A genetic survey of heavily exploited, endangered turtles: caveats on the conservation value of trade animals

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Abstract
Asian turtles face an extinction crisis, and so it is imperative that systematists accurately determine species diversity in order to guide conservation strategies effectively. We surveyed mitochondrial and nuclear DNA (mtDNA and nuDNA) variation of the heavily exploited Mauremys mutica complex, a clade of Asian turtles that contains the endangered M. mutica from Japan, Taiwan, China and Vietnam, and the critically endangered Mauremys annamensis from central Vietnam. We discovered extensive mtDNA and nuDNA variation among samples that did not correspond to the currently recognized taxonomy. Both nuDNA and mtDNA data suggest that M. mutica is paraphyletic with respect to M. annamensis. Surprisingly, M. annamensis exhibits a previously unknown mtDNA structure in the form of two clades that are paraphyletic to M. mutica. These data reveal that the currently recognized taxonomy of the mutica complex does not reflect the genetic diversity of our samples. Unfortunately, many conservation-oriented captive-breeding efforts for turtles are also based on trade samples such as the ones studied here. These efforts include plans to breed trade-rescued individuals and release their progeny into the wild. Because our genetic survey reveals that the taxonomic identity of these samples does not reflect genetic diversity, we raise serious questions about the efficacy of these programs. In order to address conservation issues and provide more accurate estimates of evolutionary lineages within Mauremys, we recommend continued surveys for wild populations of the mutica complex to provide new genetic material and additional distributional data, attempts to extract DNA from historic museum specimens and a shift in conservation focus to in situ preservation of wild populations and associated habitat.

Introduction
Asian turtles face an extinction crisis (van Dijk, Stuart & Rhodin, 2000; Turtle Conservation Fund, 2003), underscoring the importance of accurately determining species diversity to guide conservation strategies (Parham et al., 2001; Stuart & Parham, 2004). Unfortunately, determining species boundaries of Asian turtles has proven challenging because of the widespread hybridization of distinct lineages in the wild and in captivity (Parham et al., 2001; Spinks et al., 2004; Shi et al., 2005; Stuart & Parham, 2007; Spinks & Shaffer, in press), a phenomenon that is exacerbated by the pervasive transportation and captive propagation of turtles for profit (Parham et al., 2001; Shi & Parham, 2001). These challenges faced by systematists are directly relevant to the captive-breeding efforts that are increasingly being championed as one of the long-term solutions to the survival of Asian turtles (Hudson & Buhlmann, 2002; Turtle Conservation Fund, 2003).

One heavily exploited species complex in dire need of detailed systematic study is the Mauremys mutica (Cantor, 1842) complex (‘the mutica complex’ hereafter). This group of medium-sized (~20 cm), aquatic turtles is widely distributed (~2600 km west to east) from central Vietnam to the islands of southern Japan (Fig. 1a). Currently, two named species are recognized, M. mutica and Mauremys annamensis (Siebenrock, 1903), although previous studies using morphological and genetic data conflict in the inference of their relationship, and suggest that the current taxonomy may not accurately reflect lineage diversity (Honda, Yasukawa &
Despite its once-widespread distribution, *M. mutica* is listed on the IUCN Red List as endangered (IUCN, 2006) because it is one of the most heavily exploited turtles in the food and medicine trade in China (Lau & Shi, 2000; van Dijk, 2000). *Mauremys annamensis* has a much more limited distribution and is considered to be one of the world’s most endangered turtles (Turtle Conservation Fund, 2003); it has only been observed in the wild by scientists twice since 1939 (ATCN, 2006a; Parham, Stuart & Orlov, 2006). All reported localities are restricted to central and southern Vietnam, an area of intense wildlife harvesting (Le, Hoang & Le, 2004).

Establishing patterns of genetic variation among the *mutica* complex is important for guiding the usage of limited conservation resources and informing captive-breeding efforts (Parham et al., 2004; Stuart & Parham, 2004). The latter issue is especially relevant for *M. annamensis* because it is essentially unknown in the wild and trade specimens are being used in captive-breeding programs with the ultimate goal of reintroduction into the wild (Schaffer, 2004, 2006; ATCN, 2006b). Among the numerous problems associated with the translocation and release of confiscated wildlife (outlined by IUCN, 2002), the risk of genetic pollution through artificial introgression (e.g. Fitzsimmons et al., 2002) is especially high for heavily exploited Asian turtles (Buskirk, Parham & Feldman, 2005). In this study, we survey the genetic diversity within the *mutica* complex using mitochondrial and nuclear DNA (mtDNA and nuDNA) sequence data. Most of our specimens are from trade seizures, markets or turtle farms, although we also include, to our knowledge, every known-locality genetic sample obtained from the wild.

**Methods**

Specimens of *M. mutica* were morphologically diagnosed by having a weakly tricarnate to smooth carapace that is usually brown, a plastron that is marked with few or moderate black marks and a single, pale yellow temporal stripe that does not extend past the eye (Iverson & McCord, 1994; Yasukawa, Ota & Iverson, 1996). *M. annamensis* is easily diagnosed from *M. mutica* in that it has a black, moderately tricarnate carapace, plastron marked heavily with black, and two to three yellow temporal stripes that meet at the tip of the nose (Iverson & McCord, 1994; Yasukawa et al., 1996). All specimens used in this study were categorized according to these criteria.

Our sampling included five individuals previously sequenced by Parham et al. (2001) and Feldman & Parham (2004) (Supplementary Material Appendix S1). These studies included a single field-collected, known-locality specimen of *M. mutica* (from the type locality at Zhoushan Island, Zhejiang Province, China). Our study added two additional known-locality specimens of *M. mutica* from Hainan Province, China (Wanling, Qiongzhong County), eight individuals of *M. annamensis* that were confiscated from an illegal shipment within Vietnam, 12 individuals of *M. mutica* and *M. annamensis* from a turtle farm in Hainan.
implemented in PAUP
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protein 35 (R35) gene, intron 1, was amplified following samples, an (Accelrys Inc., San Diego, CA, USA). For a subset of 25 were no erroneous stop codons using Macvector v. 7.1.1 region was translated into amino acids to ensure that there directions using the same primers for amplification plus the ND4 and H-Leu (Stuart & Parham, 2004) and standard leucine (trnL)
An 892 bp fragment of mtDNA including trnL
and adjacent (profiled by Shi & Parham, 2001 and Parham & Shi, 2001) and one individual of M. annamensis from the pet trade. Thirteen of our total samples (including four outgroups) were from preserved museum specimens and 24 were photo-vouchered using digital images (Supplementary Material Appendix S1). The 24 photo-vouchered specimens were a combination of farm, illegal trade seizures and wild-caught specimens that were (at the time of this paper) either living in the care of the turtle farmer, Cuc Phuong National Park Turtle Conservation Center in Ninh Binh Province, Vietnam, or with one of us (H. S.) at Hainan Normal University, respectively. Photo-vouchers are deposited in the Museum of Vertebrate Zoology at the University of California, Berkeley (Supplementary Material Appendix S1). Although we do not have precise locality data for the M. annamensis specimens from the trade seizure, we believe that these samples were from the wild because there are no known turtle farms in Vietnam breeding M. annamensis, trade with China is unidirectional and the specimens were confiscated off a truck in northern Vietnam (Ninh Binh Province). These individuals were probably wild caught in Vietnam and therefore most likely represent lineages that are not influenced by genetic admixture in captivity.

Tissue samples in the form of liver, blood or tail tips were frozen in liquid nitrogen, stored in 95% ethanol or stored in lysis buffer. Total genomic DNA was extracted via a DNeasy Tissue Kit (Qiagen Inc., Valencia, CA, USA) following the manufacturer’s recommendations. An 892 bp fragment of mtDNA that encodes part of the NADH dehydrogenase subunit 4 (nad4) gene, the complete tRNAs histidine (trnH) and serine (trnS) and part of the tRNA leucine (trnL) was amplified by PCR using the primers L-ND4 and H-Leu (Stuart & Parham, 2004) and standard conditions. Purified PCR products were sequenced in both directions using the same primers for amplification plus the internal primers L-ND4int and H-ND4int (Stuart & Parham, 2004). Sequences were aligned and the protein-coding region was translated into amino acids to ensure that there were no erroneous stop codons using Macvector v. 7.1.1 (Accelrys Inc., San Diego, CA, USA). For a subset of 25 samples, an ~1133 bp fragment of the RNA fingerprint protein 35 (R35) gene, intron 1, was amplified following Fujita et al. (2004).

Phylogenies were reconstructed using the maximum parsimony (MP) and maximum likelihood (ML) criteria as implemented in PAUP* v. 4.0b10 (Swofford, 1998) and Bayesian inference using MrBayes v.3.1.2 (Hulsenbeck & Ronquist, 2001). For mtDNA, Cuora galbinifrons, Mauremys caspica, Mauremys nigricans and Mauremys reevesii were used as outgroups following Parham et al. (2001) and Stuart & Parham (2004), while Cuora amboinensis was used for nuDNA. Our MP analysis was conducted using the branch-and-bound algorithm, with transitions and transversions weighted equally for 1000 random addition replicates and 100 pseudoreplicates. Characters were unweighted because the third codon position transitions accumulated in a linear fashion and showed no indication of saturation. Nodal support was assessed using 1000 nonparametric bootstrap pseudoreplicates (Felsenstein, 1985), with 100 random addition sequence replicates per pseudoreplicate.

For ML analyses, Modeltest 3.5 (Posada & Crandall, 1998) was used to infer the best-fit model of sequence evolution under the hLRT criterion. Analyses were initially performed with 1000 random addition replicates with step-wise addition of taxa and tree bisection-reconnection (TBR) branch swapping. A single tree from the results was chosen, and analyses were iterated in a successive-approximations approach until the parameters stabilized (Sullivan et al., 2005). Bootstrap proportions were calculated using RAxML 2.2.3 (Stamatakis, 2006) with 1000 pseudoreplicates under the GTRCAT model of sequence evolution.

For Bayesian analysis, models were selected for each partition using MrModelTest v.2 (Nylander, 2004) under the hLRT criterion. The mtDNA dataset was partitioned using first, second and third codon positions and tRNAs (Brandley, Schmitz & Reeder, 2005) while a single model was used for the entire nuDNA dataset. Searches were run using four chains, four million generations and sampling every 1000th tree. Burn-in was estimated in the program AWTY (Wilgenbusch, Warren & Swofford, 2004) by plotting the cumulative posterior probability of nodes against the generation time. The analysis was run twice with random starting trees and the results were compared.

**Results**

**mtDNA**

An 892 bp fragment of mtDNA including nad4 and adjacent tRNAs was obtained for all samples. Products from sequencing produced single peaks and there were no erroneous stop codons within the protein-coding regions. The average nucleotide frequencies in the fragment were A = 0.349, C = 0.266, G = 0.134 and T = 0.252, showing the characteristic bias in the light strand of mtDNA against G (Kocher et al., 1989). From our dataset, 179 nucleotides were variable and 117 were parsimony informative, while uncorrected pairwise distances within our ingroup ranged from 0 to 7.5%. The MP analysis resulted in a single most parsimonious tree (length = 255; CI = 0.749; RI = 0.902). For ML, the model HKY + Γ was used with a Ti/Tv ratio = 8.7318, γ distribution shape parameter = 0.1822 and base frequencies of A = 0.3539, C = 0.2606, G = 0.1337 and T = 0.2518. After the iterative likelihood approach, the result was a single tree (−ln L = 2531.126; Ti/Tv = 8.7317; shape = 0.182171). Bayesian analyses were run under the following models: first position – HKY + Γ, second position – HKY, third position – GTR + Γ and tRNA – HKY + Γ + Γ. The first 500 generations were discarded as burn-in. Both independent Bayesian runs gave essentially identical likelihood estimates and tree topologies. The same tree topology resulted from all three analytical methods, although the support values differed (Fig. 2). Our analyses resulted in a strongly monophyletic mutica complex, with 100% support from all analyses (Fig. 2).
Contained in the mutica complex were two major, well-supported clades that differed by uncorrected pairwise sequence divergences of 6.2–7.5% (Fig. 2). One clade included the M. mutica specimen from the type locality in eastern China as well as many M. mutica specimens attributed to mainland China by the Hainan turtle farmer from whom the samples were obtained (see ‘Discussion’). Because this clade included a specimen from the type locality, we call this the ‘true mutica’ clade (Fig. 2). The second clade included mutica from Hainan and M. annamensis, and is referred to as the ‘Hainan–Vietnam’ clade. The Hainan–Vietnam clade included three haplotype groups for which monophyly is strongly supported. We refer to these clades as annamensis 1, annamensis 2 and Hainan based on either known provenance samples or dominant morphotypes contained within.

**Nu DNA**

An ~1133 bp portion of the nuclear intron R35 (Fujita et al., 2004) was collected for 25 samples. For the analyses, 31 nucleotides were variable and 14 parsimony-informative, with uncorrected pairwise distances within the ingroup ranging from 0 to 1.5%. The MP analysis resulted in a single most parsimonious tree (length = 51; CI = 0.902; RI = 0.945). For ML, the model HKY + Γ was used with a Ti/Tv ratio = 1.009, γ distribution shape parameter = 0.016 and base frequencies of A = 0.2792, C = 0.177, G = 0.212 and T = 0.3318. After the iterative likelihood approach, four equally likely trees resulted (~ln L = 1929.15; Ti/Tv = 1.041; shape = 0.016), which only differed by the placement of terminal branches. Bayesian analyses were run under the HKY + Γ model. The first 500 generations were discarded as burn-in. Both independent Bayesian runs gave essentially identical likelihood estimates and tree topologies. Similar tree topologies resulted from all three analytical methods (Fig. 3).

Within the mutica complex, three clades were recovered corresponding to taxonomy and geography: annamensis, eastern China mutica and Hainan mutica (Fig. 3). Although not all the support values were strong, M. annamensis
renders *M. mutica* paraphyletic, with eastern China *M. mutica* being more closely related to *M. annamensis* than Hainan *M. mutica*.

**Discussion**

Our study further elucidates the genetic diversity and major genetic groupings within the *mutica* complex reported by Parham et al. (2001) and Feldman & Parham (2004). We also recover a deep mitochondrial divergence (6.2–7.5%) between the eastern Chinese *M. mutica* (the true *mutica* clade) and those from the Tonkin Gulf region (The Hainan–Vietnam clade). Both mitochondrial and nuclear datasets agree that the true *mutica* clade is genetically distinct and that *M. mutica* is paraphyletic with respect to *M. annamensis*. Developing a more accurate picture of the geographic distribution of the two *mutica* clades (true *mutica* vs. Hainan–Vietnam *mutica*), and determining where they come into contact (if at all) will prove challenging because the distributional gap between known-locality specimens of both clades is in southern mainland China, the most active region in the consumption and import of turtle goods. This highlights a recurring problem associated with studying the phylogeography of Asian turtles: there are so few unambiguously field-collected specimens that establishing accurate geographical distributions is difficult (Parham & Li, 1999; Parham & Wang, 2000; Fong, Parham & Fu, 2002). However, if this distributional gap is real and ancient, it could explain the high sequence divergence between the *mutica* clades.

The high level of divergence of mtDNA used in this study between the true *mutica* and Hainan–Vietnam clade (6.2–7.5%) exceeds that between many pairs of widely accepted turtle species sequenced for the same marker (<5%; Feldman & Parham, 2002; Parham et al., 2004; Stuart & Parham, 2004). Therefore, within *M. mutica*, current taxonomy is potentially underestimating lineage diversity due to the presence of *M. mutica* in three mtDNA clades (true *mutica*, *annamensis* 1 and Hainan; Fig. 2) and two nuDNA clades (Hainan, eastern China; Fig. 3). Previous systematic studies have noted considerable regional morphological variation within *M. mutica* (Iverson & McCord, 1989, 1994), with individuals in the north-east of its range tending to be brown in coloration and black in the south-west of its range. We compared these findings with additional literature and specimens (from museums, turtle...
farms, trade seizures and markets; Supplementary Material Appendix S1 and S2). There seems to be some concordance from these results, for example, the turtle farmer’s categorizations of individuals (mutica samples 11–12, 14, 16, 26–28, 30–32) into ‘mainland’ and ‘Hainan’ were all correct based on similar criteria as Iverson & McCord (1989, 1994). However, with our limited known-locality specimens, we are unable to definitively tie morphotypes of M. mutica to geography. If consistent diagnostic characters can be adequately demonstrated, it may be justified to resurrect junior synonyms of M. mutica [e.g. Mauremys schmackeri (Boettger, 1894) for Hainan mutica and Mauremys grochovskiae (Dao, 1957) for Vietnam mutica]. But an adequately informed taxonomy of the mutica complex cannot be generated without detailed genetic and morphologic studies of specimens with reliable locality data. For now, we urge taxonomic restraint and feel that it is most judicious to maintain the current taxonomy, while treating the genetically distinct M. ‘mutica’ populations from Hainan and Vietnam as distinct units for conservation (with quotes to denote their uncertain taxonomic status) separate from true M. mutica from eastern China and M. annamensis.

Although our mtDNA and nuDNA trees have different topologies, a similar pattern arises – M. annamensis is nested within M. mutica. In the case of the mtDNA phylogeny, M. annamensis is more closely related to M. annamensis from Hainan, while the nuDNA infers M. annamensis to be more closely related to M. mutica from eastern China. Differences in the topologies may be due to biological factors (e.g. introgression or retention of ancestral polymorphisms) and/or anthropomorphic factors (e.g. translocation or artificial hybridization), but we are reluctant to favor one explanation over the other based on the available sampling. One unexpected result from our study was that M. annamensis samples seized within Vietnam had haplotypes corresponding to two distinct mitochondrial subclades (annamensis 1 and annamensis 2) that were paraphyletic to those of mutica from Hainan and Vietnam. Based on this high level of genetic diversity within M. annamensis, we predict that the range of M. annamensis may be larger than currently realized (Iverson, 1992; Parham et al., 2006). If so, this genetic break may correspond to phylogeographic patterns seen in several other Vietnamese vertebrates (Garza & Woodruff, 1992; Roos & Nadler, 2001; Stuart & Parham, 2004).

The incongruent morphological and molecular variation among our trade samples also reveals their limitation as a conservation resource. Because current captive-breeding efforts for endangered Asian turtles rely entirely on taxonomic assignments based on morphology, the potential for these programs to foster the admixture of formerly discrete genetic lineages is extremely high. In the case of M. annamensis, established programs include plans to breed trade-rescued turtles and release their progeny into the wild in Vietnam (Schaffer, 2004, 2006; ATCN, 2006b). Without a better understanding of the geographic patterns of genetic diversity in the mutica complex, these efforts may inadvertently lead to the disruption of natural population substructure through the release of animals into the incorrect geographic area, outbreeding depression and/or the release of hybrid individuals.

The next steps in resolving the genetic underpinnings of the mutica complex are to increase efforts to locate and obtain genetic material from wild-caught specimens. This study includes three known-locality genetic samples collected by one of us (H. S.), or our colleagues, but without a concerted effort to obtain more known locality samples from China and Vietnam, we do not expect this small sample size to grow in the near future. However, another potential resource for genetic material is historical museum specimens. Natural history collections worldwide house voucher specimens that were collected before the Asian turtle survival crisis. Many of these specimens have detailed locality information and could ostensibly provide genetic data for extremely rare or extinct populations (e.g. Parham et al., 2004). Unfortunately, most of these specimens are fixed with formalin, which makes DNA extraction a challenging and uncertain endeavor. Despite these difficulties, some workers have successfully extracted high quality DNA from formalin-fixed specimens (e.g. Shedlock et al., 1997; Schander & Halanych, 2002), and so with some effort and the advent of new techniques, it may be possible to unlock a trove of genetic data from museum specimens.

Conclusions

Our study illustrates that the genetic diversity seen in the mutica complex is greater than believed previously. However, the genetic divisions within this group do not match the current taxonomy. There may be multiple natural and anthropogenic forces acting simultaneously to create the patterns of variation that we observed, but our ability to untangle these forces is hindered by the fact that most available genetic material originates from the turtle trade. Unfortunately, this trade also happens to be the same source of animals for captive-breeding efforts (Hudson & Buhlmann, 2002; Schaffer, 2004, 2006; ATCN, 2006b). Based on our findings, we seriously question the probability of success and efficacy of breeding and reintroduction efforts based on trade animals (Dodd & Seigel, 1991; IUCN, 2002; Lau, 2002). This is not to say that repatriation and augmentation (Reinert, 1991) are useless tools for conservation, but rather we currently know too little about the complex systematics of most Asian turtles (e.g. Spinks & Shaffer, 2007) to proceed properly. While genetic samples obtained from trade specimens can help elucidate minimum estimates of genetic diversity, their lack of provenance and the risk of genetic admixture in captivity severely limit their utility for understanding geographic patterns of genetic diversity or captive-breeding programs that recommend releasing animals into the wild. Breeding programs are useful in preserving individuals, educating the public and gathering data on reproductive biology (Schaffer, 2006), but it is prudent to shift more attention to in situ conservation of populations and habitats and understanding the geographic and genetic
diversity through fieldwork before reintroducing turtles into
the wild.

The next steps towards unraveling the complicated patterns of incongruent molecular and morphological variation uncovered here will include: (1) intensive field surveys for new genetic material with known provenance, especially focusing on *M. annamensis* and Vietnam ‘mutica’; and (2) increased effort to extract DNA from historic and formalin-fixed museum specimens.

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**References**


**Supplementary material**

The following material is available for this article online:

Appendix S1.

Appendix S2.

This material is available as part of the online article from http://www.blackwell-synergy.com/doi/abs/10.1111/j.1469-1795.2007.00131.x

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Appendix A

A total of 37 specimens from several different sources were used in this study. Numbered specimens correspond to those in Figure 2. Ten of the DNA sequences used in this analysis were obtained from Genbank. Following is a list of all specimens used in this study with their voucher number, Genbank accession number for *nad4*, and Genbank accession number for R35 (if applicable). Outgroups: *Cuora galbinifrons* (FMNH 255695; AY364617; n/a), *Mauremys caspica* (MVZ 234281; AY337340; n/a), *M. reevesii* (MVZ 236729; EF034110; n/a), *M. nigricans* (MVZ 234641; EF034111; n/a), *C. amboinensis* (FMNH 255262; n/a; DQ386654). Ingroup:

1) *M. annamensis* (MVZ 251449; EF034098; EF587934); 2) *M. annamensis* (MVZ 238937; AY337338; EF87933) 3) *M. annamensis* (MVZ 251454; EF034103; n/a); 4) *M. annamensis* (MVZ 251456; EF034105; EF587922) 5) *Cuora X Mauremys* hybrid (MVZ 230475; AF348241; n/a); 6) *M. annamensis* (MVZ 251453; EF034102; EF587929); 7) *M. annamensis* (MVZ 251460; EF034109; EF587926); 8) *M. annamensis* (MVZ 230462; EF034113; DQ386655) 9) Vietnam *‘mutica’* (ROM 25613; AF348279; n/a); 10) Vietnam *‘mutica’* (ROM 25614; AF348280; DQ386668); 11) Hainan ‘mutica’ (MVZ 251447; EF034096; EF87929); 12) Hainan ‘mutica’ (MVZ230477; EF034105; n/a); 13) Hainan ‘mutica’ (MVZ237108; EF034104; EF587915); 14) Hainan ‘mutica’ (MVZ 251448; EF034097; EF587925); 15) Hainan ‘mutica’ (MVZ 251452; EF034101; EF587917); 16) Hainan ‘mutica’ (MVZ 251446; EF034095; EF587930); 17) Vietnam ‘mutica’ (MVZ230476; AF348278; DQ386664); 18) *M. annamensis* (MVZ 251455; EF034104; EF587923); 19) *M. annamensis* (MVZ 251457; EF034106; EF587928); 20) *M. annamensis* (MVZ 251458; EF034107; EF587924) 21) *M. annamensis* (FMNH 262238; EF034112; DQ386656) 22) *M. annamensis* (MVZ 252396; EF587914; EF587921); 23) *M.
annamensis (MVZ 251450; EF034099; EF587919); 24) M. annamensis (MVZ 251451; EF034100; n/a); 25) M. annamensis (MVZ 251459; EF034108; n/a); 26) M. mutica (MVZ 251443; EF034092; n/a); 27) M. mutica (MVZ 251444; EF034093; EF587931); 28) M. mutica (MVZ 251440; EF034089; EF587932); 29) M. mutica (MVZ 230487; AF348278; DQ386666); 30) M. mutica (MVZ 251441; EF034090; n/a); 31) M. mutica (MVZ 251442; EF034092; EF587916); 32) M. mutica (MVZ 251445; EF034094; EF587927).

Institutional abbreviations: FMNH—Field Museum of Natural History, Chicago, IL, USA; MVZ—Museum of Vertebrate Zoology, University of California, Berkeley, CA, USA; ROM—Royal Ontario Museum, Toronto, Ontario, Canada.
Appendix B

For this project, additional material to Appendix A was examined but not sequenced:


The following references provide images that aided our comparisons: Siebenrock (1903), Bourret (1941), Dao (1957), Petzold (1963), Iverson & McCord (1994), Yasukawa, Iverson, & Ota (1996).

Institutional abbreviations: CAS—California Academy of Sciences, San Francisco, CA, USA; FMNH—Field Museum of Natural History, Chicago, IL, USA; FU—Fudan University, Shanghai, China; MVZ—Museum of Vertebrate Zoology, University of California, Berkeley, CA, USA.