

**05-007R PROGRAMMATIC REPORT FORMAT (maximum of 2 pages)****Grantee:** Dr. Christopher L. Parkinson, Joshua S. Reece, University of Central Florida**Contract Number:** 05-007R**Project Title:** Integrative Marine Turtle Conservation in Florida and the Middle East**Report Period:** November 2005 to July 2006; Final Report**Project Manager(s)/Principle Investigator(s):**

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Tasks: Our goals were to genotype at least 100 loggerhead turtles (*Caretta caretta*) from Oman and compare microsatellite locus frequencies between Oman and previously described Atlantic populations to identify possible levels of connectivity between populations.

Accomplishments: Provide concise statements that summarize the progress towards accomplishing the tasks listed above. This should include deliverables (include samples if appropriate), descriptions of field and/or lab work, and descriptions of equipment purchases. Also describe any problems that were encountered and what was done to solve the problem(s).

We have genotyped 119 loggerheads (*Caretta caretta*) caught on Masirah Island, Oman, for microsatellite markers previously used in the loggerhead (Pearce 2001). The total dataset is summarized as follows:

Dataset and Populations	Number of Individuals
Pearce (2001) dataset:	
North Carolina	27
South Carolina	24
Georgia	39
Florida	291
Brazil	81
Dataset generated in this study:	
Oman	119

Our analyses include estimates of deviations from Hardy-Weinberg Equilibrium, overall F_{ST} , pair-wise F_{ST} and N_m , Nei's genetic distance to create a tree using UPGAMA. These parameters are population genetic metrics of connectivity between populations that include both female and male-mediated gene flow.

Allele frequencies for three of the four loci were significantly different from those expected under Hardy-Weinberg Equilibrium in the Oman population (Table 1) due in part to a low number of heterozygotes. Overall F_{ST} and N_m were surprisingly low (Table 2), however this depression is due largely to comparisons of the Oman populations with others in the Atlantic. In



the pairwise F_{ST} and N_m comparisons (Table 3), it is clear that the estimated number of migrants (N_m) is drastically lower for all pairwise comparisons including Oman than for those between Atlantic populations. This pattern is expected given the low level of mtDNA structure between Atlantic rookeries and thus the high level of intra-Atlantic gene flow. However, the repeated (for each locus) estimate approximately 2 migrants per generation between Oman and Atlantic rookeries is significant given their geographic isolation and putative migratory patterns. Our data support the notion that Atlantic rookeries recruit loggerheads from Oman at a frequency comparable to that between Brazilian rookeries and those of the Northwestern Atlantic and Caribbean. The management implications for this level of connectivity warrant further consideration. We suggest that future efforts center on an investigation of nuclear and additional mitochondrial markers to identify the duration of this level of gene flow over recent evolutionary time.

Table 1. Hardy-Weinberg Equilibrium

Pop	Locus	DF	ChiSq	Prob	Signif
Brazil	CC141	66	22.790	1.000	ns
Florida	CC141	105	90.455	0.843	ns
Georgia	CC141	55	50.678	0.640	ns
North Carolina	CC141	55	38.960	0.950	ns
Oman	CC141	66	294.723	0.000	***
South Carolina	CC141	55	39.394	0.944	ns
Brazil	CC176	91	79.478	0.800	ns
Florida	CC176	406	225.135	1.000	ns
Georgia	CC176	105	123.239	0.108	ns
North Carolina	CC176	91	45.288	1.000	ns
Oman	CC176	66	94.627	0.012	*
South Carolina	CC176	66	42.854	0.988	ns
Brazil	CC7	28	9.703	0.999	ns
Florida	CC7	171	229.319	0.002	**
Georgia	CC7	66	52.162	0.893	ns
North Carolina	CC7	45	41.638	0.615	ns
Oman	CC7	105	60.015	1.000	ns
South Carolina	CC7	55	42.667	0.887	ns
Brazil	DC107	28	27.836	0.473	ns
Florida	DC107	45	34.652	0.868	ns
Georgia	DC107	21	11.473	0.953	ns
North Carolina	DC107	21	17.520	0.679	ns
Oman	DC107	78	319.198	0.000	***
South Carolina	DC107	15	20.072	0.169	ns

Key: ns=not significant, * P<0.05, ** P<0.01, * P<0.001**



**Table 2. Overall F_{ST}
F Statistics and Estimates of N_m**

All Pops.	DC107	CC176	CC141	CC7	Mean
Fis	0.036	-0.027	0.050	-0.013	0.011
Fit	0.137	0.064	0.100	0.078	0.095
Fst	0.105	0.089	0.053	0.090	0.084
Nm	2.121	2.569	4.475	2.518	2.715

Table 3. Pair-Wise F_{ST} and N_m

Pop1	Pop2	Fst (via Frequency)	Nm	#Pop1	#Pop2
North Carolina	South Carolina	0.011	23.132	27	24
North Carolina	Georgia	0.011	23.230	27	39
South Carolina	Georgia	0.008	31.734	24	39
North Carolina	Florida	0.004	64.452	27	291
South Carolina	Florida	0.005	48.855	24	291
Georgia	Florida	0.006	41.885	39	291
North Carolina	Brazil	0.029	8.254	27	81
South Carolina	Brazil	0.028	8.548	24	81
Georgia	Brazil	0.041	5.877	39	81
Florida	Brazil	0.027	9.150	291	81
North Carolina	Oman	0.113	1.960	27	119
South Carolina	Oman	0.116	1.903	24	119
Georgia	Oman	0.105	2.132	39	119
Florida	Oman	0.106	2.100	291	119
Brazil	Oman	0.153	1.387	81	119

Table 4. Nei's Genetic distance and UPGMA

Caretta caretta data set Pairwise Population Matrix of Nei Genetic Distance
 North Carolina South Carolina Georgia Florida Brazil Oman

0.000						North Carolina
0.086	0.000					South Carolina
0.092	0.065	0.000				Georgia
0.031	0.040	0.056	0.000			Florida
0.175	0.172	0.283	0.154	0.000		Brazil
1.594	1.682	1.504	1.570	2.110	0.000	Oman

