

Laboratory-based surveillance of *Clostridium difficile* infection in Australian healthcare and community settings, 2013-2018

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Introduction

Clostridium difficile rose to prominence in the early 2000s with large outbreaks of the binary toxin (CDT)-positive strain, ribotype (RT) 027, in North America and Europe¹. In Australia, these strains rarely cause disease, and there is a different repertoire of circulating strains². In the ongoing national *C. difficile* Antimicrobial Resistance Surveillance (CDARS) study, we sought to describe the evolving molecular epidemiology of *C. difficile* infection (CDI) in Australian healthcare and community settings from 2013–2018.

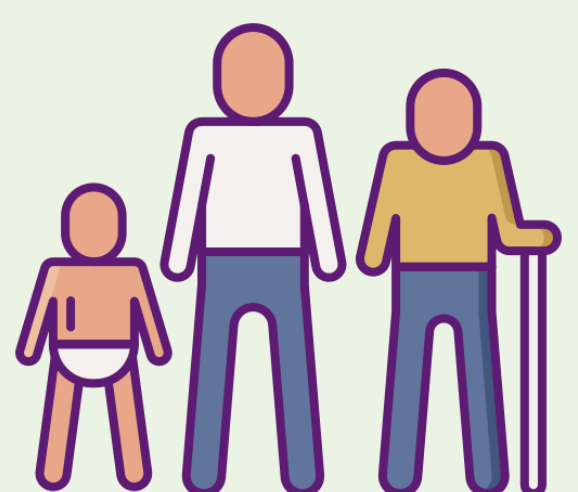
Results



- 1675 total samples
- Private laboratories – community isolates: 778 (46%)
- Public laboratories – hospital isolates: 897 (54%)



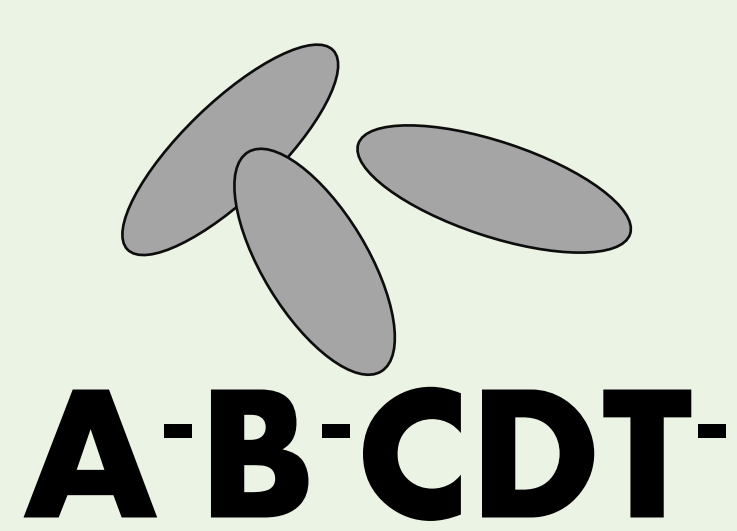
- 1523 *C. difficile* isolates recovered, RT and TP performed
- ~91% recovery rate
- 203 different RTs
- 1197 isolates assigned to internationally recognised RTs
- 49 novel *C. difficile* isolates



- ~61% females
- Ages ranged from 1 – 115 years
- Median age: 69 years [IQR 50 – 81]



- ~5% of *C. difficile* strains produced CDT
- Low numbers of epidemic RT 027 (n=2) and RT 078 (n=6) strains were found
- Strains related to epidemic RT 027 strain circulate Australia; RT 251 (n=10) and RT 244 (n=7)³⁻⁴
- Cluster of RT 126 (n=11) from VIC



- A total of 71 non-toxigenic *C. difficile* strains was recovered, the majority of which were found in the community (n=55)
- Non-toxigenic *C. difficile* strains were most likely from patients co-infected with toxigenic strains
- These were mainly RTs 010 and 039, both of which have been reported previously in lawns and composts in WA⁵

Major findings:

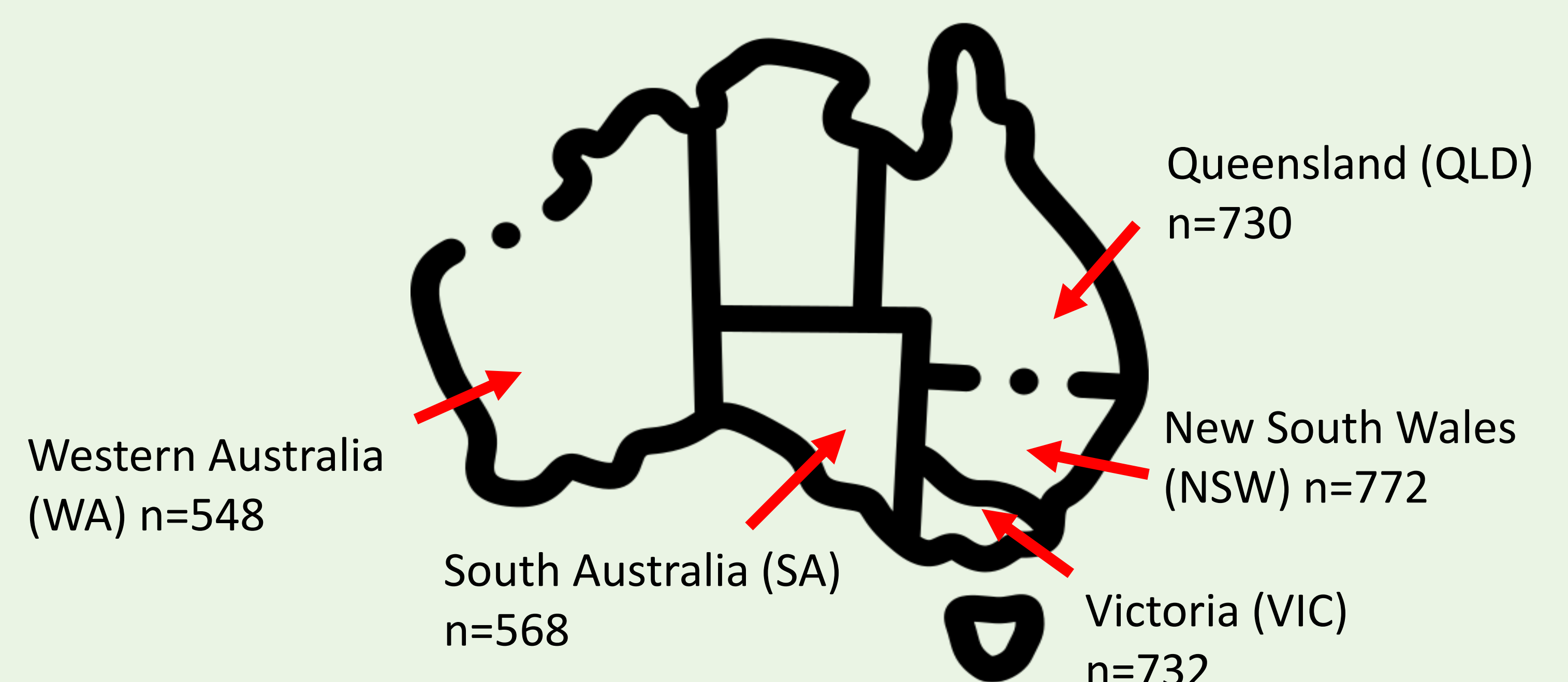
- ❖ RT 014/020 was the predominant strain type causing CDI in humans
- ❖ The top 20 *C. difficile* RTs accounted for ~74% (n=1121) of all isolates
- ❖ ~95% (n=1452) of *C. difficile* isolates produced at least one toxin, the most common TP being A+B+CDT⁻ (n=1359; ~94%)
- ❖ The most prevalent RTs found in humans have also been found in animals or in the environment (see table)

Significance & future direction

- A heterogeneous *C. difficile* strain population was identified in Australia
- *C. difficile* RT 014/020 remained the most prevalent strain causing human CDI
- The detection of identical RTs commonly isolated from humans, animals and the environment supports the notion of a One Health approach to CDI management
- Antimicrobial resistance/susceptibility profiling for these strains is underway
- Whole genome sequencing will be performed to determine the bi-directional transmission mechanisms of *C. difficile* between healthcare and community settings
- On-going surveillance of circulating *C. difficile* strains in Australia remains important for the detection of emerging strains

Study design

- Bi-annual collection phases from 2013 to 2018
- February–March and August–September to represent summer/autumn and winter/spring seasons, respectively
- 10 laboratories across Australia; one private (representing community) and one public (representing hospitals) from five states in Australia
- PCR ribotyping and toxin profiling (TP) were performed²



Top 20 *C. difficile* RTs in Australia 2013-18

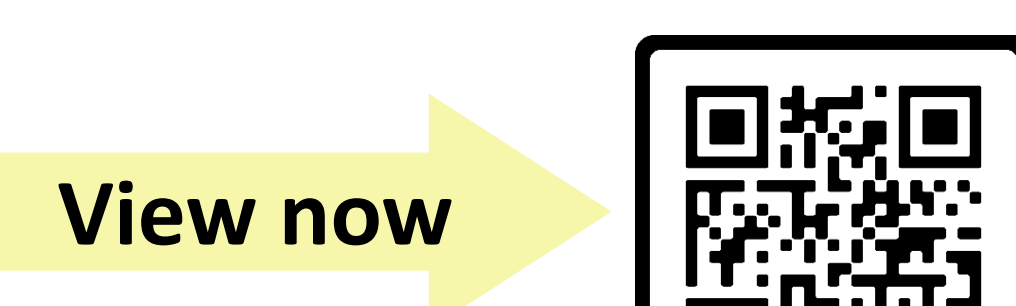
RT	TP	RT distribution							Total	%
		Site type		State						
		Private	Public	NSW	QLD	SA	VIC	WA		
014/020*	A+B+CDT ⁻	195	254	79	92	100	83	95	449	29.5
002^	A+B+CDT ⁻	82	97	76	43	24	19	17	179	11.8
056*	A+B+CDT ⁻	35	47	15	17	8	22	20	82	5.4
012	A+B+CDT ⁻	22	26	13	4	6	11	14	48	3.2
070	A+B+CDT ⁻	19	25	8	8	14	7	7	44	2.9
103	A+B+CDT ⁻	20	16	9	9	3	8	7	36	2.4
054	A+B+CDT ⁻	18	15	10	7	6	6	4	33	2.2
297/310	A+B+CDT ⁻	10	19	5	7	13	3	1	29	1.9
046	A+B+CDT ⁻	11	15	7	8	2	3	6	26	1.7
005	A+B+CDT ⁻	9	16	6	2	6	4	7	25	1.6
QX 076	A+B+CDT ⁻	12	12	3	5	4	8	4	24	1.6
106	A+B+CDT ⁻	12	9	6	7	1	4	3	21	1.4
017	A+B+CDT ⁻	9	12	4	6	4	2	5	21	1.4
043	A+B+CDT ⁻	7	11	4	2	4	7	1	18	1.2
137	A+B+CDT ⁻	10	7	3		5	4	5	17	1.1
126*	A+B+CDT ⁺	6	10	1	1	4	11		17	1.1
018	A+B+CDT ⁻	8	7	2	4	5	2	2	15	1.0
010*	A-B-CDT ⁻	12	3	4		2	5	4	15	1.0
QX 013	A+B+CDT ⁻	5	7	3	5	1	3		12	0.8
039	A-B-CDT ⁻	10	1				11		11	0.7

*Type known to be associated with animals⁶⁻⁸, food⁹ or the environment⁵; ^type known to be associated with increased morbidity and mortality¹⁰; significant increases compared to the previous study in red².

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