

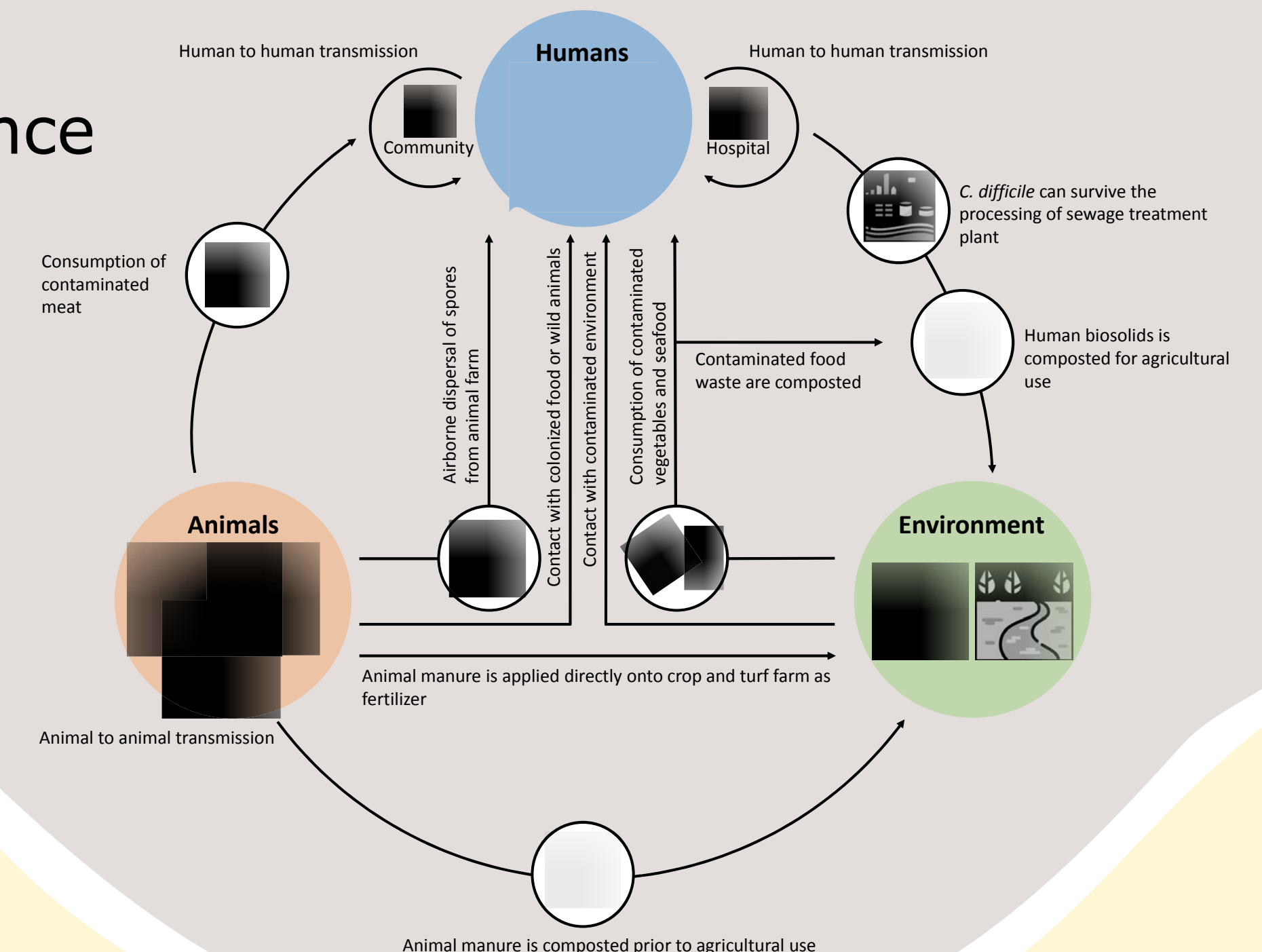
Molecular Epidemiology and Biogeographic Distribution of *Clostridium difficile* strains in Soils of Western Australia

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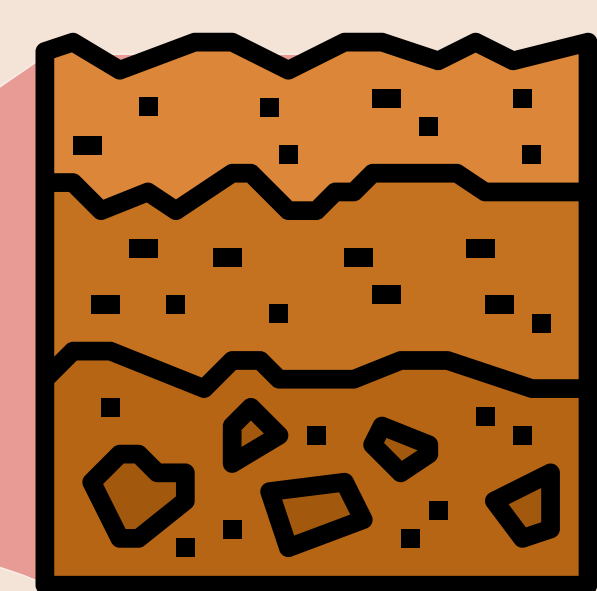
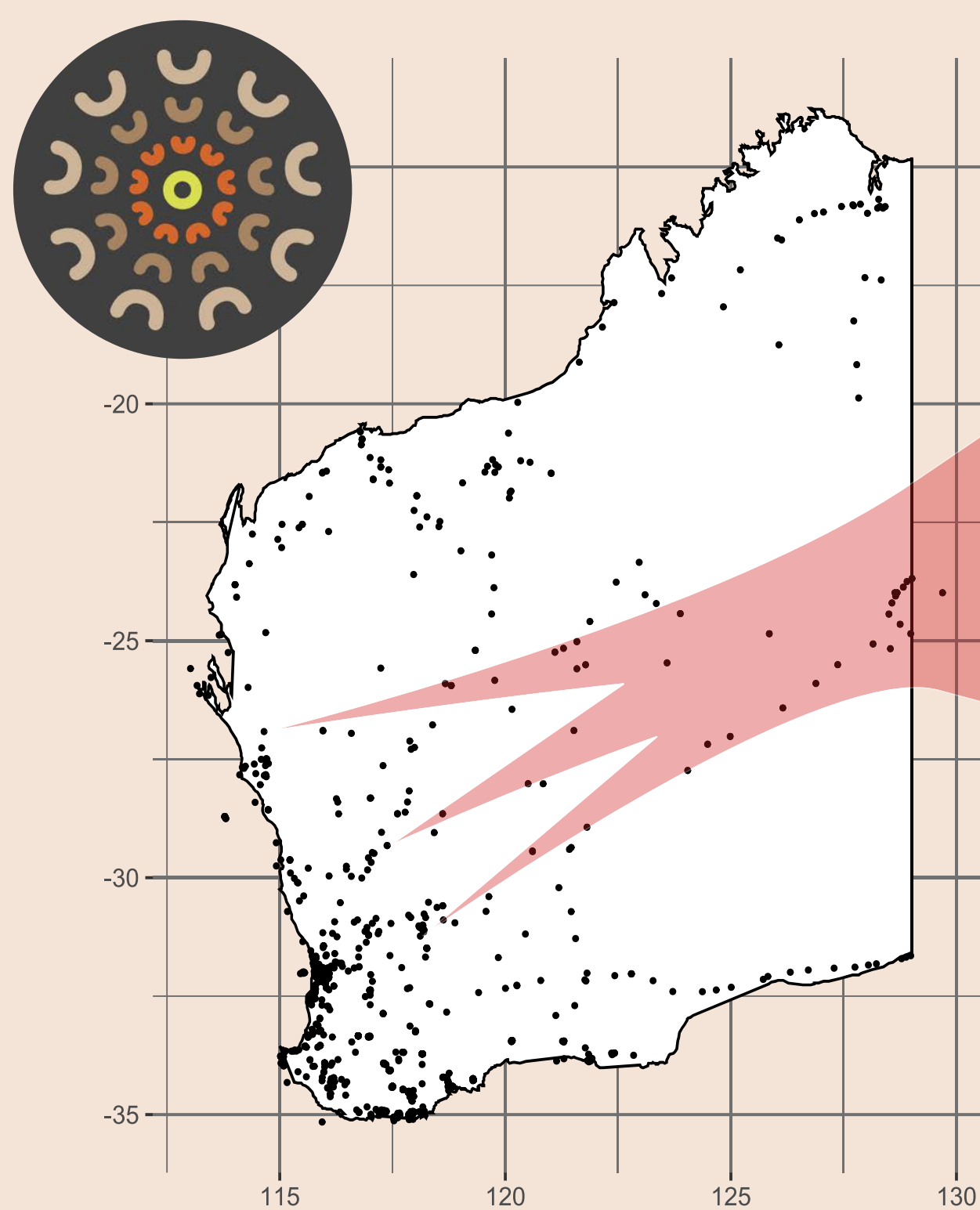
Introduction *Clostridium difficile* can be found in a variety of environmental sources worldwide. Genomic studies have shown that diverse sources of *C. difficile* play an important role in transmission. Data from Australia is particularly compelling. *C. difficile* is well established in livestock. The most common strains identified in Australian livestock are RT014 (MLST clade 1) and strains belonging to ST11 (MLST clade 5), both lineages recovered from humans in Australia and overseas. The prevalence and diversity of ST11 strains in Australian production animals suggests Australia might be the ancestral home for this lineage of One Health importance. To better understand the role of the environment in the colonisation of humans/animals in Australia, it is critical to investigate endemic sources of *C. difficile* in Australia. This study aims to describe for the first time the molecular epidemiology and biogeographic distribution of *C. difficile* in soils in Western Australia.



Methods

I. Soil collection

127 soil samples from 8 Health region areas (2,527,013 km²)



II. Isolation and Molecular characterisation

Anaerobic culture

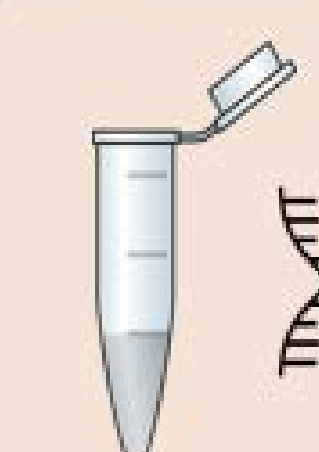
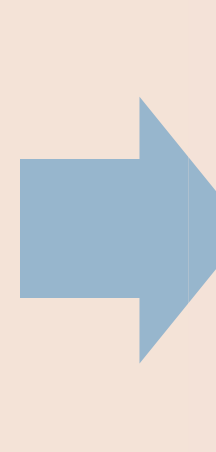


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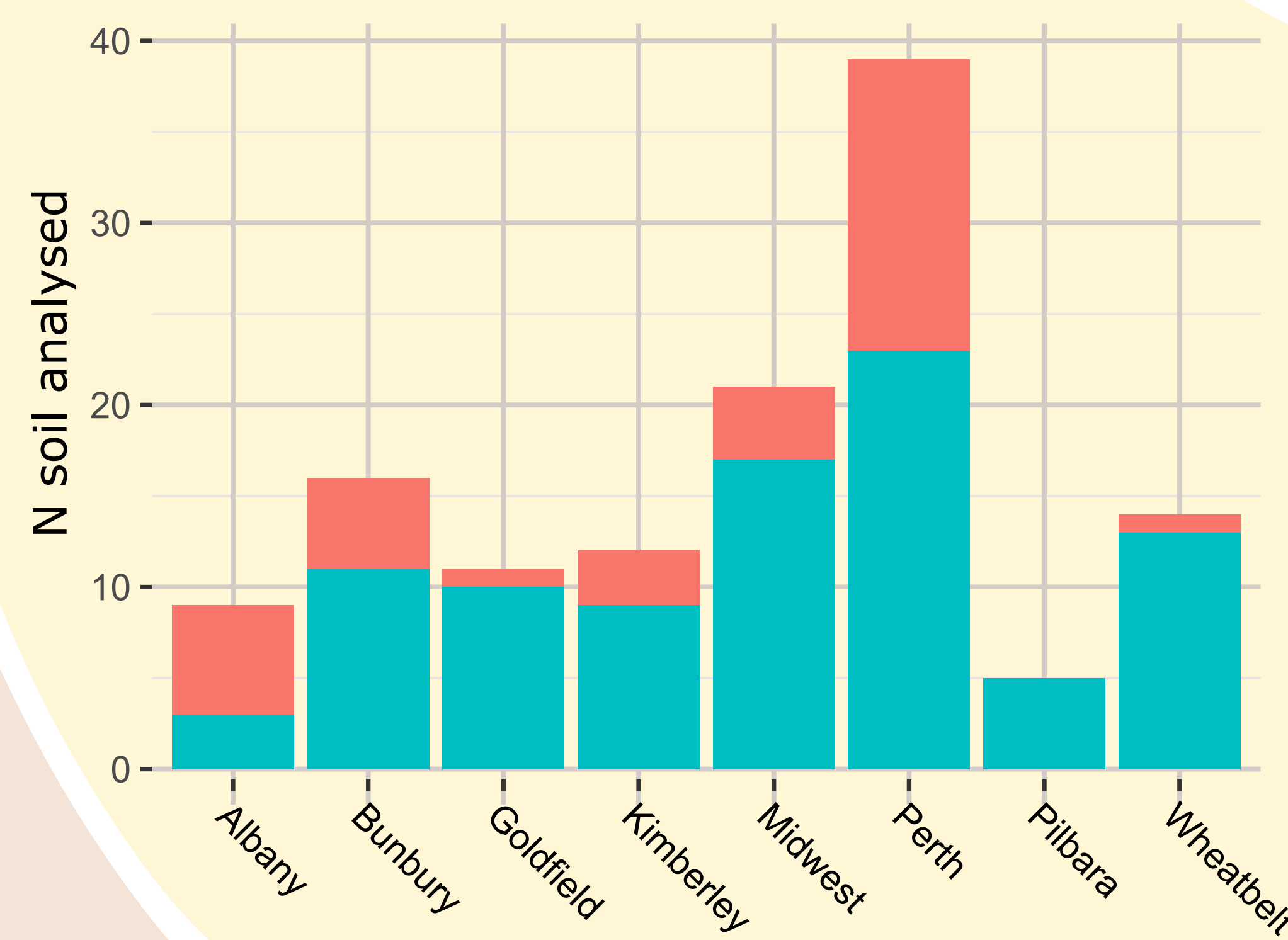
Molecular Epidemiology

- > Toxin gene profiling (*tcdA*, *tcdB*, *cdtA/B*)
- > PCR ribotype (16s-23s rRNA spacer region)

gDNA extraction



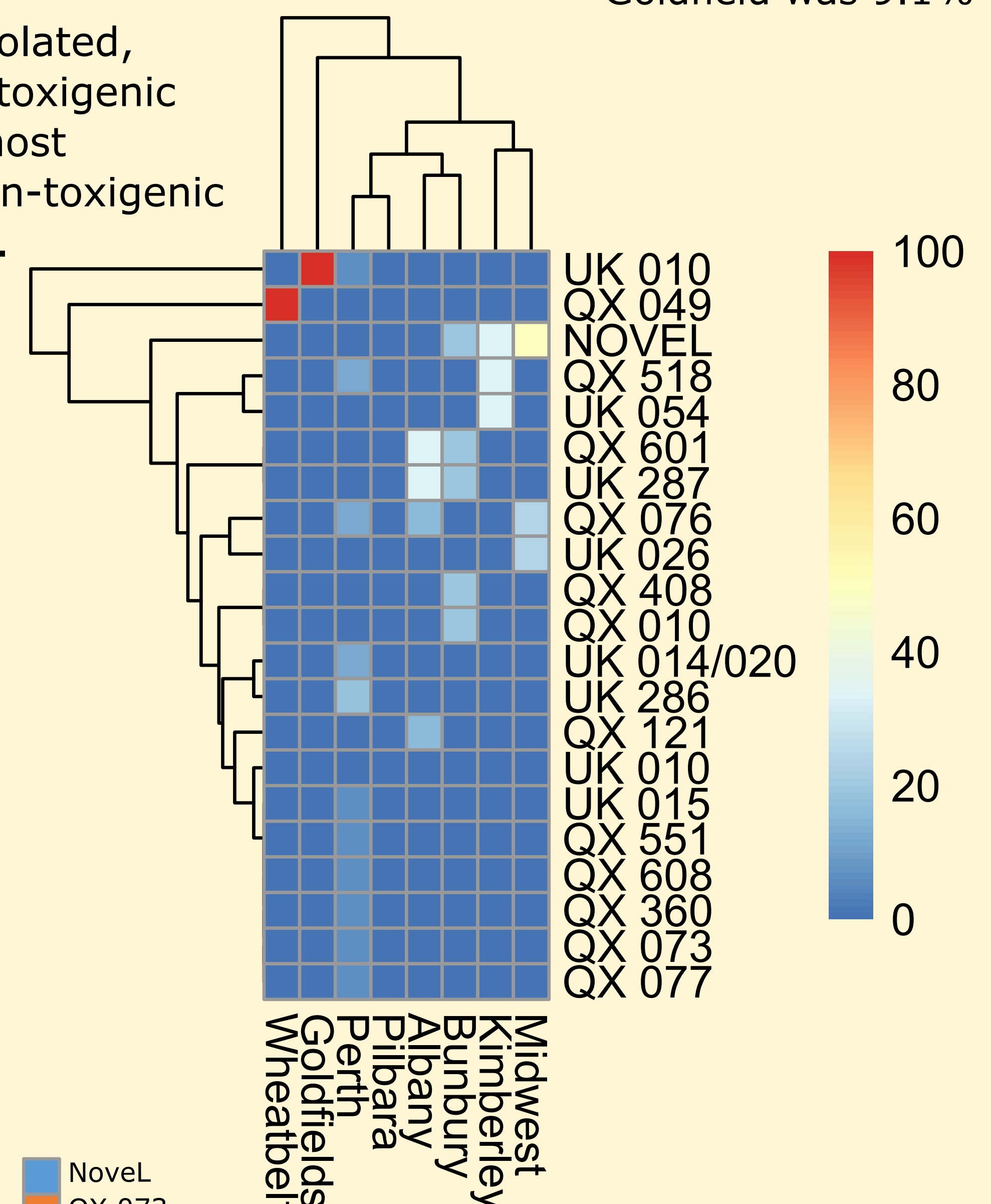
Results



Positive
Negative

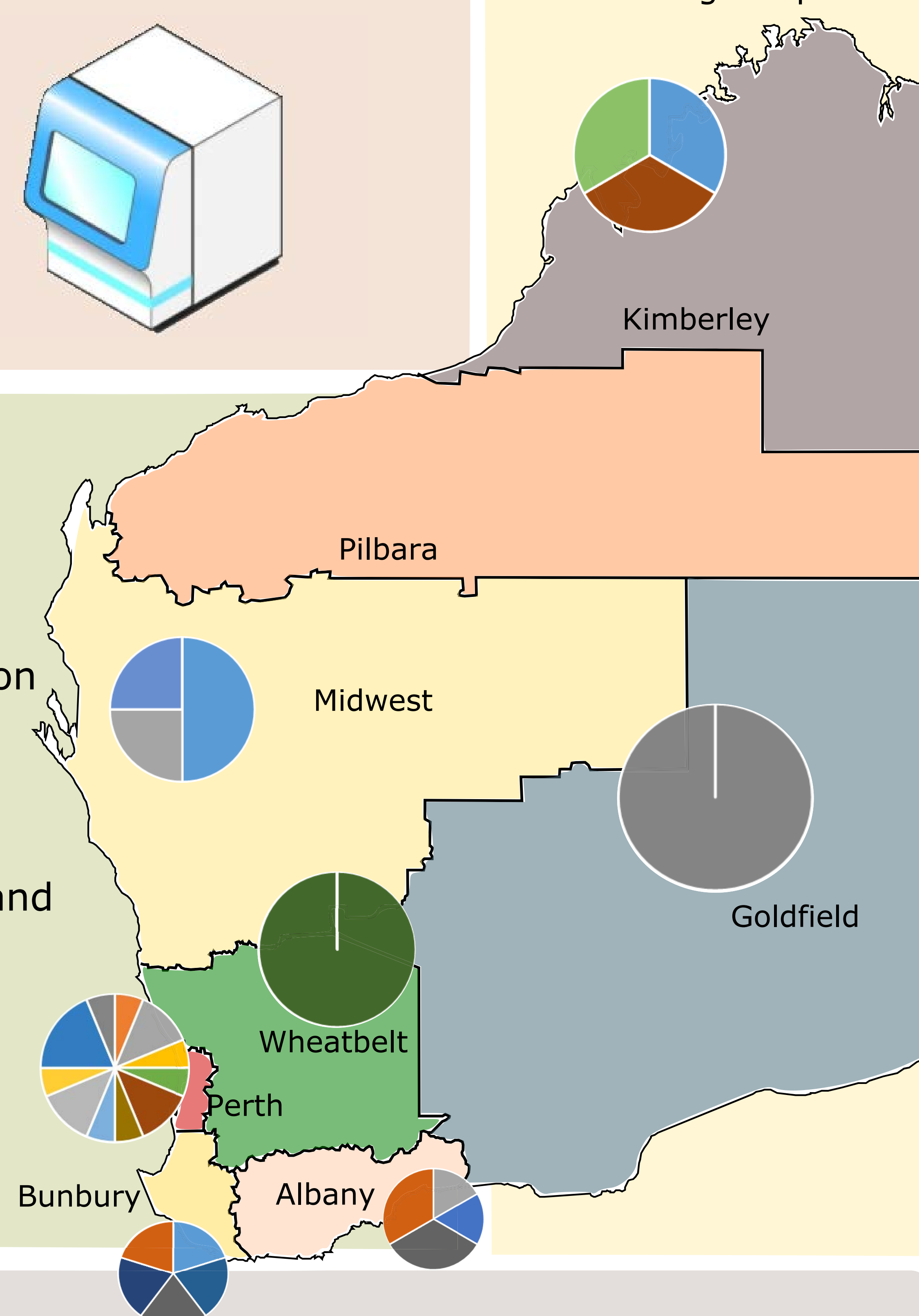
C. difficile was isolated from 28.3% of samples (36/127). It was recovered from seven of the eight health service locations. The highest prevalence was found in the Albany region (72.7%) followed by Perth Metropolitan (56.1%), Bunbury (42.1%) and Kimberley (33.3%) regions. The Midwest and Wheatbelt regions had a similar prevalence (~17%) while in the Goldfield was 9.1%

Of the 21 different RTs isolated, QX076 and QX518, both toxigenic (A+B+CDT-), were the most prevalent, followed by non-toxigenic RTs QX601, 286 and 287. Four novel strains were found, one of them with a toxigenic profile.



Discussion

This is the first study of *C. difficile* isolated from soils in Australia. The high prevalence and diverse composition of *C. difficile* strains found suggest that this environmental source may be contributing to the transmission of *C. difficile* in the community, hospital and production animal settings. These data further support the paradigm that CDI is an important One Health issue and that Australia might be the ancestral home of *C. difficile* MLST clade 5.



The highest prevalence of toxigenic strains was found in the Perth Metropolitan region (72.7%; n=8/11). The percentage of RT diversity per health region shows that Perth is the most diverse area. Isolates from Bunbury and Albany had a similar strain composition.

References

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Short Bio

Karla Cautivo is a first-year PhD candidate at Murdoch University in Western Australia. Karla did her Bachelor and Honours degrees in Chile before moving to Australia to start a research career. Her PhD work focuses on the natural history, molecular epidemiology and genomics of the enteric pathogen *Clostridium difficile*, under the supervision of Professor Thomas V. Riley and Dr Daniel R. Knight within the Department of Medical, Molecular and Forensic Science.

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