

# WHAT'S IN A TICK?

## PATTERNS OF BACTERIAL DIVERSITY IN AUSTRALIAN TICKS

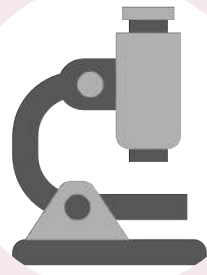
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### Introduction

Australia has been experiencing a growing pressure around the presence of an unknown tick-borne disease (TBD) in humans<sup>1,2</sup>. Molecular advances, such as next generation sequencing (NGS), have recently identified a number of candidate tick-borne pathogens in Australian <sup>3,4</sup>. 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



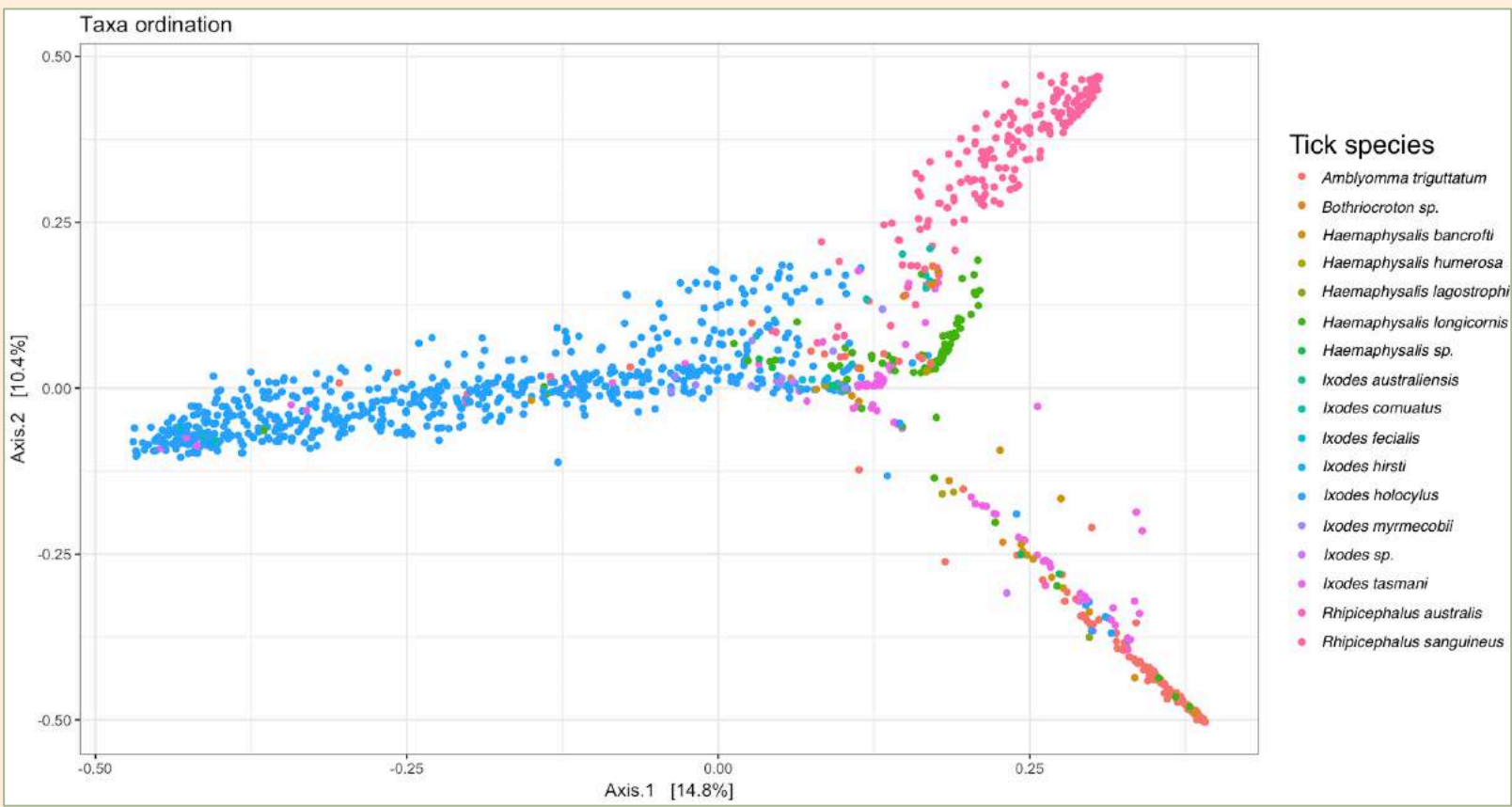
Location



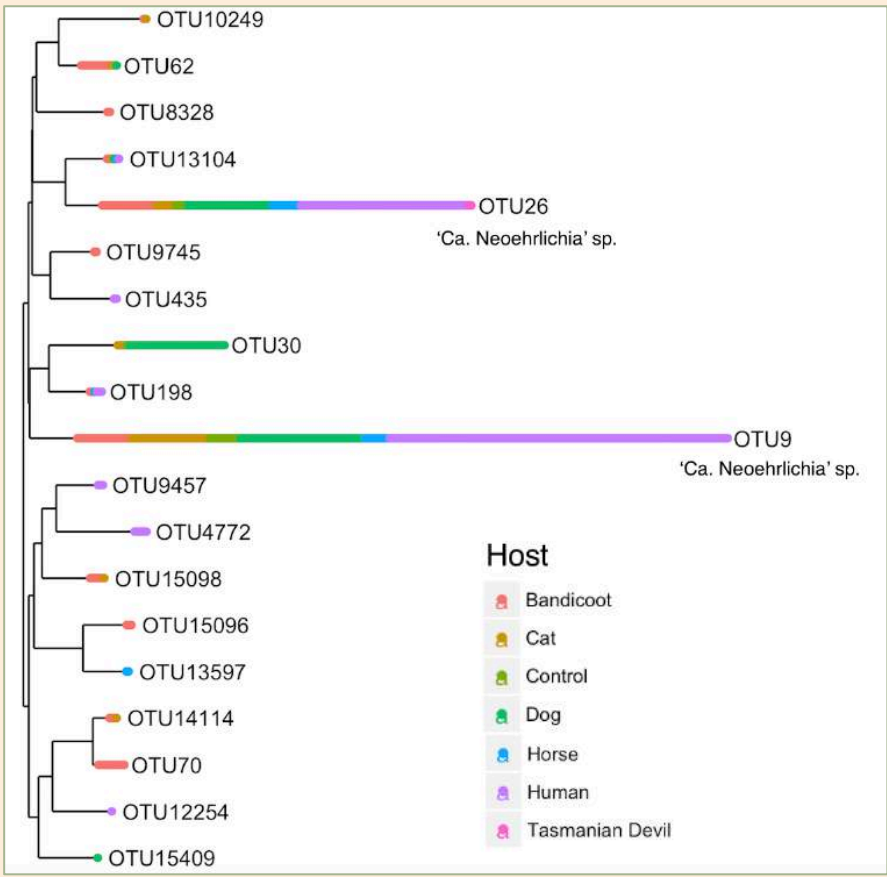
Tick species



Instar



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



**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  
UNIVERSITY



Cryptick Lab



PAWSEY  
supercomputing centre

References &  
Acknowledgments

