

**Investigating genetic population substructure of an  
Australian reptile tick, *Bothriocroton hydrosauri*,  
using highly polymorphic microsatellite markers**

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## Abstract

Despite long-term study, the mechanism explaining the parapatric distribution of two Australian reptile ticks species, *Bothriocroton hydrosauri* and *Amblyomma limbatum*, is not understood. This project aimed to use molecular genetic data to investigate aspects of the population biology of these two tick species, such as population structure and dispersal, to gain further insights into the cause and maintenance of this parapatric boundary. I developed and subsequently tested for Mendelian inheritance a suite of *B. hydrosauri* and *A. limbatum* species-specific microsatellites markers. Pedigree analysis showed one *B. hydrosauri* locus and all of the *A. limbatum* loci to be inherited in a non-Mendelian manner. Thus I could not investigate *A. limbatum* population structure and focused solely on *B. hydrosauri*.

The first part of this study tested predictions of a model formulated to explain *B. hydrosauri* transmission dynamics. The “ripple” model, based on detailed ecological and behavioural data on *B. hydrosauri* and *Tiliqua rugosa*, *B. hydrosauri*'s most common host, predicts higher relatedness among larvae than among nymphs or adults on a host, and significant spatial autocorrelation in larvae extending further than for the later life stages. The model also predicts that adult ticks are likely to encounter related partners and that this will generate inbreeding within the population. I tested those predictions using nine microsatellite loci on a sample of 848 ticks (464 larvae, 140 nymphs and 244 adults) collected from 98 *T. rugosa* hosts at the northern edge of *B. hydrosauri*'s distribution range. My data did support all of the predictions of the “ripple” model and indicated that the dynamics of transmission among hosts play an important role in parasite population structure.

The second part of this project focused on investigating the population genetic structure of *B. hydrosauri* at the edge of its geographic range and testing the predictions of a population model derived to explain *B. hydrosauri*'s parapatric boundary with *A. limbatum*. The “ridge and trough” model suggested the tick population was organised spatially into a series of “ridges” where tick density was high and “troughs” where it was low. Genetically, the expectation was to find clusters of more closely related individuals associated with the ridges. Cluster analysis of microsatellite allele frequencies and analysis of molecular variance of mitochondrial haplotype frequencies revealed the presence of four genetic clusters within a sample of 244 *B. hydrosauri* adults. As the highly genetically divergent

clusters had overlapping distributions, and in some cases were syntopic, the genetic population structure predicted for these ticks by the “ridge and trough” model was not observed. Several explanations were considered for the observed *B. hydrosauri* genetic population structure, but syntopy of the clusters suggested that assortative mating is the most likely. I speculated that the clusters have formed in allopatry, when the environment was extremely heterogeneous, such that the ticks (and their hosts) were confined to isolated patches of high-quality habitat. Given sufficient time, this could have resulted in reproductive incompatibility between ticks occupying different patches. The population structure I uncovered indicates subsequent secondary recontact of divergent groups.

Although my study allowed for a better understanding of *B. hydrosauri* biology and population structure, the reasons for the parapatric distributions of *B. hydrosauri* and *A. limbatum* are still unclear. Further research should focus on investigating the population genetic structure of *A. limbatum* at the edge of its range, as well as on performing a larger-scale study of *B. hydrosauri* population genetic structure and a more detailed investigation of the applicability of the “ridge and trough” model to this tick species. Moreover, it will be useful to inspect the population structure of both these species within the centers of their ranges and compare these findings with population structure found at the edge of the range.

## Publications and Presentations

**The thesis is based on the following articles:**

### *Journal publications*

#### **Chapter 2:**

**Guzinski J**, Saint KM, Gardner MG, Donnellan SC, Bull CM (2008) Development of microsatellite markers and analysis of their inheritance in the Australian reptile tick, *Bothriocroton hydrosauri*. *Molecular Ecology Resources*, **8**, 443-445.

#### **Chapter 3:**

**Guzinski J**, Bull CM, Donnellan SC, Gardner MG (2009) Molecular genetic data provide support for a model of transmission dynamics in an Australian reptile tick *Bothriocroton hydrosauri*. *Molecular Ecology*, **18**, 227-234.

#### **Chapter 4:**

**Guzinski J**, Bull CM, Donnellan SC and Gardner MG (in preparation) The Australian reptile tick, *Bothriocroton hydrosauri*, exhibits marked genetic population substructure at the edge of its distribution range.

### *Conference publications*

**Guzinski J**, S Donnellan and Bull CM (2008) Population genetics analysis reveals substructuring within a population of an Australian reptile tick *Bothriocroton hydrosauri*. Talk at the Genetics Society of AustralAsia 55<sup>th</sup> Annual Meeting, Adelaide, Australia.

## **Declaration**

I certify that this thesis does not incorporate without acknowledgment any material previously submitted for a degree or diploma in any university; and that to the best of my knowledge and belief it does not contain any material previously published or written by another person except where due reference is made in the text.

JARO GUZINSKI

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