

Hawksbill Genetics Explained

Molecular genetics offers a valuable set of tools for unraveling the mysteries and histories of many species. These tools have developed rapidly during the past decade, allowing scientists to gain insight into previously intractable questions. In the case of the hawksbill turtle, molecular genetics has described evolutionary patterns, stock identities, geographic distributions, and the presence of hybrids. Genetic techniques have drastically improved our understanding of hawksbill biology and, in turn, have enhanced our ability to manage the species.



A female hawksbill can mate with several males within one reproductive season; males might also have multiple mates within the same season. © R.P. VAN DAM

Recent Discoveries about Hawksbills from Genetic Studies

- Hawksbill lineages in the Indo-Pacific and Atlantic oceans are evolutionarily distinct, a notion that was established previously on a morphological basis but later discarded.
- Hawksbills, with their unique diet of sponge, belong to a carnivorous sea turtle lineage that aligns them with the loggerhead and ridley subfamilies.
- Hybridization between hawksbills and olive ridleys, loggerheads, or green turtles is sporadically observed, especially in areas where hawksbill populations have declined greatly. In Bahía, Brazil, however, hawksbill-loggerhead hybrids apparently have integrated into the normal population, constituting about 40 percent of the rookery.
- Nesting hawksbill populations are not closed, as previously thought. Rather, they share developmental and foraging grounds with individuals from multiple genetic stocks, and they migrate internationally, returning to their natal beaches to reproduce. These characteristics highlight the need for regional and multinational management schemes that take into account both nesting and foraging grounds.
- Distinctions exist among multiple nesting stocks within geographic regions. For example, there are at least 15 different nesting populations in the Caribbean region.

Clearly, genetic studies have uncovered numerous crucial clues about hawksbill populations worldwide. However, more information—particularly stock identifications for nesting populations in certain regions (for instance, the Eastern Atlantic and Indian oceans)—is necessary to solve many remaining hawksbill mysteries and to develop sound policies to conserve this species globally.

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Known Genetic Stocks of the Hawksbill Sea Turtle

In the **Pacific Ocean**, four main genetic stocks have been identified:

- Eastern Pacific (perhaps extending from Mexico to Panama)
- Northeastern Australian
- Sabah, Malaysian
- Solomon Islands

In the **Indian Ocean**, at least five genetic stocks have been identified:

- Arabian Peninsula
- Northern Red Sea
- Peninsular Malaysian
- Seychelles and Chagos Islands
- Western Australia

In the **Western Atlantic Ocean and the Caribbean Sea**, all populations analyzed to date have proven distinct. Although six stocks await final analysis, nine distinct stocks have already been identified:

- Antigua
- Barbados
- Belize
- Brazil
- Costa Rica
- Cuba
- Mexico
- Puerto Rico
- U.S. Virgin Islands

In the **Eastern Atlantic Ocean**, at least one stock occurs around the regionally important rookeries in the Democratic Republic of São Tomé and Príncipe and in Equatorial Guinea, principally on the Island of Bioko, although hawksbill nestings have been rare in recent years.