

WHAT'S IN A TICK?

PATTERNS OF BACTERIAL DIVERSITY IN AUSTRALIAN TICKS

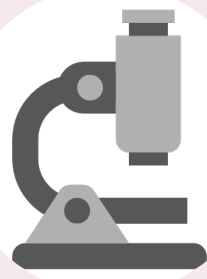
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Introduction

Australia has been experiencing a growing pressure around the presence of an unknown tick-borne disease (TBD) in humans^{1,2}. Molecular advances, such as next generation sequencing (NGS), have recently identified a number of candidate tick-borne pathogens in Australian ^{3,4}. Through a rigorous bioinformatic analysis this project aims to determine what external factors influence the bacterial communities of Australian ticks.

Bacterial agents of tick-borne disease globally include *Borrelia*, *Bartonella*, *Anaplasma*, *Ehrlichia* and 'Ca. Neoehrlichia'.



Methods

- 1 Morphological identification
- 2 Next generation sequencing
- 3 Bioinformatics
- 4 Statistical analysis

17 K
Operational
Taxonomic units

64 M
Assigned reads



Results

Factors investigated



Host



Location



Tick species



Instar

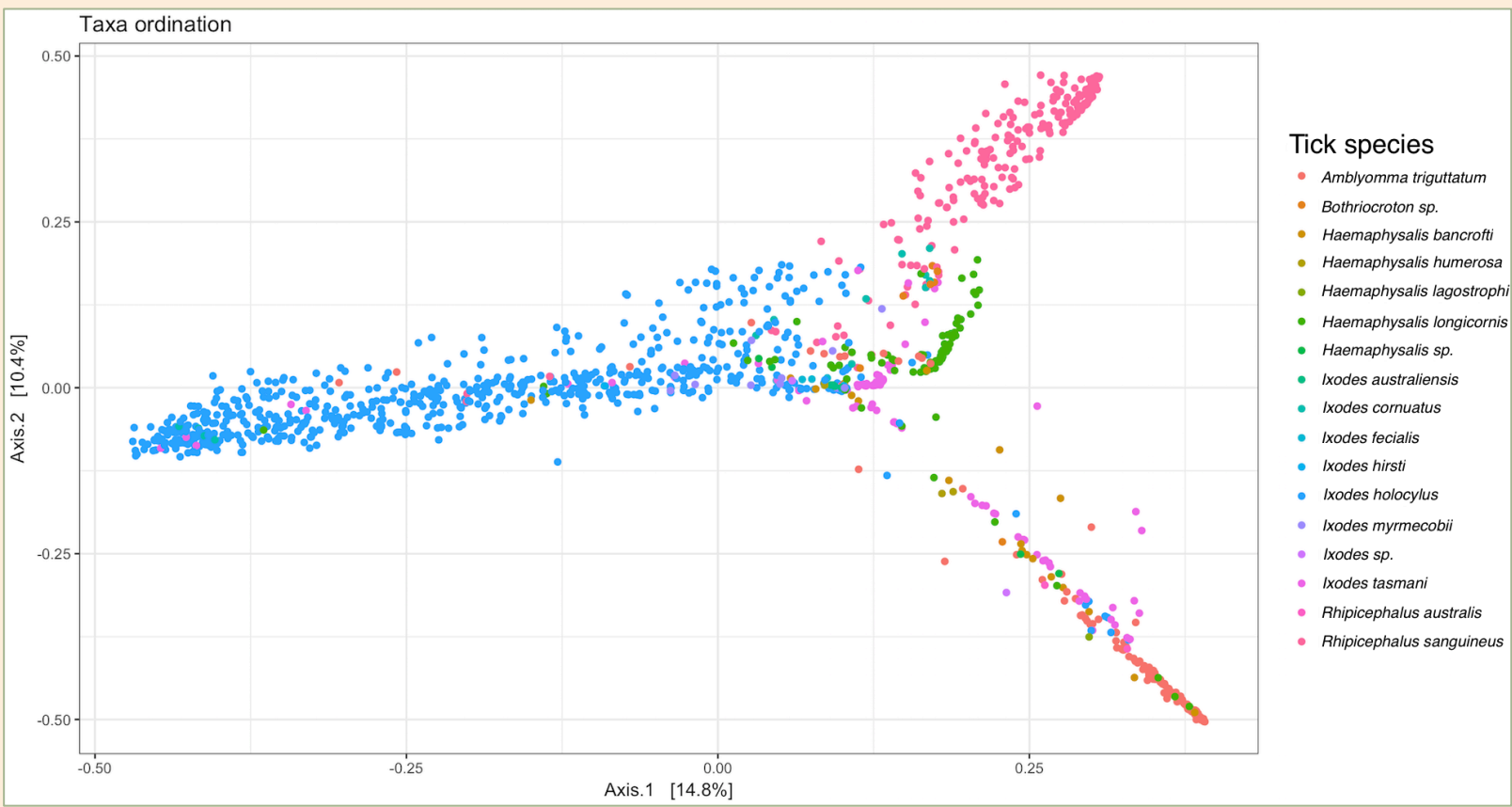


Fig 1. Ordination plot (Bray-Curtis dissimilarity), shows that tick species is the main factor influencing microbial composition of tick species.

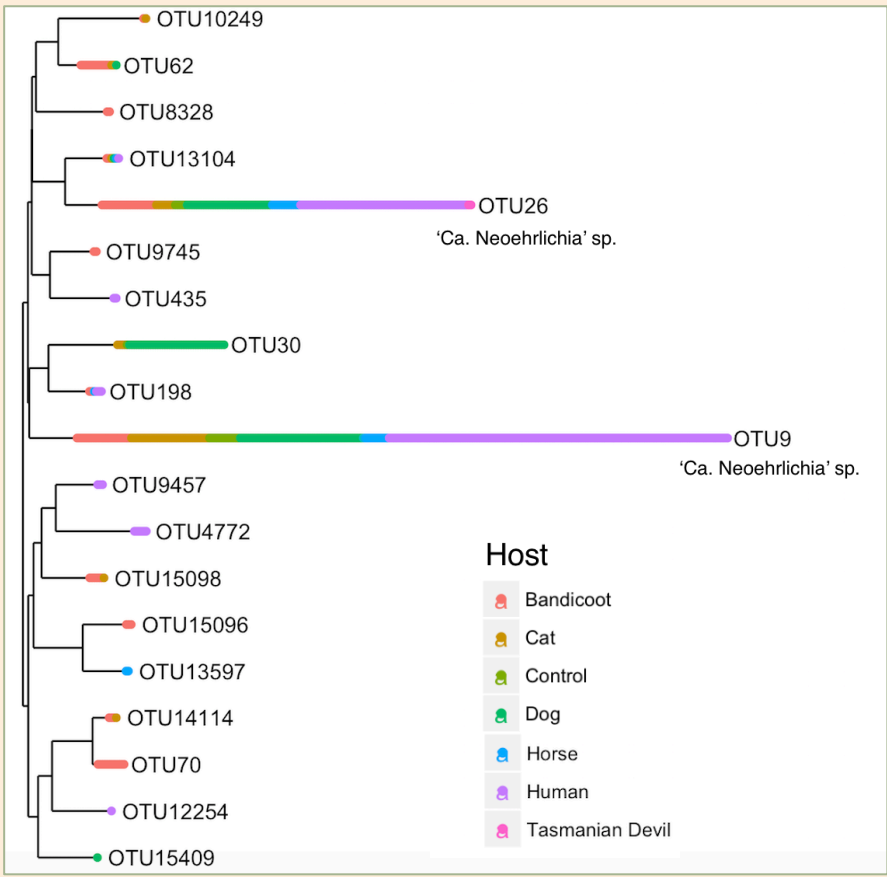


Fig 2. Presence of Anaplasmataceae bacteria among tick samples shows two dominate taxa present in ticks parasitising a diverse range of hosts

More interesting findings!
Borrelia sp. identified in two ticks.

A global emerging tick-borne pathogen 'Ca. Neoehrlichia' accounted for ~2.7% of all assigned reads.

Anaplasma sp. identified in 51 samples from ticks parasitising humans, dogs, horses and bandicoots.

30 OTUs assigned to *Rickettsia* (a known TBD in Australia) represented over 3 million assigned reads.



Murdoch
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Cryptick lab



PAWSEY
supercomputing centre

References &
Acknowledgments

