

9	GENETIC COMPOSITIONS OF GREEN TURTLES FORAGING AT BRUNEI BAY	175-192
	Juanita Joseph, Hideaki Nishizawa, Wahidah Mohd Arshaad & Syed Abdullah S. Kadir	
10	BRUNEI BAY: A POTENTIAL TRANSBOUNDARY MARINE PROTECTED AREA?	193-205
	Muhammad Ashraf Abdul Rahman, Wan Izatul Asma Wan Talaat & Mohd Hazmi Mohd Rusli	
	Index	207

GENETIC COMPOSITIONS OF GREEN TURTLES FORAGING AT BRUNEI BAY

Juanita Joseph, Hideaki Nishizawa, Wahidah Mohd Arshaad & Syed Abdullah
S. Kadir

INTRODUCTION

Green turtles (*Chelonia mydas*) are widely distributed in the tropical regions, but are considered as endangered globally because of exploitation (IUCN, 2015). It is the most abundant sea turtle species in Southeast Asia, and the major threats to its survival are poaching of eggs and bycatch in fisheries (Shanker & Pilcher, 2003). In recent years, more effort had been taken to protect nesting beaches such as the establishment of sanctuaries (Chan, 2006, 2013). However, very limited effort had been taken to protect and conserve sea turtles at their foraging grounds. Numerous times, sea turtles are illegally harvested at their foraging grounds in Southeast Asia, especially in Malaysia, Indonesia and the Philippines (Pilcher *et al.*, 2008). On top of that, conservation of green turtles in the sea is difficult because of migratory life history with wide-ranging dispersal (Hirth, 1997). Their long distance migrations present unique and complex challenges for conservation, as the migratory route often involved multiple countries, therefore jurisdictions complicates legislative and regulatory conservation policies that are effective within single nations (Campbell *et al.*, 2009). Understanding migrations and international coordination according to the migrations are required for conservation of green turtles.

Recently, population-based inferences based on genetic information, developed as mixed stock analysis (MSA) (Pella & Masuda, 2001; Bolker *et al.*, 2007), have been used for linking genetically differentiated nesting populations to foraging grounds of sea turtles (e.g. Dutton *et al.*, 2008; Dethmers *et al.*, 2010; Nishizawa *et al.*, 2013; Prosdocimi *et al.*, 2012; Naro-Maciel *et al.*, 2014). In Southeast Asia, Joseph *et al.* (2014) conducted MSA on carcass samples obtained in Mantanani for estimating the origins of illegally harvested turtles, but population-based migration between specific foraging grounds and nesting rookeries have not yet been studied.

Brunei Bay is indicated to be an important nursery, foraging and transient ground for marine animals, including sea turtles, dugongs, and coastal cetaceans (Rajamani

& Marsh, 2010, HICoE-UMT, unpublished data). Sea turtles, Irrawaddy and Indo-Pacific humpback dolphins, dugongs, finless porpoises, river otters, proboscis monkeys, saltwater crocodiles and shorebirds are observed inhabiting the area (Bali, 2005; Bali *et al.*, 2008; Jaaman, 2010; Jaaman *et al.*, 2010). Marine ecosystems in the Brunei Bay consists 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 the *Halophila* and *Halodule* species (Bali, 2005; Bujang *et al.*, 2006; Ahmad-Kamil *et al.*, 2013) attracts herbivorous marine animals such as green turtles. Because of its ecological uniqueness and economic importance, Brunei Bay is a high priority area for research and conservation of green turtles.

For understanding the utilization of Brunei Bay by green turtles, it is important to determine whether the seagrass bed in the geographically deeply indented Brunei Bay is utilized by local green turtles originating from proximate or distance rookeries in this region. Previous studies indicated that green turtles often forage in mixed aggregations drawn from various nesting populations (Bass *et al.*, 2006; Dethmers *et al.*, 2010; Nishizawa *et al.*, 2013), whereas some foraging aggregations are mainly contributed by specific populations (Dutton *et al.*, 2008; Prosdocimi *et al.*, 2012; Nishizawa *et al.*, 2013; Naro-Maciel *et al.*, 2014). Juvenile sea turtles reach their foraging grounds by transportation by oceanic current in combination with their own active swimming (Putman & Mansfield, 2015), and sea turtles in foraging grounds will return to nest at their natal regions, also known as natal homing this forms the genetic differences among rookeries (Allard *et al.*, 1994; Bowen, 1995). Therefore, knowledge of the connectivity between green turtles in nesting and foraging grounds can be used to quantify the impact of threats. On the other hand, it is also important to determine the growth stages of green turtles inhabiting the Brunei Bay. Possible ontogenetic change in foraging grounds has been suggested by green turtles in Japan (Hayashi & Nishizawa, 2015). The composition of growth stages will also be important to formulate a comprehensive management plan and policies for sea turtles in Southeast Asia.

By analyzing samples collected from the Brunei Bay foraging ground, we investigated (i) the size distributions and genetics compositions of green turtles aggregating in Brunei Bay, and (ii) natal origin of the green turtle feeding aggregation in the Brunei Bay by using MSA based on mitochondrial deoxyribonucleic acid (mtDNA) control region sequences.