubated at 37^{o}C in 5% CO_2 between 4 and 7 days. Liquid cultures were standardised by diluting with Mueller Hinton broth to between 0.030 and 0.080. Aliquots of 200 µl from each isolate were deposited into a 96 well plate and diluted serially. The original stock and dilutions were spread onto Columbia horse blood agar and incubated for 24 hours microaerobically at 42^{o}C. Once the cells had reached confluent growth, the medium was removed and the monolayer washed 3 times with warm PBS. An aliquot of 1 ml pre-warmed antibiotic-free supplemented DMEM medium was added to each well and inoculated with 100 µl 1x10^{7} colony-forming units (CFU). Following incubation in 5% CO_2 at 37°C for 4 hours, the cells were washed twice with 2 ml PBS supplemented with 4 µl (100 µl/ml) gentamicin and incubated for a further 1.5 hours. Cells were washed 3 times with PBS and an aliquot of 1 ml of warmed TrypLE (Gibco) added to each well and incubated at 37°C for 10 minutes. The lysed monolayer solution was diluted serially and spread onto Columbia horse blood agar in duplicate. Plates were incubated overnight at 42°C in a microaerobic environment and enumerated pre- and post- invasion to calculate the percentage of invaded inoculum. Assays with human HT29 cells were performed with McCoys growth media. Invasion assays were performed in triplicate and analysed using unpaired T-tests with Welch's correction.

Results and discussion

Not all reference strains are equal

Since its deposition at the NCTC there have been two main dissemination hubs of NCTC 11168. Ten of the 23 isolates we collected were obtained by contributing laboratories directly from the NCTC collection, while 13 isolates had come via another laboratory (**Figure 1**). DNA was extracted from each isolate, sequenced, and the genome was assembled (**Table S1**). All 23 isolates clustered closely in the host-generalist ST-21 lineage when compared on a maximum-likelihood phylogenetic tree (**Figure 2A;** https://microreact.org/project/NCTC11168). This suggests that despite some phenotypic heterogeneity, all isolates derived were from a recent common ancestor and no strains were misidentified during passage. Micro-evolutionary differences among closely related NCTC 11168 isolates were observed on a recombination-free phylogeny constructed using ClonalFrameML (**Figure 2B**). Genomes were compared to the original NCTC 11168 genome and as many as 281 SNP differences were observed (up to 15 genes) among collected laboratory strains and the reference (**Figure 2C; Table 1**). Although, in 21 of 23 isolates (91%) there were 32 or fewer SNP differences compared to the reference (**Table 1**). There was an average of 29 SNP differences between the laboratory strains and the reference, and fewest SNPs in any comparison was eight SNP differences (in five genes).

Under ideal storage conditions we might not expect to see any evidence of recent recombination in the laboratory reference strains. Nevertheless, we estimated the number of mutations and recombination events using Gubbins. In total, 436 of the 632 SNPs (69%) we identified were found within protein coding regions, of which 83 were synonymous mutations (19%; **Table 1**). The only isolate where we inferred any recombination was isolate **17**. This isolate has acquired four recombination blocks (combined 14,816 bp, r/m of 9.76) and lost a block of 15 genes (*Cj1319-1333*; **wgMLST supplementary file**), which includes a *maf*-family gene (*maf3/Cj1334*) involved in posttranslational modification of flagellins. Also missing were the *neuC2/Cj1328*, *neuB2/Cj1327*, *ptmA/Cj1332*, and *ptmB/Cj1331* genes involved in the addition of pseuaminic/legionaminic acid to *C. jejuni* flagellins [32, 77, 78]. A knockout mutant of the final gene in this block, *Cj1333*, demonstrated compromised agglutination and reduced invasion (in INT-407 cells)[78]. This region of the *C. jejuni* genome is prone to recombination and has shown a high level of diversity and is often

implicated in bacterial virulence [34, 35, 37, 79–82]. Isolate 17 was hyper-motile and also among the most invasive isolates when tested against chicken cell lines, but invaded human cell lines poorly (**Table 2**).

Isolate motility was tested *in vitro* [83] and phenotypic variation was observed among NCTC 11168 isolates (**Table 2**). Since its original dissemination, motile, non-motile and hyper-motile variants have been reported [25, 28, 84]. All three hyper-motile strains were passed between at least two laboratories before entering our collection. Only 50% of the isolates received by laboratories directly from the NCTC collection were motile (**Table 2**). Changes in motility can be a result of differences in the *flaA* and *flaB* genes resulting in attenuated flagella assembly [36]. However, we did not identify any non-synonymous mutations within the *flaA* or *flaB* genes. A shared frameshift mutation was identified in two hyper-motile isolates (11 and 16) within the core motor protein, *fliR* [85–87]. Isolate motility is also influenced by phase-variable gene expression as a result of upstream homopolymeric repeat regions [24, 88, 89]. Several motility associated genes (*maf1/Cj1348*, *maf4/Cj1335* and *maf7/Cj1342c*) were among 31 phase-variable regions recently identified in NCTC 11168 [90] and were among SNPs we identified in non-coding intergenic regions (196 of 632; 31%; **Table 1**). Twelve genes contained nucleotide substitutions in 10 or more NCTC 11168 isolates, of which five have been shown to be subject to phase variation [89]. Growth of motile bacteria in culture media can result in loss of motility as flagella construction is energetically expensive [91, 92]. In batch culture, rapid growth is prioritised and loss of flagella can be advantageous [93, 94].

Adequate flagella construction is an important virulence factor as, in addition to motility, flagella also contribute to invasion and secretion [95, 96], without which colonisation is impaired [28]. The ability of isolates to invade human and chicken intestinal epithelial cell lines was tested *in vitro* by gentamicin protection assay (**Figure 3AB**). Fourteen of twenty one isolates tested invaded the 8E11 chicken cell line more effectively compared to the human HT-29 cell line (**Figure 3C**). Broadly, motile and hyper-motile isolates invaded both cell lines in greater numbers **Figure 3AB**). Several genes containing SNPs in multiple isolates have been shown previously to contribute to increased invasion and virulence, including *mreB*, *cheA*, *Cj0431*, *Cj0455*, *Cj0807* and *Cj1145* [55, 81, 97]. Isolate growth was

tested at 37°C and 42°C, with all growing to a higher optical density at avian body temperature (42°C) (**Figure 3D**). Isolate 15 grew particularly poorly at 37°C. We identified the OXA-61 gene in the majority of isolates, but only two were resistant to ampicillin, according to CLSI guidelines (**Isolates 3 and 8; Table 2; Figure 3E)** [98].

The role of model strains in an age of population genomics

In most cases (21 of 23 isolates; 91%) we observed fewer than 32 SNPs among the laboratory isolate and the type strain deposited in the NCTC archive. However, even these minor changes are associated with observable phenotype differences (motility and invasion as seen here). This could be seen as a challenge to the reproducibility of experiments in different laboratories that use ostensibly identical strains [55, 97]. It is accepted among microbiologists that there is potential for variation among type strains that may display considerable genome plasticity, such as in *Helicobacter pylori* [99]. Consistent with this, variants of *C. jejuni* NCTC 11168 are defined as motile/non-motile, coloniser/non-coloniser for use in specific experiments.

Technical advances in high-throughput genome sequencing and analysis methods continue to improve understanding of *C. jejuni* from bottom-up studies that test the function of specific genes or operons, often with insertion or deletion mutants [55, 97], to top-down comparative genomic approaches in which isolates are clustered by phenotype and associated genomic variations are identified in large genome collections [50, 64, 100]. Early genome typing using DNA microarrays hinted at the level of diversity among *C. jejuni* isolates [27, 101], and comparisons of large isolate genome collections are now linking strain variation to differences in ecology [65, 102–105], epidemiology and evolution [63, 100, 106–110]. Advances in sequencing technology are helping us study genomes variation in greater depth and long read sequencing of isolate 2 identified large inversions (>90,000 bp) compared to the original finished genome (Table S1).

In conclusion, the genotypic and phenotypic differences among NCTC 11168 strains in this study, probably as a result of evolution during repeated passages, emphasises the need for laboratories to maintain isolate collections with detailed records and good culture practices. This essentially reaffirms the work of microbiology pioneers who developed practices to

minimise variation between strains and laboratories. However, in the genomics era, it may also be prudent to sequence strains more routinely, particularly as the costs continue to decline. While the interpretation of experiments using reference type strains may be adapting to more detailed genomic data and improved understanding of genome evolution, the strains themselves remain an essential resource in microbiology. The perceived power of large-scale comparative genomics and statistical genetics studies typically lies in the ability to identify genes or genetic variation that confers putative functional differences to the bacterium. Confirming these associated gene functions [56] requires traditional microbiology based upon a detailed understanding of reliable reference type control strains such as NCTC 11168.

Author statements

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Conflicts of interest

The authors declare that there are no conflicts of interest

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Consent for publication

Not applicable

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Figures and tables

Figure 1. The location of laboratories contributing *C. jejuni* NCTC11168 isolates. The most recent NCTC 11168 isolate was obtained by Swansea (isolate 13) in 2016 from the NCTC collection. Other isolates obtained directly from the NCTC collection are coloured black, isolates obtained via a second laboratory are coloured white.

Figure 2. Genetic variation among *C. jejuni* NCTC11168 genomes. (**A)** NCTC11168 isolates were contextualised with 83 previously published genomes representing the known genetic diversity in *C. jejuni* (total of 106 isolates). Genes present in 90% or more of the isolate genomes were aligned (1,359,883 bp) and a maximum-likelihood phylogeny constructed in FastTree2 with the generalized time reversible substitution model. The scale bar represents a genetic distance of 0.01. (**B)** Recombination was masked using ClonalFrame-ML to produce an alignment of the NCTC11168 isolates only (n=23; 1,555,326 bp). The scale bar represents 15 nucleotide substitutions. (**C)** The position of all nucleotide substitutions identified using SNIPPY were mapped against the original NCTC11168 genome (AL11168.1). SNPs found within coding regions (CDS) are represented with circles and SNPs located in intergenic regions are represented with an X. Gene names are given where variation was observed in 10 or more of the isolates.

Figure 3. Phenotype variation among *C. jejuni* NCTC11168 genomes. Invasion assays were carried out for strains categorised by motility phenotypes in (**A**) human HT-29 and (**B**) chicken cell lines. Comparisons were made between (**C**) invasiveness in these cell lines and (**D**) maximum growth at different temperatures. Minimum inhibitory concentration of ampicillin was determined for isolates grouped by source (**E**) and motility (**F**).

Table 1: Summary of genome differences in 23 NCTC11168 isolates.

Table 2: Summary of phenotype differences in 23 NCTC11168 isolates.

Supplementary data

Table S1: Isolate list
Table S2: Isolates used for genomic context
File S1: Alignment file: NCTC11168 isolates and 83 previously published genomes.
File S2: Alignment file: NCTC11168 isolates only.

File S3: wgMLST
File S4: SNP matrix

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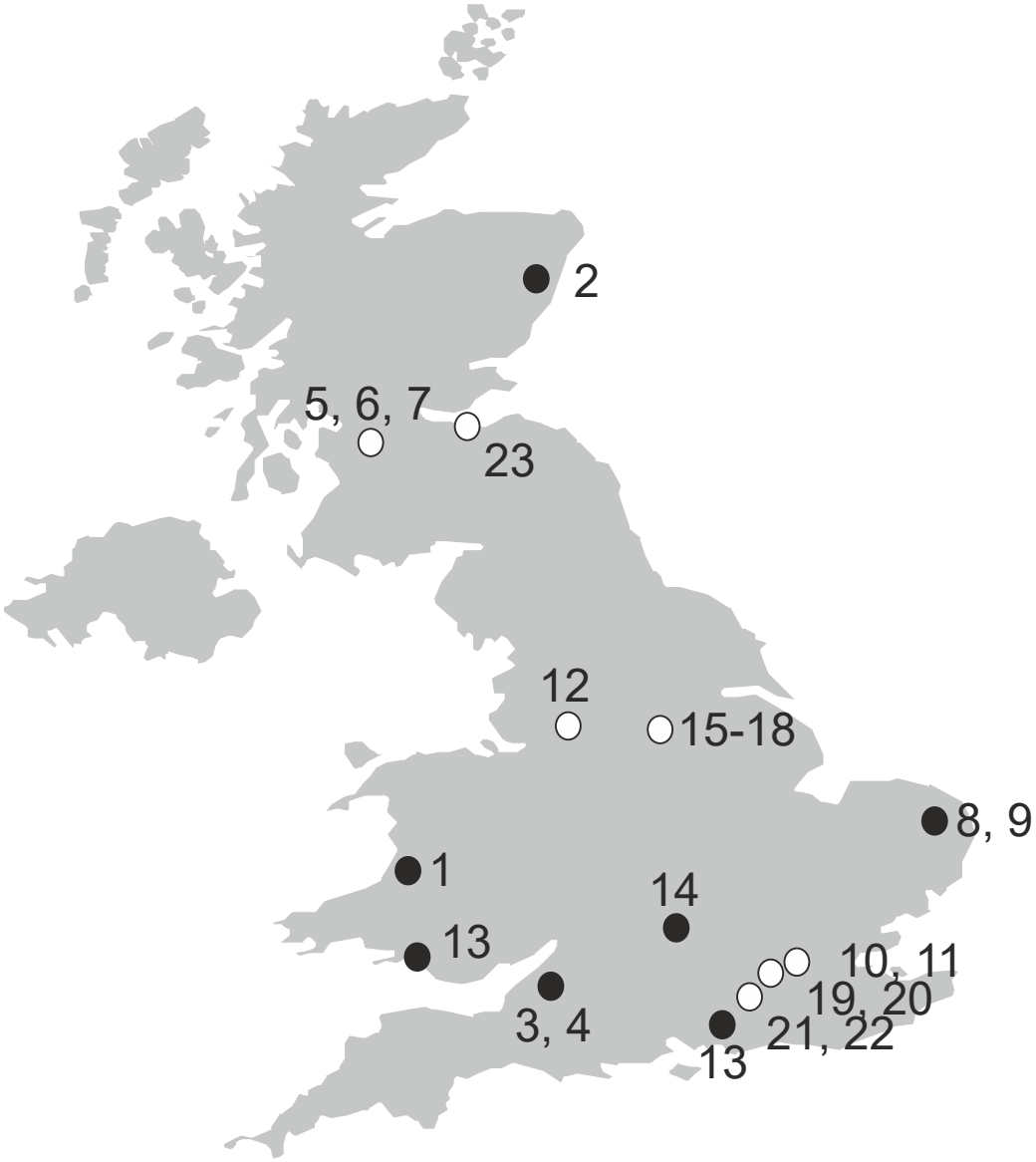

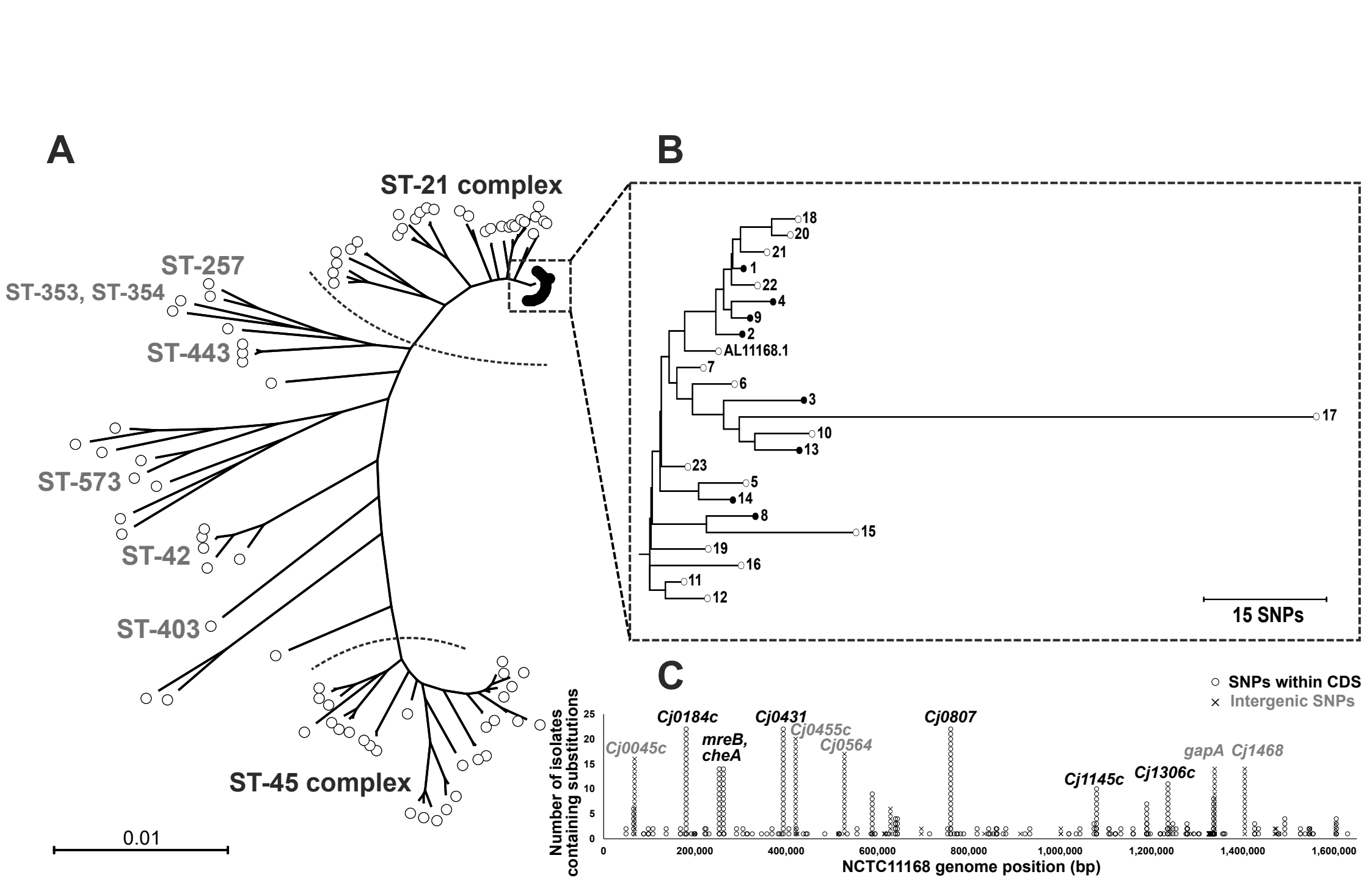
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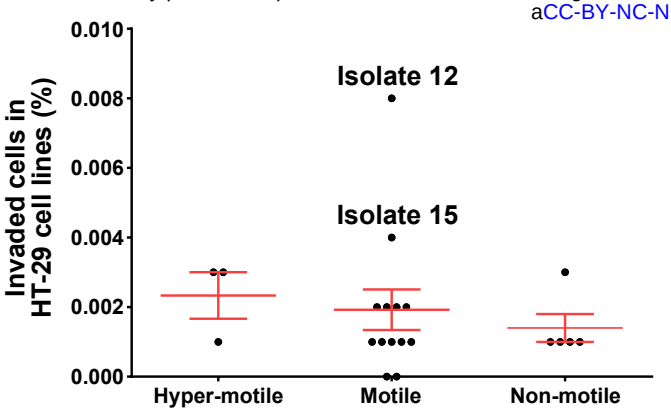

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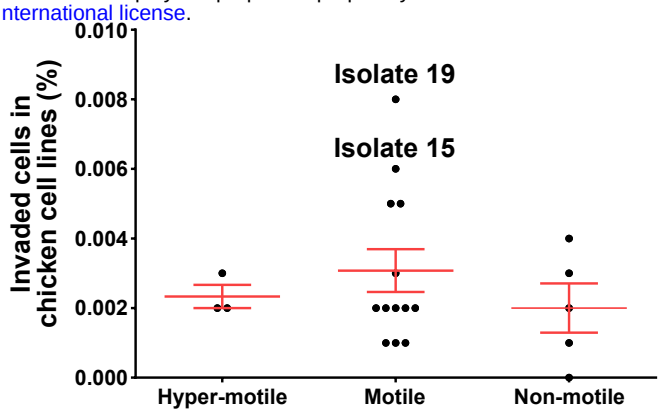

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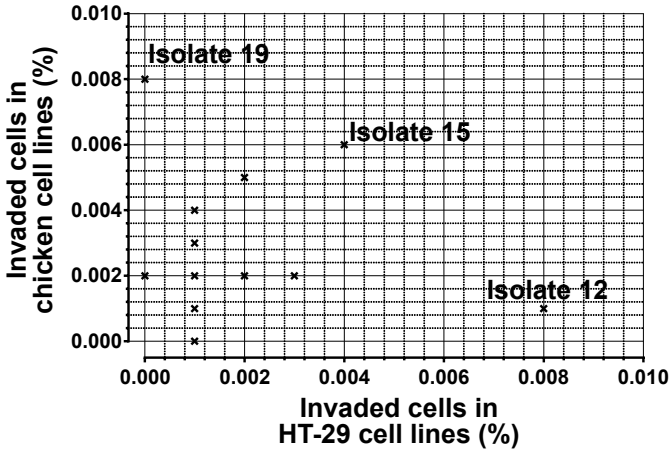

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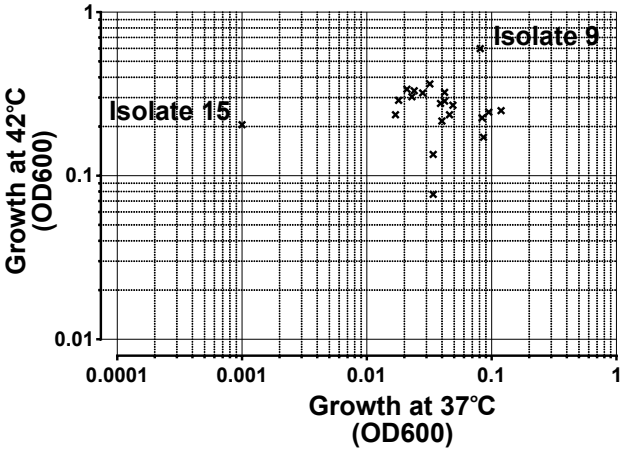

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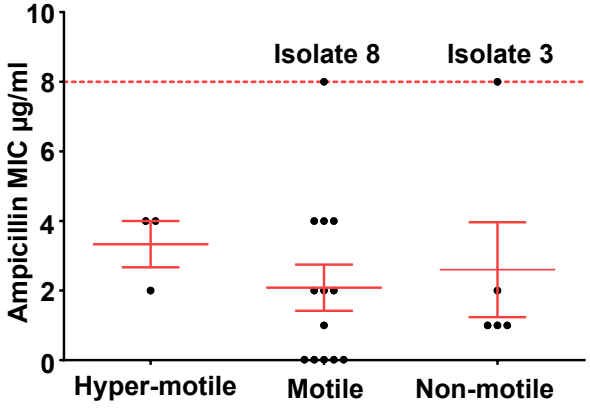

Isolate	ID	Source laboratory	Variant / comment	Aberrant phenotype*	Genome size (bp)	Total substitutions (Snippy)	Genes with substitutions (BIGS)	Number of recombination blocks (Gubbins)	Bases in recombination (Gubbins)
1	5920	Aberystwyth	Primary lab strain		1,626,801	8	5	0	0
2	5921	Aberdeen	Primary lab strain		1,626,067	11	6	0	0
3	5922	Bristol	Non-motile	✓	1,634,599	26	17	0	0
4	5923	Bristol	Hyper-motile	✓	1,626,519	22	15	0	0
5	5925	Glasgow	Hyper-motile	✓	1,625,874	11	7	0	0
6	5926	Glasgow	Original strain		1,625,293	9	9	0	0
7	5927	Glasgow	Sequenced variant		1,626,367	10	8	0	0
8	5928	Norwich	Primary lab strain		1,626,763	32	23	0	0
9	5929	Norwich	Hyper-motile	✓	1,625,378	15	11	0	0
10	5930	London	--		1,624,738	14	8	0	0
11	5931	London	Hyper-motile	✓	1,641,300	13	11	0	0
12	5932	Manchester	Hyper-motile	✓	1,628,343	12	9	0	0
13	5933	Swansea	Recently purchased		1,694,909	11	6	0	0
14	5934	Oxford	Primary lab strain		1,625,944	11	6	0	0
15	5935	Sheffield	Primary lab strain		1,625,814	59	44	0	0
16	5936	Sheffield	Hyper-motile	✓	1,626,210	18	16	0	0
17	5937	Sheffield	WT-2000		1,612,402	281	78	4	14,816
18	5938	Sheffield	WT-2010 (subcultured from WT-2000)		1,625,308	14	11	0	0
19	5939	London	Hyper-motile	✓	1,625,123	11	10	0	0
20	5940	London	[Genome previously sequenced]		1,625,478	--	--	--	--
21	5941	Surrey	Primary lab strain		1,625,755	15	9	0	0
22	5942	Surrey	--		1,624,913	17	11	0	0
23	5943	Edinburgh	--		1,626,490	12	9	0	0
Reference	AL11168.1	NCTC	Original sequenced isolate		1,641,481	--	--	0	0

***Aberrant phenotypes observed include diffrences in motility, growth and invasivness**

Isolate	ID	Source laboratory	Variant / comment	Aberrant phenotype	Observed motility	Maximum growth at 37°C (OD600)	Maximum growth at 42°C (OD600)	Invasion (HT-29 cell line)	Invasion (chicken cell line)	Ampicillin MIC (µg/ml)	blaOXA-61
1	5920	Aberystwyth	Primary lab strain		--	--	--	--	--	--	1
2	5921	Aberdeen	Primary lab strain		Non-motile	0.024	0.331	0.003	0.002	2	1
3	5922	Bristol	Non-motile	✓	Non-motile	0.032	0.364	0.001	0.001	8	1
4	5923	Bristol	Hyper-motile	✓	Motile	0.040	0.216	0.002	0.005	2	1
5	5925	Glasgow	Hyper-motile	✓	Motile	0.042	0.286	0.002	0.002	4	1
6	5926	Glasgow	Original strain		Motile	0.049	0.270	0.001	0.002	0.015	1
7	5927	Glasgow	Sequenced variant		Motile	0.039	0.277	0.002	0.002	2	1
8	5928	Norwich	Primary lab strain		Motile	0.017	0.236	0.001	0.001	8	1
9	5929	Norwich	Hyper-motile	✓	Motile	0.081	0.599	0.001	0.003	0.015	1
10	5930	London	--		Hyper-motile	0.021	0.338	0.003	0.002	4	1
11	5931	London	Hyper-motile	✓	Hyper-motile	0.034	0.135	0.003	0.002	2	1
12	5932	Manchester	Hyper-motile	✓	Motile	0.028	0.321	0.008	0.001	4	1
13	5933	Swansea	Recently purchased		Non-motile	0.119	0.250	0.001	0.003	1	1
14	5934	Oxford	Primary lab strain		Non-motile	0.042	0.323	0.001	0.004	1	1
15	5935	Sheffield	Primary lab strain		Motile	0.001	0.205	0.004	0.006	0.015	1
16	5936	Sheffield	Hyper-motile	✓	Motile	0.034	0.077	0.002	0.005	4	1
17	5937	Sheffield	WT-2000		Hyper-motile	0.023	0.304	0.001	0.003	4	1
18	5938	Sheffield	WT-2010 (subcultured from WT-2000)		Motile	0.018	0.289	0.000	0.002	0.015	1
19	5939	London	Hyper-motile	✓	Motile	0.086	0.172	0.000	0.008	1	1
20	5940	London	[Genome previously sequenced]		--	--	--	--	--	--	0
21	5941	Surrey	Primary lab strain		Non-motile	0.046	0.236	0.001	0.000	1	1
22	5942	Surrey	--		Motile	0.084	0.226	0.001	0.001	0.015	1
23	5943	Edinburgh	--		Motile	0.095	0.245	0.001	0.002	2	1
Reference	AL11168.1	NCTC	Original sequenced isolate		--	--	--	--	--	--	0

***Aberrant phenotypes observed include diffrences in motility, growth and invasivness**