LABORATORY SURVEILLANCE OF PAEDIATRIC *CLOSTRIDIUM DIFFICILE* INFECTIONS IN HEALTHCARE AND COMMUNITY SETTINGS IN AUSTRALIA, 2013-18.

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Background

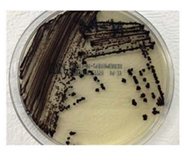
- *Clostridium difficile* is an obligately anaerobic spore-forming Gram-positive bacillus that colonises the gastrointestinal tract (GIT) and proliferates due to distortion of the GIT microbiota from antimicrobial exposure (1).
- Clinical manifestations include mild-to-moderate diarrhoea, while complications include pseudomembranous colitis and toxic megacolon (1). Asymptomatic colonisation is rare (1-7%) in healthy adults however can be frequent in infants (2-75%) (2).
- Rising rates of **hospital-acquired (HA)** and **community-acquired (CA)** *C. difficile* infection (CDI) in children have been recorded in many parts of the world (3, 4).
- Research on paediatric *C. difficile* in Australia is limited.
- CDARS (*C. difficile* Antimicrobial Resistance Surveillance) is a nation-wide longitudinal surveillance study of the molecular epidemiology and antimicrobial resistance profiles of *C. difficile* isolates in Australian healthcare settings (both **hospital** and **community**) between 2013 and 2018.

Aim

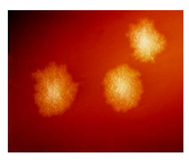
To describe the different strains of *C. difficile* circulating within the paediatric population in Australia over a period of 5 years.

Methods

- *C. difficile* isolates (or PCR positive stool samples) were sent from 10 laboratories (one public and one private laboratory per state) across 5 different states in Australia, 2013 – 2018.
- Inclusion criteria: patient ages ranged from <1 to 17 years.
- All isolates were cultured on *C. difficile* selective media (ChromID plates), then sub-cultured onto pre-reduced blood agar to be identified based on the distinctive horse dung odour, ground-glass colony morphology and the characteristic chartreuse fluorescence under long-wave UV light (360nm).



C. difficile on ChromID



C. difficile on blood agar

- PCR toxin profiling and ribotyping were performed (5, 6).
- PCR ribotypes (RTs) were then identified by comparing banding patterns to our reference library.

Results and Discussion

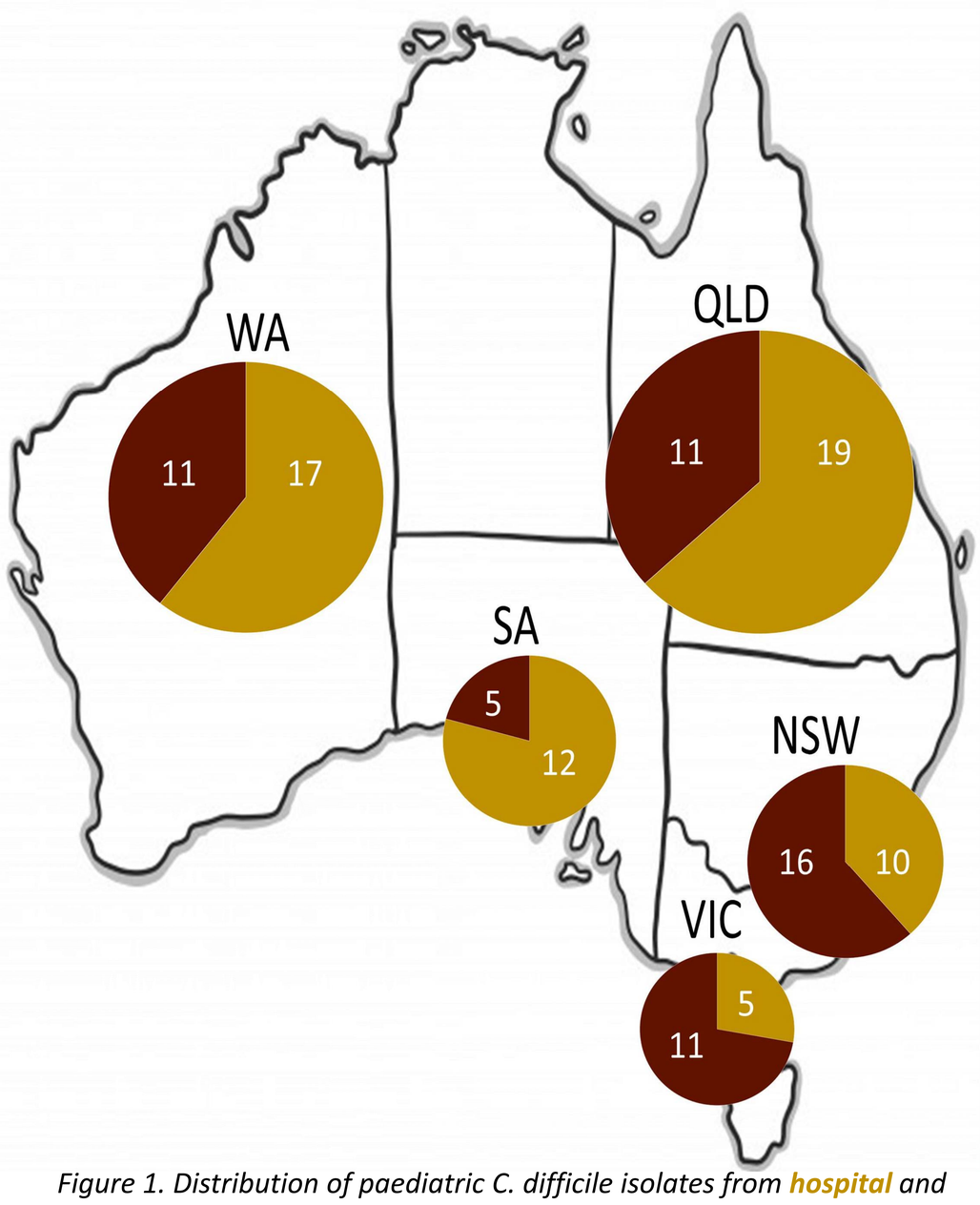
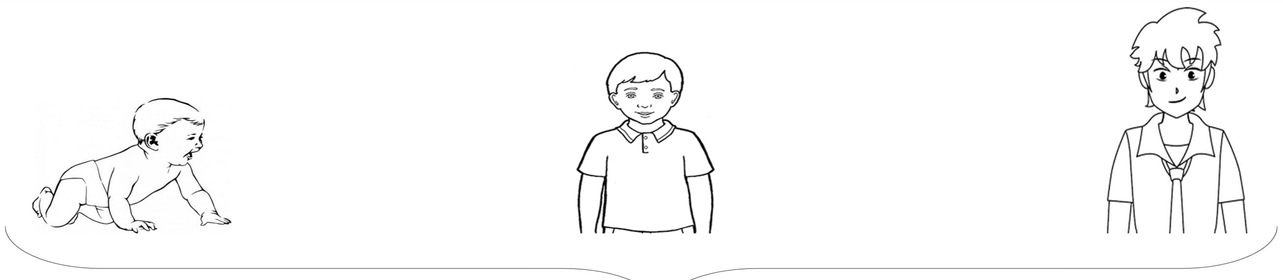


*Figure 1. Distribution of paediatric C. difficile isolates from **hospital** and **community** settings in the different states of Australia.*



- 127 of 1542 (8.2%) isolates were culture positive paediatric isolates.
- Patient demographics → median overall: 3 years old; female: 57/127 (44.9%); male: 70/127 (55.1%)
- 112 (88.2%) isolates were toxigenic (**A+B+CDT-, *n*=104**; **A+B+CDT+, *n*=6**; **A-B+CDT-, *n*=2**).
- 34 different RTs were identified.
- Most common RTs isolated were toxigenic RTs 014/020, 002, 046 and 056 (Figure 2).
- **RT 027** and **RT 244**, both epidemic strains of *C. difficile,* were isolated from an 11-year-old patient in a QLD public **hospital** and 1-year-old from the NSW **community**, respectively.
- Other binary toxin positive strains are likely to be endemic to Australia.

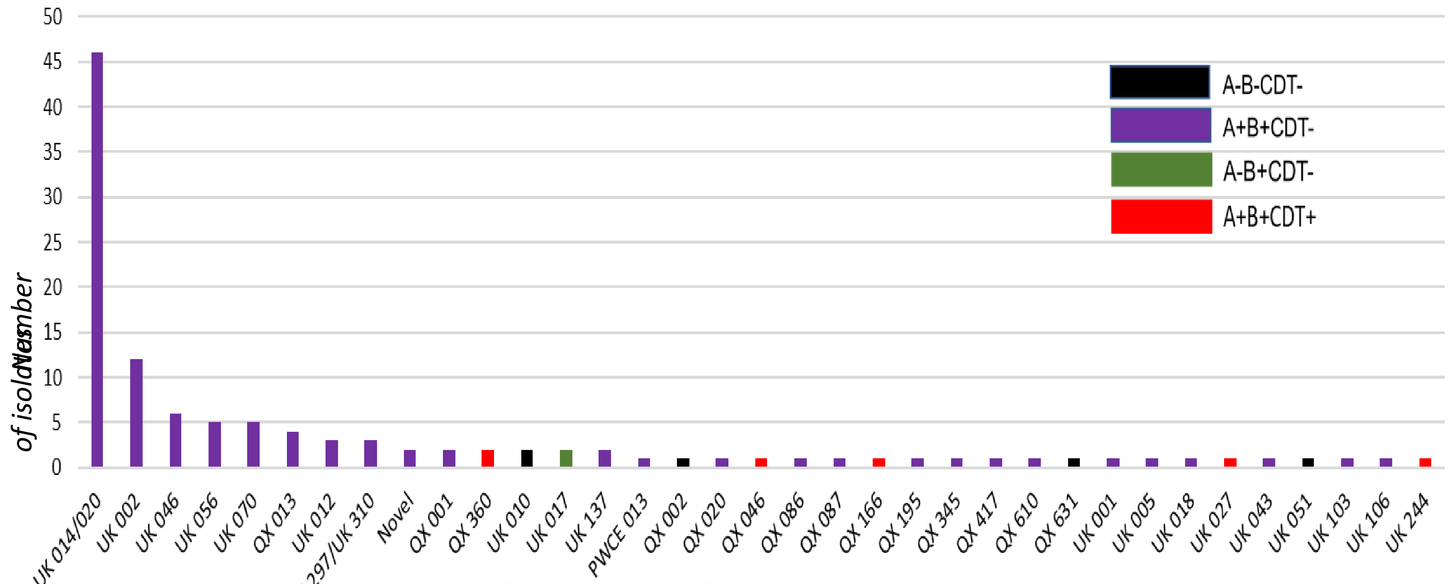


Figure 2. PCR RTs of C. difficile

- The diversity of RTs suggest the possibility of paediatrics patients acquiring infections from reservoirs located beyond **hospital** grounds (Figure 1 and 2).
- *C. difficile* RT 014 has been identified in both **CA** and **HA** CDI cases and is well-established in both human and pig populations in Australia, raising the possibility that CDI may have a zoonotic or foodborne aetiology (7). RT 020 has been isolated from lawn, mulch, compost, root vegetables and animal manure (8, 9).
- RT 046 is often found in China, however, this strain has been isolated in Australia from both human beings and other sources (10, 11).
- RT 056 has been isolated predominantly from production animals and retail root vegetables (9-11) adding further weight to a zoonotic or foodborne aetiology.
- RT 002 has been recovered frequently from CDI patients in Hong Kong (10) and is identified commonly from different **community** environmental sources in Australia (8).
- Epidemic **RT 027** has not established in Australia, however, the isolation from a 11 year old in QLD public hospital raises questions regarding possibilities of *C. difficile* transmission from overseas and whether it is capable of disseminating within local **hospital** (and **community**) grounds.

Future directions

- Distinguishing between **CA-CDI** and **HA-CDI** in children: Test for colonisation of *C. difficile* on admission (excluding neonates and infants below 1 year old).
- Finding the sources of transmission in both **community** and **hospital** settings via whole genome sequencing and core genome single nucleotide polymorphism analysis: Genomic relatedness between isolates from paediatric patients and other sources of contamination.
- Conducting antimicrobial susceptibility tests on paediatric *C. difficile* isolates.

Conclusions

1. CDI is no longer a just HA pathogen in children.

2. A heterogeneous strain population was isolated, dominated by RT 014/020 – a strain commonly isolated from human, animal and environmental sources.

3. Continued surveillance of current and emerging strains, in both rural and urban regions of Australia, is important to better understand and eventually reduce the burden of paediatric CDI.

References

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