A Cross-sectional Study Of Circulating Bacteria In Reptiles In Australia.

Sasha Herbert[1]
Lucas Huggins[1], John Stenos[2] and Simon Firestone[1]
[1] The University of Melbourne
[2] Australian Rickettsial Reference Laboratory

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Authors: S. Herbert, L. Huggins, J. Stenos, S. Firestone

Melbourne Veterinary School, Faculty of Science, University of Melbourne, Crnr Flemington Rd and Park St, Parkville, Victoria 3010, Australia
The Australian Rickettsial Reference Laboratory, Entrance 3, 59 Bellerine St. University Hospital Geelong. Geelong, VIC, 3220, Australia.

Abstract:
Research on circulating bacteria hosted by clinically healthy reptiles is sparse. Reptile-associated bacteria can be difficult to isolate and then to identify by traditional laboratory culture methods. This study uses next generation sequencing metabarcoding to characterise blood-borne bacteria in reptiles in Australia.

Method:
The doctoral study, from which this paper is drawn, has been designed to use targeted PCR, metabarcoding next generation sequencing assays and serology to detect and characterise infection of, and/or exposure to vector-borne pathogens in reptiles, their mites and ticks, and where applicable, their human carers.
The aim of this section of the study is to compare the bacterial flora found in reptile blood to provide information on the varying bacterial haemobiome of reptiles including potential pathogens and symbiotes. Blood samples in EDTA were collected from 650 squamate reptiles divided between wild and captive animals representing all Australian mainland states and territories and frozen at -80C. DNA extraction was performed using Qiagen DNEasy kits for nucleated blood cells, and quantified using a Qubit fluorometer. Conventional pcr using r16S gene primers was used for amplification of bacterial DNA. Metabarcoding next generation molecular assays using the nanopore platform was used to characterise the bacteria amplified.
Results:
In related research, antimicrobial resistant bacteria were detected in oral and cloacal swabs collected concurrently to the blood samples from 9% (95% CI: 6 - 15%) of captive reptiles sampled (66 snakes and 72 lizards). Many of the detected organisms were difficult to characterise, suggesting the need for follow-on sequencing studies. The results from the next generation sequencing of the blood samples will be discussed in detail in the presentation.