The hawksbill sea turtle (*Eretmochelys imbricata*) is seen on both foraging and nesting areas Brazilian along the Brazilian coast. Projeto TAMAR-IBAMA, the Brazilian sea turtle conservation program, has been working on nesting beaches since 1982, and on foraging grounds since 1992. To better understand the biology of hawksbills in Brazil, TAMAR has been developing both genetic and telemetry studies. These preliminary results are reported herein. The Mitochondrial DNA control region of foraging (n=93) and nesting (n=140) hawksbills, was sequenced producing ca.750pb. 17 distinct haplotypes were defined by 157 polymorphic sites. The nesting populations presented low genetic diversity indexes \( h = 0.52 \pm 0.06 \) and \( \pi = 0.009 \pm 0.005 \) with only 7 haplotypes. The juvenile foraging population in Fernando de Noronha Archipelago and Rocos Atoll presented 14 haplotypes, showing greater genetic diversity indexes \( h = 0.68 \pm 0.02 \) and \( \pi = 0.056 \pm 0.03 \) including haplotypes that suggest connectivity with the Caribbean and west Africa.

The Satellite Telemetry studies started on February 2005, and 6 out of the 15 tracked hawksbills are still transmitting. The Program STAT (*Satellite Tracking and Analysis Tool*) has been used to monitor the turtles, and daily data sent by the Argos system is analyzed. Maps to visualize the turtle’s movements are produced after the received data has been filtered in order to provide quality information. Geographic references such as bathymetry are added to the individual maps enabling to track each turtle’s migratory route. The hawksbills monitored have remained along the coast, distributing themselves throughout
the northeastern and northern Brazilian coast. A complete analysis will be made after the end of the data collection.