

Poster 07

Population genetic structure of Green turtles nesting in Japan

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Green turtles (*Chelonia mydas*) are long-lived reptiles with a circumtropical distribution. Studies of mitochondrial DNA (mtDNA) have indicated nesting females are philopatric to their natal regions and phylogeographical population structures (Bowen *et al.* 1992; Lahanas *et al.* 1994; Encalada *et al.* 1996; Dethmers *et al.* 2006). Japan is located in the northern limit of Pacific green turtle breeding area, and the nesting sites exist in the Ryukyu Archipelago and the Ogasawara Group (Tokyo Metropolitan Fisheries Experiment Station 1986, Kamezaki 1999). The previous studies in the Japanese nesting populations suggested that there were at least three genetically differentiated stocks (Naito 2006, Nishizawa *et al.* 2011). In the present study we collected the samples in the Amami and Okinawa Islands, located in the central Ryukyus, and analyzed population differentiation among nesting regions by comparing haplotype compositions of the mtDNA control regions (384 bp). Although clear phylogeographical structure was diminished by the occurrence of several divergent haplotypes within nesting populations, the haplotype compositions showed the significant differentiation among regions. These results suggested that there were several regional management units in the Japanese nesting populations.