

Constructing Haplotype Networks to Investigate the Impact of Host Dispersal on the Genetic Structure of an Understudied Parasitic Trematode

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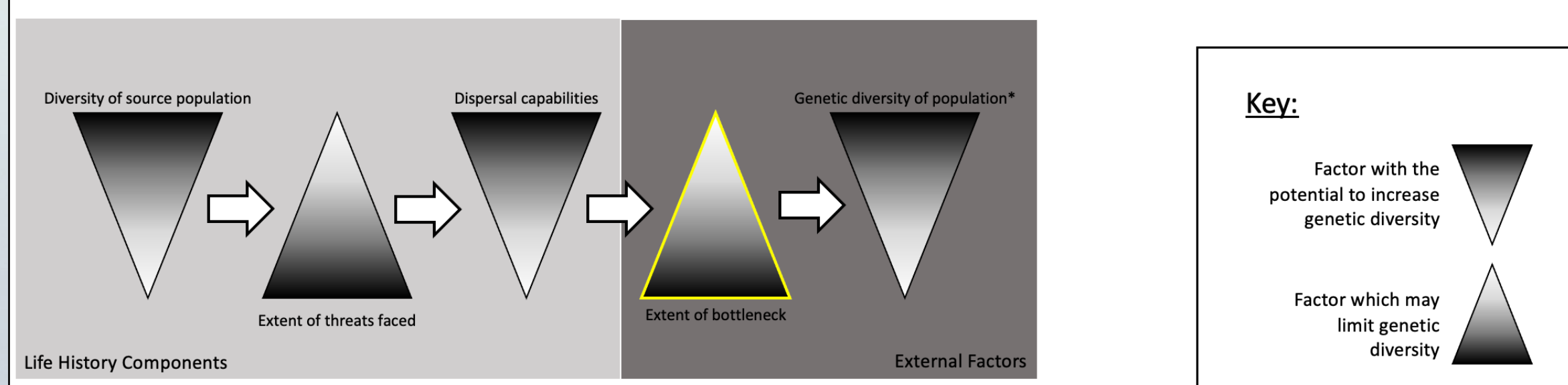
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BACKGROUND

- Coevolution: patterns of interactions between two major groups of organisms with a close and evident ecological relationship⁵
- Parasites exhibit a specific form of reciprocal selection
- 80% of all described species are described as parasites¹²
- Digenean trematodes are parasites which exhibit complex, multi-host life cycles¹
- Dispersal rates of trematodes and other endoparasites are often directly associated with that of their host²
- Low rates of dispersal can lead to strong coevolutionary dynamics between hosts and parasites over time^{8,10,11}
- Understanding genetic structure of host and parasite populations has been described as a prerequisite to making inferences about evolution of parasitic symbioses¹⁰
- Diamondback terrapins form isolated subpopulations through their range due to limited dispersal capabilities and high site fidelity⁹, providing the perfect system to study how these variables present themselves in parasites' genomes

(a) Free Living/Host Species:



(b) Parasite Species:

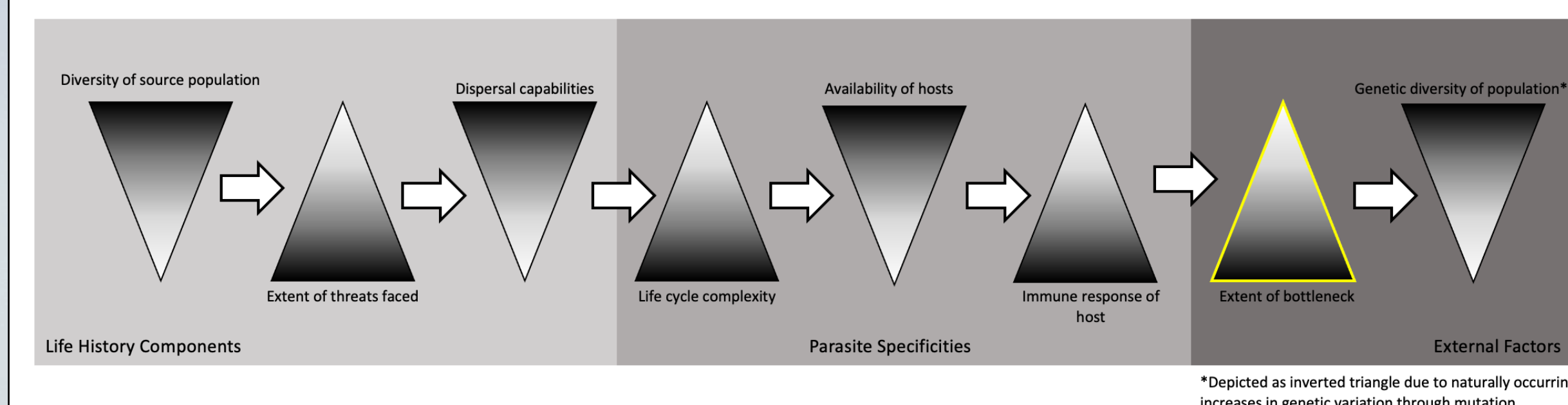


Figure 1: (left) Theoretical illustration of the processes which may affect genetic diversity of parasites and hosts during genetic bottleneck. Adapted from Blakeslee (2019).

EXPECTED RESULTS & INTELLECTUAL MERIT

Hypothesis: The genetic structure of *P. malaclemys* will more closely resemble that of *M. terrapin* (definitive host) than *T. obsoleta* (intermediate host)

- Supported by literature stating that the genetic structure of trematodes will be directly associated with the host species exhibiting the highest dispersal rate³
- However, if an obvious correlation exists between haplotypes of *T. obsoleta* and *P. malaclemys*, it may hint at missing information about the life cycle of the parasite or researchers' understanding of the system

This study aims to:

1. Support conservation of the endangered diamondback terrapin by providing additional insight into its unique ecology and demographics
2. Serve as a case study on the effects of genetic bottleneck of a host on parasites' genetic diversity
3. Provide a better understanding of the genetic structure of parasites exhibiting complex life cycles

STUDY SYSTEM

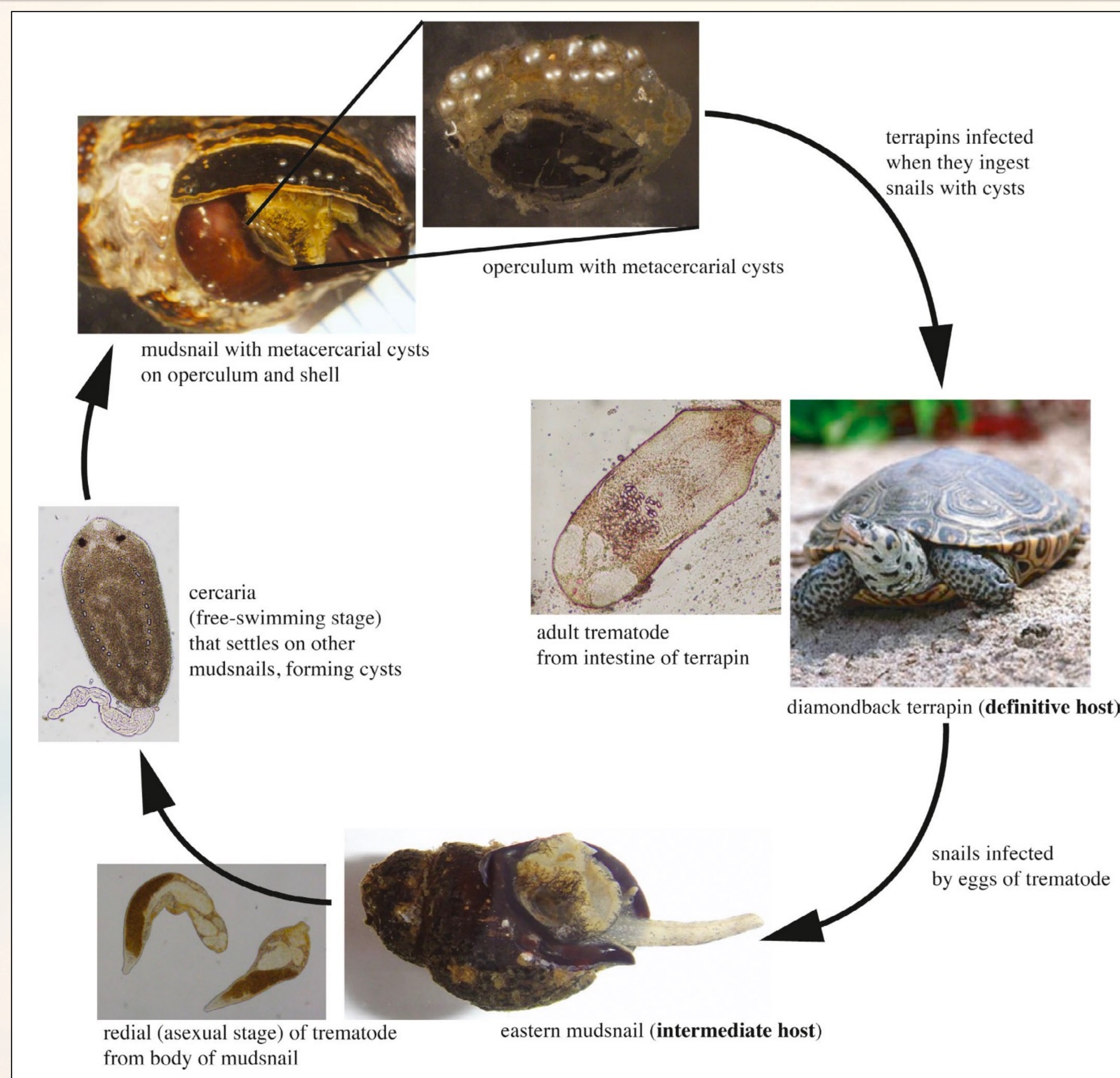


Figure 2: (above) The life cycle of *P. malaclemys*, including stages dependent on intermediate host *Tritia obsoleta* and endangered definitive host *Malaclemys terrapin*. From Eugene et al (2021).

METHODS

1. Collection of genetic samples from multiple populations of *T. obsoleta* and *P. malaclemys* within Chesapeake Bay (appx. 38.3°N)
2. Sample preparation; DNA extraction and amplification via PCR (Table 1)
3. Sending DNA samples for sequencing of the COX1 mitochondrial marker
4. Sequence alignment and haplotype network construction
5. Statistical comparison of haplotype networks for *T. obsoleta* and *P. malaclemys*
6. Visual comparison of haplotype networks to novel terrapin regionalities (Figure 2)
7. Repeating in other regions, as time and resources allow

Figure 3: (right) Subspecies as described by Ernst & Bury (1982) labeled A through G⁶. Four regions of terrapin genetic diversity 1-4 as described by Hart et al (2014)⁹. Modified from Hart et al (2014)⁹; images from iNaturalist.

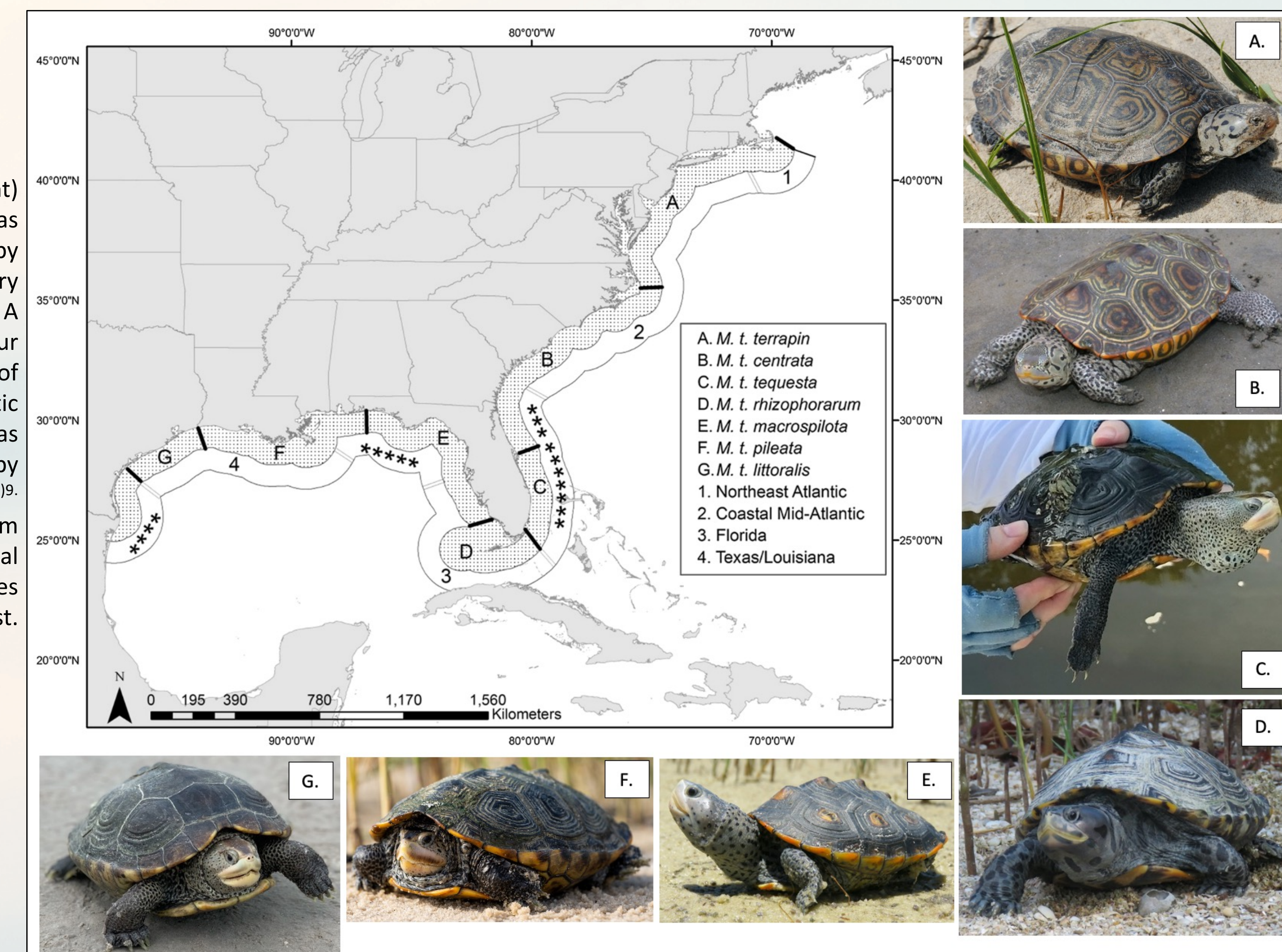


Table 1: (right) Forward and reverse primers to be used in this study, per species. Adapted from Blakeslee et al (2019).

Species	Marker	Fragment Size (bp)	Forward Primer	Reverse Primer	Root Species (Genbank Accession Number; Citation)
<i>Tritia obsoleta</i>	COI	546	TCGTGCTGAACCTGGACAC	CCCCAGTAAATACAGGCAAA	<i>Cyclope neritea</i> (AY789981.1; Simon-Bouhet et al., 2006)
<i>Austrotilharzia variegata</i>	COI	571	CGCCTCTGCTGTGTGTGAA	AAACCCCAACACTCACCAAA	<i>Fasciola hepatica</i> (X15613.1; Garey et al. 1989)
<i>Himantula quistensis</i>	COI	522	CTGCGTCGGTTTGTGTAGGT	TCCCAACACACAAATAGCC	<i>Fasciola hepatica</i> (X15613.1; Garey et al. 1989)
<i>Lapocordulia setiferoides</i>	COI	514	CCCCCTTGTCGAGTGGGGAT	TGCAGTATGCATCCAAACCCACC	<i>Fasciola hepatica</i> (X15613.1; Garey et al. 1989)
<i>Zoogonotus latus</i>	COI	535	CCGCTTTATCTTCTGTGGA	TATGCATATCCAAACCAACC	<i>Fasciola hepatica</i> (X15613.1; Garey et al. 1989)

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ACKNOWLEDGMENTS

I'd like to thank my advisor Dr. Mike McCoy and committee member Dr. April Blakeslee for their support of this thesis, as well as the other members of the McCoy Lab for their feedback during the development of my project. I'd also like to thank my family and partner for their limitless support despite listening to incessant information about turtles for years. -GJM

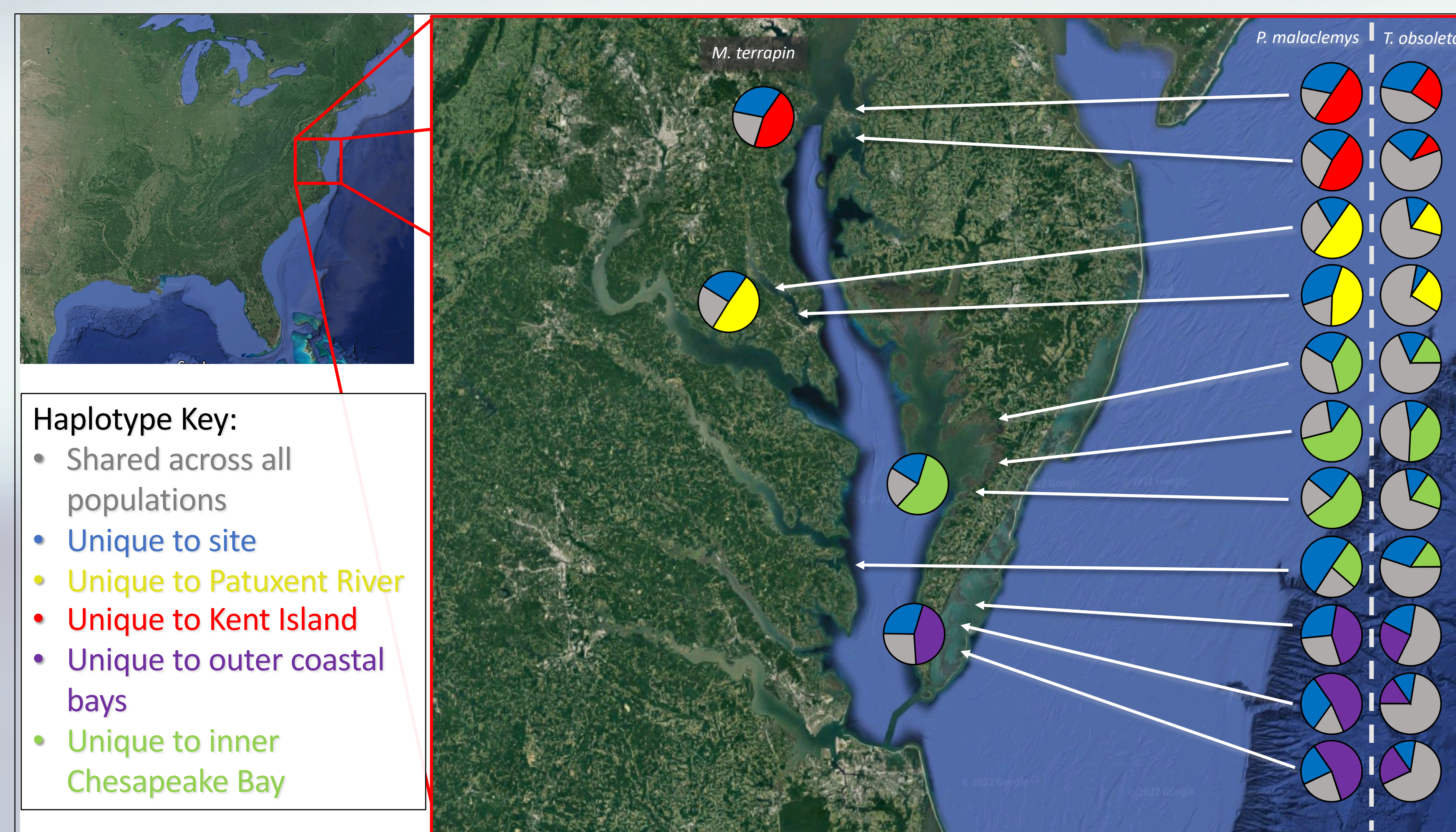


Figure 4: (above) Haplotype map showing hypothetical expected results. The genetic variation of *P. malaclemys* significantly differs from that of *T. obsoleta*, hinting that the parasites' genetic structure and dispersal is facilitated by definitive host *M. terrapin*