

Species-Wide Genetic Atlas of Antimicrobial Resistance in *Clostridioides difficile*

Korakrit Imwattana¹, César Rodríguez², Thomas V Riley^{1,3,4,5} and Daniel R Knight^{1,3}

¹ School of Biomedical Sciences, The University of Western Australia, Western Australia
² Facultad de Microbiología & Centro de Investigación en Enfermedades Tropicales (CIET), Universidad de Costa Rica, Costa Rica
³ School of Veterinary and Life Sciences, Murdoch University, Western Australia
⁴ School of Medical and Health Sciences, Edith Cowan University, Western Australia
⁵ Department of Microbiology, PathWest Laboratory Medicine, Queen Elizabeth II Medical Centre, Western Australia

Background and Objectives

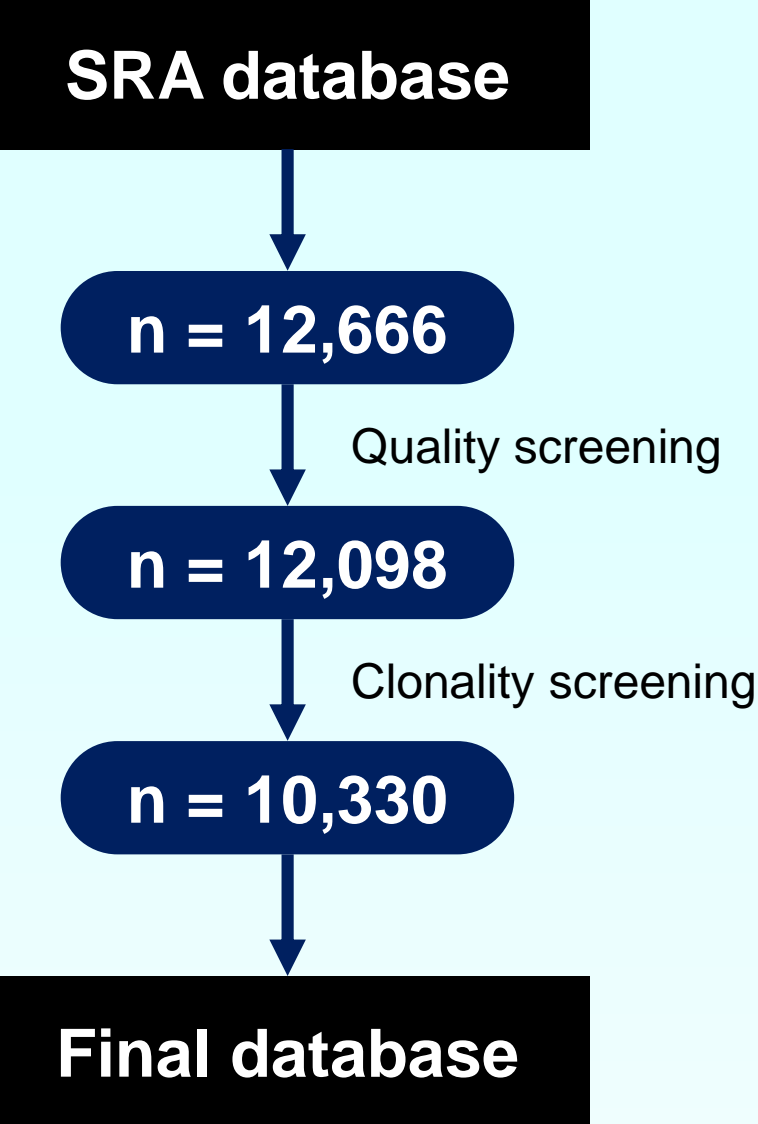
Antimicrobial resistance (AMR) plays an important role in the spread and pathogenesis of *Clostridioides difficile* infection (CDI). An association between AMR and CDI outbreaks has been identified^{1,2,3}, however, such studies have been limited to a few strains in limited geographical regions.

This study aimed to investigate the prevalence of AMR genotypes in the global population of *C. difficile*.

Methods

- All publicly available genomes were downloaded.
- All non-redundant genomes were screened for quality and contamination using kraken2⁴.
- Genomes of epidemic strains (sequence types (STs) 1, 2, 11 and 37) were screened for clonality (nucleotide identity > 99.98%) using SRST2⁵ and Sketch⁶, respectively.
- All remaining genomes were interrogated against several AMR databases.[#]

Sample size



Gene databases[#]

Gene alleles

- MLST alleles⁷
- *gyrA*/*gyrB*⁷ (Fluoroquinolones)
- *rpoB*⁷ (Rifamycins)
- *pbp1* & *pbp3*^{*} (Carbapenems)

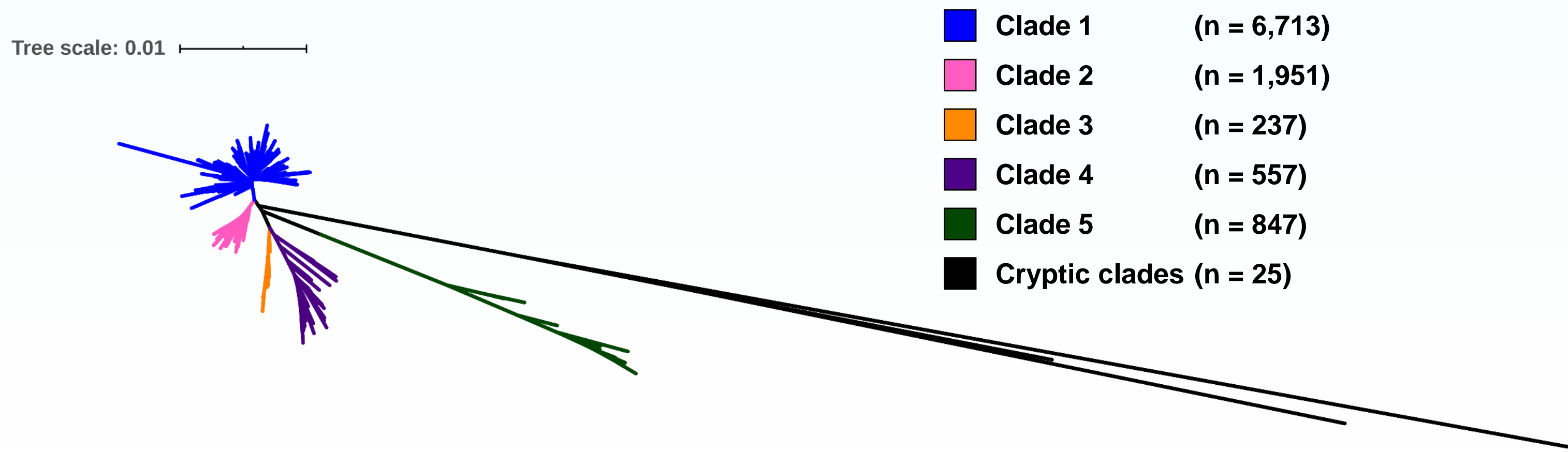
Accessory genes

- ARGannot⁸
- Resfinder⁹
- ^{*} customised databases

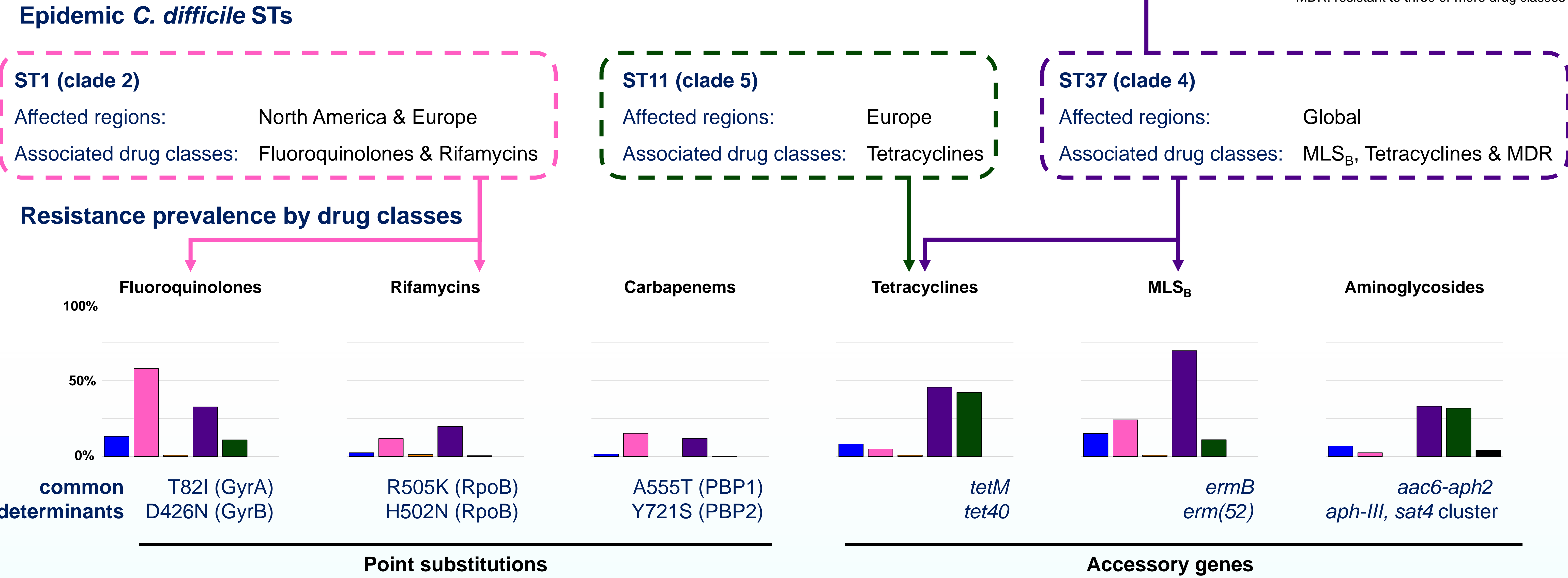
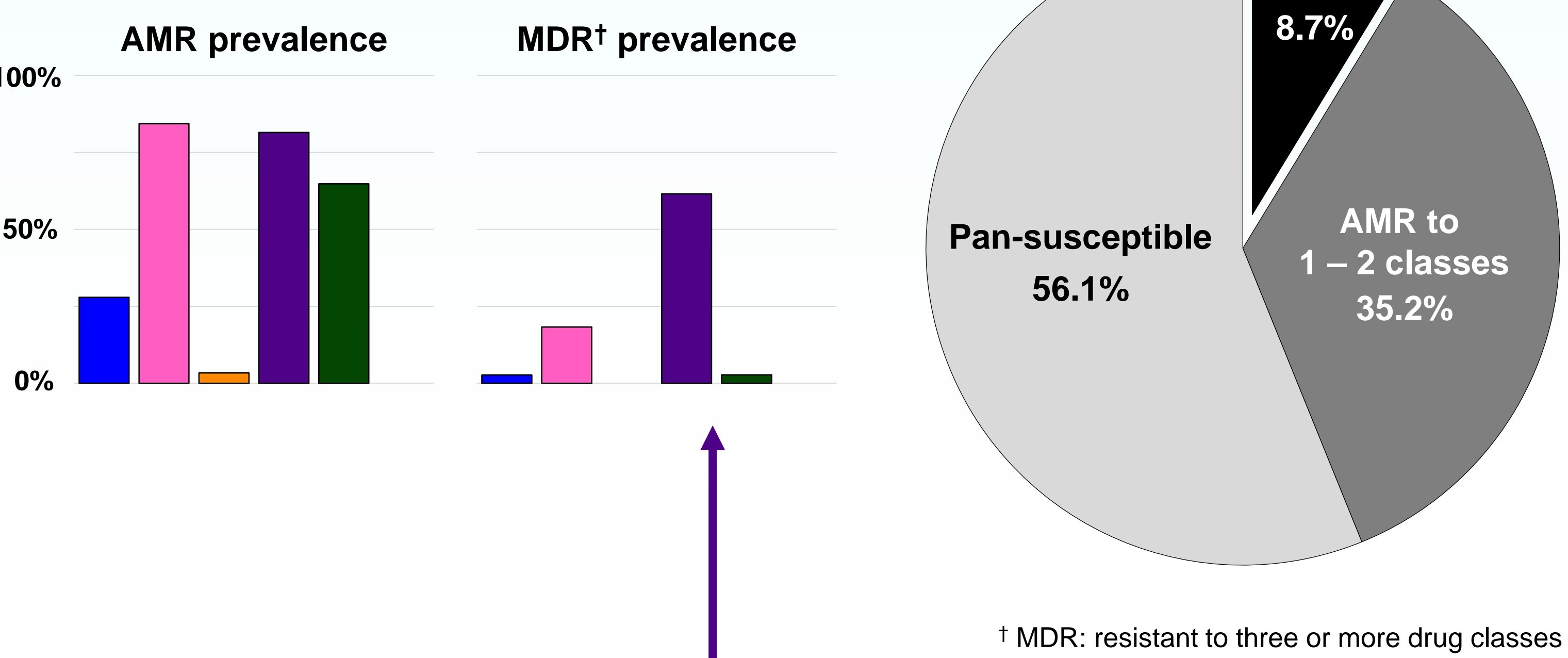
Detailed methods available here

Results

1. Population structure of *C. difficile*



2. Overall AMR prevalence



Conclusion

There was a higher prevalence of AMR among epidemic *C. difficile* lineages. Despite its intrinsic resistance, some *C. difficile* strains carried aminoglycoside resistance genes, suggesting its role as a reservoir of AMR genes.



References

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