



What can knowing something about the evolution of *Clostridium difficile* teach you about infection prevention and control?

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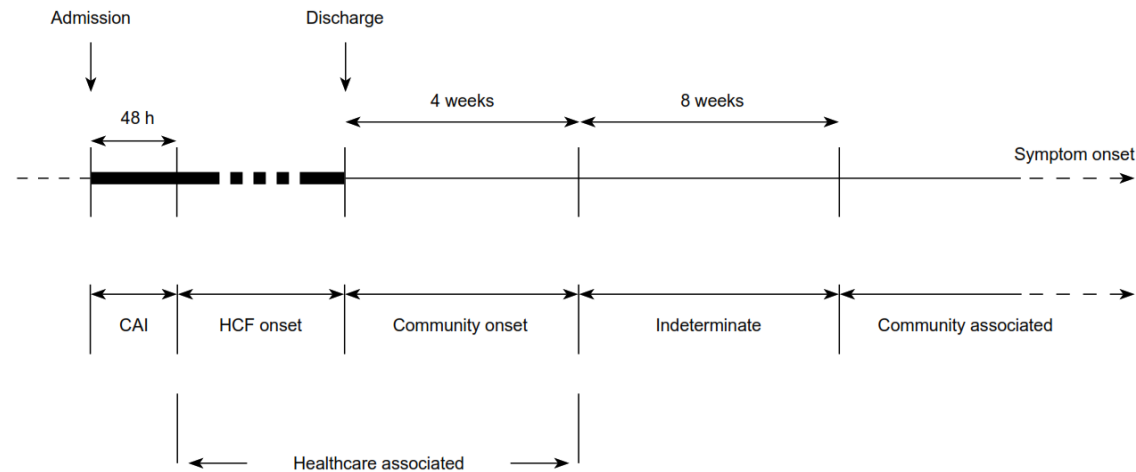
October 15, 2025

Outline

- Definitions
- History
- Animal reservoirs
- Environmental sources
- One Health

Community-associated vs community-acquired

Adapted with permission from McDonald LC, Coignard B, Dubberke E, et al. Recommendations for surveillance of *Clostridium difficile*-associated disease. *Infect Control Hosp Epidemiol* 2007;28:140–45.



CAI, community-associated infection; HCF, healthcare facility

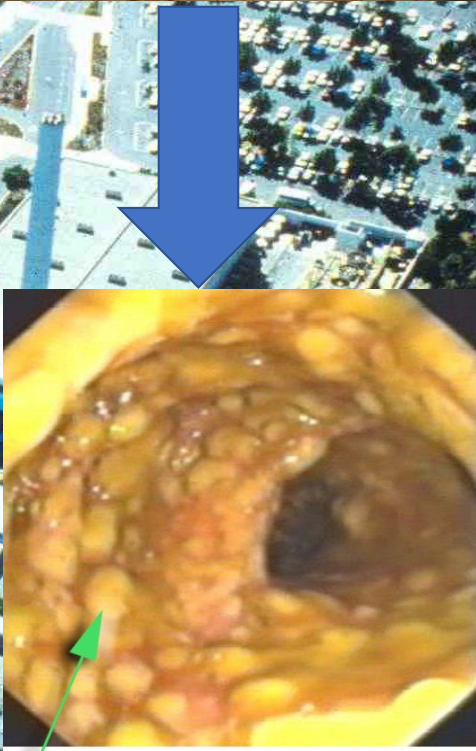
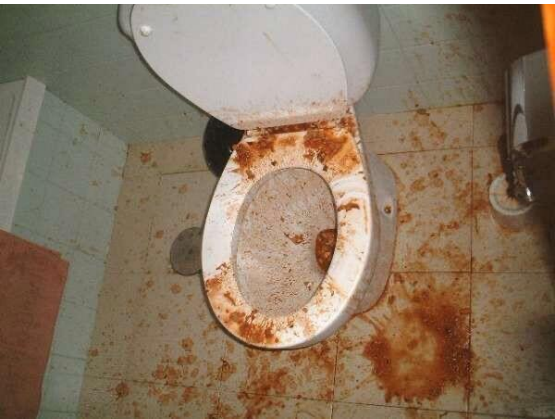
Source vs reservoir

The reservoir of an organism is the site where it resides, metabolizes and multiplies. The source of the organism is the site from which it is transmitted to a susceptible host, either directly or indirectly through an intermediary object.

The reservoir may or may not be the source from which an agent is transferred to a host. (Brachman P, *Medical Microbiology* Ed. S Baron 1996)



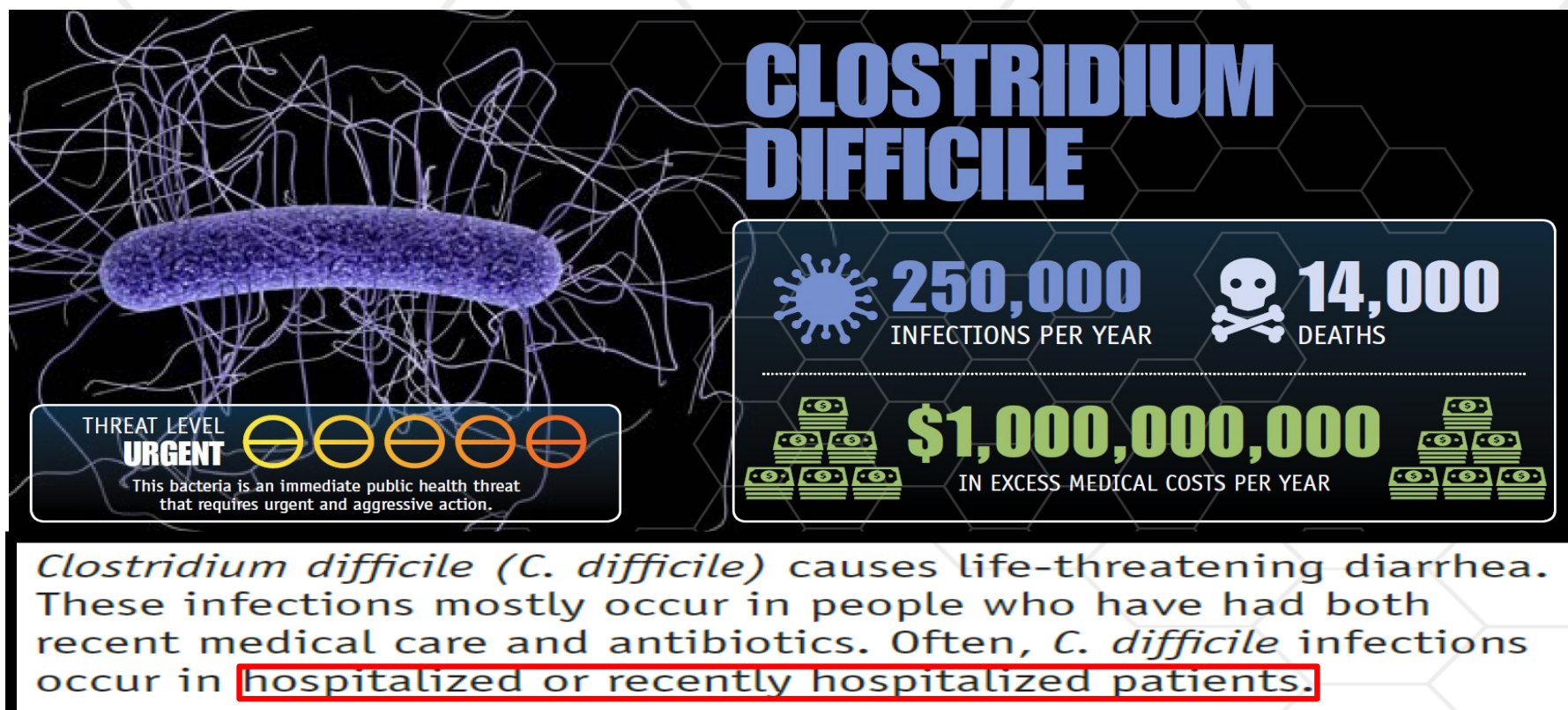
Antimicrobials



Urgent Threats

CDC, Dec 2013

- *Clostridium difficile*
- Carbapenem-resistant Enterobacteriaceae (CRE)
- Drug-resistant *Neisseria gonorrhoeae*



2019 CDC Report



Urgent Threats

These germs are public health threats that require urgent and aggressive action:



CARBAPENEM-RESISTANT
ACINETOBACTER



CANDIDA AURIS



CLOSTRIDIoidES DIFFICILE



CARBAPENEM-RESISTANT
ENTEROBACTERIACEAE



DRUG-RESISTANT
NEISSERIA GONORRHOEAE

CLOSTRIDIoidES DIFFICILE

THREAT LEVEL URGENT



223,900
Estimated cases
in hospitalized
patients in 2017



12,800
Estimated
deaths in 2017



\$1B
Estimated attributable
healthcare costs in 2017

Clostridioides difficile (*C. difficile*) bacteria can cause life-threatening diarrhea. Infections occur most often in people who have taken antibiotics for other conditions. It is the most common healthcare-associated infection.

WHAT YOU NEED TO KNOW

- While healthcare-associated *C. difficile* cases are decreasing, community-associated cases are not.
- Strategies to reduce *C. difficile* infections include improving antibiotic use, infection control, and healthcare facility cleaning and disinfection.
- *C. difficile* infections are more common and tend to be more severe in older patients.

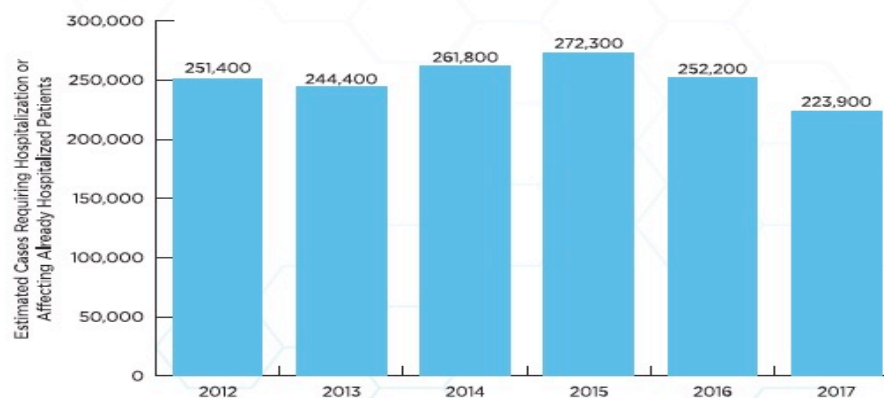
Previously *Clostridium difficile*. Also called *C. diff*. Cost includes hospital-onset cases only.



U.S. Department of
Health and Human Services
Centers for Disease
Control and Prevention

CASES OVER TIME

Continued appropriate infection control, antibiotic use, and diagnostic testing are important to maintain decreases in *C. difficile* cases.



Clostridium difficile (also named *Clostridioides difficile* (Lawson et al., 2016))

- An ancient genus, hundreds of millions of years old - anaerobic
- The population structure of *C. difficile* consists of at least 8 clades, each of which includes toxigenic strains (Griffiths et al. 2010; Dingle et al. 2011; Stabler et al. 2012).
- Genes for toxins A & B are contained on a 19.6-kB Pathogenicity Locus (PaLoc), absent in non-toxigenic strains
- When present, the PaLoc is always found at the same chromosomal location (Braun et al. 1996; Dingle et al. 2011) and it is tempting to conclude that the PaLoc was stably integrated before the clades diverged – but evidence says otherwise.
- However, nontoxigenic strains are present throughout the *C. difficile* population, occasionally sharing the same multilocus sequence type (ST) as toxigenic strains (Dingle et al. 2011).
- This irregular distribution resembles that of an MGE and some evidence of a phage.



Pangaea was the super-continent that existed during the late Paleozoic roughly 300 million years ago. It was surrounded by a super-ocean called Panthalassa.

CONTINENTAL DRIFT OF PLATES



225 Million Years Ago



150 Million Years Ago



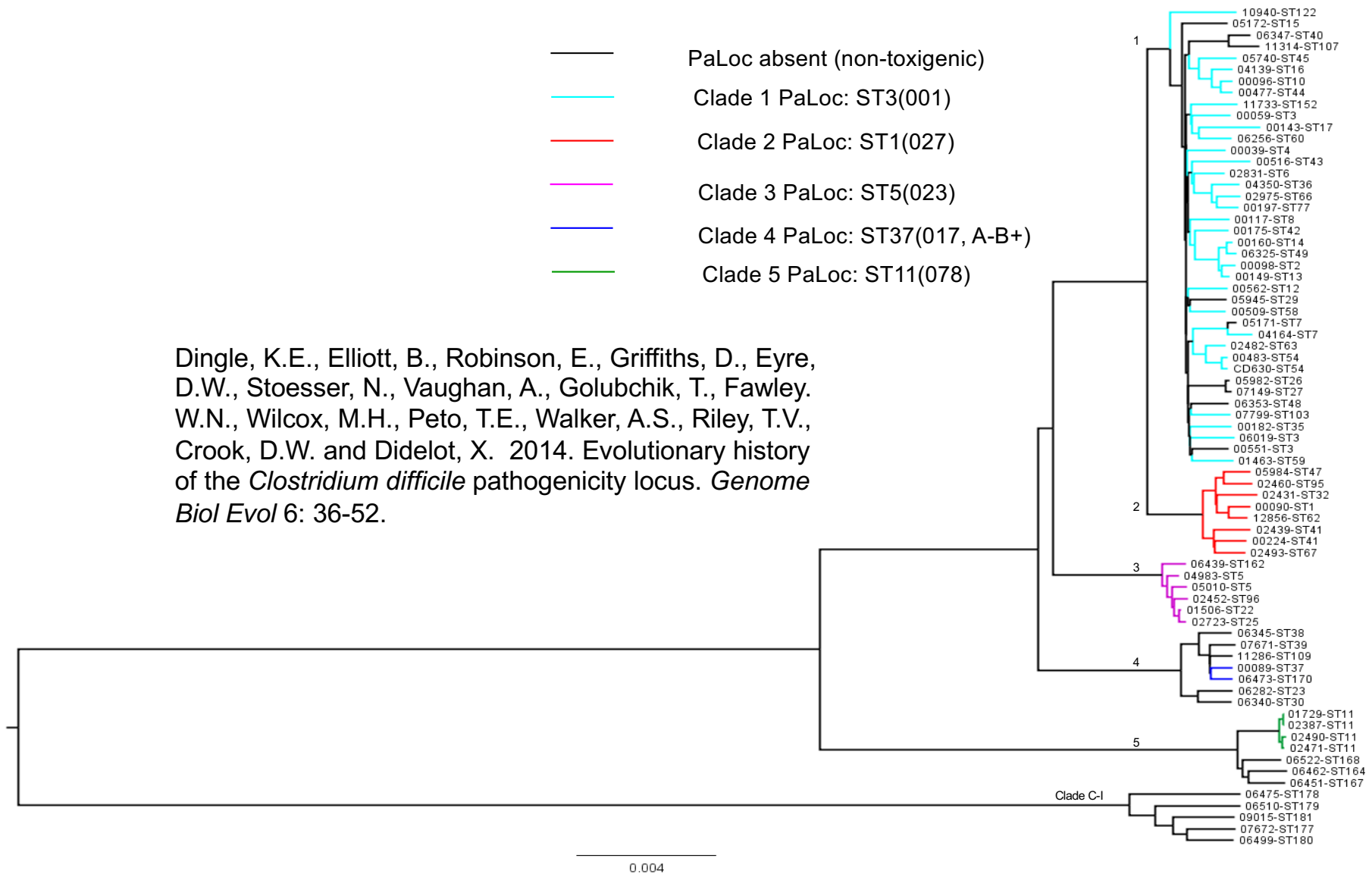
100 Million Years Ago



Earth Today

Dingle, K.E., Elliott, B., Robinson, E., Griffiths, D., Eyre, D.W., Stoesser, N., Vaughan, A., Golubchik, T., Fawley, W.N., Wilcox, M.H., Peto, T.E., Walker, A.S., Riley, T.V., Crook, D.W. and Didelot, X. 2014. Evolutionary history of the *Clostridium difficile* pathogenicity locus. *Genome Biol Evol* 6: 36-52.

- PaLoc absent (non-toxicogenic)
- Clade 1 PaLoc: ST3(001)
- Clade 2 PaLoc: ST1(027)
- Clade 3 PaLoc: ST5(023)
- Clade 4 PaLoc: ST37(017, A-B+)
- Clade 5 PaLoc: ST11(078)



Dan Knight



ST3 (C1) vs. all clades (FastANI)

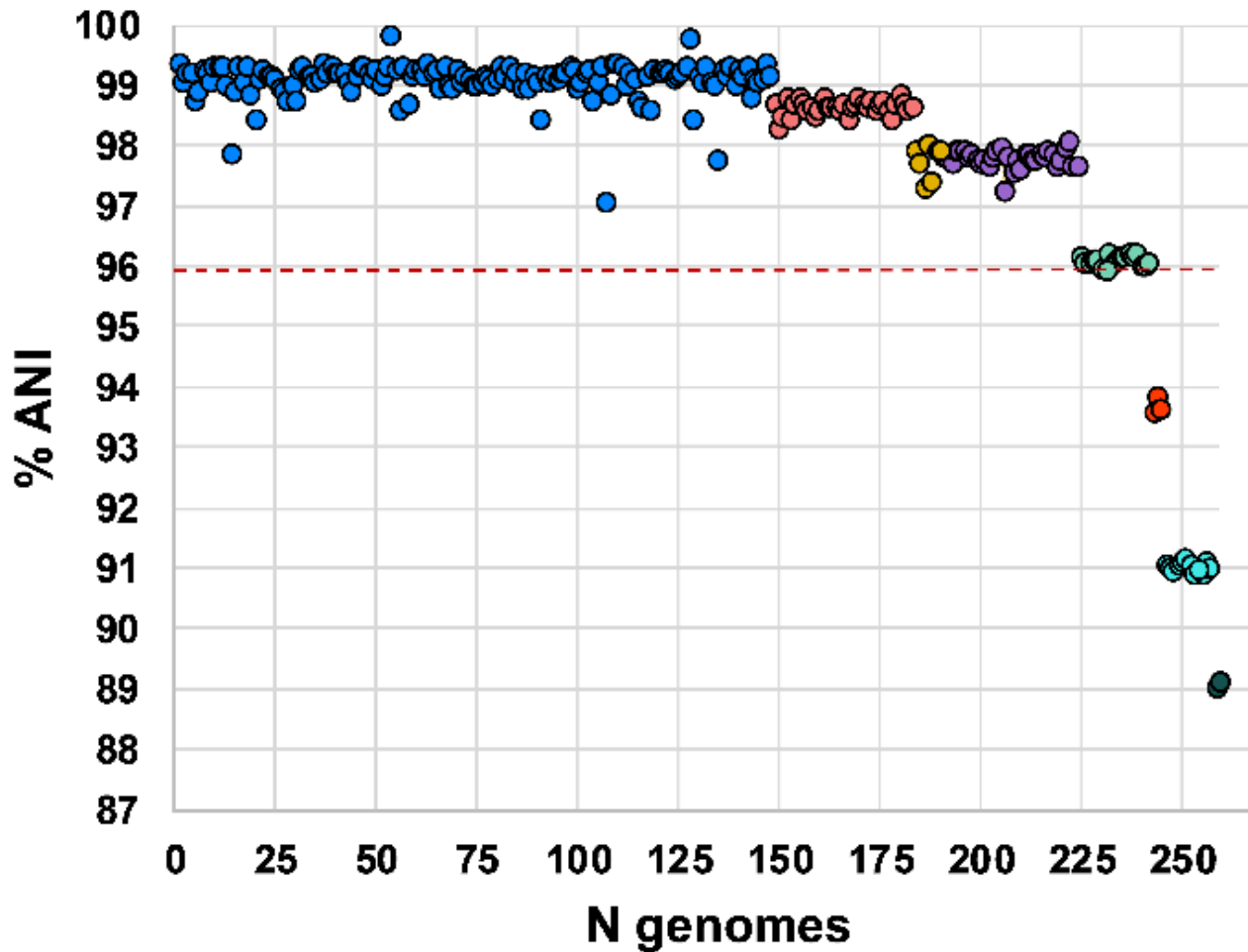


Figure 3. Species-wide average nucleotide identity (ANI) analysis.

Knight et al. eLife 2021;10:e64325.
DOI: <https://doi.org/10.7554/eLife.64325>

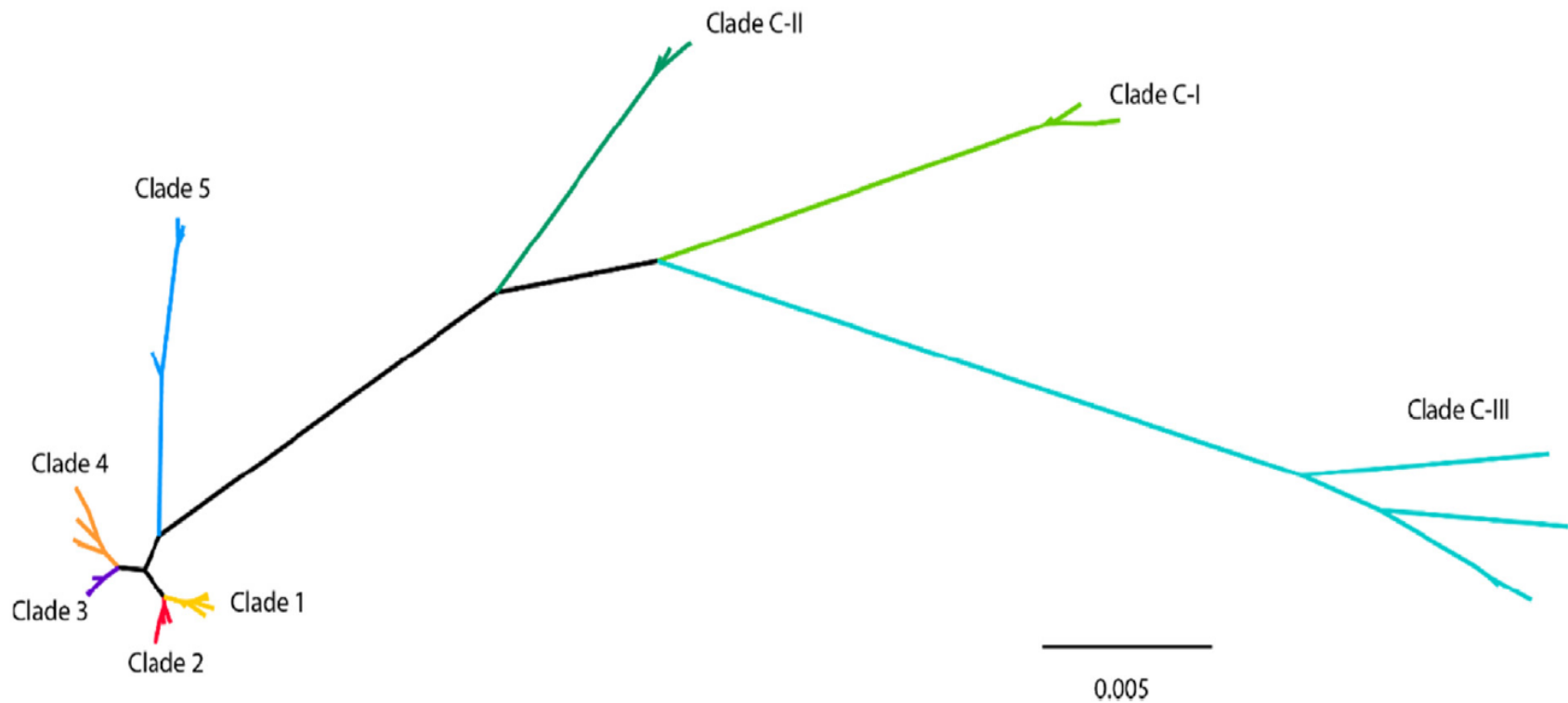
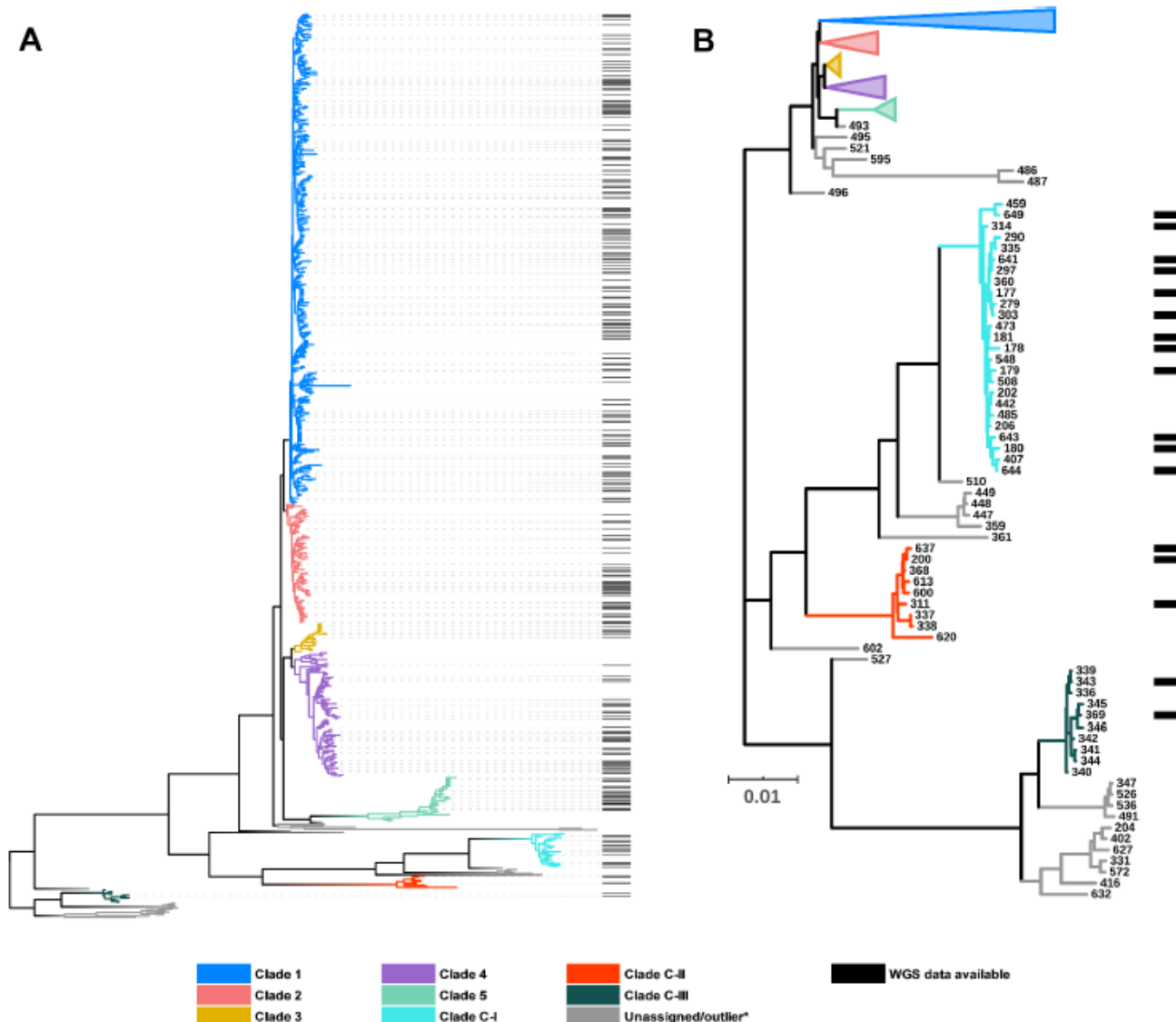


Fig. 2. Maximum likelihood tree generated using MLST data from all known clades present in the PubMLST database. The evolutionary history was inferred by using the Maximum Likelihood method based on the Tamura-Nei model. The tree with the highest log likelihood (-8568.3698) is shown. Initial tree(s) for the heuristic search were obtained by applying the Neighbor-Joining method to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Evolutionary analyses were conducted in MEGA6 (Tamura et al., 2013).

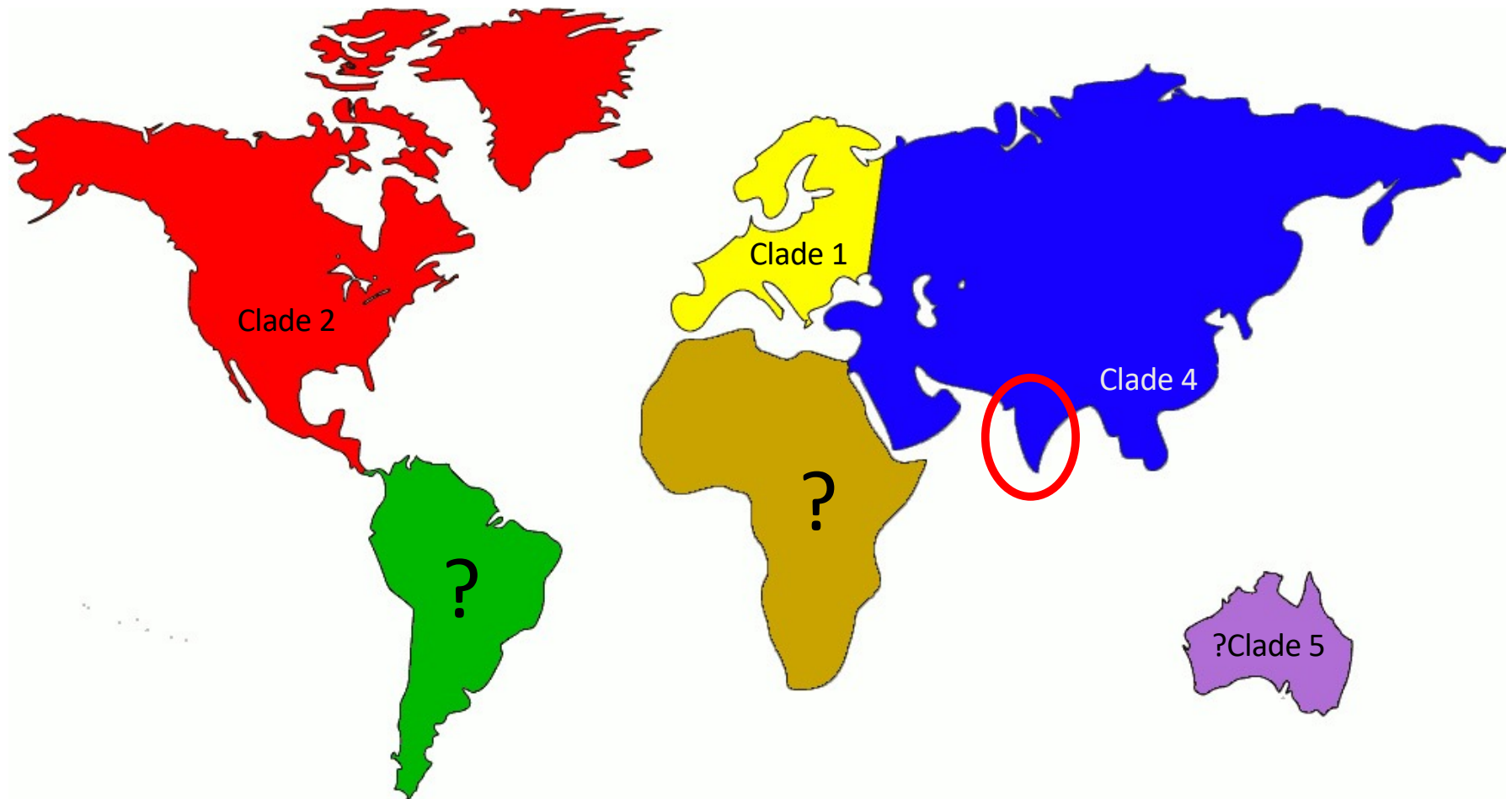


Taxonomic placement of cryptic clades predates *C. difficile* emergence by millions of years

Previous studies using BEAST have estimated the common ancestor of C1–5 existed between 1 to 85 or 12 to 14 million years ago (mya) (He et al., 2010; Kumar et al., 2019). Here, we used an alternative Bayesian approach, BactDating (Xavier Didalot), to estimate the age of all eight *C. difficile* clades currently described. The last common ancestor for *C. difficile* clades C1–5 was estimated to have existed between 1.11 and 6.71 mya. In contrast, all three cryptic clades were estimated to have emerged millions of years prior to the common ancestor of C1–5.

Knight et al. eLife 2021;10:e64325.
DOI: <https://doi.org/10.7554/eLife.64325>

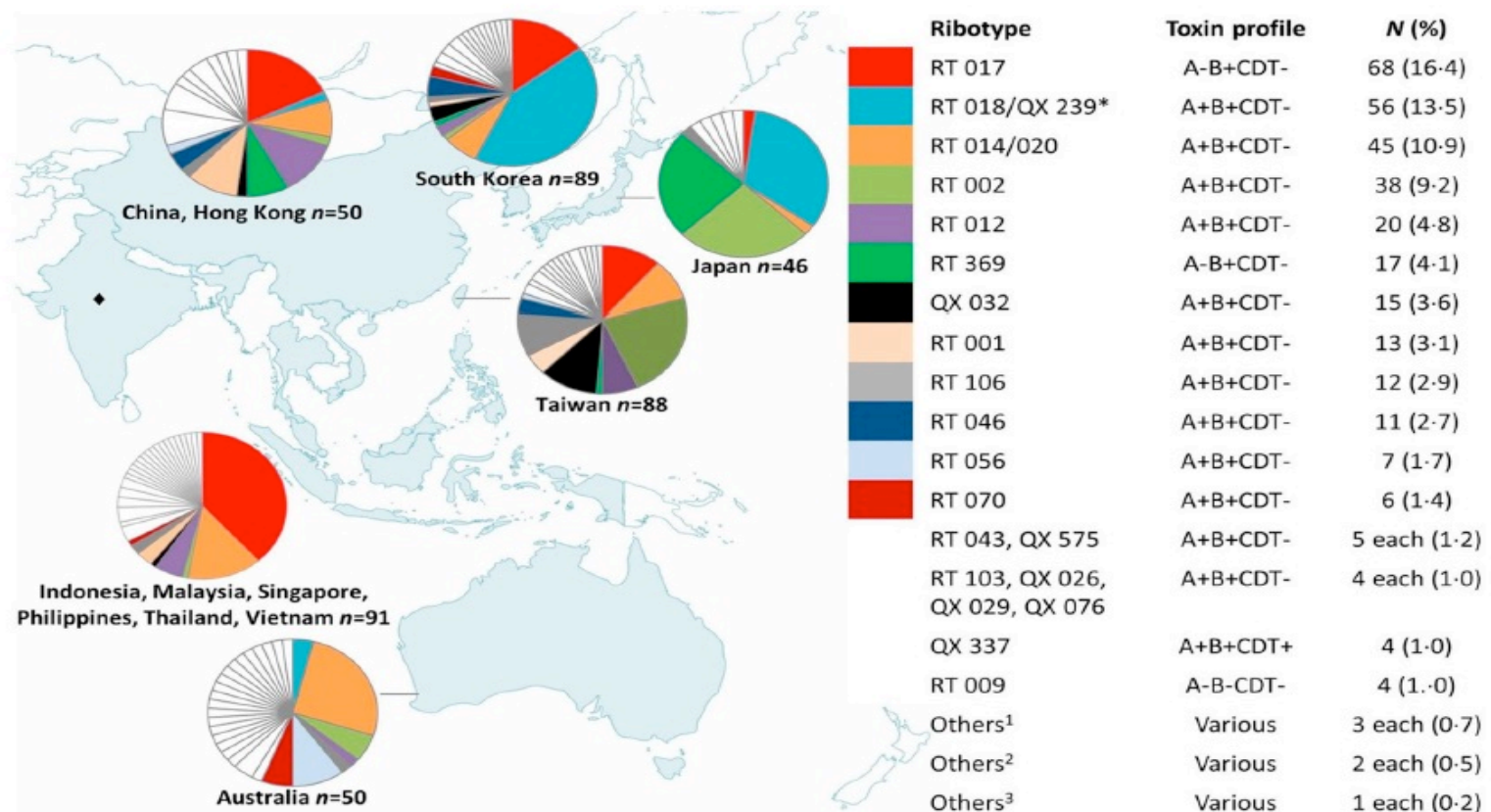
Phylogeographical tropism of *C. difficile*





Clostridioides difficile infection in the Asia-Pacific region

Deirdre A. Collins^{1b a}, Kyung Mok Sohn^{2b}, Yuan Wu^{3c}, Kentaro Ouchi^{1b d}, Yoshikazu Ishii^{4e,f}, Briony Elliott^{5a}, Thomas V. Riley^{1b a,g}, Kazuhiro Tateda^{4e,f,h} and for the *Clostridioides difficile* Asia-Pacific Study Group*



Emergence and global spread of epidemic healthcare-associated *Clostridium difficile*

Miao He¹, Fabio Miyajima^{2,3}, Paul Roberts^{2,3}, Louise Ellison¹, Derek J Pickard¹, Melissa J Martin⁴, Thomas R Connor¹, Simon R Harris¹, Derek Fairley⁵, Kathleen B Bamford^{6,7}, Stephanie D'Arc^{6,7}, Jon Brazier⁸, Derek Brown⁹, John E Coia⁹, Gill Douce⁹, Dale Gerding¹⁰, Hee Jung Kim¹¹, Tse Hsien Koh¹², Haru Kato¹³, Mitsutoshi Senoh¹³, Tom Louie¹⁴, Stephen Michell¹⁵, Emma Butt¹⁵, Sharon J Peacock^{1,16–18}, Nick M Brown^{17,18}, Tom Riley¹⁹, Glen Songer²⁰, Mark Wilcox²¹, Munir Pirmohamed^{2,3}, Ed Kuijper²², Peter Hawkey²³, Brendan W Wren⁴, Gordon Dougan¹, Julian Parkhill¹ & Trevor D Lawley¹

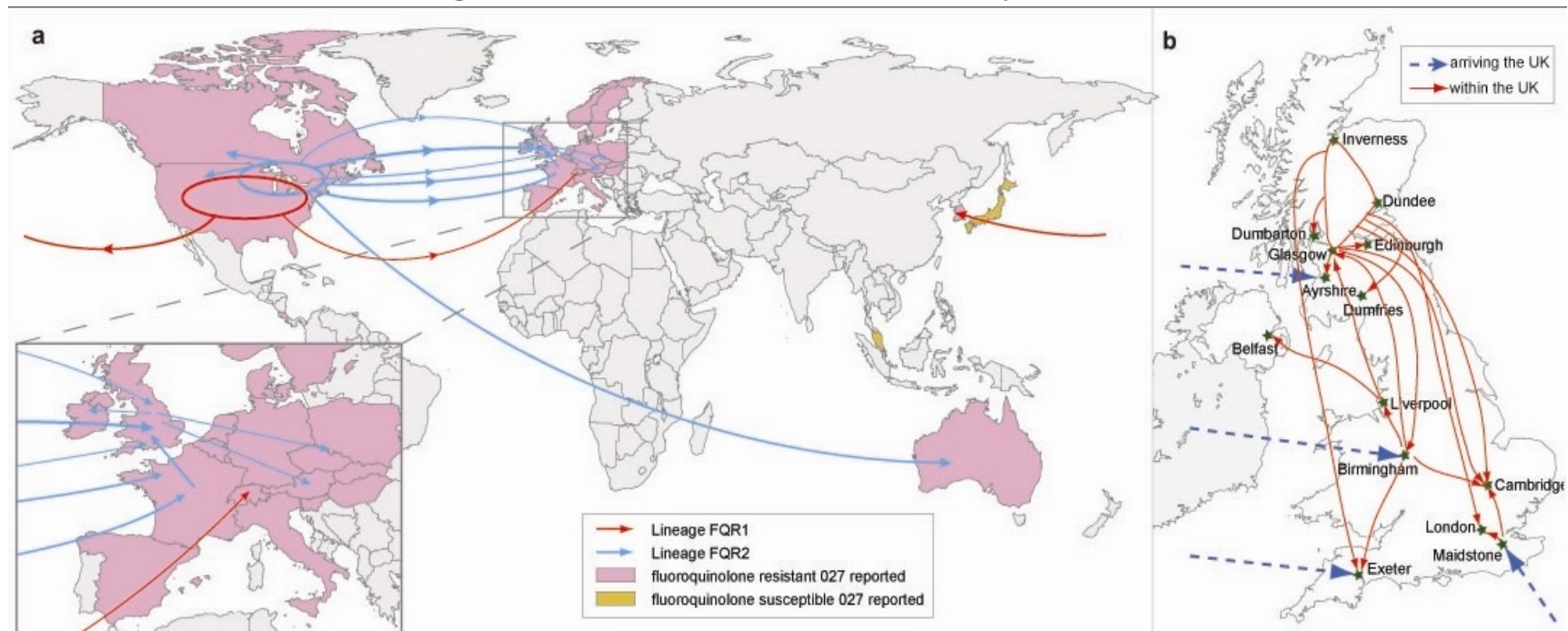


Figure 5: PCR types of *C. difficile* in hospital patients in England and Wales: referrals to ARL 1995- 2003

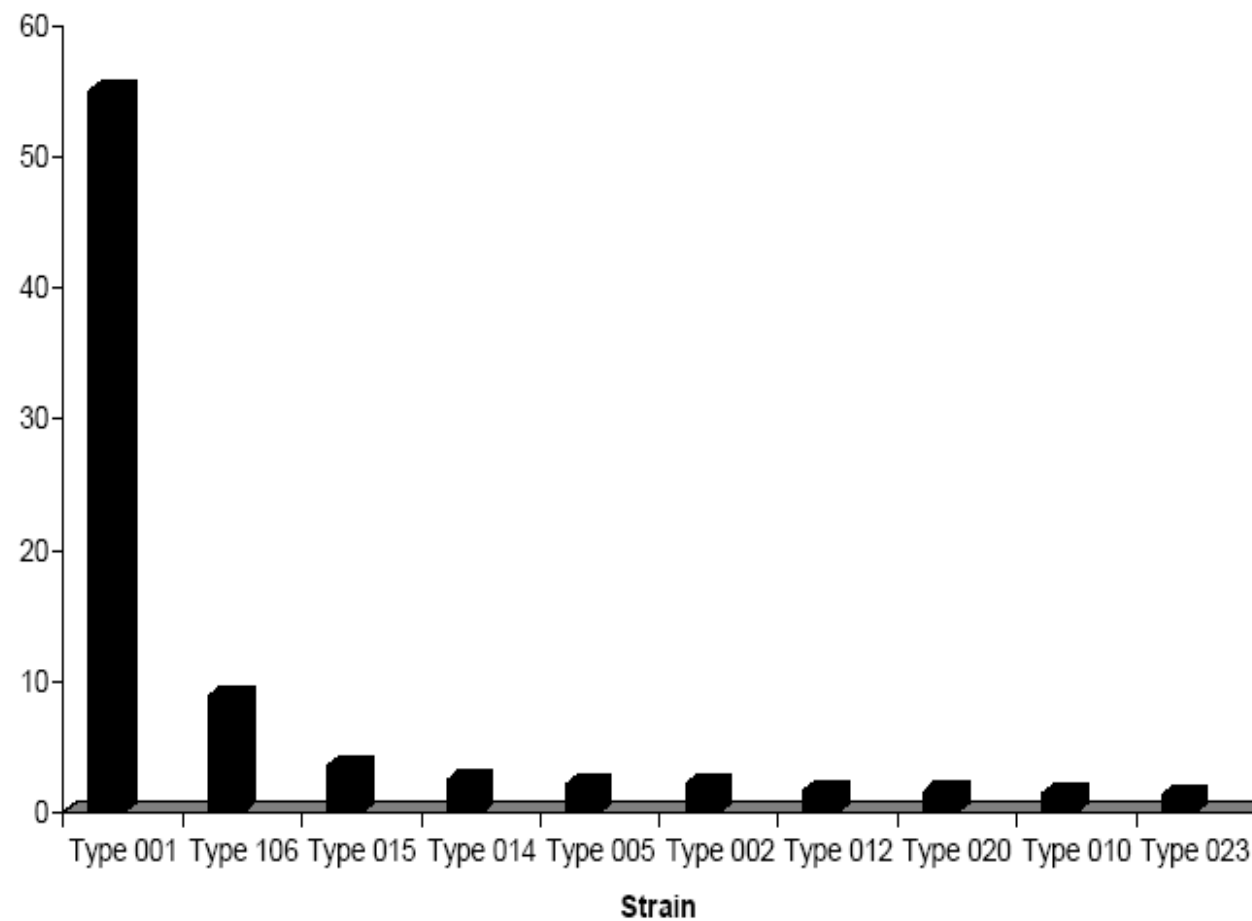
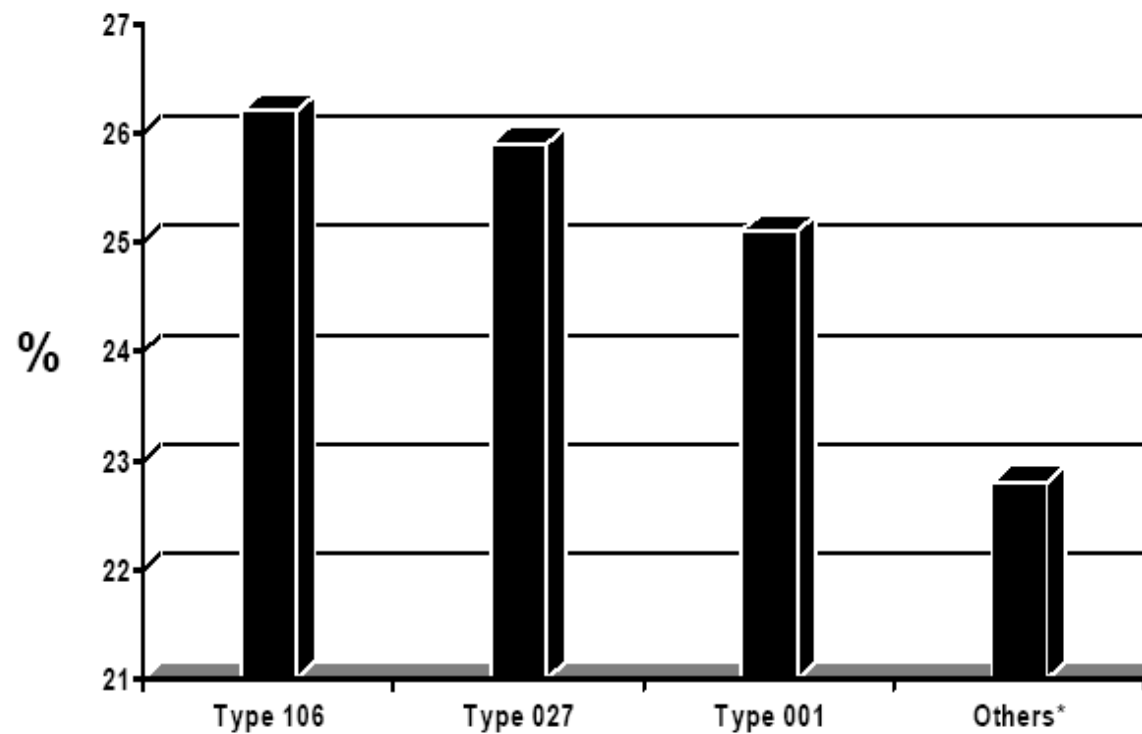


Figure 4: PCR types of *C. difficile* in hospital patients in England January-December 2005: samples from the random sampling surveillance scheme (n=881)



* 200 isolates consisting of 22 different PCR ribotypes

Table 1

Notable types within the phylogenetic clades.

Clade	Notable types
1	UK 014 (ST-2), ^a UK 020 (ST-14) ^a , UK 002 (ST-8), ^a UK 015 (ST-44), ^a UK 018 (ST-17) ^a
2	UK 027 (ST-1), ^b UK 244 (ST-41), ^b UK 176 (ST-1), ^b UK 251 (ST-231) ^b
3	UK 023 (ST-5) ^b
4	UK 017 (ST-37) ^c , UK 047 (ST-37) ^c
5	UK 078 (ST-11), ^b UK 126 (ST-11), ^b UK 033 (ST-11), ^d UK 237 (ST-167) ^e
C-I	ST-181, ^e ST-206 ^e
C-II	ST-200, ^{c,g}
C-III	Unknown ^f

NB: Where ribotypes are associated with multiple sequence types, the most common sequence types is given (Dingle et al., 2011; Stabler et al., 2012).

^a Toxin profile: A + B + CDT −.

^b Toxin profile: A + B + CDT +.

^c Toxin profile: A − B + CDT −.

^d Toxin profile: A − B − CDT +.

^e Toxin profile: A − B + CDT +.

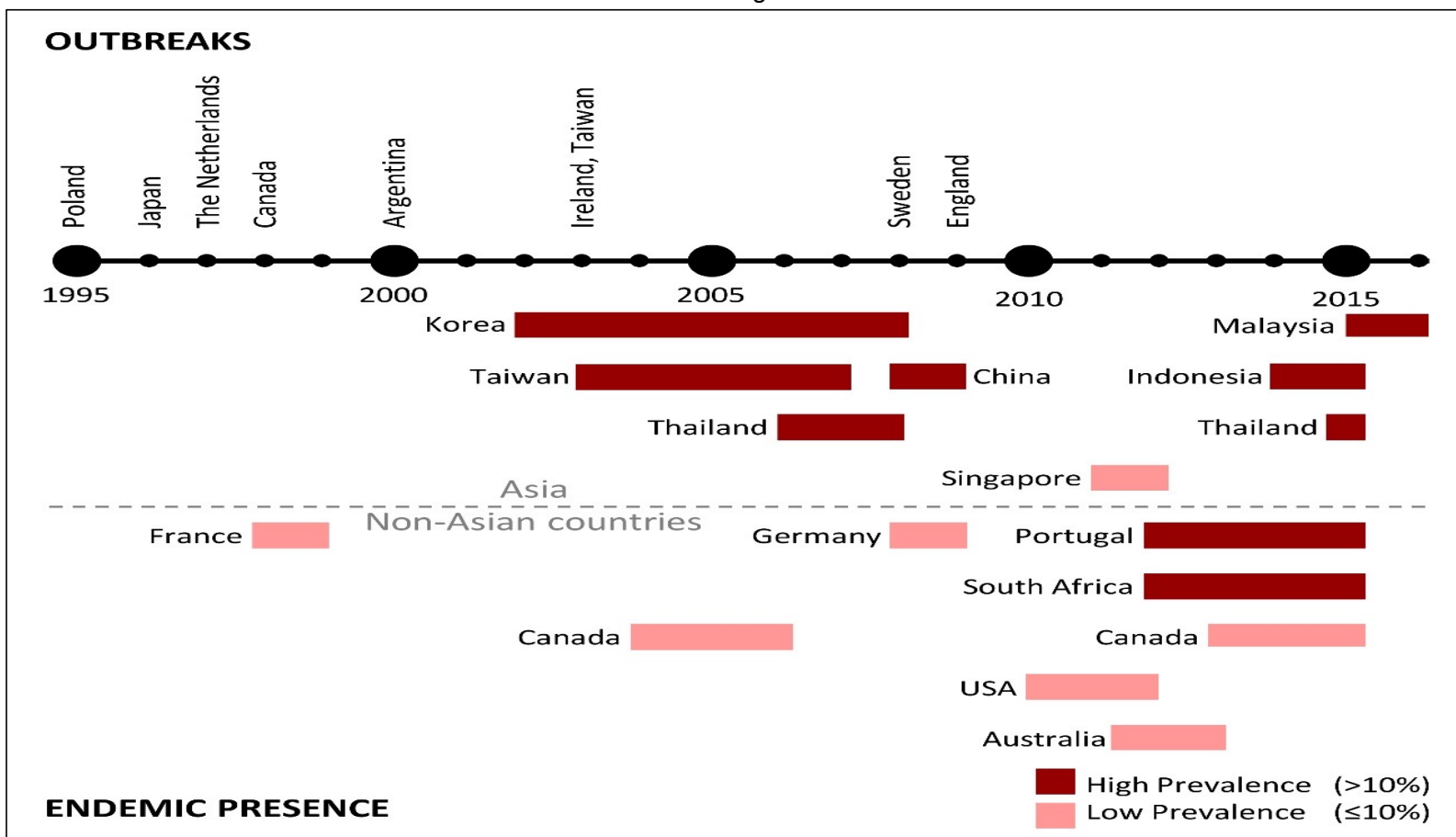
^f Very little is known about the three cryptic clades. Although some do contain unusual toxigenic strains, the majority are apparently non-toxigenic.

^g Toxin profile: A + B − CDT − (unusual monotoxin locus).

Comparative Genome Analysis and Global Phylogeny of the Toxin Variant *Clostridium difficile* PCR Ribotype 017 Reveals the Evolution of Two Independent Sublineages

M. D. Cairns,^{a,b,c} M. D. Preston,^d C. L. Hall,^a D. N. Gerding,^{e,s} P. M. Hawkey,^{f,g}
H. Kato,^h H. Kim,ⁱ E. J. Kuijper,^j T. D. Lawley,^k H. Pituch,^l S. Reid,^m B. Kullin,^m
T. V. Riley,ⁿ K. Solomon,^{o,p} P. J. Tsai,^{q,t} J. S. Weese,^r  R. A. Stabler,^a B. W. Wren^a

“Phylogeographic analyses show a North American origin for RT017, as has been found for the recently emerged epidemic RT027 lineage.”



Timeline of *C. difficile* RT 017 reports around the world. Outbreaks refer to an increase in the regional prevalence of RT 017, which is confirmed either to be clonal or with evidence suggesting that isolates came from the same source. Endemic presence refers to prevalence reports that were not associated with outbreaks.

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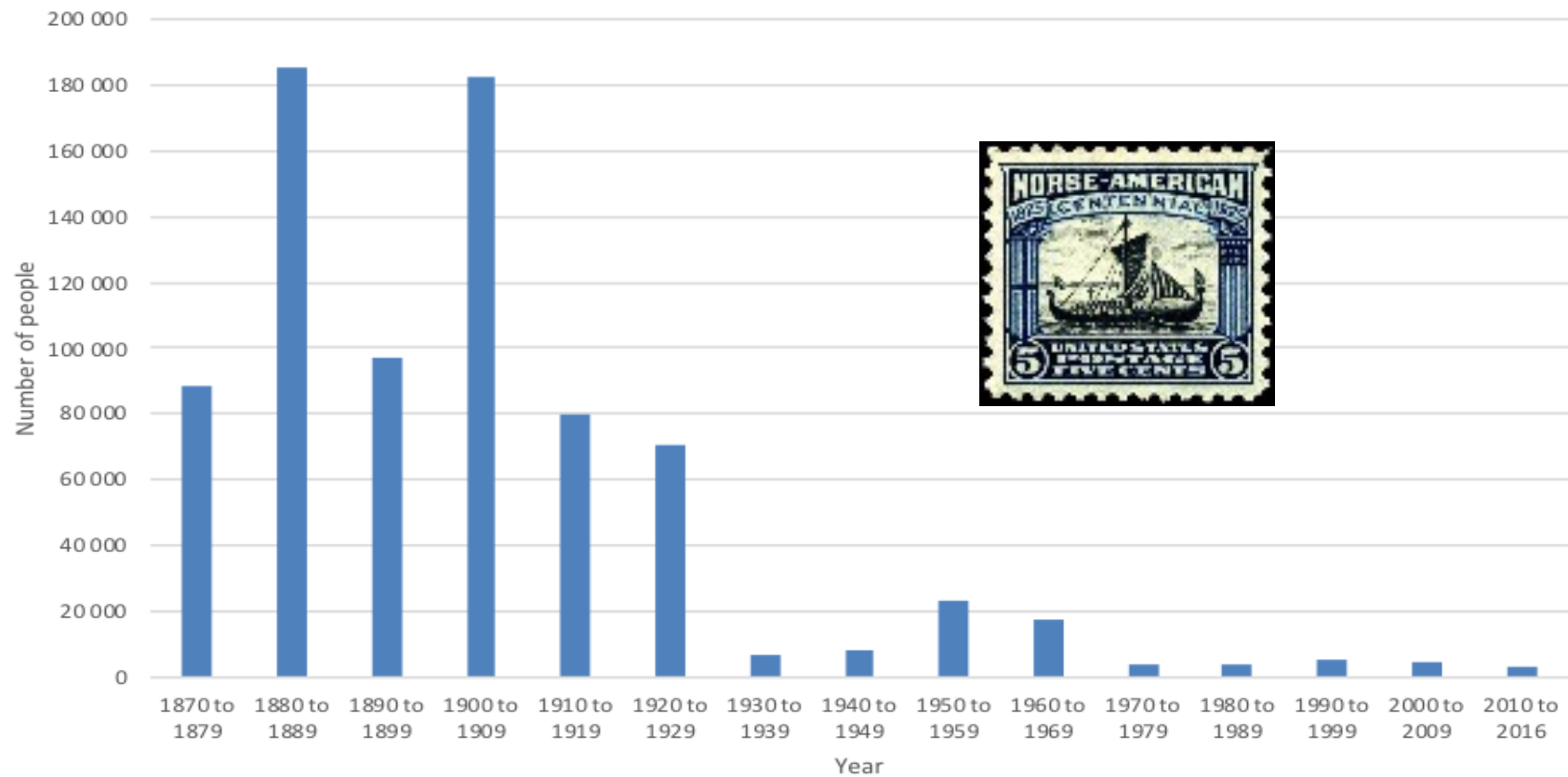
Agents in San Francisco,
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NEUBIT & CO., PRINTERS.

The period between 1848 and 1855 is known in the U.S. as California Gold Rush. The rush started when James W. Marshall found gold at Sutter's Mill in California. 300,000 Chinese came and made up 10% of the Californian population at the time.

Number of Norwegian persons obtaining lawful permanent resident status in the USA from 1870 to 2016



Office of Immigration Statistics, U. S. Department of Homeland Security. (2016). *2016 Yearbook of Immigration Statistics*. Retrieved from: <https://www.dhs.gov/immigrationstatistics/yearbook/2016>

The NGO Eurogroup for Animals (2021) estimated that in 2019, over 1.6 billion livestock (mainly ovine, bovine, poultry and pigs) were transported alive across the EU and beyond its borders by road, sea, rail, and air for trade purposes.



Animal transport as regulated in Europe: a work in progress as viewed by an NGO

Nikita Bachelard

La Fondation Droit Animal, Ethique et Sciences (LFDA), Paris, France

Animal Frontiers, Volume 12, Issue 1, February 2022,
Pages 16–24, <https://doi.org/10.1093/af/vfac010>



Knight, D.R., Squire, M.M., Collins, D.A. and Riley, T.V. 2017. Genome analysis of *Clostridium difficile* PCR ribotype 014 lineage in Australian pigs and humans reveals a diverse genetic repertoire and signatures of long-range interspecies transmission. *Front Microbiol* 7: 2138. doi: 10.3389/fmicb.2016.02138

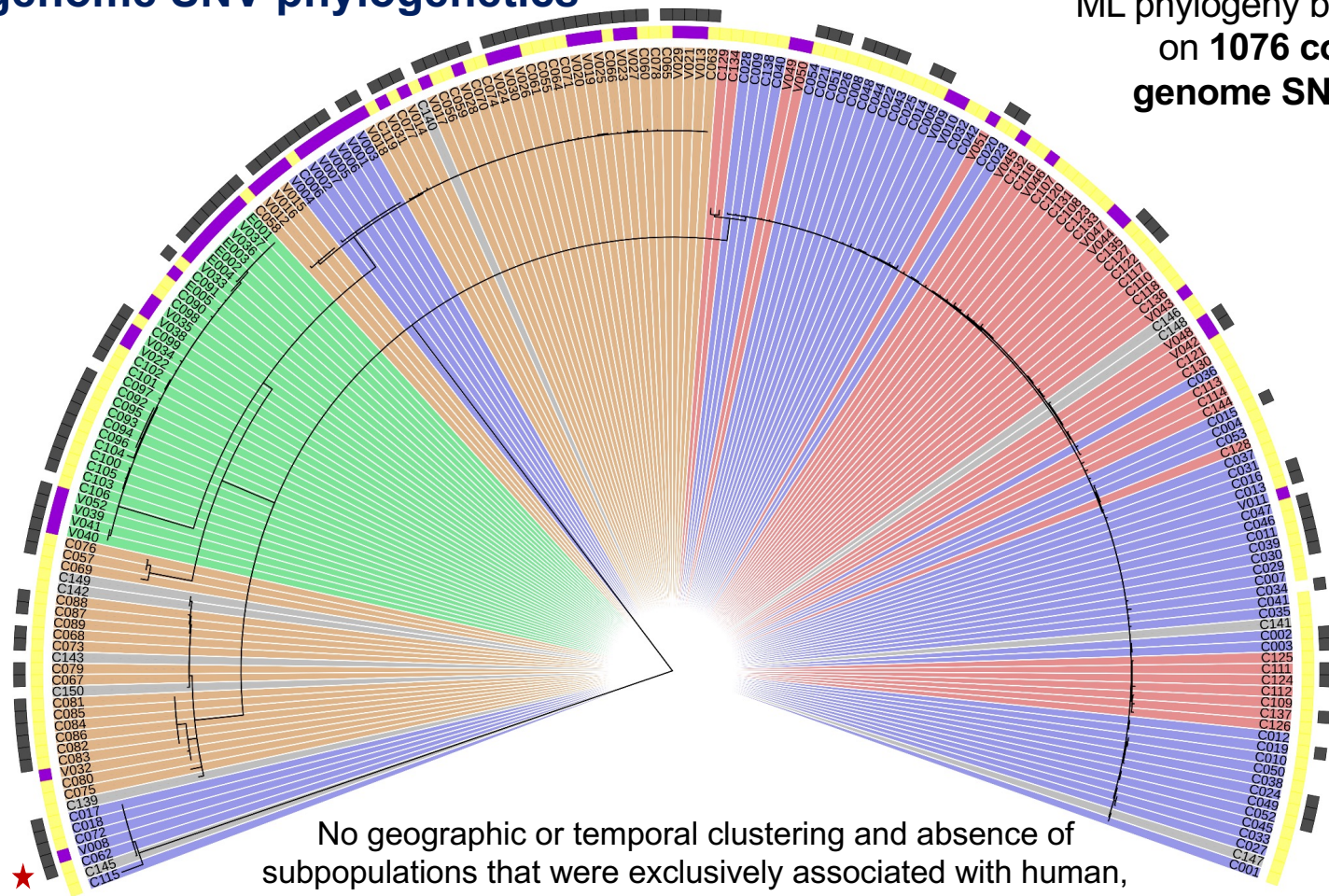
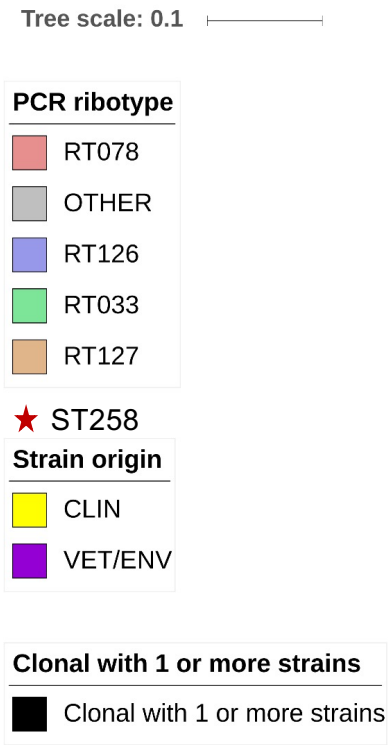


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Comparative phylogenetic, genomic and antibiogram analysis of RT014 isolated from humans (n=9) and piglets (n=9) in Victoria, Australian 2013																												
KEY: present ● absent ○					Toxin genes				AMR genes						Tn			Bacteriophages							slpA allele			
Isolate ID	Host species	RT	ST	MLST Clade	tcdA	tcdB	cdtLoc	ΔtcdC	ermB	tetW	tetM	aph3'-III	sat4	ant6	Tn6194	Tn5397	TnB1230-like	ΦCD27	ΦC2	ΦCDMH1	ΦCD38-2	ΦCD6356	ΦMMP02	Bacillus G	Clostr_c_st	7	9	
ESP146	Porcine	14	49	1	●	●	○	○	●	●	●	●	●	○	●	●	●	●	○	○	○	○	●	●	○	○	○	●
ESP148	Porcine	14	49	1	●	●	○	○	●	●	●	●	●	●	●	●	●	●	○	○	○	●	●	○	○	○	○	●
ESP150	Porcine	14	49	1	●	●	○	○	●	●	●	●	●	○	●	●	●	●	○	●	○	○	●	○	○	○	○	●
ESP152	Porcine	14	49	1	●	●	○	○	●	●	●	●	●	○	●	●	●	●	○	○	○	○	●	○	○	○	○	●
ESP154	Porcine	14	49	1	●	●	○	○	●	●	●	●	●	○	●	●	●	●	○	○	○	○	●	○	●	○	○	●
ESP156	Porcine	14	49	1	●	●	○	○	●	●	●	●	●	○	●	●	●	●	○	●	○	○	●	○	○	○	○	●
ESP158	Porcine	14	49	1	●	●	○	○	●	●	●	●	●	○	●	●	●	●	○	○	○	○	●	●	●	○	○	●
ESP160	Porcine	14	13	1	●	●	○	○	○	●	○	●	○	○	○	○	○	●	○	○	○	○	○	○	○	○	○	●
ESP162	Porcine	14	13	1	●	●	○	○	○	●	○	●	○	○	○	○	○	●	○	○	○	○	○	○	○	○	○	●
SQ0120	Human	14	13	1	●	●	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	○	●	○	●	○	●
SQ0114	Human	14	2	1	●	●	○	○	○	○	○	○	○	○	○	○	○	○	○	●	○	○	○	○	○	○	○	○
SQ0116	Human	14	2	1	●	●	○	○	○	○	○	○	○	○	○	○	○	○	○	●	○	○	○	○	○	○	○	○
SQ0118	Human	14	2	1	●	●	○	○	○	○	○	○	○	○	○	○	○	○	○	●	○	○	○	○	○	○	○	○
SQ0126	Human	14	2	1	●	●	○	○	○	○	○	○	○	○	○	○	○	○	○	●	○	○	○	○	○	○	○	○
SQ0341	Human	14	2	1	●	●	○	○	○	○	○	○	○	○	○	○	○	○	○	●	○	○	○	○	○	○	○	○
SQ0342	Human	14	2	1	●	●	○	○	○	○	○	○	○	○	○	○	○	○	○	●	○	○	○	○	○	○	○	○
SQ0348	Human	14	2	1	●	●	○	○	○	○	○	○	○	○	○	○	○	○	○	●	○	○	○	○	○	○	○	○
SQ0352	Human	14	2	1	●	●	○	○	○	○	○	○	○	○	○	○	○	○	○	●	○	○	○	○	○	○	○	○

C. difficile ST11 core genome SNV phylogenetics

ML phylogeny built on 1076 core genome SNVs



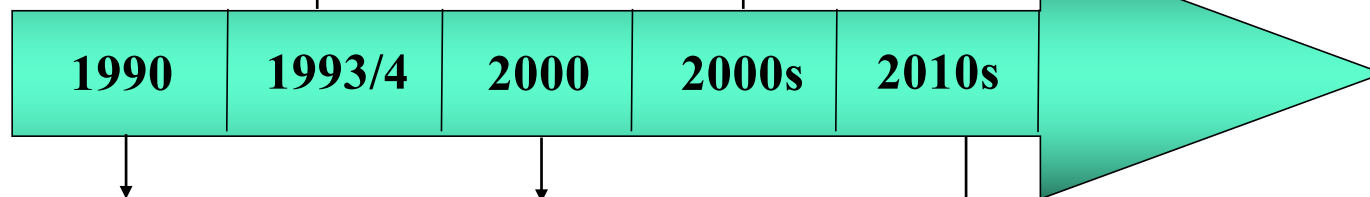
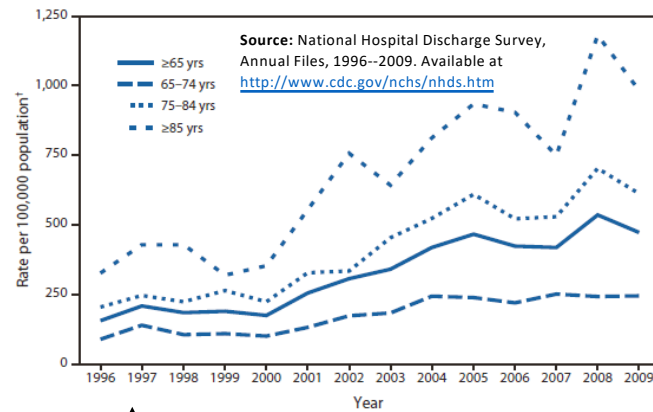
No geographic or temporal clustering and absence of subpopulations that were exclusively associated with human, porcine or bovine hosts

Evolutionary and Genomic Insights into *Clostridioides difficile* Sequence Type 11: a Diverse Zoonotic and Antimicrobial-Resistant Lineage of Global One Health Importance

© Daniel R. Knight,^a Brian Kullin,^b Grace O. Androga,^{c,d} Frederic Barbut,^a Catherine Eckert,^{a,f} Stuart Johnson,^g Patrizia Spigaglia,^h Kazuhiro Tateda,ⁱ Pei-Jane Tsai,^j Thomas V. Riley^{a,k,l}



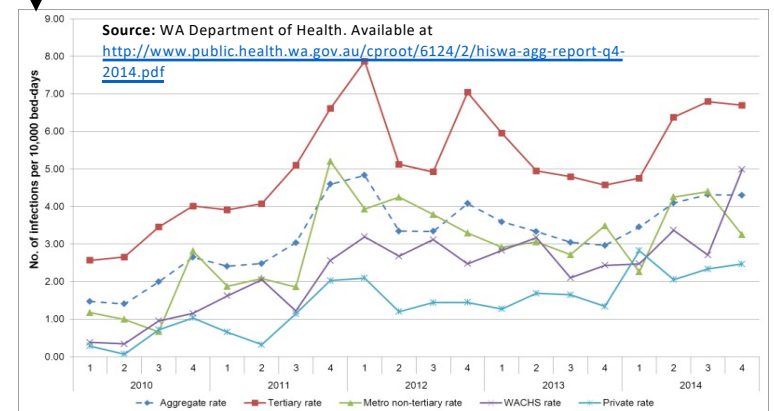
Ribotype 027 mutates to FQ resistance in 2 places independently (He *et al.* 2013)



Community infection completely missed in North America!

Ceftiofur licensed for animal use in North America

Ceftiofur licensed for animal use in Australia



***C. difficile* infection in Australia**

Surveillance

- Mandatory since 2010
- Counts numbers of “hospital identified” CDI
- Includes a proportion of CA-CDI
- No requirement to determine source but many hospitals do
- But use McDonald “interim” definitions from 2007!
- No estimation of severity
- This all needs revision

Incidence: 4.00/10,000 patient days (PD)
23.8/100,000 population

Prevalence: 7% of all diarrhoeal specimens

Mortality: 7%

Length of stay: 16.8 days

Costs: \$12,000-19,000 per case

- **>8,500 cases per year***
- **~600 deaths per year**
- **≥\$107 million per year in costs**
- **14% of all hospital-associated infections**

*This is an underestimation of case numbers in Australia, since counts are of hospital-identified CDI alone, not accounting for CDI cases detected or undiagnosed in the community.



Deirdre Collins

ACSQH, 2022
Cheng et al., 2016
Putsathit et al., 2015
Collins et al., 2016
Chen et al., 2017
Bond et al., 2017



Research

Increasing incidence of *Clostridium difficile* infection, Australia, 2011–2012

Claudia Slimings
BSc, PGDipHlthSci, PhD,
Associate Professor



Global rates of hospital-associated *Clostridium difficile* infection

Abstract

(Slimings et al Med J Aust 2014; 200: 272–276)

In some parts of the world 50% of CDI is now community-associated - ~25% in Australia in 2011/12

AUSTRALIAN COMMISSION ON SAFETY AND QUALITY IN HEALTH CARE

***Clostridioides difficile* infection: Data snapshot report: 2020 and 2021**

What do the analyses show about CDI in Australia?

In Australian public hospitals:

- separations with a CDI diagnosis increased by 29% from 2020 and 2021
- community-onset CDI (pre-existing CDI symptoms on admission) accounted for over 80% of separations
- healthcare-associated hospital-onset CDI accounted for less than 20% of all CDI diagnoses.

What do these findings mean and why are they important?

The findings from this report suggest that:

- community-onset CDI is a significant health problem in Australia
- hospital-based strategies to prevent healthcare-associated hospital-onset CDI are effective
- changes in CDI rates coinciding with the response to COVID-19 may be linked to improved IPC strategies and changes in access to healthcare during the pandemic.

***Clostridioides difficile* infection (CDI) - Information for primary health providers**

Published on
9 October 2024

CDI is a community health issue

Background information for clinicians

Clostridioides difficile (*C. difficile*) is a spore-forming bacterium that causes diarrhoea, commonly after exposure to antimicrobial agents.³ Exposure to other medications, such as proton pump inhibitors and immunosuppressant agents can independently contribute to CDI for some patients.^{4, 5}

C. difficile is typically found in the gastrointestinal tracts of many young animal species, humans, and contaminates the natural environment including agriculture and food production, as well as in built environments.^{6, 7} Transmission of *C. difficile* occurs by ingestion of spores, either through person-to-person contact, or animal-to-person contact. *C. difficile* spores can also survive on environmental surfaces for extended periods of time and can be transferred from person-to person by contaminated hands or equipment.⁷

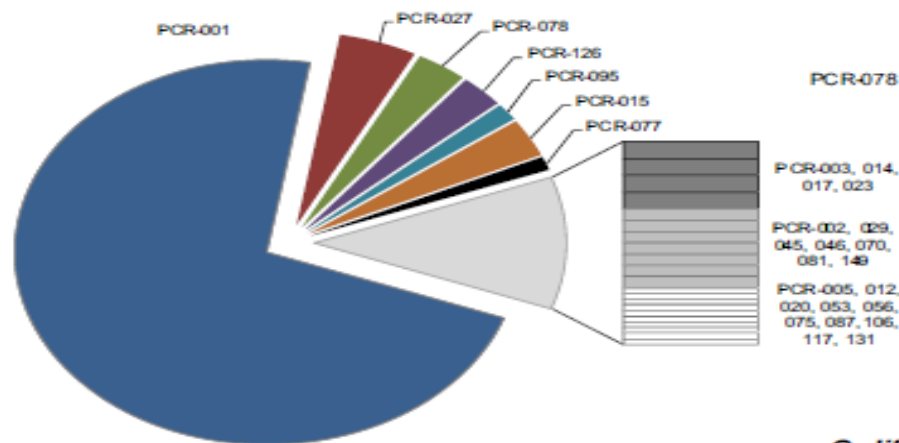
Animal reservoirs

- Companion animals
- Food animals
- Horses
- Wild animals
- Reptiles
- Birds

Food sources

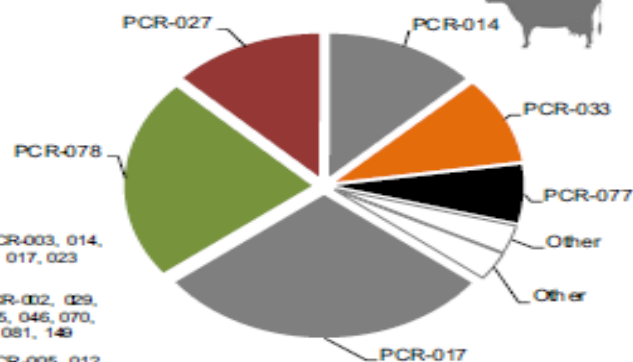


Hospitals, Germany

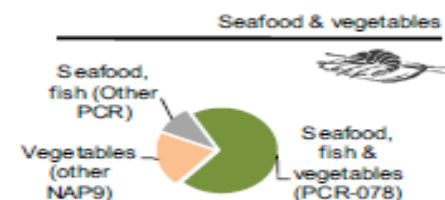
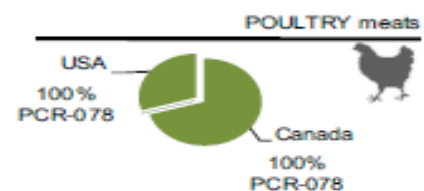
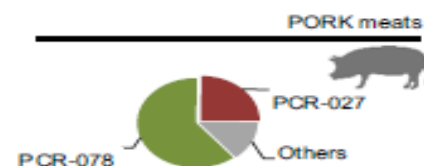
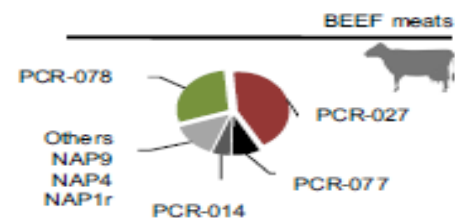


C. difficile in calves at the farm, 102 farms, Canada

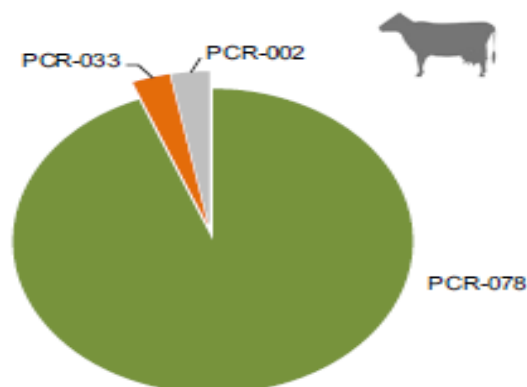
May-September 2004



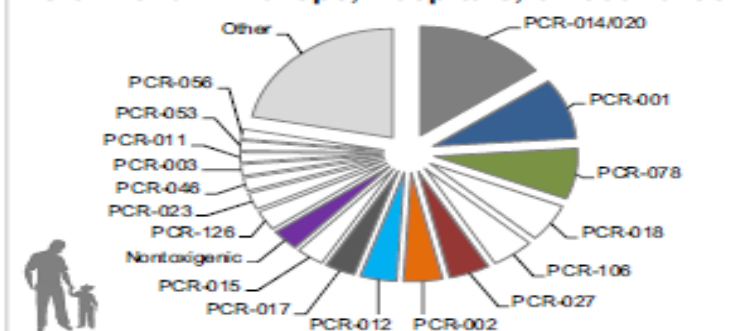
C. difficile in foods North America



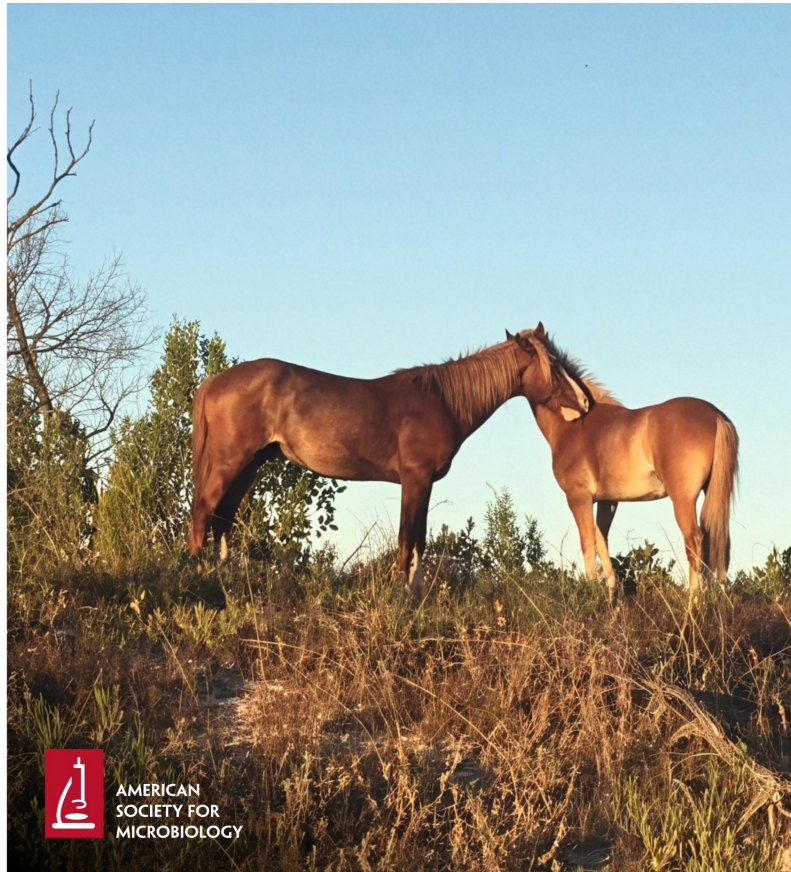
C. difficile in calves shipped to a single farm, USA



C. difficile in Europe, hospitals, 34 countries



Applied and Environmental Microbiology



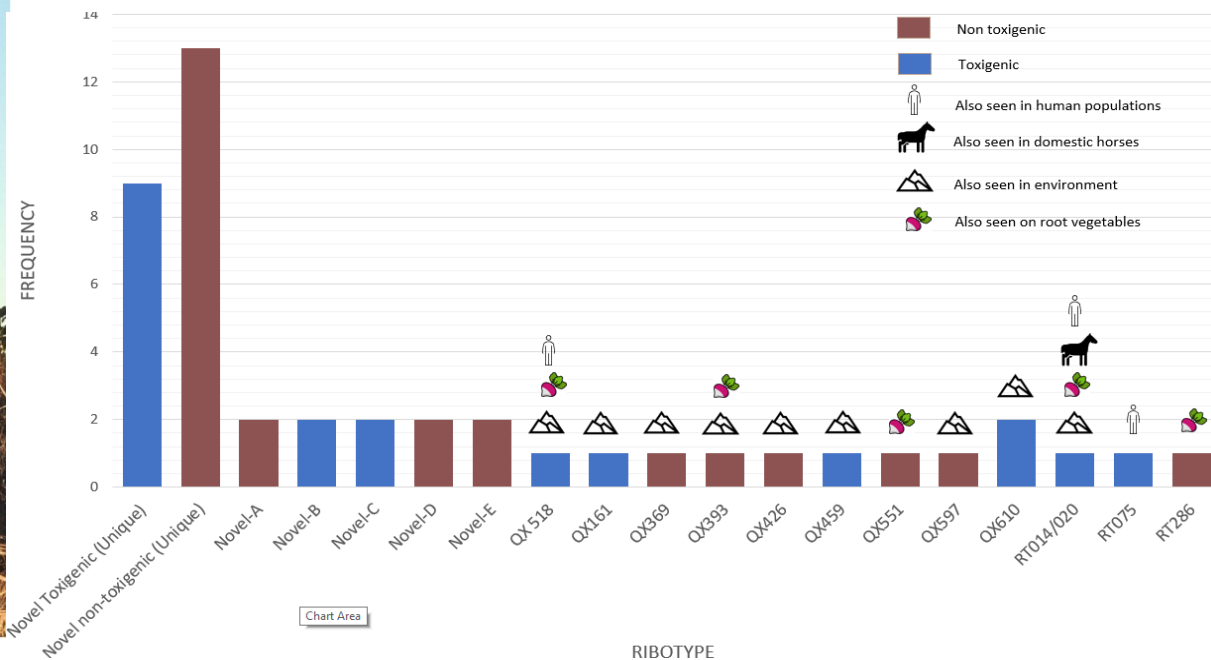
A JOURNAL BY THE AMERICAN SOCIETY FOR MICROBIOLOGY

Clostridioides difficile in feral horse populations in Australia



Natasza M. R. Hain-Saunders¹ Daniel R. Knight, Andrea Harvey,
Mieghan Bruce, Brian A. Hampson and Thomas V. Riley

C. difficile was isolated from 45 of the 380 samples (11.8%)—forty
ribotypes (RTs) were identified, 28 of which (70%) were novel.





Environmental sources

- Soil
- Water
- Wastewater
- Gardens – home
- Gardens – vegetable (home or commercial)
- Parks



October 2023 Volume 89 Issue 10



Applied and Environmental
Microbiology

Environmental Microbiology | Full-Length Text

Biogeographic distribution and molecular epidemiology of *Clostridioides (Clostridium) difficile* in Western Australian soils

Karla Cautivo-Reyes,¹ Daniel R. Knight,^{2,3} Deborah Bowle,⁴ Benjamin Moreira-Grez,⁴ Andrew S. Whiteley,⁵ Thomas V. Riley^{1,2,3,6}

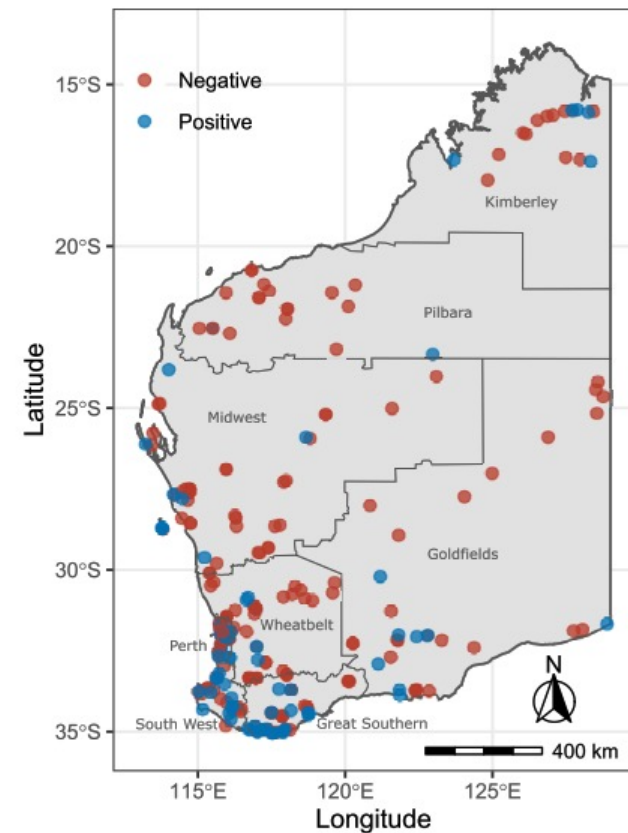
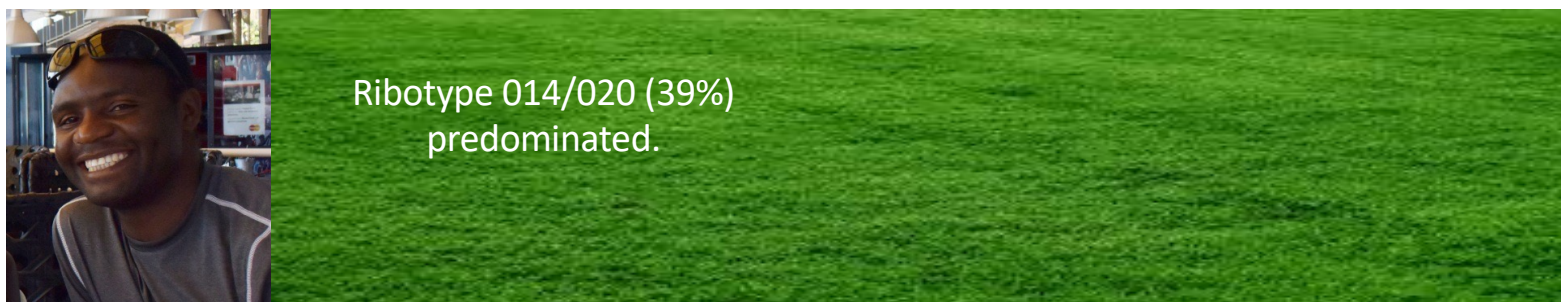


FIG 1 Biogeographic distribution of *C. difficile* positive soil samples ($n = 100/321$) ;

Variable	Variable categories	<i>C. difficile</i> number isolated (%)	Univariable model	Covariate Odds ratios (95% CI) [†]	
			Odds ratios (95% CI) [†]	Sampling site	<i>P</i> value [‡]
Age [‡]	Old lawn (n = 113)	53 (47)	Referent		
	New lawn (n = 198)	129 (65)	2.11 (1.32–3.4)	2.30 (1.16–4.57)	0.015 [‡]
Area	Extra-large (n = 85)	53 (62)	Referent		
	Large (n = 53)	26 (49)	0.58 (0.28–1.16)	0.49 (0.16–1.49)	0.7
	Medium (n = 101)	60 (59)	0.88 (0.49–1.59)	1.02 (0.42–2.51)	0.7
	Small (n = 72)	43 (60)	0.89 (0.47–1.71)	0.88 (0.32–2.43)	0.7
Location	North (n = 161)	98 (60.9)	Referent		
	South (n = 150)	84 (56)	1.22 (0.78–1.92)	1.25 (0.61–2.59)	0.99
Season	Autumn (n = 224)	135 (60.3)	Referent		
	Winter (n = 87)	47 (54)	0.77 (0.47–1.28)	0.67 (0.28–1.62)	0.52

Table 1. The relationship between the prevalence of *C. difficile* in lawn and the age of the lawn, its size, sampling site, location, postcode, and season in Perth.





Lauren Bloomfield

Community- and healthcare-associated infections in females in WA, by age group, 2010 – 2014

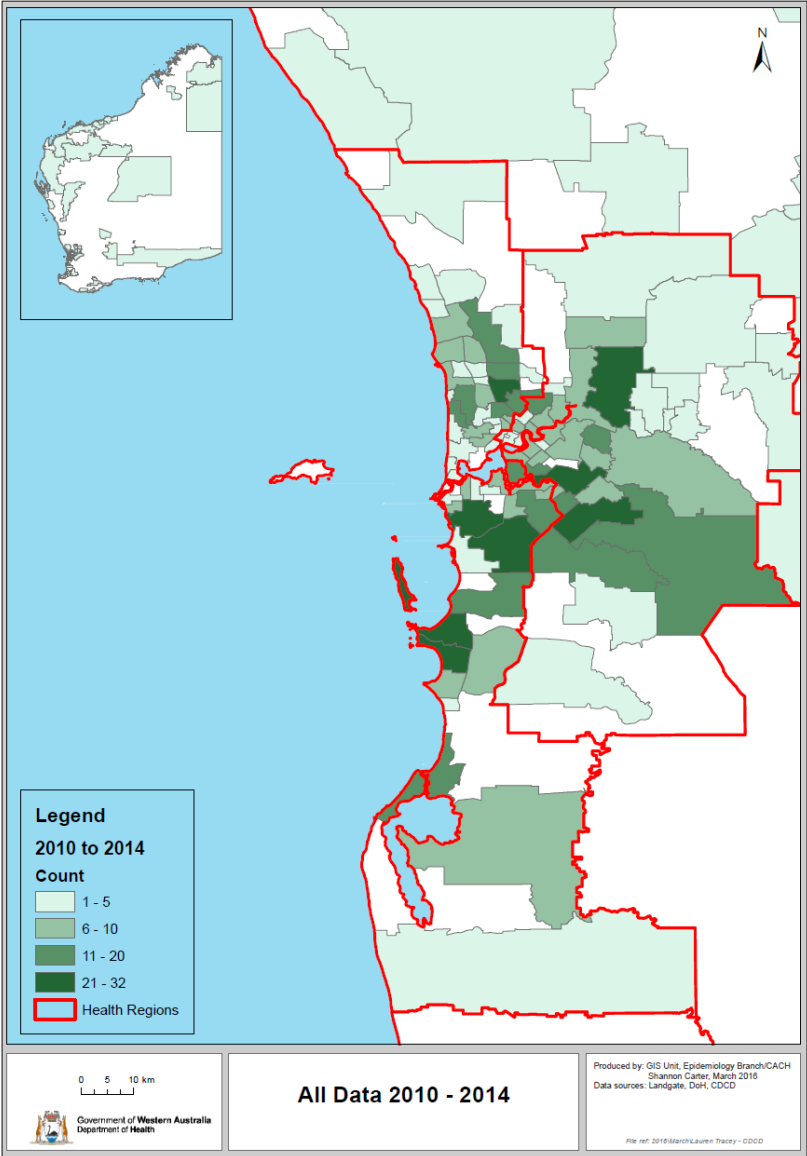
Age group	CAI n (%)	HAI HCFO n (%)	OR (CI ₉₅)
2 - 19 years	29 (43.9)	37 (56.1)	0.92 (0.48 – 1.76)
20 - 39 years	109 (67.2)	53 (32.7)	1.90 (1.19 – 3.05)
40 - 59 years	100 (39.3)	154 (60.6)	1.13 (0.77 – 1.67)
60 - 79 years	141 (31.8)	303 (68.2)	1.18 (0.88 – 1.58)
80+ years	116 (27.9)	300 (72.1)	0.86 (0.61 – 1.21)
Total	495 (57.0)	847 (52.8)	1.09 (0.93 – 1.30)



Maybe confounded by young families.



Food preparation
Washing, creating aerosols!
Contaminating benches
Preliminary study of 30 kitchens in affluent part of Perth - 10% positive

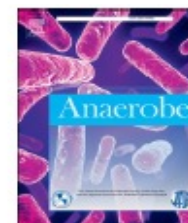




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Clostridioides difficile (including epidemiology)

Prevalence and molecular types of *Clostridioides (Clostridium) difficile* on Australian retail vegetables and household surfaces

Deirdre A. Collins^{a,b,*}, Su Chen Lim^{a,b}, Jessica Chisholm^b, Molly Lattin^c, Linda Selvey^c, Simon Reid^c, Thomas V. Riley^{a,b,d}

Table 2

RTs of *C. difficile* isolated from household environmental and potato swabs, Queensland (QLD) and Western Australia (WA).

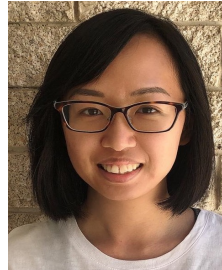
Ribotype	QLD			WA			Total (%)
	Chopping board	Fridge/pantry	Unwashed potato	Chopping board	Fridge/pantry	Unwashed potato	
QX 690						5	5 (13.2)
056 ^a		1	1		2		4 (10.5)
010	1	1					2 (5.3)
QX 014 ^a			2				2 (5.3)
QX 551			1			1	2 (5.3)
002 ^a					2		2 (5.3)
014/020 ^a					1		1 (2.6)
078 ^b			1				1 (2.6)
106 ^a		1					1 (2.6)
286						1	1 (2.6)
Others	3	2	4	1	3	4	17 (44.7)
Total	4	5	9	1	8	11	38 (100.0)

^a Toxigenic strain (A+B+CDT-).

^b Toxigenic strain (A + B + CDT+).

Gardening centres

~30% of samples positive for *C. difficile*
 Some obvious like animal manures
 Some less obvious like compost/mulch
 But expired vegetables from large stores going into compost/mulch



Su-Chen Lim

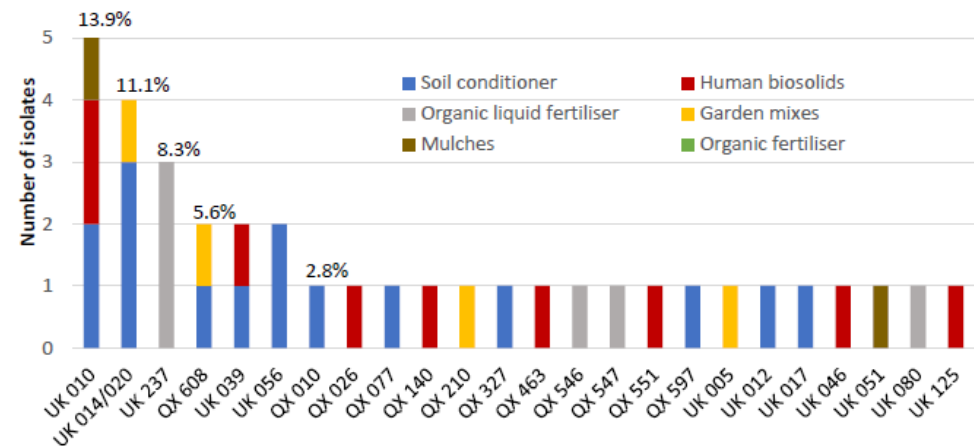


Figure 1. PCR ribotype of *C. difficile* isolates in gardening products

DOI: 10.1111/jam.15408

ORIGINAL ARTICLE

J Appl Microbiol. 2022;133:1156–1168.



Whole-genome sequencing links *Clostridium* (*Clostridioides*) *difficile* in a single hospital to diverse environmental sources in the community

Su-Chen Lim¹ | Deirdre A. Collins¹ | Korakrit Imwattana^{2,3} | Daniel R. Knight^{2,4} | Sicilia Perumalsamy² | Natasza M. R. Hain-Saunders^{1,4} | Papanin Putsathit¹ | David Speers^{2,5} | Thomas V. Riley^{1,2,4,5}

environmental microbiology reports
 Environmental Microbiology Reports (2020) 12(6), 672–680
 doi:10.1111/1758-2229.12889

Brief Report

***Clostridium difficile* in soil conditioners, mulches and garden mixes with evidence of a clonal relationship with historical food and clinical isolates**



Spore-Forming *Clostridium (Clostridioides) difficile* in Wastewater Treatment Plants in Western Australia

Jessica M. Chisholm,^a Papanin Putsathit,^b Thomas V. Riley,^{a,b,c,d} Su-Chen Lim^{a,b}

TABLE 1 Characteristics of wastewater treatment plants and the prevalence of *C. difficile*

WWTP ^a	Treatment process	Final effluent receiving body	Final biosolids application	Prevalence, % (n)			
				Influent	Effluent	Irrigation	Biosolids
W1	Preliminary, primary, secondary	Ocean		100 (11/11)	54.5 (6/11)		
W2	Preliminary, primary, secondary, anaerobic digestion of biosolids	Ocean, groundwater	Agricultural land	100 (11/11)	75.0 (3/4)		90.0 (9/10) ^b
W3	Preliminary, primary, secondary	Woodlot/wetland		87.5 (7/8)	30.0 (3/10)		
W4	Preliminary, primary, secondary	Groundwater		90.9 (10/11)	45.5 (5/11)		
W5	Preliminary, primary, secondary	Ocean, W7	Agricultural land	81.8 (9/11)	18.2 (2/11)		100 (14/14) ^c
W6	Preliminary, primary, secondary	Groundwater		100 (10/10)	81.8 (9/11)		
W7	Microfiltration, reverse osmosis membrane	Ocean, groundwater	Agricultural land	75.0 (9/12)	0.0 (0/4)		100 (12/12) ^c
W8	Preliminary, primary, secondary	Groundwater	Agricultural land	90.0 (9/10)	60.0 (6/10)		100 (12/12) ^c
W9	Preliminary, primary, secondary, filtration, chlorination, fluoridation, ultraviolet disinfection	Sport grounds, creek		90.9 (10/11)	10.0 (1/10)		
W10	Preliminary, primary	Ocean		90.0 (9/10)	100 (4/4)		
W11	Preliminary, primary, secondary, chlorination, lime amendment of biosolids	Ocean, sport grounds	Agricultural land	90.0 (9/10)	66.7 (6/9)	40.0 (2/5)	72.7 (8/11) ^d
W12	Preliminary, primary, secondary, anaerobic digestion of biosolids	Ocean, W7	Agricultural land	90.9 (10/11)	55.6 (5/9)		100 (11/11) ^b
Total				90.5 (114/126)	48.1 (50/104)	40.0 (2/5)	94.3 (66/70)

^aWWTP, wastewater treatment plant.

^bAnaerobically digested biosolids.

^cUntreated biosolids.

^dLime-amended biosolids.

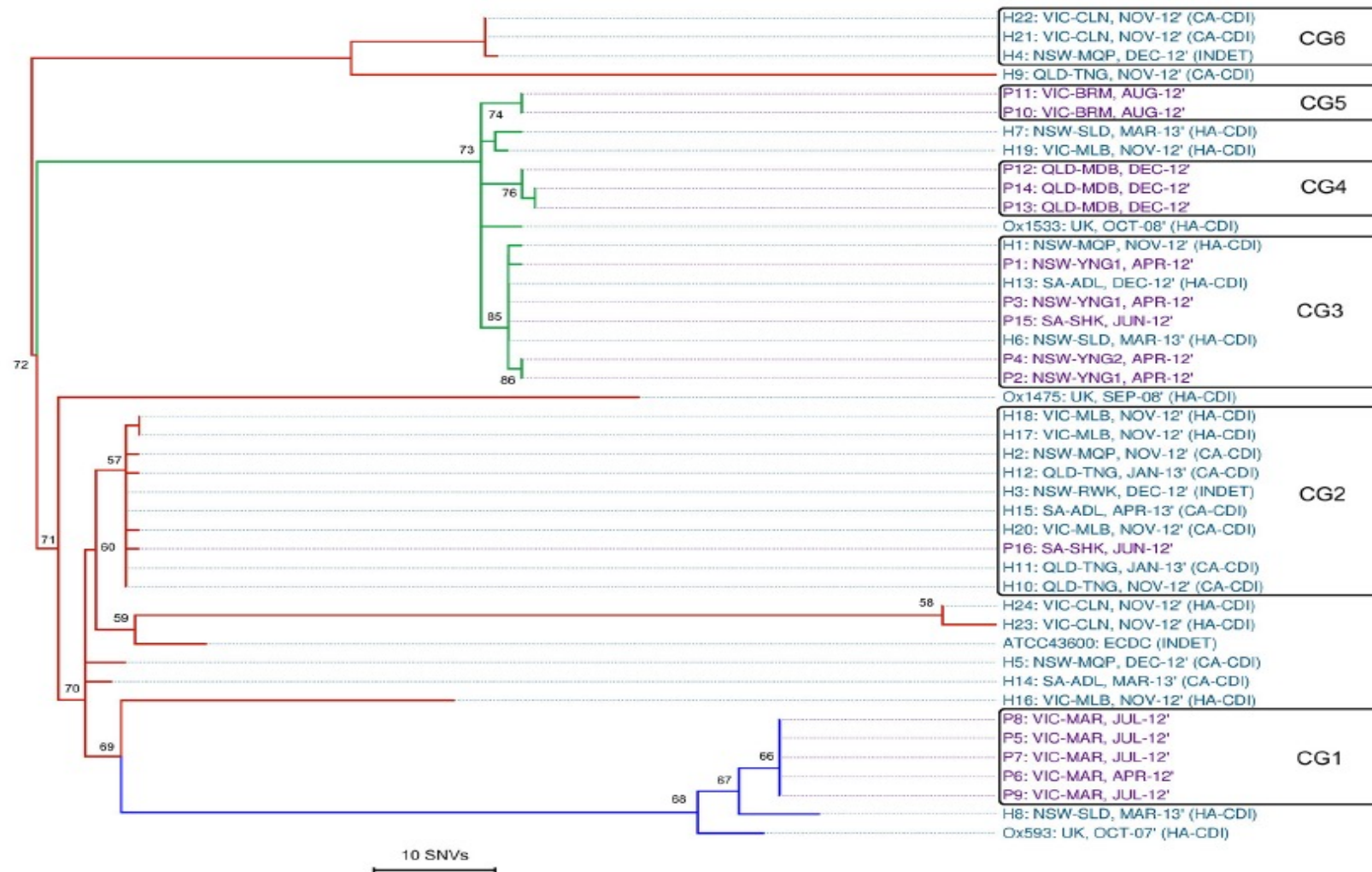


FIGURE 3 | Single nucleotide variant analysis of 44 *C. difficile* RT014.

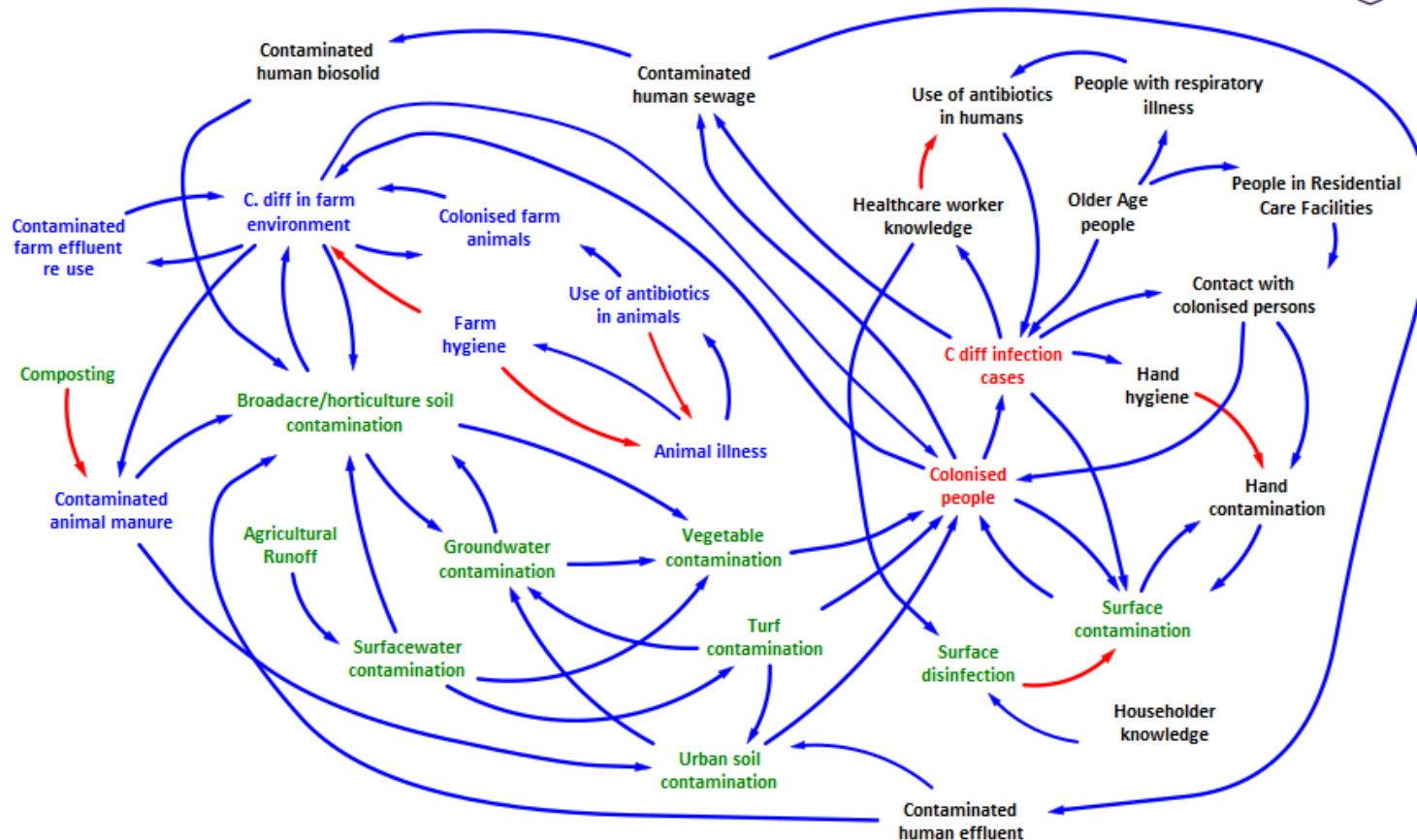
Systems Dynamics was the One Health approach chosen

The modelling process used in Systems Thinking is iterative, and often participatory, to achieve consensus on the problem being modelled and to ensure the system structure is realistically replicated, revealing system behaviour that often deviates from initial expectations.

The process involved the following key steps:

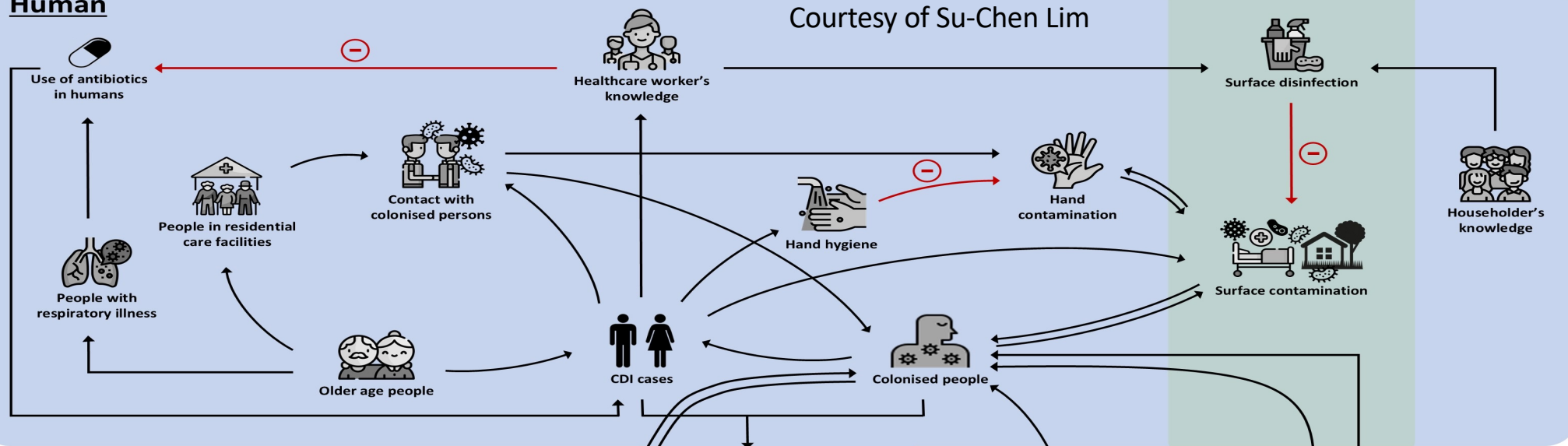
- Stakeholder identification and problem scoping
- Identifying key variables and their relationships
- Building a Causal Loop Diagram
- Identifying feedback loops
- Iceberg model development and analysis
- Leverage points (intervention strategies)

Courtesy of Oz Sahin, Simon Reid and Russell Richards @

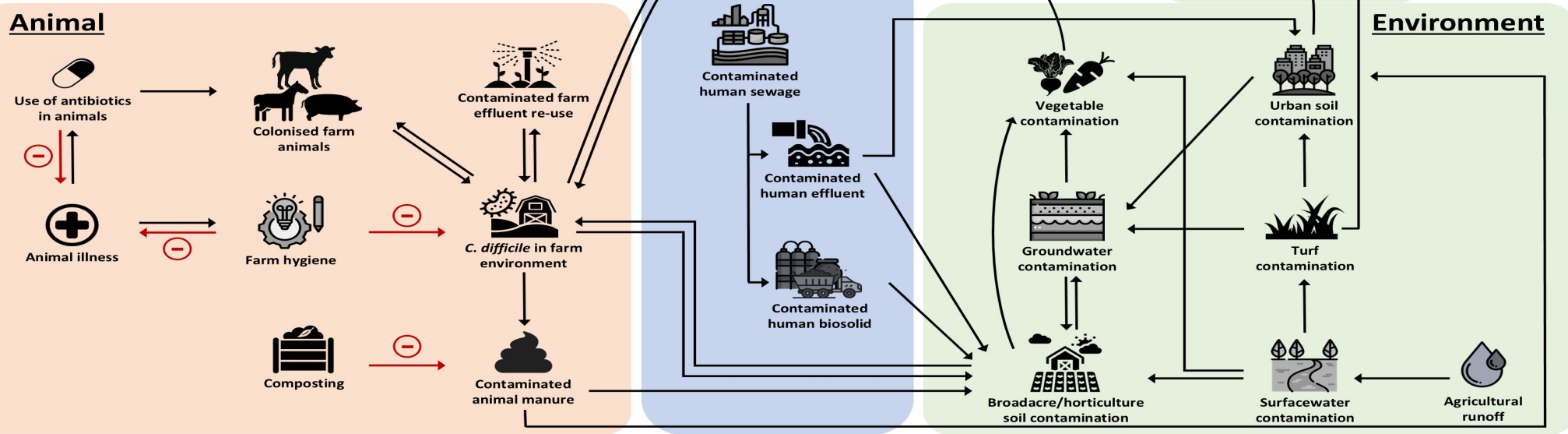


Summary Causal Loop Diagram showing the key feedback loops associated with the transmission of *Clostridioides difficile* in Australia. Arrows denote the direction of the causal relationship. A blue arrow denotes a “positive (+)/same” relationship (both change in the same direction), and a red arrow denotes a “negative (-)/opposite” relationship (variables change in opposite directions, i.e. an increase in one causes a decrease in the other)

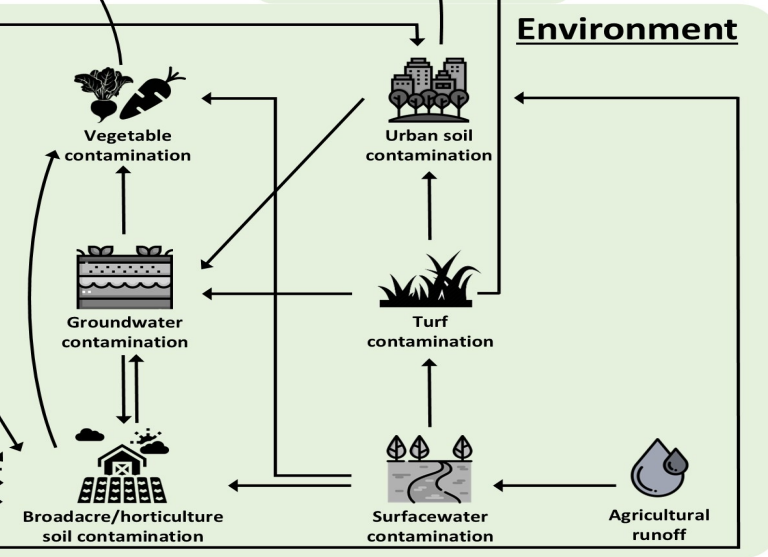
Human



Animal



Environment



What does this teach us about IP & C?

CDI not just a hospital issue, it's a worldwide public health issue.

Geography is a guide to what strains of *C. difficile* will be found.

Knowing the strain (RT or better ST) helpful.

Each jurisdiction needs to understand its own back yard ie needs a reference laboratory!

Many sources of *C. difficile* other than food important (such as gardens/lawn/WWTP effluent).

Anywhere there is manure there is a problem!

Putting antimicrobials into production animals is not a good idea.

In Australia, we need a good study of CA-CDI involving GPs.

Requires a One Health approach.

One Health

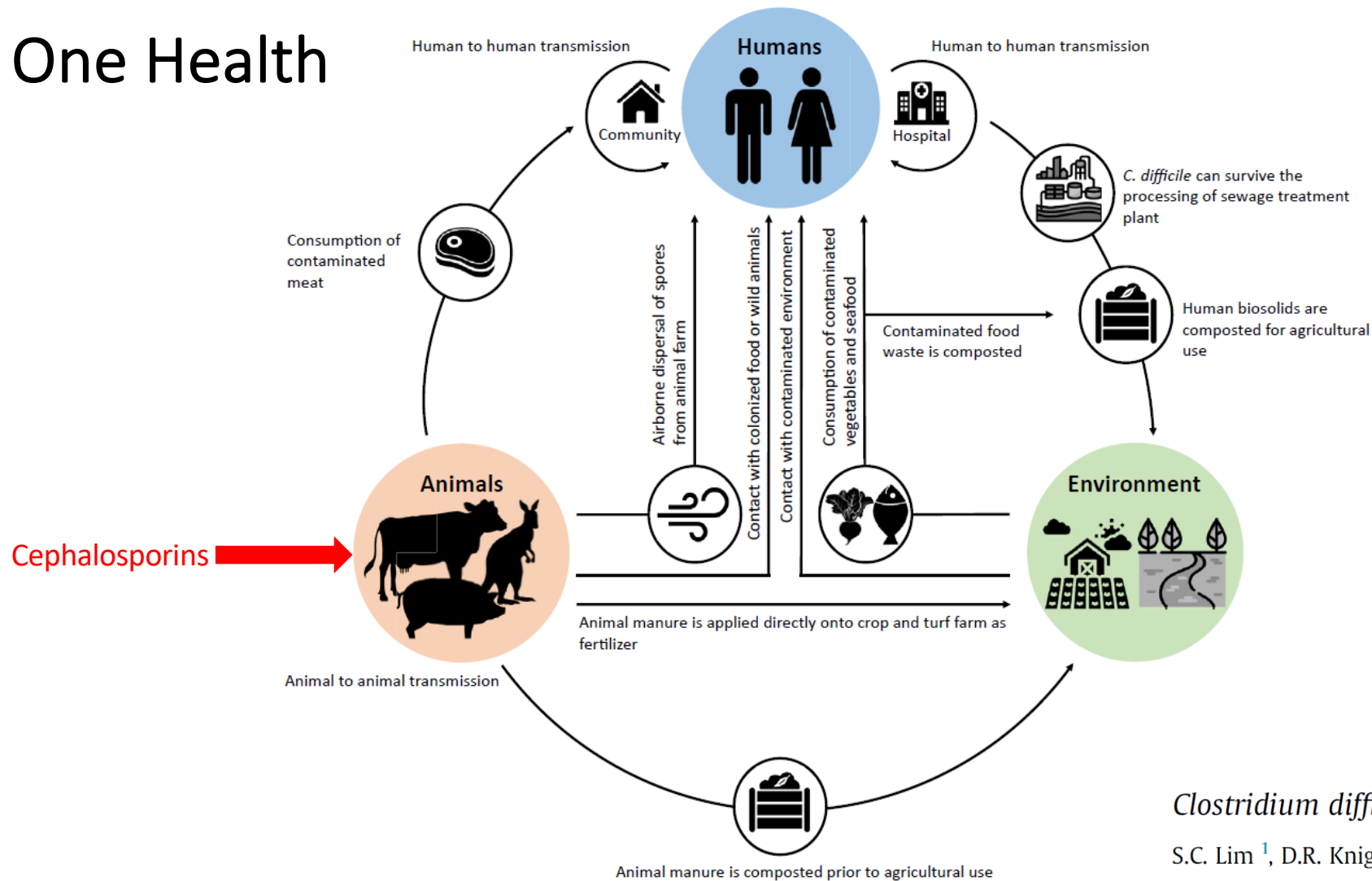


Fig. 2. Transmission of *Clostridium difficile*.

Clostridium difficile and One Health

S.C. Lim¹, D.R. Knight², T.V. Riley^{1, 2, 3, 4, *}

Clin Microbiol Infect 2020;26:857

Acknowledgements

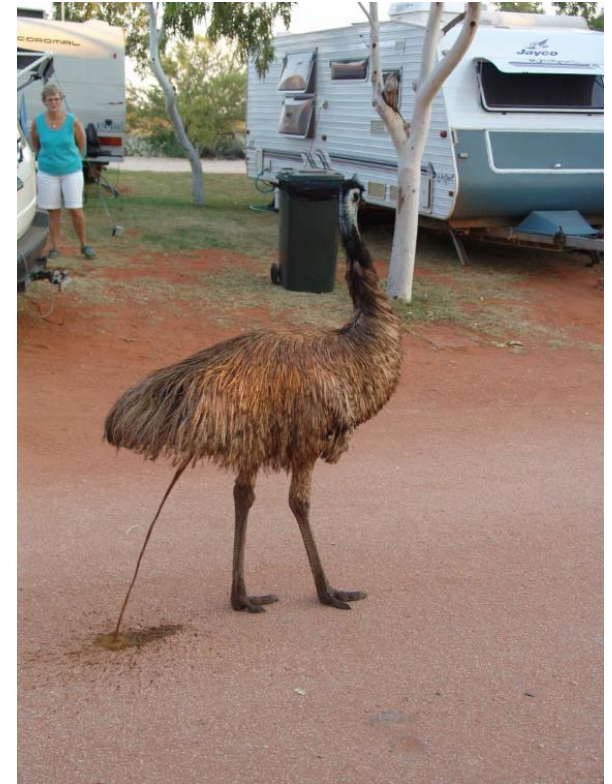
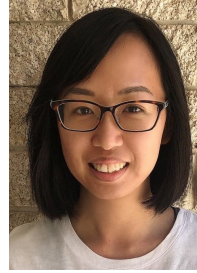
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Leeds University (Mark Wilcox)
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OCTOBER

- 2 ... Sustainable Healthcare and IPC: Can They Co-Exist? (an IFIC teleclass)
Afro-European Teleclass With Dr. Graham Pike, UK, and Profa. Dra. Camila Quartim de Moraes Bruna, Brazil
- 7 ... Clean Hospitals Day 2025: Human Factors and Collaboration
Afro-European Teleclass With Dr. Alexandra Peters, Switzerland, and Dr. Martina Močenić, Croatia
- 15 ... What Can Knowing Something About the Evolution of *Clostridium difficile* Teach Us About IPAC?
Australasian Teleclass With Prof. Thomas Riley, Australia
- 23 ... Discussion: Are Current Healthcare Cleaning Guidelines Sufficient to Fight Antimicrobial Resistance Spread?
With Dr. Jon Otter, UK & Dr. Curtis Donskey, US
- 28 ... Research Priorities to Strengthen Environmental Cleaning in Healthcare Facilities: the CLEAN Group
Afro-European Teleclass Consensus
With Dr. Giorgia Gon, UK

NOVEMBER

- 11 ... The Use of Faecal Microbiota Transplant as Treatment for *Clostridium difficile*
Afro-European Teleclass With Simon Goldenberg, UK
- 13 ... Solve the LTC Outbreak!
With Steven J. Schweon
- 19 ... Special Lecture for World Toilet Day

DECEMBER

- 4 ... What's On a Surface Doesn't Stay On a Surface - The Dynamics and Risk of Microbial Resuspension From Surfaces
With Prof. Charles Gerba, US
- 16 ... Patience, Patients and Persistent Antimicrobial Resistance
Afro-European Teleclass With Colm Dunne, UK
- 18 ... Empowering Patients to Prevent Healthcare-Associated Infections
With Dr. Curtis Donskey, US

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