

Transmission of antimicrobial resistance in the gut microbiome of subsocial insects

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INTRODUCTION

Antimicrobial resistance:

- major threat to global health
- harboured by pathogenic & commensal bacteria
- transmission in populations not fully understood

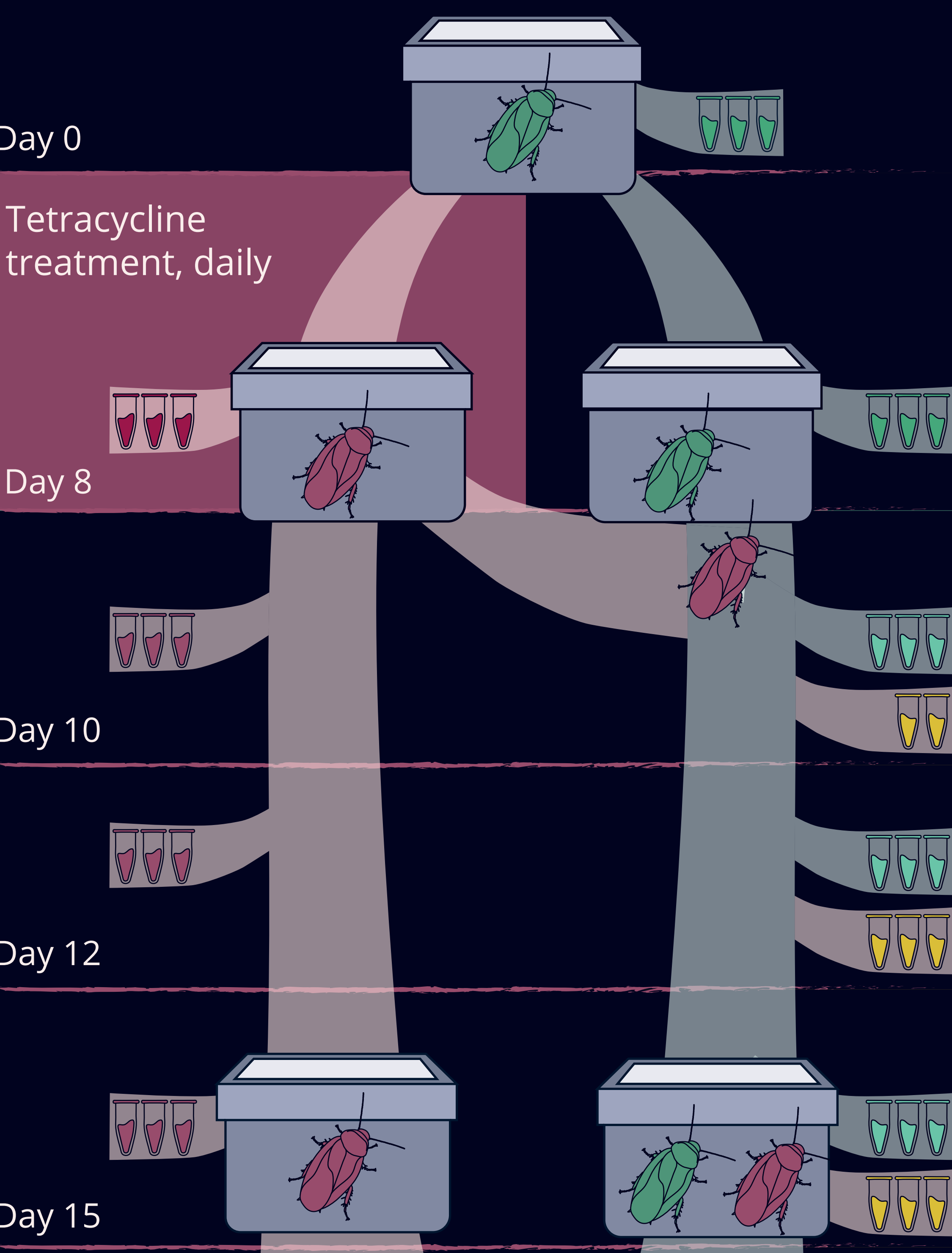
Semisocial cockroach microbiomes:

- species: *Pycnoschelus surinamensis*
- diverse gut microbiome & semisocial lifestyle
- potential organism for antimicrobial resistance studies

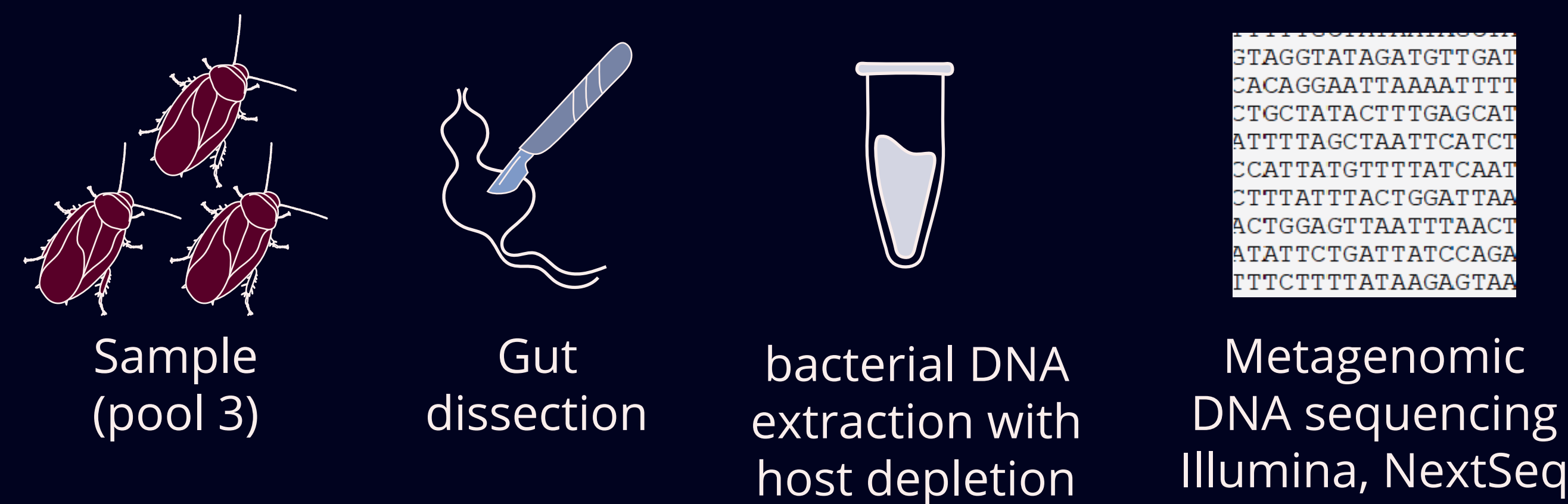
Goal:
Evaluate the effect of tetracycline on gut microbiome and the transmission of resistance between treated and not-treated populations

METHODS

EXPERIMENTAL SETUP



SAMPLE PROCESSING



BIOINFORMATIC PROCESSING

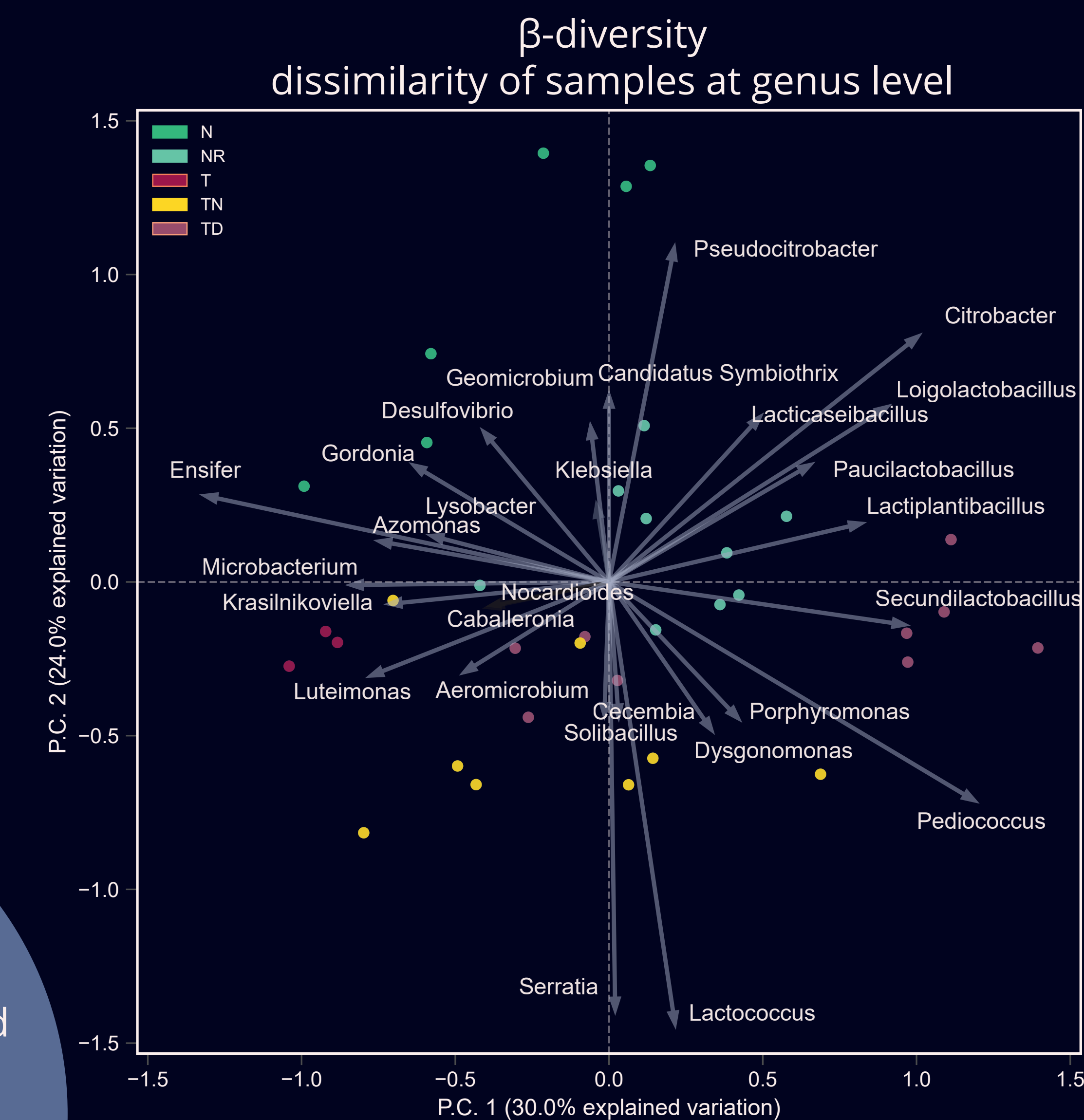
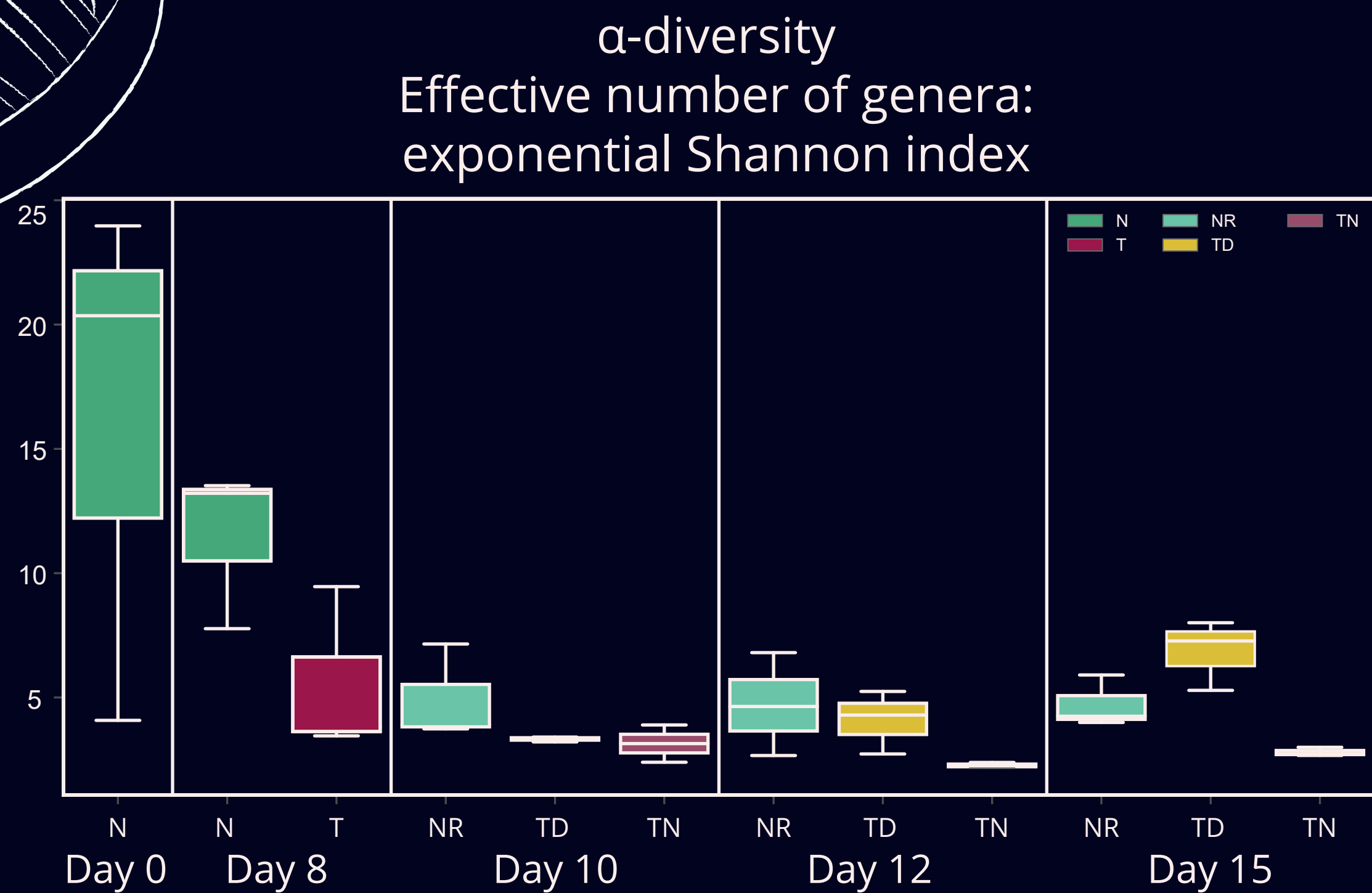
Data stored & analysis performed on Computerome 2.0
Data trimming pipeline with FastQC & bbdutk2

Sequences aligned & mapped with KMA:

- genomic database (taxonomic identification)
- ResFinder database (antimicrobial resistance genes)

ANALYSES AND RESULTS

BACTERIAL COMMUNITY



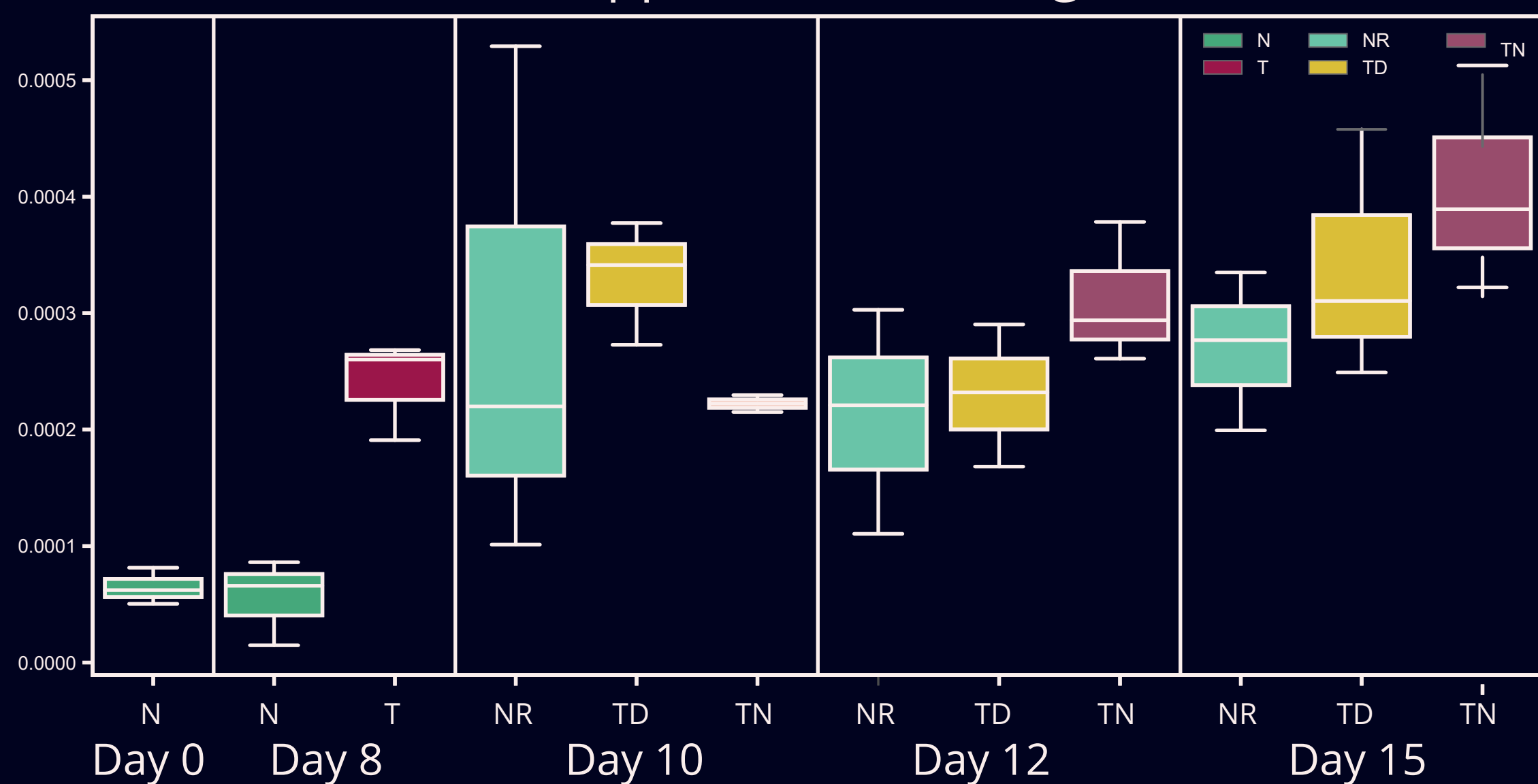
CONCLUSIONS

Antimicrobial treatment and bacterial transmission affected the AMR gene profile and the composition of the bacterial community.

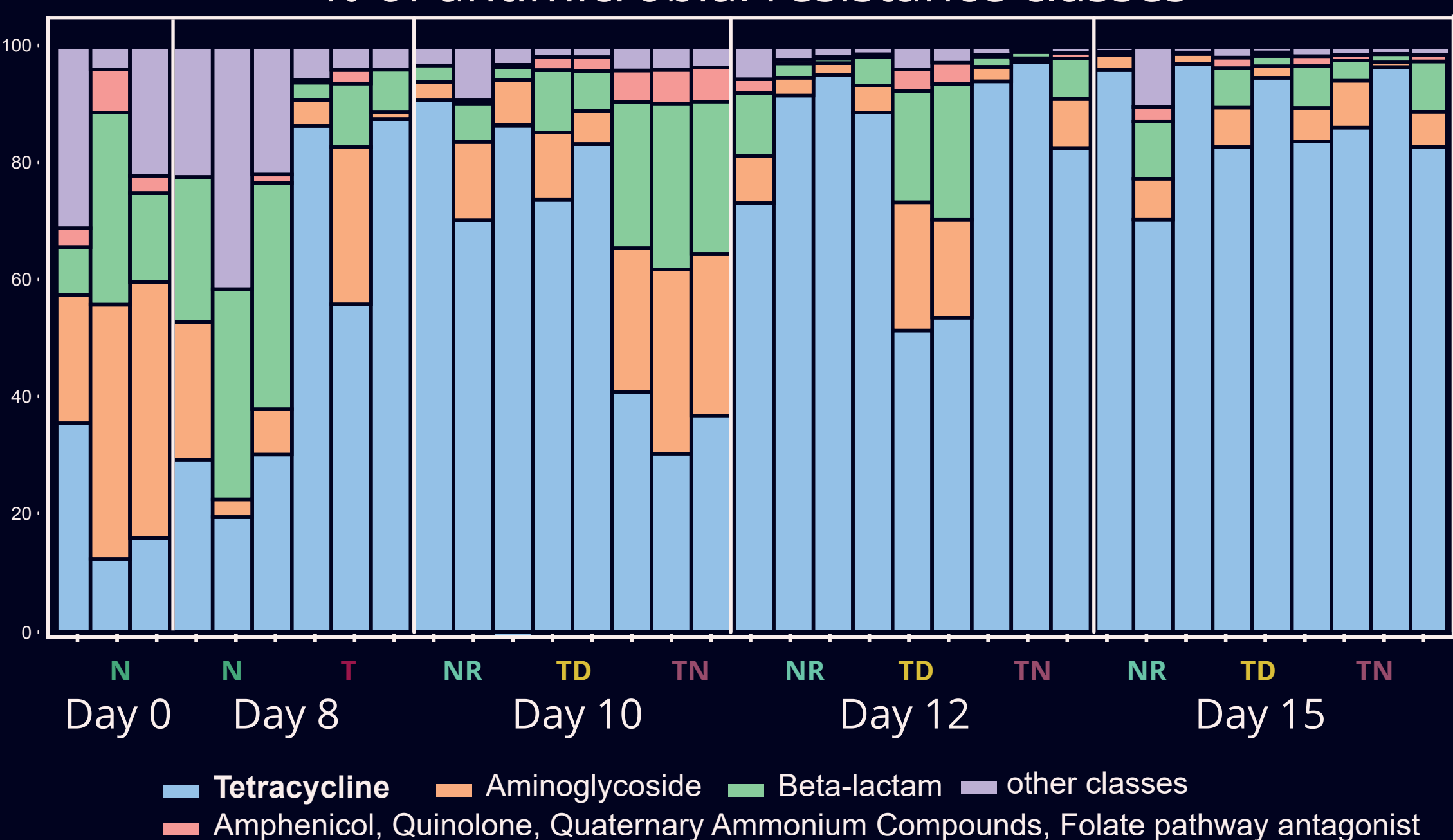
Cockroaches are a promising candidate for experiments on AMR transmission.

ANTIMICROBIAL RESISTANCE

Ratio of reads mapped to tetracycline resistance genes vs. reads mapped to bacterial genomes



% of antimicrobial resistance classes



ACKNOWLEDGEMENTS

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