Final Report for Research Work Order 167 entitled:

Population Genetic Structure of Marine Turtles, *Eretmochelys imbricata* and *Caretta caretta*, in the Southeastern United States and adjacent Caribbean region

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Introduction

The goals of this project were three-fold:

1. Development of microsatellite assays for loggerhead, *Caretta caretta*, nesting populations in the Southeastern United States

2. Development of microsatellite assays for hawksbill, *Eretmochelys imbricata*, nesting populations in the Caribbean

3. Mitochondrial DNA (mtDNA) analysis of hawksbill, *Eretmochelys imbricata*, nesting and foraging populations in the Caribbean

The main objective are to elucidate male migratory behavior through the use of nuclear DNA analysis and to improve methodology and databases for Mixed Stock Analysis (MSA) of hawksbill and loggerhead turtles utilizing maximum likelihood algorithms.

Results - Summary

Much progress has been made in the collection of samples from nesting and foraging populations of hawksbills and loggerheads. In addition, many of the samples that have been collected during the work period have been sequenced to determine their mtDNA haplotype and added to the databases on hawksbills (n=283 new samples) and loggerheads (n=78 new samples).

The microsatellite analyses have proceeded more slowly, but some preliminary data has been generated. From this intitial work it was determined that we needed to screen and develop more microsatellite loci for loggerhead populations in the Atlantic.

Hawksbills

Nesting Locations

Listed below is a synopsis of the new data that has been gathered regarding nesting populations in the Caribbean.

Location	Number of Individuals	Haplotype
Brasil	4	A (1), Hybrids (3)
Mexico	34	Q
USVI	16	A (1) , F (15)
Barbados	30	A (9)
Puerto Rico	1	F
Venezuela	7	A
Costa Rica	5	Not completed yet
Total	**97**	**71**

Foraging Locations

In addition to the analysis of more nesting females we have been able to increase the sample sizes of some foraging locations and also to add additional foraging sites from the Caribbean. Unfortunately in some cases, such as Venezuela, we may not be able to increase the sample size to complete the analysis. Delays in permit processes have prevented furthur research at this location. The work at Fernando de Noronha is continuing, but no further resources from RWO 167 will be dedicated in the South Atlantic.

Dominican Republic

Haplotype	*# of Individuals*
A	45
F	28
G	2
J	1
L	1
Q	7
Alpha	6
Total	**90**

Texas Strandings of live or dead juveniles

Haplotype	*# of Individuals*
F	3
Q	33
TX1	1
Total	**37**

St. Croix, US Virgin Islands

Haplotype	*# of Individuals*
A	26
B	2
F	15
N	5
Q	5
Alpha	3
Gamma	1
EA1	1
Total	**58**

Los Roques, Venezuela

Haplotype	*# of Individuals*
A	17
F	6
Total	**23**

Fernando De Noronha, Brazil

Haplotype	*# of Individuals*
A	2
EA1	1
EA2	1
Total	**4**

Loggerheads

Nesting Locations

Unlike the work on hawksbill populations, our efforts to date have been directed primarily towards increasing sample sizes for U.S. locations and accessing unsampled nesting locations. Additional locations have been sampled but are not included here, because they will be analyzed under the auspices of other funding sources. Larger sample sizes of nesting populations are imperative for the analysis of these populations using nuclear DNA.

Location	*# of Individuals*	*Haplotype*
Brazil:		
Bahia	45	D (39), BR1 (6)
Espirito Santo	32	D (31), BR2 (1)
Bahamas:		
Great Inagua	1	B
Florida:		
Sarasota	20	Not processed yet
Panhandle	8	Not processed yet

Conclusions

Much progress has been made and many gaps have been filled in our sampling of both hawksbill and loggerhead nesting populations. The analysis of multiple hawksbill foraging grounds will provide much needed information of migratory pattems in this endangered species. The increased sample size for loggerheads will allow characterization of male mediated gene flow, and may provide additional dividends in 1)resolving additional management units (fine-scale population structure) between Florida and North Carolina, and 2) provide an additional pool of genetic markers for mixed stock analysis.