Whole genome sequence analysis of *Clostridium difficile* ribotype 017 strains in hospital patients in Cape Town, South Africa

Brian R. Kullin[1], Daniel R. Knight[2], Sharon J. Reid[1], Valerie R. Abratt[1], Thomas V. Riley[2,3,4]

[1]Dept of Molecular and Cell Biology, University of Cape Town, Cape Town, South Africa;
[2]Medical, Molecular and Forensic Sciences, Murdoch University, Murdoch, Western Australia (WA);
[3]Edith Cowan University, Joondalup, WA; [4]PathWest Laboratory Medicine, Nedlands, WA

Introduction

- *Clostridium difficile* PCR ribotype (RT) 017 was the predominant RT in patients attending hospitals in the Cape Town metropole in 2014-2015[1]
- Preliminary multilocus variable-number tandem-repeat analysis showed a high level of inter-strain relatedness, indicative of possible patient-to-patient transmission
- *In vitro* antimicrobial susceptibility testing revealed multidrug resistance for the majority of the isolates

Aims

To carry out WGS analysis of *C. difficile* RT017 strains from Cape Town hospitals to examine strain transmission and the genetic basis of antimicrobial resistance (AMR)

Methods

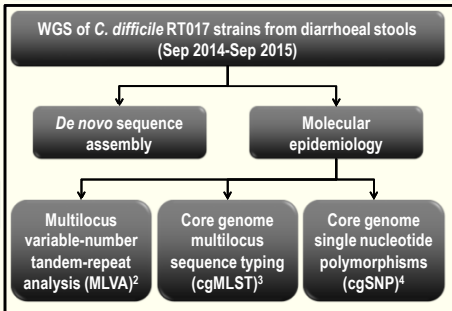


Figure 1: Flowchart of methods

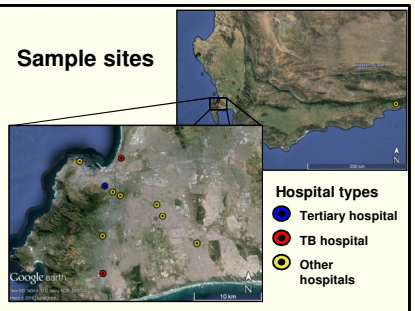


Figure 2: Locations of participating hospitals in Cape Town

Results

SA RT017 *C. difficile* strains harboured a number of AMR determinants

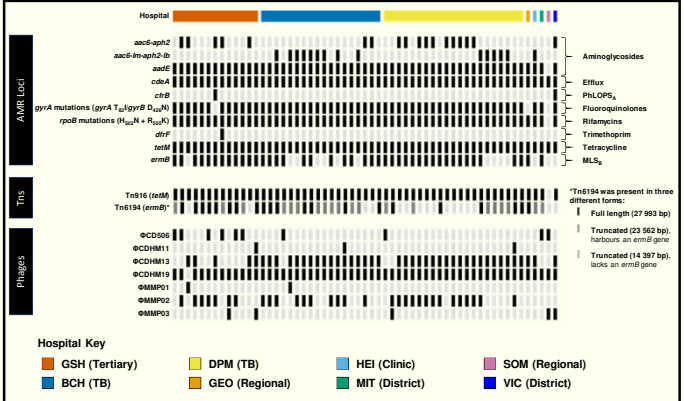


Figure 3: Antimicrobial resistance (AMR) loci and predicted intact prophages present in South African RT017 isolates. The presence and absence of AMR loci, transposons and phages is indicated in each case by black and grey bars respectively. **Note:** Three distinct versions of the Tn6194 transposon were present as indicated by the different bars.

High resolution profiling identified 182 high-quality biallelic SNPs

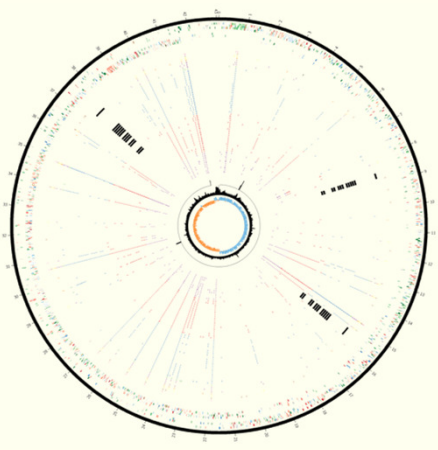
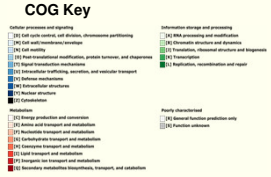


Figure 4: SNPs between *C. difficile* M68 and 57 South African RT017 isolates. The outermost ring represents position with respect to the M68 *C. difficile* reference genome. The next six rings represent annotated genes on the forward strand (first 3 rings) and the reverse strand (next 3 rings), coloured according to the respective COG function. The two innermost rings represent GC skew (<0% orange, >0% blue) and GC content (black histogram). The third ring represents SNP density in 10 kbp windows. The remaining 57 rings represent the location of SNPs in each strain, coloured according to hospital. Finally, regions of recombination identified by the Gubbins algorithm are represented by black blocks.

COG Key



High-resolution typing suggested intra- as well as inter-hospital strain transmission

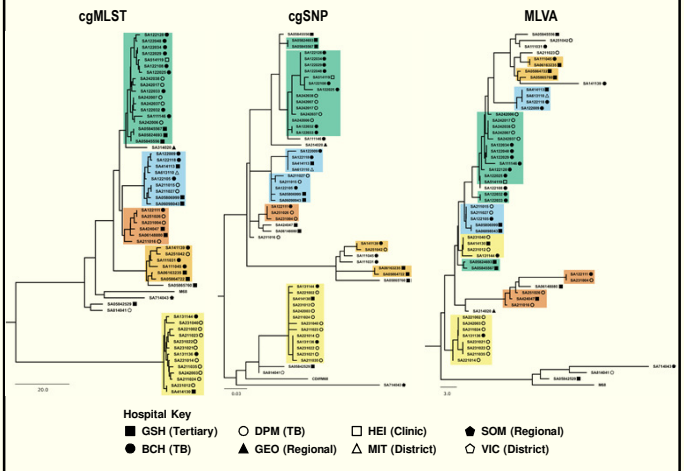


Figure 5: Clustering of isolates by cgMLST, cgSNP and MLVA. Shaded areas represent clusters of clonally-related strains identified by each method. Similar colours are used to facilitate visual comparison between methods. The following cutoffs were used to classify clonally-related strains: cgMLST ≤ 6 loci different, cgSNP ≤ 2 single nucleotide variants, MLVA ≤ 2 summed tandem repeat distance.

cgMLST and cgSNP typing methods were highly congruent

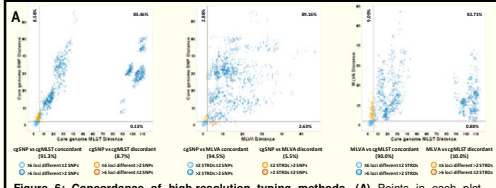


Figure 6: Concordance of high-resolution typing methods. (A) Points in each plot represent pairwise comparisons for every pair of isolates using each of the three typing methods. **(B)** Diversity [Simpson's index] and congruence measurements (adjusted non-directional [Rand] and directional [Wallace] coefficients).

Strains isolated from the same hospital were not more closely related than strains isolated from different hospitals

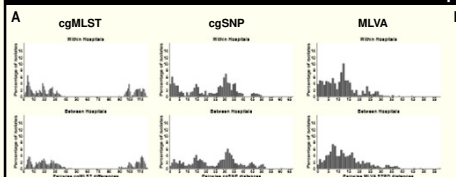


Figure 7: Pairwise comparisons between isolates. (A) Distances according to cgMLST, cgSNP and MLVA between every pair of isolates stratified according to whether the pair was isolated from the same ("Within Hospitals") or different ("Between Hospitals"). **(B)** Proportions of isolates for which the closest related strain was isolated from the same hospital, a different hospital or both.

Conclusions

This is the first study to carry out a detailed genomic analysis of South African *C. difficile* strains. The results suggest that:

1. SA RT017 isolates harboured a diverse array of antimicrobial resistance determinants, which was correlated with phenotypic resistance to moxifloxacin, erythromycin, rifampicin and tetracycline
2. Clonally-related RT017 strains were circulating within patients attending public hospitals in the Cape Town area during the study period
3. WGS-based methods (cgSNP and cgMLST) provided similar levels of resolution when used to analyse RT017 strains, whereas MLVA had higher discriminatory power but was a poor predictor of clustering by the WGS-based methods

References

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Funding sources

National Research Foundation
Australia Awards
Carnegie Corporation of New York

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