

Attn: Ms. Miri Tatarata
Delegation for the Environment,
Government of French Polynesia

November 16, 2006

**SUMMARY REPORT OF GENETIC ANALYSIS OF GREEN TURTLE (*CHELONIA MYDAS*)
SAMPLES FROM FRENCH POLYNESIA**

Background

The NOAA-Fisheries has been conducting a Pacific-wide genetic survey of green turtles in collaboration with numerous international partners in order to examine and define stock structure and identify management units for conservation. Work is ongoing to adequately sample all the nesting populations in the Pacific, however considerable progress has been made in obtaining representative samples from rookeries in the eastern, central Pacific, and some areas in Micronesia and the western Pacific. In addition, data from nesting populations in Australasia and Melanesia have recently become available (Demethers et al 2006). Taken together with our unpublished data these provide a framework to interpret the results obtained from samples analyzed from the Society Islands in French Polynesia. This report is intended to provide an update, and a basis for future planning.

Methods and Results

In 1996, a total of 35 samples were collected from green turtles. Skin samples were collected by George Balazs (NOAA-Fisheries Pacific Islands Science Center-PISC) in collaboration with French Polynesia colleagues. Samples were archived and analyzed at the Marine Turtle Genetics Laboratory at the NOAA-Fisheries Southwest Fisheries Science Center in La Jolla, California, USA. The control region of mitochondrial DNA (mtDNA) was sequenced from 28 of the samples and haplotypes were identified based on alignment with a 384bp reference fragment (Norman et al. 1994; Dutton et al., <http://swfsc.noaa.gov/prd-turtles.aspx>). The animals sampled were siblings from three different clutches, and therefore the haplotype frequencies are not representative of the French Polynesia nesting population as a whole, since each sibling will have identical mtDNA and haplotypes obtained from hatchlings from one clutch represent one individual (the mother who laid the clutch) of the nesting population. We identified 3 different haplotypes among the samples we have analyzed, suggesting that the turtles came from at least 3 different clutches (Table 1).

Haplotype CmP20 has also been identified at nesting populations in Micronesia, Melanesia, Australia (Timor Sea), and Taiwan (Demethers et al. 2006; Dutton et al., unpublished; Norman et al. 1994), as well as previously from limited sampling from French Polynesia (Norman et al. 2004). The two additional new haplotypes we found, CmP22 and CmP23, we have also identified among green turtles nesting in Samoa.

Conclusions and Future Work

The limited presence of these haplotypes in French Polynesia and Samoa suggests the likelihood that the regional nesting populations may be demographically and genetically isolated from other regional Pacific stocks that have been identified to date. However, a larger number of samples will be needed from key nesting sites around French Polynesia, and other South Pacific Islands to fully describe the genetic stock structure and management units for conservation. The three haplotypes identified here for French Polynesia (CmP20, CmP22 & CmP23), have also been found among the juvenile and sub-adult populations foraging around Fiji (Dutton et al, unpublished). Mortality due to harvest at these foraging areas will impact the nesting stocks these animals belong to. Additional sampling from nesting populations will provide baseline data that is needed to identify the source breeding populations that turtles frequenting these foraging areas come from.

We continue to be interested in partnering with the Government of French Polynesia to obtain a representative sample set from nesting sites in your region, and extend an offer of technical assistance and laboratory support for the continuation of this research in coordination with our colleague George Balazs.

Please let me know if you have any questions, and accept my best wishes.

Sincerely,



Peter Dutton, Ph.D.
Leader, Marine Turtle Research Program
Tel: 1-858-546-5636
FAX: 1-858-546-7003
Email: Peter.Dutton@noaa.gov

Cc George Balazs, NOAA-Fisheries PISC

Table 1. MtDNA haplotypes and information on samples collected from captive green turtles on Tahiti in 1996. Lab ID. refers to archive specimen no. catalogued at the NOAA-Southwest Fisheries Science Center Tissue and DNA collection. Haplotype nomenclature follows <http://swfsc.noaa.gov/prd-turtles.aspx>

LAB ID	FIELD ID	LOCATION	SCL	CCL	HAPLOTYPE
6705	P822	SCILLY	72.5	63.0	Cmp22
6706	P823	SCILLY	74.0	67.0	Cmp20
6707	P824	SCILLY	71.0	66.5	Cmp20
6708	P829	SCILLY	87.0	79.0	Cmp23
6709	P830	SCILLY	79.5	72.5	Cmp20
6710	P848	SCILLY	71.5	62.5	Cmp20
6711	P849	SCILLY	76.0	69.0	Cmp20
6712	P868	SCILLY	65.5	59.0	Cmp20
6713	P875	MOPELIA	69.0	63.5	Cmp20
6715	P877	MOPELIA	76.0	68.0	Cmp20
6716	P878	MOPELIA	70.5	65.0	Cmp20
6717	P880	MOPELIA	74.5	71.0	Cmp20
6718	P884	MOPELIA	80.0	72.0	Cmp20
6719	P885	MOPELIA	68.0	62.0	Cmp20
6720	P895	MOPELIA	72.0	67.5	Cmp20
6721	S723	MOPELIA	68.0	34.0	Cmp20
6722	S725	MOPELIA	68.0	60.0	Cmp20
6723	S730	MOPELIA	69.0	64.0	Cmp20
6724	S732	MOPELIA	68.5	62.0	Cmp20
6726	S951	MOPELIA	73.0	63.0	Cmp23
6727	S952	MOPELIA	90.0	78.5	Cmp23
6728	S953	MOPELIA	82.0	71.5	Cmp23
6729	S954	MOPELIA	87.0	74.0	Cmp23
6730	S955	MOPELIA	72.0	64.5	Cmp23
6731	S956	MOPELIA	83.0	76.5	Cmp23
6732	S957	MOPELIA	84.0	76.0	Cmp23
6733	S962	MOPELIA	88.5	78.0	Cmp23
6734	S963	MOPELIA	81.5	75.0	Cmp23