

COMMENTARIES AND REVIEWS

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Chelonian Conservation and Biology, 1997, 2(3):438–439
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Movement of Hawksbill Turtles — a Different Perspective on the DNA Data

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Whether hawksbill turtles (*Eretmochelys imbricata*) are relatively sedentary or move between nesting beaches and distant foraging areas is of more than academic interest. It has implications for both harvesting and conservation. If the hawksbills nesting on a beach in one country feed in waters of another country, then harvesting in either country could decrease the number of animals available in the other country. Likewise, conservation efforts in one country could be affected by practices in the other country.

Bowen et al. (1996) analyzed the mitochondrial (mt) DNA of hawksbill turtles in a foraging area off Mona Island, Puerto Rico. They concluded that this population was not primarily composed of turtles nesting nearby on Mona Island itself but was drawn from nesting populations “throughout the Caribbean” and that “these data indicate that a hawksbill turtle harvest on feeding grounds will reduce nesting populations throughout the Caribbean region.”

The basis of this view was a comparison of haplotypes of turtles at the foraging area with those of turtles from 7 nesting areas: Belize, Yucatan (Mexico), U.S. Virgin Islands, Antigua, Barbados, Bahia (Brazil), and Mona Island (Puerto Rico). In addition to the point that these sites do not cover the nesting areas of this species throughout the Caribbean, there are other reasons for thinking more about the conclusions of Bowen et al., or at the least wanting to see more extensive data.

The most common haplotype found by Bowen et al. in the 41 specimens from the Mona Island foraging ground was F (18 of 41 turtles, Table 1). This haplotype is also common in hawksbills nesting in the U.S. Virgin Islands (Buck Island), ca. 350 km from Mona Island. Therefore, while it may be true that the Mona

Island feeding population “is not drawn primarily from the proximal nesting colony,” i.e., the beaches on Mona Island itself, “or any single assayed nesting colony,” it cannot be excluded that many of the turtles feeding at Mona Island come from fairly nearby. Table 3 in Bowen et al. estimates the contribution from the Virgin Islands as 51.0% of the Mona Island feeding colony. Adding on 12.7% for the Mona Island nesting beaches, 63.7% or nearly two thirds of the turtles at this foraging area appear to come from relatively close nesting areas, and not from throughout the Caribbean.

Doubtless, Bowen et al. would have preferred to have had additional samples from some other areas. Nevertheless, the argument they give as to why “the presence of unsampled beaches may not have been an overwhelming limitation” is interesting. They cite work by Broderick et al. (1994) indicating that hawksbill turtles may move between nesting beaches separated by several hundred km (100–750 km). “Hence when one nesting beach is sampled for mtDNA analysis, it probably represents an extended nesting population including several adjacent sites” (Bowen et al., 1996).

This looks like trying to have it both ways at once. If unsampled beaches are not a problem because they will be represented by genetically similar hawksbills in an extended population nesting over several nesting beaches, then it seems inconsistent to put so much weight on the point that many of the turtles feeding off Mona Island do not actually nest on Mona Island itself. The turtles foraging off Mona Island may, primarily (nearly two thirds), come from the same nesting population.

But what of the other third? When one sees haplotypes in the Mona Island foraging area that are not found on the beaches there, or on the nearby Virgin Islands, such as haplotypes B and Q (Table 1), does that not prove that at least some of the turtles are coming from distant places? Perhaps the most striking indication of foragers coming from distant nesting areas is the presence of 7 cases of haplotype Q found at the Mona Island foraging area. In the 7 nesting areas sampled, haplotype Q was found only in the Yucatan where it appeared to be relatively com-

Table 1. Hawksbill haplotypes from 7 nesting beaches and 1 foraging area. Data from Table 2 of Bowen et al. (1996) listing the nesting areas in order of geographic proximity to the foraging area.

Location	Haplotype																				
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U
Mona Is. foraging	7	1				18						1		3			7				
Mona Is. nesting	1					1				2	1	1	2	6	1						
Virgin Is. nesting	1					14															
Antigua nesting	9	4	2																		
Barbados nesting	11			1	3																
Yucatan nesting																2	13				
Belize nesting						11	1	1	1												
Bahia nesting	4																	6	2	1	1

mon. This points to the possibility of the Yucatan nesting colony making a sizeable (18.9% in Table 3 of Bowen et al.) contribution to the Mona Island foraging population, though some other unsampled population could also have been the source of the Q haplotype.

However, without contesting the logic of this argument, one may wonder how much confidence should be placed in the adequacy of the data set on which it is based. The sample size for the Mona Island nesting area was only 15. If one were to cut this sample size in half, by randomly removing animals from the Mona Island nesting row in Table 1, then some of the 8 haplotypes found would probably have been missed, and the appearance of the foraging turtles coming from elsewhere would have been more striking. Conversely, if one were to double the sample size, then it seems quite likely that more haplotypes would be detected, perhaps the Q haplotype or others not so far found on Mona Island. The point is that these sample sizes are small — too small to exclude the possibility that, for instance, haplotype Q found in nesters at Yucatan might also show up in nesters on Mona Island or nearby beaches.

Given the bureaucratic and other obstacles in doing this kind of research, Bowen et al. have performed a valuable service; they have provided a starting point for discussion and further work on this aspect of hawksbill demography. But, at present, perhaps the matter of hawksbill movements in the Caribbean is less definite than the impression given by a casual reading of their paper. It might be appropriate if some of the conclusions in that paper were also less definite. For instance, after mentioning the trade of hawksbill products from Cuba and Panama to Japan, Bowen et al. state: "In the light of the results obtained here, the organized harvest of adults and juveniles on coastal feeding grounds...may be especially damaging, as this type of fishery will diminish reproductive populations throughout the region." It seems that some consideration of the amount of harvesting and the effects of the harvest on the resource might also be relevant here. For instance, in Cuba there has been a harvest of hawksbill turtles for more than 25 years, with at least some government records of the numbers taken. It would be worth trying to find out whether

that harvest has been sustainable or not, before asserting that such harvests "will diminish reproductive populations throughout the region."

In this context, another point to be considered is that the assessment of relative contributions from different nesting beaches to a foraging area does not relate to the numbers of turtles nesting in a particular area. Suppose that further work established beyond reasonable doubt that there are haplotypes at a foraging area that are only found in nesting turtles at a particular distant beach. Then, for example, if there are large numbers of hawksbills nesting in the Yucatan, even if haplotypes unique to Yucatan nesters show up fairly often at the foraging Mona Island population, these may not represent many turtles as a percentage of the Yucatan output. Removal of turtles contributing a certain proportion to the Mona Island foraging ground would not have an effect of a corresponding proportion at the nesting beach.

In summary, the data available at present are a useful start, but can be interpreted in different ways. Is the glass half empty or half full? Some hawksbills may indeed come to Mona Island from distant places, but there are also indications that most of them come from relatively nearby.

Acknowledgments. — I thank M.H. Godfrey for criticism.

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Received: 29 September 1996

Reviewed: 4 March 1997

Revised and Accepted: 12 March 1997