

## **Defining Turtle Diversity: Proceedings of a Workshop on Genetics, Ethics, and Taxonomy of Freshwater Turtles and Tortoises**

### **EXECUTIVE SUMMARY**

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Genetic data, in combination with strong field studies, form one of the cornerstones of evolutionary, conservation, and population biology. Turtles are particularly well suited to benefit from the insights that genetics can bring to important management issues. With only 313 currently recognized extant species worldwide, turtles are a manageable group from a phylogenetic perspective, such that conservation and management biologists are able to identify species complexes that will benefit from additional genetic analyses. Additionally, field studies of threatened and endangered turtles have identified conservation and management questions needing genetic answers. Given the severe survival threats facing the world's turtle and tortoise fauna, it is clear that the research and conservation communities, more than ever before, need to work together to help identify, manage, and renew the world's depleted turtle populations.

Freshwater turtles and tortoises have received considerable attention from the genetics research community, and several important trends came out of the comprehensive literature analyses by FitzSimmons and Hart, and Engstrom et al. First, the vast majority of work to date has been based on mitochondrial (mt) DNA, with input from the nuclear genome coming from population level analyses of microsatellite data and (in the older literature) allozymes. Given the recent work from several groups demonstrating that mtDNA can be strongly affected by hybridization, introgression, and incomplete lineage sorting, the genetics community needs to continue efforts to develop new nuclear DNA tools that will allow testing of phylogenetic, phylogeographic, and population genetic hypotheses with independent datasets. In addition, taxonomic and geographical biases exist in the areas of concentration of genetic research on turtles. In particular, North American turtles have received most of the research attention to date. While this focus is related to the high concentration of the genetics research community in North America, most of the critically important conservation problems are for non-North American taxa. The call by FitzSimmons and Hart for renewed research attention in other regions of the world is essential, both for filling in basic gaps in our knowledge of turtle genetics and to address the most crucial conservation needs faced by worldwide turtle and tortoise populations.

McGaugh et al. point out the stunning new tools that are becoming available for genetic studies, ranging from indi-

vidual paternity analysis to deep phylogenetics to identifying genes associated with unique phenotypes. Many of these newest tools are just being applied to turtles, and the possibilities for asking and answering new questions are truly astonishing. As new genomic-level resources for turtles become available, it should become both easier and less expensive to achieve these new research goals. The availability of the first full genomic sequence for a turtle (*Chrysemys picta*, scheduled for delivery in 2008) will be a huge boost for this research agenda.

The Turtle Taxonomy Working Group (TTWG) focused on the important issues surrounding the scientific names that we apply to turtles, what they should represent, and their value in scientific communication and conservation biology; in essence, how do we recognize and define turtle diversity? Particularly as molecular genetic data have been applied to phylogenetic problems, the names that we apply to monophyletic groups (clades) at the genus level or higher have become quite unstable in recent years. While many of these taxonomic changes may be positive, too much change can lead to instability that is at odds with effective communication and conservation legislation. The TTWG recommended a set of "Guidelines for Best Scientific Practices for Revising Taxonomy" that could serve to stabilize taxonomy by recognizing the role that scientific nomenclature plays in biology, and the ways that we can use names to effectively communicate critical biological knowledge.

As we have continued to discover and investigate more of the world's turtle populations, and applied increasingly refined morphologic and genetic characters and criteria for recognizing and documenting chelonian diversity, the number of distinct turtle taxa have grown dramatically. The Turtle Taxonomy Working Group, in a separate chapter, documents this diversity by providing a complete, up-to-date list of all currently recognized extant or recently extinct turtle species and subspecies (consisting of 319 species and 146 additional subspecies, for 465 total turtle taxa), including a list of over 100 issues in turtle taxonomy that have either undergone recent taxonomic change or are in dispute or in need of some type of resolution. Of the currently recognized modern turtle taxa, 6 species plus 3 additional subspecies (9 total taxa) have gone extinct since 1500 AD, leaving us currently with 313 living turtle species, 143 additional living subspecies, and 456 living turtle taxa.

Assembling a complete phylogenetic tree for all species of turtles is a critical goal, and Iverson et al. summarize the literature to date on turtle phylogeny. They then go on to construct a set of supertrees that stand as the best composite hypotheses on turtle phylogeny assembled to date. Progress in the last 20 years on turtle phylogenetics has been incredible, and we can anticipate that in another decade turtles will emerge as one of the most completely understood clades of vertebrates. Major accomplishments include progress on the “backbone tree” of turtles, and phylogenetic relationships within Trionychidae, Geoemydidae, and Testudinidae. Given both the high species diversity and conservation concerns with these three families, this progress is important and timely. As Iverson et al. emphasize, much of this progress relies on mtDNA, and an infusion of nuclear DNA data and analyses will represent the next major step forward in assembling a true Tree of Life for turtles.

Conservation genetics is a theme that runs throughout this monograph, and is particularly emphasized by the Turtle Conservation Genetics Working Group. Key areas where population genetics approaches have been effective for turtle conservation include the identification of management units and cryptic lineages, understanding gene flow among natural populations, and forensic research on the exploitation of endangered taxa. One of the most important outcomes of this work has been in strengthening the working relationship between research biologists, agency and management scientists, and the captive breeding communities.

Syed et al. consider a related way in which the genetics and conservation communities work together for common goals through captive breeding and assurance colonies. Both *in-situ* and *ex-situ* captive management programs have provided a valuable hedge against extinction in the form of strong captive breeding programs, and some of the world’s most endangered turtles (ranging from the Madagascar ploughshare tortoise, *Astrochelys yniphora*, to the critically endangered Australian western swamp turtle, *Pseudemydura umbrina*) are now being propagated and repatriated into the wild. Genetics plays a key role by identifying cryptic lineages that require independent management, as well as guidance in avoiding close inbreeding and resultant inbreeding depression. All of these approaches to conservation effectively use genetic technologies to help conserve turtles, and they represent a rich history of sharing resources and material across a variety of partners that has benefited turtle conservation as a discipline.

Another theme, and one that is often overlooked in academic treatises, is an explicit focus on ethical considerations in research programs. Two groups consider ethics from rather different vantage points in this volume. Burke et al. take a broad view of legal considerations—given the sometimes conflicting and confusing laws surrounding domestic and international research, how can individual researchers move forward with their work and respect the critical laws that govern and manage endangered species? The answers are not always simple, but they are important

and need to be addressed by anyone who works on natural populations. A related theme explored by Lehn et al. is the ethics surrounding vouchering—that is, collecting representative material for long-term storage in standard specimen-based museums. Traditional voucher specimens constitute the physical record by which we often judge historical changes in species’ ranges, and they are an absolute necessity for work in systematics and taxonomic descriptions requiring type specimens. However, as turtles become increasingly rare in the wild, euthanizing specimens as vouchers is often in direct conflict with the stated goals of conservation and management. These are difficult issues, and both Burke et al. and Lehn et al. consider the material already available in traditional museum collections, alternative media such as digital photographs or tissue samples, and investigator responsibilities in considering how traditional and non-traditional specimen acquisition should proceed.

Finally, one must consider the issue of data distribution in an Internet-driven world. The turtle community currently has several useful Internet resources, including the EmySystem site, and Kiester and Bock discuss how such a website can be developed as an improved portal to important data, advances, and issues related to conservation and organismal biology. They identify and discuss three key challenges: continuous content update, quality assurance and control, and synthesis and integration. All of these are issues that must be dealt with, and Kiester and Bock offer a concrete proposal for a website that would serve the needs of the turtle research and conservation communities into the future.

We have clearly made enormous strides in the last two decades in the use of genetics to further our understanding of evolutionary history, current demography, and conservation biology of the world’s turtle and tortoise fauna. Major challenges still remain, particularly if we are to prevent the further loss to extinction of the relatively few species of turtles currently living on earth. However, we are coming to understand the species and lineages that require the most urgent conservation, and we can see clear, demonstrable progress in populations of taxa ranging from giant Galapagos tortoises to diminutive swamp turtles. Genetics has played a key role in some of these successes, and will continue to do so in the future, particularly as genomic resources become increasingly available.

The stakeholders in the international turtle conservation community include individuals and institutions from the diverse research and conservation communities of academics, non-governmental organizations, governmental agencies, international organizations and regulatory bodies, philanthropic foundations, zoos and aquaria, and private herpetoculturists. Collaboration between these various stakeholders who work with or care for turtles is the key to current and future progress, and the turtle community has been a leader in establishing and fostering such collaborative efforts. We are proud of these efforts, and continue to encourage them as we focus on expanding and accelerating progress for turtle conservation worldwide.