Prevalence and diversity of *Salmonella* in wild reptiles


Raina M. Fitzpatrick | West High School, Knoxville TN and Benjamin M. Fitzpatrick | Ecology & Evolutionary Biology, University of Tennessee, Knoxville TN

Questions

1. How common is *Salmonella* in wild reptiles?
2. Does prevalence vary among host species?
3. Do different host species carry different *Salmonella* genotypes?

Introduction

Reptiles are known carriers of *Salmonella* (Fig. 1), and transmission from pets to humans has been a substantial concern. However, it is not known how prevalent *Salmonella* is among wild reptiles if they often carry strains that infect humans. This pathogen is not known to be harmful to reptiles except in particular circumstances involving *S. enterica* in captive snakes. Since *S. enterica* is often found in asymptomatic reptiles, it might be a normal symbiote in the wild. A pattern of host specificity in the wild would be consistent with host-symbiote coevolution.

Methods

- Sampling was systematic: We sought a diversity of aquatic and terrestrial species of turtles, snakes, and lizards (Table 1).
- Aquatic turtles were trapped in 3rd Creek and an urban pond in Knoxville, TN.
- Snakes, skinks, and box turtles were captured by hand on the UT campus, 3rd Creek Greenway, and other urban parks.
- Microbiological samples were taken from cloacae with sterile swabs.
- Presence of *Salmonella* was determined by PCR of enriched cultures using primers for the *Salmonella*-specific hiiA gene (highly invasive locus A) [3].
- DNA sequences from positive samples were compared to 42 hiiA sequences available on GenBank.

Results

- *Salmonella* was detected in 67% of samples (Table 1).
- None of the hosts showed obvious symptoms of disease.
- Prevalence was different among different host species (Table 1).
- Different host species tended to carry different *Salmonella* genotypes (Table 2).
- All *Salmonella* detected grouped within *S. enterica enterica* (Fig. 2).
- Genotypes associated with *S. odoratus* were unusual (Fig. 2).

Discussion

Our sample was restricted to urban parks and one creek in Knoxville, TN, so we are hesitant to generalize from these findings. However, there is a suggestive pattern of higher prevalence in aquatic vs. terrestrial reptile species (Table 1). It makes sense that transmission of *Salmonella* would be more efficient and widespread in water.

Most of the *Salmonella* genotypes found in wild reptiles were similar to *S. enterica* serovars commonly isolated from clinical samples (Fig. 2). The hiiA gene sequence alone cannot discriminate more finely among most known serovars. Even so, we can see a strong pattern of host specificity in our sample. In particular, one of the genotypes associated with *S. odoratus* appears to have evolved more rapidly than normal for hiiA. As this gene plays a crucial role in host cell invasion, more detailed analysis might shed light on the nature of host-symbiote interactions and coevolution.

Table 1. Prevalence of *Salmonella* among reptiles in Knox Co, TN. Replication is inadequate to confirm association between prevalence and habitat, but the distribution is non-random (RxC test P = 0.0019)

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Table 2. Association between reptile host species and *Salmonella* genotypes of the hiiA gene (RxC test P = 0.0001)

<table>
<thead>
<tr>
<th>Host</th>
<th>E. fasciatus</th>
<th>N. sipedon</th>
<th>S. dekayi</th>
<th>S. odoratus</th>
<th>Tr. scripta</th>
<th>Te. carolina</th>
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Fig 1. Pet red-edared sliders (*Trachemys scripta*) are famous as sources of *Salmonella* infections in young children, who might be tempted to kiss a hatchling like this. But little is known about *Salmonella* in wild turtles and other reptiles.

Photo credit: Matt Niemiller

Fig 2. Evolutionary relationships among *Salmonella* hiiA gene sequences.

Numbers by nodes are posterior probability support values (only values > 0.75 are shown). Highlighted tips are sequences found in our sample, all others were obtained from GenBank. Genotypes within the subspecies *S. enterica enterica* are labeled by serovar (e.g., *S. enterica* ST003b and 10 other serovars, not shown), all other tips represent unique sequences.

We estimated the gene tree using MrBayes [7] with a GTR+I+G model, two independent runs of 4 linked chains, 1.5e10 burn-in steps, and 1000 trees sampled from the last 1.0e7 post-burn-in steps for each run.

Works Cited