Modern Genetics Reveals Ancient Diversity in the Loggerhead

What makes a loggerhead turtle a loggerhead turtle? Over the years, "loggerhead" has meant many different things. At one time, the term "loggerhead" included the Ridley turtles. More recently, it encompassed two different subspecies (*Caretta caretta caretta* and *Caretta caretta gigas*).

Owing largely to modern genetics, the identity of loggerhead turtles is no longer ambiguous. We now know that the loggerhead turtle, *Caretta caretta,* is in fact a single species. But what does this mean for the loggerhead—and for its conservation and management?

Life is certainly not simple, and much like the loggerhead's genetic structure, our knowledge of loggerhead genetics is continually evolving.

Using mitochondrial DNA sequence analysis, scientists have been able to identify different genetic stocks that represent rookeries or groups of rookeries that are genetically isolated from each other, as detailed in the inset on the following page. These studies have also traced the relationships among different stocks and have proposed scenarios of how the different lineages have evolved. Today's lineages can all be traced back to a common ancestral stock that existed approximately 3 million years ago, when the Atlantic Ocean was separated from the Indo-Pacific Ocean by the formation of the Panama Isthmus.

Since then, geographic, environmental, and biological forces (natal homing, for example) have shaped dispersal patterns, extinctions, and recolonization events. All of these events have left clues in the loggerhead's DNA, and these continue to be revealed through ongoing studies. The global genetic diversity that we now see in loggerhead turtles has evolved over the last three million years as they adapted to changing climate and geography to colonize new rookeries, while other rookeries disappeared. This genetic diversity is reflected in the current population structure as we understand it. Although we know a great deal about loggerhead genetics, a complete understanding will require new research that targets the many genetically unknown populations.

Genetic markers have also been used as tags to map transoceanic migrations and to uncover the linkages between foraging areas—enabling researchers to identify the stock origin of turtles that are caught incidentally by fishers on the high seas and in coastal areas. These studies have revealed a great deal. Loggerheads born of the North Pacific (Japanese) stock, for example, spend part of their lives some 7,000 miles away off the coast of Baja California, Mexico. Similarly, studies suggest that loggerheads of the eastern Australian stock may inhabit waters off Peru and Chile—more than 10,000 miles from their natal shores. In the Atlantic, juvenile loggerheads born on the shores of

A loggerhead swims off the coast of Florida, U.S.A. Loggerheads of the Florida peninsula genetic stock generally grow to be larger than those from the Mediterranean genetic stocks. © BRIAN SKERRY / NATIONAL GEOGRAPHIC

the United States venture into the Mediterranean and eventually return to reside in coastal U.S. waters. New genetic data suggest that these larger juveniles generally take residence near their natal beaches, where the females return to nest as adults.

The most important fact that we have learned in the field of loggerhead genetics is this: conserving the loggerhead is less about protecting the species at the global scale and more about focusing on the survival of each of the many distinct parts that make up the loggerhead species. After all, genetic diversity is the key to a species' ability to adapt and persist through environmental change—a truth that bears even greater poignancy amid today's changing climate.

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The Known Genetic Stocks of the Loggerhead Sea Turtle

In the **Pacific Ocean,** there appear to be three main genetic stocks:

1. a western Australian stock;
2. an eastern Australian stock, possibly including turtles born in New Caledonia; and
3. a North Pacific or Japanese stock including all loggerhead rookeries in the Japanese archipelago.

In the **Atlantic Ocean** and **Caribbean Sea** the loggerhead stock structure appears to be divided among at least eight genetic stocks:

1. a northern U.S.A. stock, including rookeries from southern Virginia, southward to the northern Florida border;
2. a Florida peninsula, U.S.A. stock, which includes rookeries from the northeastern Florida border through southwestern Florida (Pinellas County);
3. a Dry Tortugas stock including islands west of Key West;
4. a northern gulf (U.S.A.) stock that extends from northwestern Florida into Texas;
5. a Cay Sal Bank, western Bahamas stock;
6. a Quintana Roo, Mexico stock, including all loggerhead rookeries on Mexico's Yucatan Peninsula;
7. a Brazilian stock; and
8. a Cape Verde stock.

The genetic composition of loggerheads that nest through much of the **wider Caribbean region** remains unknown due to lack of research. This category includes loggerheads born of beaches in Caribbean Central America, the Bahamian Archipelago, Cuba, Colombia, Venezuela, and the eastern Caribbean islands.

Similarly, the loggerhead populations along the **western African coast** remain a mystery in many regards.

In the **Mediterranean Sea** there are two distinct genetic stocks: one that centers on rookeries in Turkey, and a second that centers on Greece. **Libya** also hosts a large loggerhead population, whose genetic composition remains unknown but may prove to be distinct.

The genetic structure of loggerhead rookeries in the **Indian Ocean** is somewhat less clear.

It is apparent, however, that the **South African rookery** is a distinct genetic stock (and may include sites in Mozambique), and rookeries in **Oman** and **Yemen** also represent a distinct genetic stock. It is unclear where the nesting beaches in Madagascar and Sri Lanka fall.