

TITLE: Spatial and temporal genetic variation among size classes of green turtles (*Chelonia mydas*) provides information on oceanic dispersal and population dynamics

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ABSTRACT:

MEPS Marine Ecology Progress Series Contact the journal Facebook Twitter RSS Mailing List Subscribe to our mailing list via Mailchimp HomeLatest VolumeAbout the JournalEditorsTheme Sections MEPS 543:241-256 (2016) - DOI: <https://doi.org/10.3354/meps11521> Spatial and temporal genetic variation among size classes of green turtles (*Chelonia mydas*) provides information on oceanic dispersal and population dynamics Michael P. Jensen^{1,8,*}, Ian Bell², Colin J. Limpus³, Mark Hamann⁴, Stephen Ambar⁵, Terrence Whap⁶, Charles David⁷, Nancy N. FitzSimmons^{1,9} ¹Institute for Applied Ecology, Faculty of Applied Science, University of Canberra, Canberra, ACT 2601, Australia ²Queensland Department of Environment and Heritage Protection, Townsville, Qld 4810, Australia ³Threatened Species Unit, Department of Environment and Heritage Protection, PO Box 2454, Brisbane, Qld 4001, Australia ⁴College of Marine and Environmental Sciences, James Cook University, Townsville, Qld 4811, Australia ⁵Former Ranger, Hammond Island Community, Torres Strait, Qld 4801, Australia ⁶Traditional Owner, Mabuiag Island, Torres Strait, Qld 4575, Australia ⁷Traditional Owner, Iama Island, Torres Strait, Qld 4875, Australia ⁸Present address: Marine Mammal and Turtle Division, Southwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, 8901 La Jolla Shores Dr., La Jolla, CA 92037, USA ⁹Present address: Australian Rivers Institute, Griffith University, Nathan, Qld 4111, Australia *Corresponding author: michael.jensen@noaa.gov

ABSTRACT: Migratory marine species present challenges for conservation because of complex threats within their pelagic dispersal zones, including coastal foraging areas and extensive migration pathways, or at breeding grounds. To better understand the connectivity between green turtle rookeries and foraging populations, we sequenced the mtDNA control region of 987 turtles from 6 major foraging grounds on a ~2300 km longitudinal transect off eastern Australia, and used mixed stock analysis (MSA) to estimate their natal origins. We investigated variation in natal origins within different size classes and over spatial and temporal scales and compared this to approximately 30 yr of mark-recapture data. For adult turtles, we found that the northern Great Barrier Reef (nGBR) genetic stock dominated in the northern feeding grounds while the southern Great Barrier Reef (sGBR) and Coral Sea stocks dominated in the south, with a changeover of dominating stock occurring between 14° and 20°S. However, at the 3 most northern feeding grounds, we found an unexpected decrease (17-30%) in the proportion of nGBR turtles among small immature turtles relative to large immatures and adults. Four possible hypotheses were explored, with the 2 most plausible being that (1) small immature turtles from the sGBR and other rookeries first settle in nGBR feeding grounds, but later shift to other feeding grounds as they mature, or (2) a reduced hatching success for decades from the main nGBR rookery at Raine Island has resulted in reduced recruitment into the nGBR feeding ground from this stock. These results may indicate an alarming reduction in hatching success at the largest known green turtle rookery in the world. **KEY WORDS:** Mixed stock analysis · Migration · Management · Mitochondrial DNA · Genetics

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