**INTRODUCTION**

Clostridium (Clostridioides) difficile is a Gram-positive, spore-forming, rod-shaped anaerobic bacterium that is found in the environment and the gastrointestinal tracts of young individuals (both human and non-human). It is the causative agent of pseudomembranous colitis and a predominant cause of life-threatening antimicrobial-associated diarrhoea worldwide [1]. C. difficile infection (CDI) has been thought of as a healthcare-associated infection, and its increasing incidence, severity and recurrence make it a major healthcare threat [2]. In recent years, community-acquired CDI (CA-CDI) has emerged as a significant health problem, accounting for ~50% of all CDI cases [3]. Possible sources of CA-CDI are soil, food and water contaminated with strains of C. difficile from animals. More broadly, contaminated home gardens and shoe soles could contribute to the dissemination of C. difficile spores in the community.

**AIM:** To assess the prevalence of C. difficile in home gardens, including soil, compost, manure and shoe soles samples collected from community home gardens in Western Australia (WA).

**MATERIALS AND METHODS**

In total, 97 samples consisting of soil (n=48), compost (n=15), manure (n=12) and shoe sole swabs (n=22) were collected from 23 homes in 22 suburbs of Perth, WA, during 2018. Approximately 5 g of soil/compost samples were enriched in 90 mL brain heart infusion broth (BHIB) (supplemented with 1 g/L taurocholate, cefoxitin (10 mg/L) and cycloserine (200 mg/L) which was pre-reduced for 4 h in an anaerobic chamber, and incubated at 35°C for 5 days with the lids loose, followed by alcohol shock and plating onto ChromID agar plates (bioMerieux). Viable counts of C. difficile from soil, compost and manure were determined from a subset of samples. The total number of colony forming units (CFU) in 100 µL were converted to CFU/mL and multiplied with the average maximum viable counts were in enrichment procedure). RT 014/020, RT 014 and RT 010). Two-thirds (67%, 65/97) of the isolates were toxigenic (A+B+CDT+, n=1; A+B−CDT−, n=27; A−B+CDT+, n=1; A+B−CDT−, n=4).

**RESULTS**

Two-thirds (67%, 65/97) of home garden samples were positive for C. difficile (Fig 1), yielding 87 isolates. Among them, 38% (33/87) of the isolates were toxigenic (A+B+CDT+, n=1; A+B−CDT−, n=27; A−B+CDT+, n=1; A+B−CDT−, n=4).

26 different PCR ribotypes (RTs) were identified. The toxigenic C. difficile strain, UK 014/020, was the most prevalent (20.7%, 18/87) (Fig 2). RT 014/020 was also the only RT found in all sources (soil, compost, manure and shoe soles). Of note, 21.8% (19/87) of the isolates produced white colonies on ChromID plates, indicating that the ylack esculin hydrolysis enzyme. Of these, four were toxigenic but produced only toxin A (A+B−CDT−) and 5 isolates were UK 125 (A−B−CDT−).

Both esculin hydrolysis negative and positive colonies were recovered from the same samples with mixed RTs (RT 014/020, RT 014 and RT 010). Through direct culture method, 41% (40/97) of C. difficile were recovered (the rest recovered only after a culture enrichment procedure).

The average maximum C. difficile viable counts were in compost (2028 CFU/g) followed by manure (619 CFU/g) and soil (554 CFU/g).

**CONCLUSIONS**

A high prevalence of C. difficile in home gardens and the RTs 014/020, 056, 054, 010 and 103 identified from this study had been isolated from humans with CDI in WA dearly indicated that home gardens may be a possible reservoir for the dissemination of C. difficile spores in the environment which subsequently cause CA-CDI.

Our findings highlight the importance of a "One Health" approach to dealing with CDI.

Further investigation is required to compare the relatedness of these isolates with isolates from CA-CDI cases by whole genome sequencing.

**REFERENCES**