TABLE 3. Diet overlap index among *Rana catesbeiana* size class groups and overlap percentages (in parentheses). Rec-met. = recently metamorphosed.

Size Class	Rec-met.	Juveniles	Sub-adults	Adults
Rec-met.	-	0.79 (64%)	0.54(39%)	0.18 (27%)
Juveniles		-	0.76 (60%)	0.20 (36%)
Sub-adults			-	0.64 (54%)

P = 0.000) and pos-hoc Bonferroni test found significant mean differences between adults and all other categories ($\alpha = 0.05$). There was significant and positive relationship between Bullfrog length (SVL) and prey length (r = 0.578, N = 338, P = 0.01). Bullfrog size explained only 33% of the prey size variability. The remainder of the variation is probably due to other factors including behaviour, physiological needs, prey availability and habitat use.

Rana catesbeiana has a generalist diet, but probably has a preference for some prey items such as Odonata, Coleoptera, Hymenoptera, and vertebrates (fish and frogs). There was a tendency to increase vertebrate consumption as bullfrog size increased. It was observed mainly in large frogs (sub-adults and adults). Cannibalism can have strong effects on reducing population size and community structure (Fox 1975).

The diet of Bullfrogs introduced into Colombia mostly consisted of insects (56%), with vertebrates constituting only 2% of the diet (Daza and Castro 1999). However, in Japan it was found that adults fed mainly on crayfish (49.6%) with vertebrates not represented in the diet (Hirai 2004).

Our results confirmed that *R. catesbeiana* is an opportunistic species, with both invertebrates and vertebrates comprising the diet. Differences in diet are related to differences in body size and microhabitat selection (Wu 2005). This invasive species may affect native amphibians as predators, competitors, agents of habitat change, and disease reservoirs. Therefore, management and control should be attempted.

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Absence of Cloacal Shedding of *Salmonella* in Wild Red-eared Sliders (*Trachemys scripta elegans*)

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Salmonella is a zoonotic bacterium that causes gastrointestinal disease in humans and can be carried asymptomatically by animals (Chiodini and Sundberg 1981). While most human infections are caused by the consumption of contaminated food (Tauxe 1991), reptiles are also a source of infection and may cause as many as 70,000 human cases annually in the United States (Mermin et al. 2004). Public health concerns have led to studies to identify the rate of *Salmonella* shedding in captive turtles from zoos (Otis and Behler 1973), commercial turtle farms (Siebeling et al. 1984), and private collections (Abalem de Sá and Solari

2001). Comparatively little is known, however, about *Salmonella* infections in wild, free-ranging turtles. Generally, wild turtles are believed to shed *Salmonella* at lower rates than captive turtles because they either lack exposure to stressors that increase shedding rates or because they are not natural carriers of the bacterium (Du Ponte et al. 1978; Richards et al. 2004; Saelinger et al. 2006). A few recent studies on wild chelonians have, however, reported a high prevalence of *Salmonella* in turtles (Chambers and Hulse 2006; Gaertner et al. 2008), with wild turtles having similar prevalence of *Salmonella* infection to captive turtles (Gaertner et al. 2008).

We examined the prevalence of *Salmonella* in wild Red-eared Sliders (*Trachemys scripta elegans*). Red-eared Sliders are common in the pet trade, and numerous studies have quantified *Salmonella* shedding rates in this species in captivity (Abalem de Sá and Solari 2001; Chassis et al. 1986; McCoy and Seidler 1973; Otis and Behler 1973; Pasmans et al. 2002a). They are also notorious as a globally invasive species, and they inhabit a variety of aquatic habitats. Our goal was to estimate the prevalence of *Salmonella* in wild Red-eared Sliders in Illinois where they inhabit a variety of natural water bodies and man-made agricultural ponds. We hypothesized that the prevalence of *Salmonella* in turtles would differ among habitat types because turtles might have experienced persistent stressors in man-made habitats, which might have increased shedding rates, or because man-made habitats might have increased infection risk directly. Such a result would have public health implications, and might help to explain variation in shedding rates observed among previous studies of wild turtles.

Turtles were sampled from water bodies in southern Illinois, a region characterized primarily by a mosaic landscape of forest, grassland, and intensive row crop agriculture. Five natural ponds (37.0688°N–37.1080°N, 88.5934°W–88.4677°W; NAD83) and five artificial ponds were sampled (37.4622°N–37.4089°N, 88.6900°W–88.6508°W; NAD83). Natural ponds, oxbow lakes along the Ohio River floodplain, were large (mean ± S.E.: 28.4 ± 11.5 ha), and supported a high diversity of fishes (Readel, unpubl. data) as well as diverse turtle assemblages (Dreslik et al. 2005). Artificial ponds, built in the 1970s as agricultural retention ponds, were small (1.1 ± 0.3 ha), contained only common lentic turtle species, and have been stocked with game fish (Readel, unpubl. data). Both habitat types were used as public or semi-public fishing grounds, and Red-eared Slider turtle abundance (trap-hours required to capture one turtle) was similar between sites (natural: 33.8 ± 9.5; manmade: 41.5 ± 13.7; Readel, unpubl. data).

Turtles were captured using baited hoop traps and were held in individual bleach-decontaminated tubs up to 4 h until sampling. Cloacal swabs were collected from turtles by rubbing a sterile polyester swab against the inner cloacal lining to obtain fecal material. Each swab was then agitated into 10 mL of selenite cystine broth (Edge Biologicals, Memphis, Tennessee, USA) that was incubated for 18 h at 37°C and then plated on xylose lysine desoxycholate (XLD) agar (Edge Biologicals, Memphis, Tennessee, USA) to isolate individual bacterial colonies. Plates were incubated at 37°C for 24 h and suspect colonies (colonies morphologically consistent with *Salmonella*) were inoculated into 0.2 ml tubes containing tryptic soy agar (Becton, Dickinson and Company, Sparks, Maryland, USA) for transport to the laboratory. If suspect colonies were not present after 24 h, plates were incubated at room temperature for an additional 24 h. Colonies were re-streaked on XLD agar and re-isolated in the laboratory.

All suspect colonies were subjected to a diagnostic PCR for *Salmonella*. Isolated colonies were inoculated into 0.5 ml of Luria-Bertani broth (Becton, Dickinson and Company, Sparks, Maryland, USA), which was incubated for 18 h at 37°C. Bacterial cells were then pelleted by centrifugation, and DNA was extracted using the DNeasy Mini Kit (Qiagen, Valencia, California, USA) eluted in a 100 μl volume, according to the manufacturer's protocol. The *Salmonella* specific primer pair invA-1 (5´- ACAGTGCTCGTTTACGACCTGAAT) and invA-2 (5´- AGACGACTGGTACTGATCGATAAT) was used to amplify a 243 bp segment of the *Salmonella* invA gene, which has been shown to be both sensitive and specific for this bacterial genus (Chiu and Ou 1996). As an internal control for DNA extraction and amplification, another published PCR primer pair of 16S-F (5´- AGACTGCTACGGGAGGCAGCAGT) and 16S-R (5´- GTTGCGCTCGTTGCGGGACTTAA) was used to amplify a 755 bp fragment of the 16S ribosomal RNA subunit gene, which is present in all bacteria (Villalobo and Torres 1998). PCRs were conducted in 12.5 μl volumes containing 1X DyNAzyme EXT buffer (Finnzymes OY, Finland), 3.5 mM MgCl2, 200 μM dNTPs, 0.3 μM each of primers 16S-F and 16S-R, 0.06 μM each of primers invA-1 and invA-2, and 0.125 units of DyNAzyme EXT DNA polymerase (Finnzymes OY, Finland). Reactions were cycled in an i-Cycler thermocycler (BioRad Inc, Hercules, California, USA) at 94°C for 2 minutes, then for 30 cycles at 94° C for 30 seconds, 57°C for 30 seconds, and 72°C for 45 seconds, followed by a final 72°C 4-minute extension step and an indefinite 4°C soak. A sample of wild-type *Salmonella typhimurium* DNA from the University of Illinois Veterinary Diagnostic Laboratory was used as a positive control, and sterile, distilled water was used as a negative control. Amplicons were visualized by electrophoresis in 1.5% agarose /TAE buffer followed by ethidium bromide staining and digital imaging under ultraviolet light. Samples were considered positive only if PCR produced both the 243 bp invA band and the 755 bp internal control 16S rRNA band. To confirm amplification of the correct gene, one invA PCR product from the positive control isolate was purified using the Zymoclean Gel DNA Recovery Kit (Zymo Research, Orange, California, USA) and submitted to the University of Illinois, Biotechnology Center for sequencing. The resulting sequence was compared to published sequence data (BLAST tool from the National Center for Biotechnology Information).

One hundred wild Red-eared Sliders were captured between June 18–29, 2006. Fifty turtles were captured from natural ponds and an equal number were captured from artificial ponds. Suspect colonies (colonies that were morphological consistent with *Salmonella* on XLD agar) were recovered from nine of 50 turtles in natural ponds and 12 of 50 turtles in artificial ponds.

PCR testing of suspect colonies failed to yield amplicons of the invA gene in any suspect colony, although amplifications of the internal control 16S rRNA fragment yielded positive results in all cases. Our *Salmonella* positive control yielded amplicons of both invA and 16S, and DNA sequencing confirmed that we had indeed amplified invA. These results demonstrated that DNA extraction and PCR were universally successful. The prevalence of

Salmonella spp. in the turtles sampled was therefore 0%, with an upper 95% confidence limit of 4.4% for the entire population of 100 turtles (calculated using the modified Wald method; Agresti and Coull 1998). All suspect colonies were, therefore, likely to be normal enteric organisms that produce hydrogen sulfide.

The absence of *Salmonella* in wild turtles in our study was consistent with findings of other studies on wild turtles in the United States that have reported a prevalence of 0–8% (Brenner et al. 2002; Harwood et al. 1999; Jackson et al. 1969; Richards et al. 2004; Saelinger et al. 2006), but was lower than those reported from Spain (12–15%; Hidalgo-Vila et al. 2006), Pennsylvania (100%; Chambers and Hulse 2006), and Texas (51%; Gaertner et al. 2008). Studies on captive turtles have reported *Salmonella* in 12–41% of *T. scripta* (Abalem de Sá and Solari 2001; Chassis et al. 1986; McCoy and Seidler 1973; Otis and Behler 1973; Pasmans et al. 2002a), and in 3–72% of all turtle species (Abalem de Sá and Solar 2001; Cambre et al. 1980; Corrente et al. 2004; Geue and Löschner 2002; Jackson and Jackson 1971; Nakadai et al. 2005; Onderka and Finlayson 1985; Otis and Behler 1973; Pasmans et al. 2002a). Our results supported the conclusion that the prevalence of *Salmonella* is low in wild compared to captive turtles.

Turtles might be natural carriers of *Salmonella*, but rarely shed the bacterium unless physiologically stressed (Du Ponte et al. 1978; Richards et al. 2004; Saelinger et al. 2006). In this study, artificial habitats were not associated with increased shedding in wild Red-eared Slider turtles. The habitats in which our turtles resided might not have experienced stress levels high enough to activate shedding. Alternatively, wild turtles may not be natural carriers of *Salmonella*, but rather only become infected through their environment (Richards et al. 2004; Saelinger et al. 2006). For instance, wild turtles admitted to a veterinary hospital were not shedding *Salmonella* upon entrance or after three wk in captivity, and gastrointestinal mucosal samples from dead or euthanized wild turtles were also negative (Saelinger et al. 2006), suggesting that these turtles were not carriers of *Salmonella* before capture (Saelinger et al. 2006). Our results were consistent with another study that found no effect of habitat on the prevalence of *Salmonella* in aquatic turtles (Gaertner et al. 2008).

Our methods might have limited our ability to detect turtles with occult *Salmonella* infection, because we did not sacrifice turtles and sample regions of their gastrointestinal tracts where *Salmonella* can reside (Pasmans et al. 2002b). However, we used methods that were similar to previous studies (Corrente et al. 2004; Saelinger et al. 2006). Corrente et al. (2004), for example, showed that the quantity of feces on swabs was not correlated with a greater recovery rate, because of the efficiency of the enrichment step. Repeated culture with several media over time may have increased our chance of detecting intermittently shed organisms like *Salmonella* (Smith et al. 2002). Nevertheless, our failure to detect *Salmonella* in any of the 100 turtles indicated that, if the bacterium existed in this population, its point prevalence was below 4.4%.

Overall, our results were consistent with previous observations that wild turtles have low prevalence or shedding rates of *Salmonella*, and that these rates are lower than in captive turtles. To the extent that our results can be generalized, the public health problem of zoonotic salmonellosis of turtle origin may be largely characteristic of farmed and otherwise captive turtle populations; wild turtles may not represent an important source of the bacterium, even in habitats that are artificial and/or impacted by human activity. Red-eared Sliders, a notoriously ecologically plastic (and globally invasive) species may be able to adapt to areas of high human impact without serious health-related consequences. It remains to be seen whether other, less adaptable turtle species show similar patterns.

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Diet and Reproduction of the Lizard *Tropidurus etheridgei* in Rocky Areas of Central Brazil

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Lizards of the genus *Tropidurus* occur throughout South America, mainly in open habitats such as Caatinga and Cerrado, occupying a wide variety of microhabitats (Rodrigues 1987). Many *Tropidurus* species (e.g., *T. oreadicus*, *T. hispidus*, *T. torquatus,* and *T. etheridgei*) are abundant, widespread, and ecologically diverse (Rodrigues 1987). *Tropidurus* are diurnal, heliophilous, sit and wait predators, consuming a wide variety of arthropods and occasionally vertebrates (Bergallo and Rocha 1993; Colli et al. 1992; Rocha and Siqueira 2008). With few exceptions, reproduction of *Tropidurus* species is non-continuous, occurring during the dry-wet season (Van Sluys et al. 2002) and involves a sexual dimorphism, both in color and size (Wiederhecker et al. 2002).

Although several aspects of life history of some *Tropidurus* species have been studied (e.g., Bergallo and Rocha 1994; Carpenter 1977), little is known about geographic variation in ecological attributes of the widely distributed species *T. etheridgei*.

Wide-ranging lizards often exhibit geographic variation in life-history and ecological traits (Qualls and Shine 1997). Understanding sources of this variation is essential for understanding the success and evolution of lizard species (e.g., Vitt and Colli 1994). Moreover, modification or the maintenance of ecological attributes between different populations of the same species may indicate the influence of historical or ecological factors on the structure of lizard communities (Vitt et al. 1998).

Tropidurus etheridgei is a medium-sized lizard distributed in the dry habitats of the Chaco, the Cerrado and the Pantanal regions, in Brazil, Paraguay, Bolivia and Argentina (Cei 1993; Rodrigues 1987). In spite of following the same patterns of other *Tropidurus* with a seasonal reproductive cycle, sexual dimorphism in color and shape and a generalized diet, there are some differences in the biology of *T. etheridgei* between the Chaco (Cruz 1997; Cruz et al. 1998) and the Cerrado (Vitt 1991) populations, mainly with respect to diet, reproduction and habitat use. However, information about populations in these two regions is limited. Herein, we describe the reproduction and diet of *T. etheridgei* in rocky areas of the Pantanal, Western Brazil. In addition, we compare reproductive and feeding data to those reported for *T. etheridgei* in the Chaco and the Cerrado regions.

Materials and Methods.—The study was conducted in three rocky areas (19.1802778°S, 57.5381111°W; 19.1672222°S,