

**No genetic divergence between green turtle (*Chelonia mydas*)  
nesting populations from the Andaman Sea and the Gulf of Thailand**

Kongkiat Kittiwattanawong<sup>1)</sup>, Somchai Mananasup<sup>2)</sup>, Masato Kinoshita<sup>3)</sup> &  
Kouji Nakayama<sup>4)</sup>

*1) Phuket Marine*

*Biological Center, Phuket 83000, Thailand. E-mail: kongkiat\_k@hotmail.com*

*2) Sea Turtle Conservation Station, Department of Fisheries, Mannai Island,  
Rayong 21190 Thailand. E-mail: mannai@loxinfo.co.th*

*3) Department of Fisheries, Faculty of Agriculture, Kyoto University, Sakyo-ku,  
Kyoto 606-8520, Japan. E-mail: kinoshit@kais.kyoto-u.ac.jp*

*4) Laboratory of Marine Stock-enhancement Biology, Division of Applied  
Biosciences, Graduate School of Agriculture, Kyoto 606-8502, Japan. E-mail:  
nakayama@kais.kais.kyoto-u.ac.jp*

Nucleotide sequences from the control region of the mitochondrial (mt) DNA were analyzed for Thai green turtles (*Chelonia mydas*) to reveal population genetic structure. Four primers were employed i.e. Green15552F (GTGTC CACAC AAAC T AACTA CCT), Green16300R (GTCTC GGATT TAGGG GTTTG GCG), Green15579F (CTGCC GTGCC CAACA GAACA), and Green16087R (CCAGT TTCAC TGAAT CGGCA). The aligned sequences contained 438 base pairs (bp) with 254 polymorphic sites. There were 8 haplotypes assigned from the 49 green turtles sampled from the Andaman Sea (19 individuals) and the Gulf of Thailand (30 individuals). Low genetic divergence between the nesting green turtle populations of the Gulf of Thailand and the Andaman Sea was detected in both haplotypic ( $G_{st}=0.00311$ ) and nucleotide levels ( $N_{st}=0.02838$ ) as well as genetic distance ( $D_{TN}=0.016\pm 0.003$ ). Haplotype frequencies were not significantly different between the two nesting sites. The result was in contrast with a finding using satellite telemetry that discovered separated home ranges. Recent population separation and/or highly conservation of the studied mtDNA region might be an explanation.