

# A Phylogeny of *Ixodes* Genus (Hard-Bodied Ticks)

Jewel E. Voyer, Dr. Rachel Schwartz  
Department of Biological Sciences,  
University of Rhode Island

## Introduction

- *Ixodes* and human health
- Known for being host of many pathogens
- Lack of previous phylogeny data
- Morphology
- rRNA genome
- Mitochondrial sequencing
- Small number of species
- Having a strong phylogeny of the *Ixodes* genus can provide for evidence of evolutionary relationships within the genus and the pathogens each species carries

## Methods

- Identify phylogenetic markers
- Obtain Genomic sequence data from ENA
- Larger sample size, N = 20
- Whole genome files
- Trim data
- Align to composite genome
- Use RAxML
- Gives Newick tree description
- Find root
- Determine the bootstrapping and maximum likelihood

SNP Identification from Short Read Sequences (SISRS) software

## Discussion

- Clades comparable to previous publications
- Phylogeny shows new information
- Good bootstrap support
- May indicate some rapid radiation of the species
- Future Work
  - Determine if there is more genomic information
  - Compare with parasites each species carries to see indications of evolutionary relationships

## Results

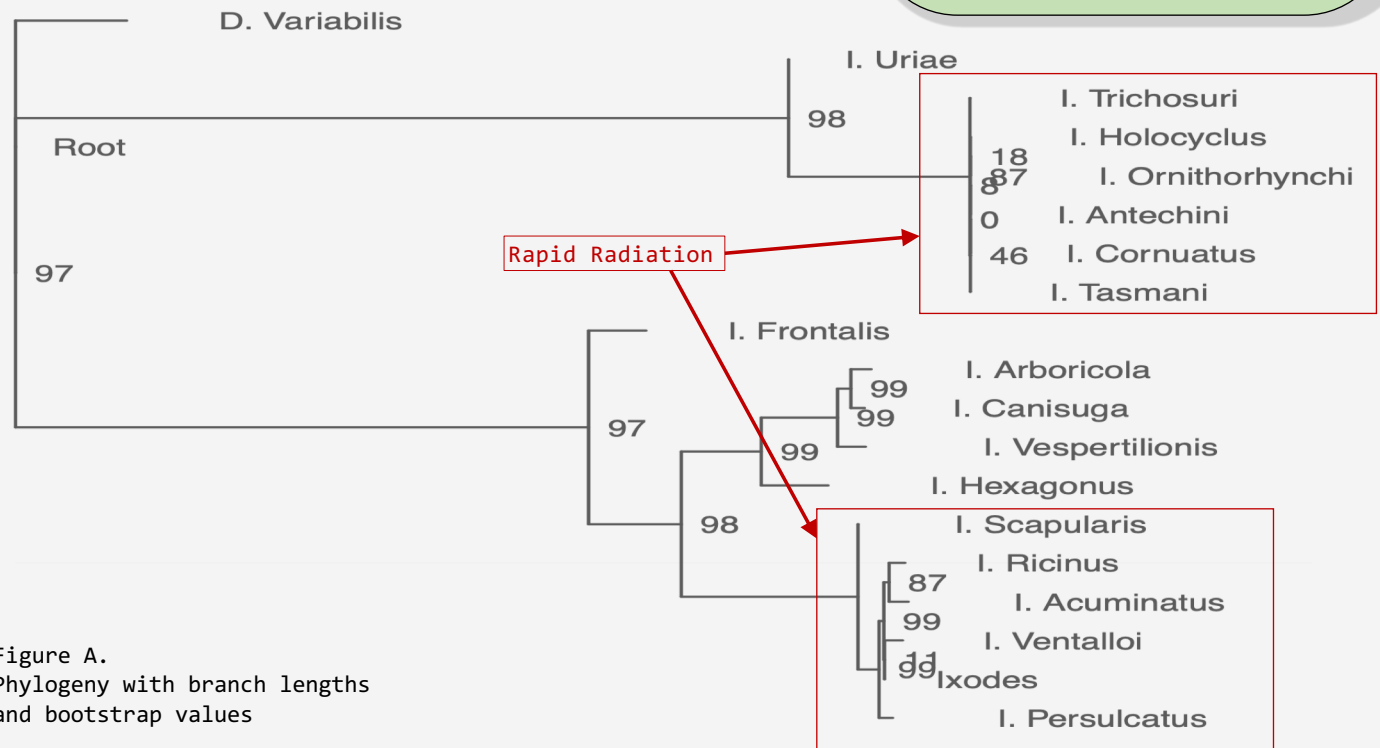


Figure A.  
Phylogeny with branch lengths  
and bootstrap values