Supplemental Table 1. Incidence rates per 100 000 person-years among Calgary residents with ST1193 blood stream infections

Sex	Age	2016		2018		*P*-value
		IR	95% CI	IR	95% CI	
Males	0-4 yr	2.3	[0.1-12.7]	2.5	[0.1-14.2]	1.00
	5-14 yr	0.0	[0.0-4.9]	0.0	[0.0-4.5]	1.00
	15-19 yr	0.0	[0.0-10.7]	0.0	[0.0-10.6]	1.00
	20-24 yr	0.0	[0.0-9.2]	0.0	[0.0-9.5]	1.00
	25-34 yr	0.9	[0.0-5.2]	0.0	[0.0-3.7]	1.00
	35-44 yr	0.0	[0.0-3.5]	0.9	[0.0-5.2]	1.00
	45-54 yr	2.3	[0.3-8.3]	1.2	[0.0-6.5]	1.00
	55-64 yr	7.2	[2.3-16.9]	9.4	[3.8-19.3]	0.77
	65-74 yr	15.8	[5.8-34.5]	15.4	[6.2-31.8]	1.00
	75+ yr	17.9	[4.9-45.7]	28.7	[11.5-59.2]	0.55
	Any	3.1	[1.8-4.8]	3.8	[2.4-5.6]	0.54
Females	0-4 yr	0.0	[0.0-8.8]	0.0	[0.0-10.0]	1.00
	5-14 yr	0.0	[0.0-5.2]	0.0	[0.0-4.8]	1.00
	15-19 yr	0.0	[0.0-11.4]	0.0	[0.0-11.5]	1.00
	20-24 yr	0.0	[0.0-9.9]	0.0	[0.0-10.2]	1.00
	25-34 yr	0.0	[0.0-3.5]	2.0	[0.2-7.2]	0.24
	35-44 yr	0.0	[0.0-3.6]	0.9	[0.0-5.2]	1.00
	45-54 yr	1.2	[0.0-6.6]	0.0	[0.0-4.4]	1.00
	55-64 yr	2.9	[0.4-10.5]	2.6	[0.3-9.5]	1.00
	65-74 yr	2.5	[0.1-13.8]	4.1	[0.5-14.6]	1.00
	75+ yr	9.8	[2.0-28.5]	37.8	[19.6-66.1]	**0.03**
	Any	1.1	[0.5-2.4]	3.0	[1.8-4.7]	**0.03**
Overall	0-4 yr	1.2	[0.0-6.5]	1.3	[0.0-7.3]	1.00
	5-14 yr	0.0	[0.0-2.5]	0.0	[0.0-2.3]	1.00
	15-19 yr	0.0	[0.0-5.5]	0.0	[0.0-5.5]	1.00
	20-24 yr	0.0	[0.0-4.8]	0.0	[0.0-4.9]	1.00
	25-34 yr	0.5	[0.0-2.6]	1.0	[0.1-3.6]	0.61

35-44 yr	0.0	[0.0-1.8]	0.9	[0.1-3.4]	0.50
45-54 yr	1.8	[0.4-5.1]	0.6	[0.0-3.3]	0.62
55-64 yr	5.1	[2.0-10.5]	6.0	[2.7-11.3]	0.81
65-74 yr	8.9	[3.6-18.4]	9.5	[4.3-18.0]	1.00
75+ yr	13.2	[5.3-27.2]	33.9	[20.4-52.9]	**0.03**
Any	1.0	[0.7-1.5]	1.7	[1.3-2.3]	**0.05**
LTC residents	10.1	[0.3-56.2]	93.5	[44.8-171.9]	**0.01**

LTC; long term care residents that includes those from nursing homes and special care facilities.

Supplemental Table 2. Genomic analysis of ST1193 isolates causing blood stream infections in Calgary (2016 and 2018).

	Isolates
	n=67[#] (%)
Serotype:	
O75:H5	67 (100%)
fimH:	
64	67 (100%)
K capsular types:	
K1	64 (96%)
K5	3 (4%)
QRDR mutations:	
gyrA S83L	66 (98%)
gyrA D87N	66 (98%)
parC S80I	67 (100%)
parE L416F	64 (96%)
B-lactamases:	
CTX-M-15	7 (10%)
CTX-M-14	1 (1%)
CTX-M-27	6 (9%)
CTX-M-55	3 (4%)
OXA-1	3 (4%)
TEM-1	48 (72%)
CMY-42	3 (4%)
CMY-2	2 (3%)
Aminoglycoside modifying enzymes:	
aac(3)-IIa	3 (4%)
aac(3)-IId	15 (22%)
aac(6')-Ib-cr	3 (4%)
aadA1	1 (1%)
aadA2	1 (1%)

aadA5	15 (22%)
aph(3'')-Ib	41 (61%)
aph(6)-Id	41 (61%)
Others AMR determinants:	
mcr-1.2	1 (1%)
mph(A)	27 (42%)
erm(B)	3 (4%)
dfrA8	1 (1%)
dfrA12	1 (1%)
dfrA17	38 (57%)
sul1	20 (30%)
sul2	41 (61%)
tetA	14 (21%)
tetB	14 (21%)
Plasmid types:	
Col (B512)	62 (93%)
Col (MP18)	3 (4%)
Col156	20 (30%)
ColpVC	9 (13%)
FIA	56 (84%)
FIB	63 (94%)
FII	5 (7%)
IncI1	14 (21%)
IncX4	2 (3%)
IncB/O/K/Z	5 (7%)
pMLST plasmid types*:	
F-:A-: B1	1 (1%)
F-:A-: B10	2 (3%)
F-:A-: B20	2 (3%)
F-:A1: B-	1 (1%)
F-:A1: B1	8 (12%)

F-:A1: B10	41 (61%)
F-:A1: B20	5 (7%)
F-:A1: B49	1 (1%)
F2:A-: B10	1 (1%)
F29:A1: B10	1 (1%)
F35: A1: B10	1 (1%)
F95: A1: B10	1 (1%)
Virulence genes	

QRDRs; quinolone resistance-determining regions, AMR; antimicrobial resistance determinants

*Two isolates were negative with pMLST.

#One ST1193 isolate had less than 20 times coverage and were excluded from genomic analysis. One isolate was a double locus variant of ST1193 (i.e., ST11316), contained *fimH*27, was positive for *bla*$_{\text{TEM-1,}}$ and *sul1,* tested negative for *parC, gyrA* and *parE* mutations.

Supplementary Data

Genomic analysis

The Nextera XT DNA sample preparation kit (Illumina, San Diego, CA, USA) was used to prepare libraries for sequencing. Samples were multiplexed and sequenced on an Illumina NextSeq500 for 300 cycles (151 bp paired end).

Draft genomes were obtained using SPAdes [1]. To define the presence of genes and mutations, BLAST [2] in combination with following databases or typing schemes were accessed: NCBI Bacterial Antimicrobial Resistance Reference Gene Database (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA313047), ResFinder[3], PlasmidFinder[4], MLST[5], and virulence finder[6].

A recombination-free, core SNP-based phylogenetic tree was computed after alignment against E. coli MCJCHV-1 ST11937 using the RedDog pipeline [7]. https://github.com/katholt/RedDog Recombination sites identified with Gubbins[8], and prophages with PHASTER[9], were removed. Core SNPs and sites that were present in all genomes, were included to create a maximum-likelihood tree using RAxML with the GTR GAMMA substitution model.[10] The tree was visualized using iTOL v5[11].

A phylogeny-free population genetics approach of core SNPs and hierarchal clustering analysis with the BAPS program (Bayesian Analysis of Population Structure), were used to identify clades within ST1193.[12] The hierarchal BAPS clustering analysis[12] was conducted with 3 nested levels with *a priori* upper bound of the number of clusters between one fourth to one half of the total number of isolates. We defined clades using the second level of clustering.

Statistical analysis

Denominator data were retrieved from the 2016 and 2018 City of Calgary Civic Census. As the 2018 Census does not stratify the population according to age and gender, it was assumed that the age-gender distribution of 2018 was identical to one observed in 2019. For spatial analysis, postal codes were mapped to the Calgary region defined according to the City of Calgary Census by Community. Non-residential areas were excluded from the analysis. Global Moran tests were used to infer presence of spatial autocorrelation of ST1193 blood stream infections using aggregated data. Spatial Poisson models were subsequently used to estimate associations between number of long-term care facilities in a community and ST1193 blood stream infections. The 95% credible intervals were used for inference, as described [13]. Analyses were carried out in R version 3.4.2 [14] using the *sf*, *tmap* and R2BayesX packages [15-17]. Projection 3776 was used for plots. For all analyses, statistical significance was set at 5% level.

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