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Original research article

Genetic stock compositions and natal origin of green turtle (*Chelonia mydas*) foraging at Brunei Bay

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ABSTRACT

Knowledge of genetics composition and growth stages of endangered green turtles, as well as the connectivity between nesting and foraging grounds is important for effective conservation. A total of 42 green turtles were captured at Brunei Bay with curved carapace length ranging from 43.8 to 102.0 cm, and most sampled individuals were adults and large juveniles. Twelve haplotypes were revealed in mitochondrial DNA control region sequences. Most haplotypes contained identical sequences to haplotypes previously found in rookeries in the Western Pacific, Southeast Asia, and the Indian Ocean. Haplotype and nucleotide diversity indices of the Brunei Bay were 0.8444 ± 0.0390 and 0.009350 ± 0.004964, respectively. Mixed-stock analysis (for both uninformative and informative prior weighting by population size) estimated the main contribution from the Southeast Asian rookeries of the Sulu Sea (mean $\geq$ 45.31%), Peninsular Malaysia (mean $\geq$ 17.42%), and Sarawak (mean $\geq$ 12.46%). Particularly, contribution from the Sulu Sea rookery was estimated to be the highest and lower confidence intervals were more than zero ($\geq$24.36%). When estimating contributions by region rather than individual rookeries, results showed that Brunei Bay was sourced mainly from the Southeast Asian rookeries. The results suggest an ontogenetic shift in foraging grounds and provide conservation implications for Southeast Asian green turtles.

1. Introduction

Green turtles (*Chelonia mydas*) are widely distributed in tropical regions, but are considered endangered globally because of exploitation (IUCN, 2015). The green turtle is the most abundant sea turtle species in Southeast Asia, but poaching of eggs and bycatch in fisheries are major threats to green turtle survival (Shanker and Pilcher, 2003). To prevent egg poaching,

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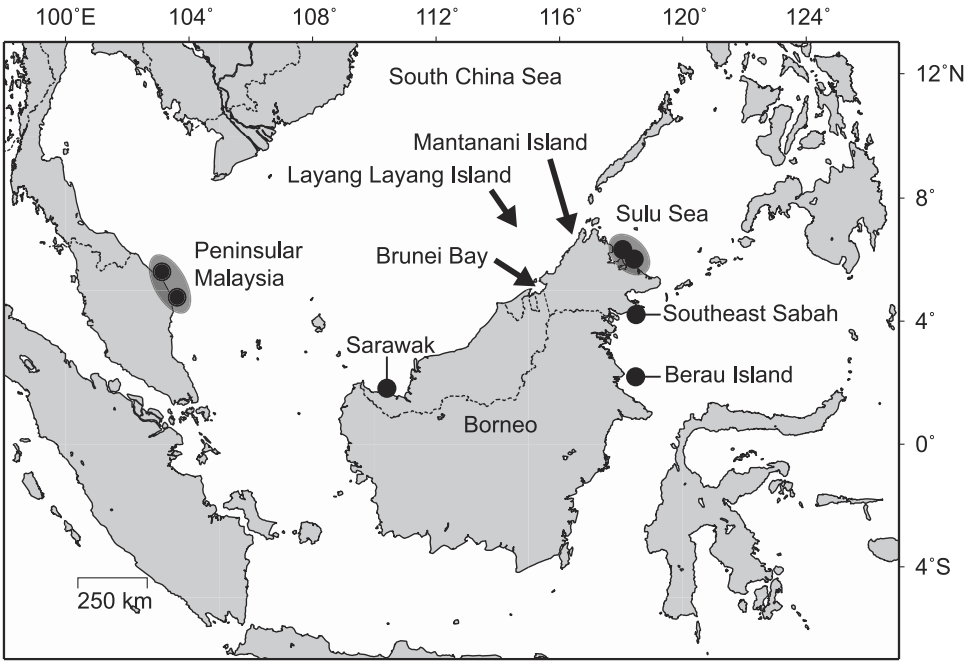

Fig. 1. Location of Brunei Bay and other foraging grounds (i.e., Mantanani Island and Layang Layang Island) and possible source rookeries (black circles) in Southeast Asia.

sanctuaries were established for example at Sabah in 1984, Sarawak in 1999, and Redang Island in 2005 (Chan, 2006, 2013). On the other hand, conservation of green turtles in the sea is difficult because of the migratory life history and wide-range dispersal of this species (Hirth, 1997). Their long-distance migrations present complex challenges for conservation because the migratory route often involves multiple countries; therefore, jurisdictions complicate legislative and regulatory conservation policies that are effective within single nations (Campbell et al., 2009). An understanding of these migrations and the establishment of international coordination according to these migrations are required for the conservation of green turtles.

Mark-recapture is a traditional approach that provides direct evidence for the movement between two capture sites. Tagging of sea turtles has been practiced globally, including in Southeast Asia (e.g. Pilcher, 2010). Satellite tracking is another method that provides direct evidence of movement and information on migratory routes. Satellite tracking research in Malaysia has shown that green turtles migrate from their nesting beaches at Redang Island in Peninsular Malaysia to foraging grounds around Borneo or Bangka Island (Luschi et al., 1996; Liew et al., 2000). Although tagging and telemetry studies provide useful information on demography, site fidelity, and migration, the available data are individual-based and biased toward intensively surveyed locations. To understand the links between foraging grounds and nesting beaches of sea turtles by tagging and telemetry, insights come mainly from individual adult females. Population-based inference based on genetic information, developed as mixed-stock analysis (MSA) (Pella and Masuda, 2001; Bolker et al., 2007), has recently been used to link genetically differentiated nesting populations to foraging grounds of sea turtles (e.g. Dutton et al., 2008; Dethmers et al., 2010; Prosdocimi et al., 2012; Nishizawa et al., 2013; Naro-Maciel et al., 2014). In Southeast Asia, Joseph et al. (2014) conducted MSA on carcass samples obtained in Mantanani Island to estimate the origins of illegally harvested turtles. In addition, Jensen et al. (in press-a) have recently estimated the origins of immature green turtles foraging at Mantanani Island and Layang Layang Island. However, there are several other foraging grounds in Southeast Asia and population-based migration between these foraging grounds and nesting rookeries are required to be determined for better understanding of green turtle migration in Southeast Asia.

In Southeast Asia, Brunei Bay (4°45′–5°02′N, 114°58′–115°10′E) (Fig. 1) is known to be an important nursery, foraging, and transient ground for marine animals, including sea turtles, dugongs, and coastal cetaceans (Rajamani and Marsh, 2010; HICOE-UMT, unpublished data). Marine ecosystems in Brunei Bay consist of mangrove forests, seagrass beds, coral reefs, estuarine, mudflats, and continental slope (Bali, 2005; Bujang et al., 2006; Jaaman et al., 2010; Ahmad-Kamil et al., 2013), and the seagrass bed dominated by *Halophila* and *Halodule* species (Bali, 2005; Bujang et al., 2006; Ahmad-Kamil et al., 2013) attracts herbivorous marine animals such as green turtles. At the same time, Brunei Bay has high amounts of fish resources. The fishing industry is ranked second in economic importance to the petroleum and hydrocarbon industry in the area (Department of Fisheries Sabah, 2010). Because of the ecological uniqueness and economic importance, Brunei Bay is a high-priority area for research and conservation of green turtles.

To characterize the utilization of Brunei Bay by green turtles, we explored whether the seagrass bed in the geographically deeply indented Brunei Bay is utilized by green turtles originating from the proximate or distal rookeries. Previous studies