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The Indian Ocean Turtle Newsletter was initiated to provide a forum for exchange of information on sea turtle biology and conservation, management and education and awareness activities in the Indian subcontinent, Indian Ocean region, and south/southeast Asia. The newsletter also intends to cover related aspects such as coastal zone management, fisheries and marine biology.

The newsletter is distributed free of cost to a network of government and non-government organisations and individuals in the region. All articles are also freely available in PDF and HTML formats on the website. Readers can submit names and addresses of individuals, NGOs, research institutions, schools and colleges, etc. for inclusion in the mailing list.

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Cover photograph: Olive ridley hatchling at Orissa in 2008.

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EDITORIAL

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Molecular genetics has contributed greatly to our understanding of sea turtle biology and conservation efforts, and is the focus of two major papers in Issue 20 (July 2014) of IOTN. FitzSimmons and Limpus (pg 2) presents the location of genetic stocks of all sea turtle species in the Indo-Pacific region and compares genetic stock/Management Units with the Regional Management Units proposed by Wallace *et al.* (2011; PLoS ONE6: e24510), while Phillott and Gamage (pg 19) provide a summary of genetics studies, including structure of nesting and foraging populations of all species, mating systems, DNA barcoding and identification of the source of illegal tortoiseshell products, conducted to date in

the Indian Ocean and southeast Asia. Both papers identify gaps in our knowledge of sea turtle mating systems, stock structure, and management units. IOTN readers currently conducting, or considering, research in molecular genetics are encouraged to use longer (~800bp), more informative mtDNA sequences and contribute their sequences both to GenBank and the SWFSC database so as to ensure consistent haplotype designations and avoid confusion among ocean basins. Submitting details of your ongoing genetics project to the IOSEA Marine Turtle MoU Genetics Directory (see Resources of Interest) will also facilitate collaboration and dissemination of information within our region.

CALL FOR SUBMISSIONS

The Indian Ocean Turtle Newsletter was initiated to provide a forum for exchange of information on sea turtle biology and conservation, management and education and awareness activities in the Indian subcontinent, Indian Ocean region, and south/southeast Asia. Issue 21 of IOTN will be a special joint issue with Marine Turtle Newsletter with a focus on fisheries bycatch; if you would like to submit a research article, project profile, note or announcement, please email material to iotn.editors@gmail.com before 1st November 2014. Guidelines for submission can be found on the last page of this newsletter or at <http://www.iotn.org/submission.php>.

ARTICLES



MARINE TURTLE GENETIC STOCKS OF THE INDO-PACIFIC: IDENTIFYING BOUNDARIES AND KNOWLEDGE GAPS

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INTRODUCTION

Effective management of marine species has been challenging in part because of the cryptic nature of diverse life stages and the complexity of aquatic dispersal that is mediated by oceanographic features. This makes it difficult to define population boundaries or to understand population dynamics, particularly for marine migratory species where knowledge of migratory routes and population interactions during different life stages can be difficult to elucidate. Because of this, management for conservation of marine species has often taken place without the knowledge of exactly what is being managed. Are aggregations of individuals part of a single isolated population, a complex metapopulation, or do they come from a collection of independent populations that only share foraging habitats or migratory corridors? As our ability to define marine populations has improved through linking mark-recapture techniques, population genetics, satellite telemetry and isotope studies to oceanographic data, so too has the need to apply these findings to conservation management.

Conservation of marine turtle populations relies on being able to define populations and understand the geographic extent of habitat use throughout individual life history phases that may include oceanic or benthic developmental habitats, and extensive individual, population and species-level variation in the size and location of foraging home ranges and subsequent adult breeding migrations. To understand and manage populations requires determining whether a population nests at a single beach or island, or nests at multiple beaches. From an ecological perspective, populations are considered to be functionally independent, such that demographic processes are mostly independent of other populations and there is limited gene flow among different populations (Palsbøll *et al.*, 2007). Populations are often comprised of sub-populations that

are typically recognised as different spatial or temporal groupings of individuals. Examples of this include the many distinct rookeries that comprise the Northwest Shelf green turtle population (Dethmers *et al.*, 2006) or the western Pacific leatherback population that nests across sites in Indonesia, Papua New Guinea, and the Solomon Islands, and shows behavioural differences in foraging behaviour among summer and winter nesting groups (Dutton *et al.*, 1999; Benson *et al.*, 2011). Continued gene flow among sub-populations is at a high enough level that sub-populations share demographic features and are not distinguished genetically.

From the perspective of conservation management, populations are also considered to be groupings of animals that function independently in the near term (tens or hundreds of years) and can thus be thought of as 'Management Units' (MU) or 'genetic stocks' (Moritz, 1994). Use of these terms, as well as the terms 'population' and 'sub-population', can be problematic due to different usage, thus it is necessary to clarify what is meant. In the IUCN Red List process, 'population' is defined to mean the entire taxon (species) and, more specifically, the definition only considers adults that are contributing to future generations (IUCN, 2010). What ecologists would consider as populations are instead defined as 'sub-populations' within the IUCN Red List assessments (IUCN, 2010). The term 'stock' can be problematic as it is often used in fisheries management to represent different geographic aggregations of fish that are commercially fished, without regard to whether they constitute a single population or mixed populations that share a feeding ground (Carvalho & Hauser, 1994). With regard to marine turtle populations, the term 'Regional Management Unit' (RMU) has been introduced for the purpose of setting conservation priorities (Wallace *et al.*, 2011), yet the units that are defined are often inconsistent with a Management Unit (Moritz, 1994) approach (FitzSimmons, In Press). For the purposes of this paper,

the terms population, Management Unit, and genetic stock are considered to be synonymous and the basis for effective marine turtle conservation management.

Several Management Units have been defined for marine turtles within the Indo-Pacific (e.g., Dethmers *et al.*, 2006; Bourjea *et al.*, 2007; Pittard, 2010). The location of foraging grounds and migratory routes are known for some genetic stocks (e.g., Benson *et al.*, 2011), but many knowledge gaps remain. Because of limited tissue sampling for genetic studies, there are genetic stocks yet to be identified and additional sampling is needed to determine the geographic range of rookeries used by each genetic stock. For example, the defined green turtle genetic stock for Papua New Guinea, was based on a single location in the northeast at Long Island (Dethmers *et al.*, 2006), but further research by Velez-Zuazo *et al.* (2006) showed that this stock extended a further 2000 kms westward to include rookeries off the northwest coast of Papua, Indonesia. Mark-recapture tagging studies have provided considerable information on the habitat range of genetic stocks (Limpus, 1997) and the use of satellite telemetry has been a valuable source of data on populations, particularly where there are limited mark-recapture records (e.g., Lushci *et al.*, 2006; Benson *et al.*, 2011). Genetic analyses of foraging aggregations of turtles have added to this knowledge by providing estimates of the proportional representation of genetic stocks at different foraging areas (Dethmers *et al.*, 2010; Jensen, 2010; Nishizawa *et al.*, 2013), but the efforts required to sample sufficient numbers of turtles at foraging grounds means that few studies have been conducted to date. These studies are particularly valuable if there are substantial levels of mortality at foraging areas as it allows the proportional assignment of mortality to the different genetic stocks that share the feeding ground (Jensen *et al.*, 2010).

This paper aims to summarise the present state of knowledge for all species of marine turtle populations within the Indo-Pacific in terms of the distribution of rookeries, the relative size of rookeries, and how rookeries are grouped into genetic stocks. Information on the international extent of foraging areas or migratory routes is provided from mark-recapture data, satellite telemetry data, or genetic studies that indicate a genetic stock uses habitat across international borders. Data are provided as species-specific maps to show the locations of genetic stocks and to identify areas where there are knowledge gaps. This paper has been also been provided to the secretariat of the Indian Ocean South East Asia Memorandum of Understanding (IOSEA) to be included on the website (<http://www.ioseaturtles.org/>) and updated periodically with input from IOSEA affiliates.

METHODS

Rookery location and estimated rookery size were taken from the published literature, unpublished reports, theses, conference proceedings, and personal communications from researchers throughout the Indo-Pacific. These data have been generated using GIS software (ArcView) and used to construct the maps shown in Figures 1-6. In these Figures, nesting locations are shown as dots that denote recorded nesting sites. The size of the dot is scaled, with the smallest dots representing 1-10 nesting females per year to the largest dots representing tens of thousands of females per year for *Caretta caretta*, *Chelonia mydas* and *Lepidochelys* spp., or thousands of females per year for *Dermochelys coriacea*, *Eretmochelys imbricata* and *Natator depressus*. Crosses denote recorded nesting sites for which the size of the nesting population has not been quantified. Nesting sites demonstrated to be a part of the same genetic stock are encircled and the abbreviated name of the genetic stock is identified (see Table 1).

Designations of genetic stocks were taken from the published literature, unpublished reports, theses and conference proceedings. In all cases, these studies used a definition of genetic stocks following the Management Unit (MU) concept as provided by Moritz (1994). Following Moritz (1994), marine turtle MUs are recognised by having significant allele frequency differences, such as observed in mitochondrial (mt) DNA haplotype frequencies (e.g., Dethmers *et al.*, 2006), nuclear microsatellite allele frequencies (e.g., FitzSimmons *et al.*, 1997b), or SNPs (single nucleotide polymorphisms) allele frequencies (e.g., Roden *et al.*, 2013). If the null hypothesis that sampled rookeries have the same mtDNA haplotype frequencies cannot be rejected, then they are considered as being grouped into the same genetic stock. If the null hypothesis is rejected when comparing two rookeries, or groups of rookeries, then they are designated as separate genetic stocks. This is done on the basis that significant genetic differentiation indicates limited gene flow and that populations are thus expected to function with demographic independence (Moritz, 1994; Palsbøll *et al.*, 2007). Data from mtDNA are particularly useful for conservation management of marine turtle populations because the matrilineal inheritance of the mtDNA means that the data reflect the history and relationships among rookeries (Avice, 1995). Application of nuclear genetic markers (microsatellites and SNPs) can be beneficial for understanding male-mediated gene flow among populations and male migratory behaviour relative to females. When used in regional studies, they have contributed to the designation of genetic stocks, mostly with similar results (FitzSimmons

et al., 1997b; Pittard, 2010; Roden *et al.*, 2013).

RESULTS

In total, 57 genetic stocks have been identified for all species of marine turtles within the Indo-Pacific, but many regional or species-specific gaps remain (Tables 1-2, Figures 1-6). For 37 (65%) of these stocks, some habitat use outside of the country(s) where the rookeries are located have been identified through tag recovery data, satellite telemetry data, or genetic stock analyses. International habitat use by various genetic stocks was recorded for all species, emphasising the need for international cooperation in marine turtle conservation efforts. The designated genetic stocks represent not only the demographically independent marine turtle populations within the Indo-Pacific, they also represent unique combinations of genetic diversity within the region.

Caretta caretta

Five genetic stocks of loggerhead turtles have been identified (Table 1, Figure 1) in the Indo-Pacific (Hatase *et al.*, 2002; Shamblin *et al.*, 2014). At present, genetic studies of the southwest Pacific stock do not uncover any differences between rookeries in eastern Australia and New Caledonia (FitzSimmons *et al.*, unpubl. data), although tagging of females suggests that these regions function as independent populations (Limpus, 2008a). Frequency differences among mtDNA haplotypes distinguish rookeries in Japan, eastern and western Australia as forming three unique populations, though the level of divergence among mtDNA haplotypes in the eastern Indian Ocean and western Pacific Ocean is low. Only one shared haplotype, found in one turtle in Japan, has been observed in both Australia and Japan (Hatase *et al.*, 2002). In contrast, there is high genetic divergence between the Japan/Australia/New Caledonia genetic lineages and the highly divergent Oman and South Africa lineages (Shamblin *et al.*, 2014). Additional sampling is needed for the southwest Pacific Ocean and to determine whether the Sri Lanka rookeries form an additional genetic stock, and to clarify whether rookeries in Yemen are part of the northwest Indian Ocean stock.

Genetic analyses have been conducted on some loggerhead turtle feeding ground samples, stranded turtles and turtles caught by fisheries. This includes feeding grounds in Western Australia and Queensland (Pacioni *et al.*, 2012, unpubl. data), stranded turtles in Australia (FitzSimmons *et al.*, unpubl. data), and fisheries bycatch samples in Peru (Boyle *et al.*, 2009). The latter study confirmed an hypothesis that loggerhead turtles from rookeries in eastern Australia and New

Caledonia are traversing the south Pacific and are caught by long-line fisheries off the coast of Peru.

Chelonia mydas

Green turtles have the largest number of genetic stocks identified within the Indo-Pacific, with 30 different stocks designated to date (Figure 2). This reflects a high level of genetic diversity found in the region, including at least five divergent genetic lineages (Dethmers *et al.*, 2006; Bourjea *et al.*, 2007). Dethmers *et al.* (2006) analysed 27 rookeries and determined there were 17 management units among sample sites in the western Indian Ocean, SE Asia and western Pacific. The Scott Reef genetic stock (Dethmers *et al.*, 2006) has been expanded to include Browse Island (Jensen, 2010) and the genetic stock identified from Long Island in northeast Papua New Guinea has been expanded to include all of northern New Guinea (Velez-Zuazo *et al.*, 2006). Research by Mahardika *et al.* (2007) suggests that the northeast Borneo and east Borneo genetic stocks, identified by Dethmers *et al.* (2006) as the SE Sabah and Berau Islands management units, may constitute a single genetic stock, although work by Arshaad & Kadir (2009) supports the designation of at least two stocks. In the southwestern Indian Ocean, Bourjea *et al.* (2007) identified four genetic stocks that include the Arabian Peninsula, the northern Mozambique Channel, Europa and Juan de Novo. There is some evidence that there may be additional genetic differentiation within the genetic stock of the northern Mozambique Channel, but further sampling in the region is required (Bourjea *et al.*, 2007).

Regional genetic studies have identified additional genetic stocks in the Indo-Pacific. These include genetic stocks at Coburg Peninsula in the Northern Territory, Australia and the Cocos (Keeling) Islands (Jensen, 2010). In the northwestern Pacific and South China Sea, three genetic stocks have been identified to exist in Japan, southeast Taiwan and southwest Taiwan (Cheng *et al.*, 2008; Nishizawa *et al.*, 2011). Genetic differentiation identified two stocks in Taiwan, which was somewhat unexpected, given the two island rookeries are only ~250 km distant from each other. However, a similar result of genetic differentiation was found between the Ashmore Reef and Scott/Browse genetic stocks in the Arafura Sea, which are comprised of island rookeries ~225 km distant (Dethmers *et al.*, 2006; Jensen, 2010). Most surprisingly, there was a high level of genetic differentiation (no haplotypes were shared between the sites) between the Taiwan stocks, although the sample size was small (n = 14) for one site and additional sampling is needed. The most striking result was found by Nishizawa *et al.* (2011), who uncovered mtDNA genetic differentiation between

rookeries on two islands in Japan where sample sites were located only 40 – 60 kms apart. They recommended further study to confirm this, so these rookeries are considered a single stock at present. In contrast to these geographically limited genetic stocks, the North West Shelf stock in Western Australia encompasses over 1000 kms between the furthest rookeries sampled (Dethmers *et al.*, 2010) and the northern New Guinea stock includes rookeries over 2000 kms apart (Velez-Zuazo *et al.*, 2006).

Genetic studies of rookeries in Thailand did not find significant genetic divergence between rookeries at Khram Island in the Gulf of Thailand and Huyon Island in the Andaman Sea (Kittiwattanawong *et al.*, 2003), even though these are separated by >2300 km of coastline. It was suggested that these results could be due to low levels of gene flow through the Malacca Straits after colonisation by a common ancestor (Kittiwattanawong *et al.*, 2003). This explanation is problematic given that each of the rookeries is genetically divergent from the intermediately located Peninsular Malaysia stock. Satellite telemetry of post-nesting turtles shows behavioural differences between the two rookeries in the location of their foraging grounds (Kittiwattanawong *et al.*, 2002, 2003; Kittiwattanawong & Manansap, 2009), suggesting demographic independence of the two rookeries, although additional telemetry data are needed. As suggested, a lack of genetic differentiation can occur when populations are colonised from the same ancestral population, and too few generations have occurred to develop differentiation through genetic drift and new mutations (Avice, 2000). Alternatively, genetic similarities may reflect the random nature of colonisation from multiple source populations that result in demographically separate populations appearing to be similar. The most common haplotype in Thailand rookeries is shared among all rookeries throughout the region, the second most common haplotype is observed in several Malaysian stocks and none of the other six haplotypes observed at lower frequencies are shared between the two Thailand rookeries. Colonisation of the Sunda Shelf in the last 8,000 years as sea levels dropped would have occurred from multiple source populations, which could have led to the Thailand rookeries appearing to be similar, as suggested for loggerhead populations on the east and west coast of Florida (Encalada *et al.*, 1998). A similar situation of no observed genetic divergence occurs between two hawksbill populations in Australia (nQLd, nEA; Table 1), but due to differences in nesting seasonality, they are considered as separate genetic stocks (Limpus, 2009a). We provisionally consider the two rookeries sampled in Thailand as separate stocks based on behavioral differences in foraging locations (Kittiwattanawong & Manansap, 2009) and their

differentiation from the Peninsular Malaysia stock.

Mixed stock analyses of mtDNA data have been conducted for several green turtle foraging grounds in the Indo-Pacific to determine the proportional contribution of different genetic stocks to shared foraging grounds. Foraging grounds have been analysed in the southwest Pacific Ocean (Jensen, 2010; Read *et al.*, In Press), northwest Pacific Ocean (Nishizawa *et al.*, 2013), western Indian Ocean (Jensen, 2010), Arafura and Timor seas (Dethmers *et al.*, 2010), South China Sea (Jensen, 2010) and the Celebes Sea (Mahardija *et al.*, 2007). Considerable variation in results exists, with some foraging ground aggregations being composed mostly of turtles from the nearest genetic stock (i.e., Aru, Gulf of Capentaria, nGBR; Dethmers *et al.*, 2010; Jensen, 2010) while other aggregations include significant numbers of turtles from genetic stocks over 1,000 km distant (i.e., New Caledonia and Japan; Nishizawa *et al.*, 2013; Read *et al.*, In Press). Unfortunately, the presence of a high proportion of shared mtDNA haplotypes in the Indo-Pacific often precludes firm conclusions about the origins of turtles at foraging grounds. Instead, most knowledge on the international dispersal of post-nesting turtles has come from tag recovery data (Table 1 references). Genetic analyses have been conducted on green turtles harvested in Bali and Australia (Moritz *et al.*, 2002), demonstrating that the Bali harvest harvests turtles from a broad geographic region and includes turtles originating from other countries, whereas the nGBR harvest primarily has a local impact (Moritz, 2002; Jensen, 2010).

Important knowledge gaps remain, with several large, isolated rookeries not yet analysed, and regions where additional sampling of rookeries would help clarify stock boundaries (see Figure 2). Additional green turtle genetic stocks are likely to be found in the Indo-Pacific, particularly if the rookeries are located more than 500 km from rookeries used by other genetic stocks (Dethmers *et al.*, 2006). Mixed stock analyses of feeding grounds will require large sample sizes (Jensen, 2001) and will be most effective if conducted as regional transects (e.g., Dethmers *et al.*, 2010; Jensen, 2010) that incorporate knowledge of the complex ocean currents of the region.

Dermochelys coriacea

Population genetic studies have identified three genetic stocks in the Indo-Pacific, but many gaps remain in the sampling of low-density rookeries throughout the region. Stocks are identified in the southwest Indian Ocean, northeast Indian Ocean (Malaysia, Nicobar Islands) and western Pacific Ocean (Dutton *et al.*, 1997, 2007; Shanker *et al.*, 2011) (Table 2, Figure 3). The

grouping of Malaysia and Nicobar is tentative as it is based on only nine samples from Malaysia (Dutton *et al.*, 1999) and there is some evidence that they forage in different areas (Limpus, 1997; Shanker, pers. comm. 2014, data at seaturtle.org/stat/). Additional sampling is needed in many areas to determine the boundaries of the nesting regions for each stock. Satellite telemetry has revealed the extensive foraging range of the western Pacific Ocean stock, with differential migratory behaviour observed between austral summer and winter nesting turtles (Benson *et al.*, 2011). Although it is speculated that demographic differences may exist between austral summer and winter nesting turtles, nesting throughout the year among western Pacific Ocean turtles would allow for sufficient gene flow such that the stock is considered a meta-population (Benson *et al.*, 2011). Ongoing satellite telemetry of post-nesting females from the northeast Indian Ocean stock is similarly demonstrating a wide dispersal of individuals to foraging areas in several countries (Shanker, pers. comm. 2014, data at atseaturtle.org/stat/) and suggests the origins for at least some of the stranded leatherback turtles along the western Australia coast (Prince, 2004).

Eretmochelys imbricata

Population genetic studies of hawksbill turtles in the Indo-Pacific have revealed the presence of at least nine genetic stocks (Mortimer & Broderick, 1999; FitzSimmons, 2010; Arshaad & Kadir, 2009, Tabib *et al.*, 2011, 2014). Interesting results include the possible separation of stocks within the Arabian Gulf and the grouping of distant rookeries in Seychelles and Chagos (FitzSimmons, 2010; Tabib, 2014). The Gulf of Thailand stock is proposed, but additional samples are needed to confirm this (Arshaad & Kadir, 2009). The north Queensland and northeast Arnhem Land stocks could not be differentiated with genetic analyses, but are separated on the basis of that the turtles in those populations nest at different times of year (Limpus, 2009a). There are severe knowledge gaps in the genetic study of hawksbill turtle rookeries throughout the Indo-Pacific (Figure 4). Foraging ground mixed stock analyses have been conducted for some areas (FitzSimmons, 2010), but most data on the use of foraging grounds across international borders comes from limited tag recovery data of post-nesting females (Table 1 references).

Lepidochelys olivacea

Separate genetic stocks have been identified in six regions that include the eastern India coast, Sri Lanka, Andaman and Nicobar Islands (India), Peninsular

Malaysia, western Northern Territory (Australia) and western Cape York Peninsula (Australia) (Bowen *et al.*, 1998; Shanker *et al.*, 2004; Jensen *et al.*, 2013; Shanker *et al.*, 2011). Preliminary data from nesting turtles in Indonesia have been provided that suggest substantial variation from the Australian rookeries (I. B. W. Adnyana *et al.*, unpublished data, reported in Jensen *et al.*, 2013). Many important sampling gaps exist, particularly in Africa, Oman, western India, northeast Indian Ocean, the South China Sea, Arafura Sea and Timor Sea (Figure 5). As observed in other species, the geographic extent of genetic stocks is highly variable, such as the grouping of many rookeries along the eastern India coast into a single genetic stock, whereas turtles nesting in nearby in Sri Lanka are genetically differentiated into a separate stock (Shanker *et al.*, 2004).

Information on the use of internationally dispersed foraging grounds by particular stocks is limited, given there are no published genetic studies of olive ridley turtles sampled at feeding grounds in the Indo-Pacific and few tag recovery records of turtles found outside of the countries they were tagged in. Jensen *et al.* (2013) analysed mtDNA variation in olive ridley turtles that had become entangled in discarded fishing nets (ghost nets) that drifted ashore in the Gulf of Carpentaria. It appears that the nets are entangling turtles from Australian and Indonesian stocks at shared feeding grounds in the Arafura Sea, and thus have a broad impact. Satellite tagging of post-nesting females from Northern Australia supports the hypothesis of shared feeding grounds, given that some tracked females entered Indonesian waters (Whiting *et al.*, 2007). Considerably more genetic, tagging and satellite telemetry studies are needed to better understand the dynamics of olive ridley populations within the Indo-Pacific.

Natator depressus

Five genetic stocks of flatback turtles have been identified (Pittard, 2010), all of which nest only within Australia (Table 1, Figure 6). Some of these stocks use feeding grounds in Indonesia and Papua New Guinea (Limpus, 2007). Within the eastern Queensland and Arafura Sea genetic stocks there is evidence of restricted gene flow among at least some pairs of rookeries that have been sampled (Pittard, 2010). Some rookeries may be more independent than can be uncovered by genetic studies at present. Additional sampling along the northwest coast of Western Australia Kimberley region will help determine the boundary between the winter nesting genetic stock sampled at Cape Domett (Joseph Bonaparte Gulf stock) and the summer nesting stock sampled at Eco Beach (southwest Kimberley stock).

Several satellite telemetry studies of post-nesting females are being conducted and reveal extensive migrations, mostly within Australian waters (see seaturtle.org/stat/).

DISCUSSION

Considerable progress has been made to define population boundaries and understand migratory behaviour of marine turtles within the Indo-Pacific, which has supported international efforts in conservation management. Genetic studies have led to the identification of 57 genetic stocks that are considered as separate management units in that the loss of nesting females in one stock will not be replaced readily by nesting turtles from another stock. Over two-thirds (68%) of the genetic stocks have turtles that either breed in more than one country, or breed and forage in different countries, thus international cooperation is critical for understanding and protecting marine turtle populations in the Indo-Pacific.

One important conclusion from population genetic studies is the inability to predict which rookeries are grouped together as a genetic stock, unless tagging efforts have been extensive and cover a large number of rookeries in a region. Stock boundaries have varied hugely, separating rookeries <60 kms distant, to the grouping of rookeries >2000 kms apart; thus filling in knowledge gaps needs to be quantitative, and cannot be assumed. Similarly, tagging and satellite telemetry studies of migratory turtles have provided important data on the broader geographic range of a stock at foraging locations and migratory pathways, but unless studies are extensive, it is not possible to quantify the extent to which stocks use different locations. Genetic studies using mixed stock analyses have provided quantification of how stocks are distributed in benthic as well as pelagic habitats. These studies have been particularly important in allowing quantification of stock-specific impacts from human disturbance, such as incidental capture in fisheries or directed take (Bowen *et al.*, 1995; Jensen *et al.*, 2012). One of the largest remaining gaps is the lack of understanding about the pelagic phase of post-hatchling and juvenile turtles in the Indo-Pacific, and genetic studies can provide important insights if samples can be obtained (e.g., Boyle *et al.*, 2009).

Genetic stocks/Management Units versus Regional Management Units

Most of the designations of genetic stocks have been based upon rejecting a hypothesis that sampled rookeries share the same mtDNA haplotype frequencies. Palsbøll *et al.* (2011) argue that a more effective approach would be to

set a threshold level of dispersal as the criteria for defining management units. For marine turtle genetic stocks, dispersal would relate to the number of females that migrate between two rookeries, or groups of rookeries, being analysed. From a genetic perspective, the question becomes not just whether two populations are genetically divergent, but by how much. The authors acknowledge however, that empirical links between dispersal and demographic independence are poorly known for most species (Waples & Gaggiotti, 2006), and that species-specific models linking demographic parameters and population genetic estimations are needed. Setting a threshold level of dispersal has been done for the identification of salmon stocks by the IUCN Salmon Specialist Group, who determined the appropriate threshold level to be less than one migrant per year. Theoretical analyses are needed to link a threshold level of dispersal to the equivalent level of genetic divergence as observed in genetic studies. For sockeye salmon (*Onchorhynchus nerka*) the threshold of one migrant per year was determined to equate to a genetic divergence of $F_{ST} = 0.04$ using nuclear microsatellite data (IUCN, 2014), where $F_{ST} = 0$ for identical populations and $F_{ST} = 1$ for populations that do not share any of the same alleles. If the same approach is taken for defining marine turtle stocks, then rookeries known to have (on average) one female per year that has switched between two rookeries, then these rookeries can be defined as part of the same genetic stock. To determine an F_{ST} threshold for defining marine turtle stocks requires establishing the relationships among dispersal, gene flow, generation time and genetic divergence using empirical data. At present, the designation of genetic stocks based upon rejecting a null hypothesis of no genetic divergence is likely to be a valid, and probably conservative, approach for defining marine turtle populations.

An alternate approach for defining 'units' for management, known as Regional Management Units (RMUs), was proposed by Wallace *et al.* (2010) and used for setting global conservation priorities (Wallace *et al.*, 2011). In general, this approach does not take a population level perspective, but instead groups populations into regional constructs, largely based upon the sharing of foraging areas. While the RMU process aims to be informative by incorporating a variety of data sources and provides distribution maps of habitat use (Wallace *et al.*, 2010), the resultant RMUs may comprise a single population, multiple populations, or unknown populations, thus it is not clear what is being managed. Within the Indo-Pacific 31 RMUs have been defined, which include eight putative RMUs where data were lacking (Wallace *et al.*, 2010). In comparison to the 57 genetic stocks identified to date within the Indo-Pacific,

and with the expectation that more will be defined, the RMU approach is clearly different. Olive ridley turtle populations are reduced from six genetic stocks (with more expected) to four RMUs, with a west Pacific RMU that includes the western Pacific, all of southeast Asia, Australia and the western Indian Ocean. Additionally, there are two northeast Indian RMUs that separate turtles based on whether or not they nest in arribadas (Wallace *et al.*, 2010). Most of the seven hawksbill turtle RMUs are putative so do not bear scrutiny, but the five flatback turtle genetic stocks have been reduced to three RMUs (Wallace *et al.*, 2010), one of which includes geographically distant stocks that nest at different times of the year. The biggest discrepancy is for green turtle populations in the Indo-Pacific; with 30 genetic stocks reduced to eight RMUs (Wallace *et al.*, 2010). One RMU that stands out as inappropriate is the southwest Pacific RMU, which includes the New Caledonia, Coral Sea, southern Great Barrier Reef, northern Great Barrier Reef and northern New Guinea genetic stocks (Wallace *et al.*, 2010). This includes stocks (sGBR, nGBR) that are highly genetically divergent and known to function with complete demographic independence, other than the sharing of feeding grounds in some locations (Limpus, 2008b). Because leatherback turtle genetic stocks tend to use several nesting beaches within a large region, and loggerhead turtle genetic stocks are quite isolated from each other, the RMU approach for these two species in the Indo-Pacific does not differ from a genetic approach, with the exception that the RMU approach presents putative stocks.

Rather than benefitting the local or regional management of marine turtle populations, the RMU approach has the potential in some areas and for some species to de-emphasise the importance of monitoring and managing from an ecologically sound population perspective. We argue for the need to maintain the focus of management at the level of the genetic stock because critically, nesting habitats used by a specific population (genetic stock, MU) would not readily be recolonised by migrants from other genetic stocks in the near term if local extinction occurs (Moritz, 1994; Palsbøll *et al.*, 2007). Additionally, the distribution of genetic divergence in the Indo-Pacific emphasises the importance of prioritizing the conservation of genetic stocks, not simply based on the size of the stock, but also by the unique combination of genetic diversity found within genetic stocks. For example, some genetic stocks are known to only support tens of females per year while other stocks support tens of thousands of females, but from a biodiversity perspective they may be equally significant. For example, the much smaller non-arribada olive ridley populations of the Indo-Pacific contain more

genetic diversity than the large arribada population in India (Shanker *et al.*, 2004, 2011; Jensen *et al.*, 2013).

Management for turtle conservation at a genetic stock level involves a two-step process of first identifying which rookeries group together to form a genetic stock, and then identifying the nearshore and oceanic habitat used by each population with a combination of genetic, tagging and telemetry data. This combined approach provides managers with the information needed to prioritise actions based on threats to nesting beaches and feeding grounds for each population. It also provides more specific information to be used when negotiating internationally regarding these shared populations. Rather than relying on the RMU maps given in Wallace *et al.* (2010), countries should develop maps for each genetic stock indicating rookery locations and habitat use in pelagic and benthic environments. This has recently been done in Australia for incorporation into a revised marine turtle recovery plan. For the advancement of marine turtle conservation and management in the Indo-Pacific, we urge the continued progress in delineating marine turtle genetic stocks in the Indo-Pacific and using that information as the basis for targeting further research, monitoring and international collaboration to achieve better management outcomes for marine turtles.

Literature cited

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Table 1. Marine turtle genetic stocks found within the geographic region included within the Indian Ocean-South-East Asian Marine Turtle Memorandum of Understanding, shown by species, stock and country, with known links between nesting and foraging populations across international borders. Countries shown in italics are those with rookeries presumed to be a part of a particular stock but this has not been confirmed by tagging or genetic studies. Genetic stocks identified with an asterisk show evidence of some genetic differentiation among some rookeries within the stock.

Species/Genetic Stock	Country-nesting	Other Countries- feeding grounds	Other countries-post-hatchling/juvenile pelagic	References
<i>Caretta caretta</i>				
northwest Pacific Ocean (nwPac)	Japan	Philippines	Mexico, USA	deVeyra, 1994; Bowen <i>et al.</i> , 1995; Hatase <i>et al.</i> , 2002; Limpus, 2008a
southwest Pacific Ocean (swPac)	Australia, New Caledonia	Indonesia, Papua New Guinea, Solomon Islands	Peru	Limpus <i>et al.</i> , 1992; FitzSimmons <i>et al.</i> , 1996; Kelez <i>et al.</i> , 2003; Alfaro-Shigueto <i>et al.</i> , 2004; Boyle <i>et al.</i> , 2009; Limpus, 2008a; Limpus <i>et al.</i> , database ¹
southeast Indian Ocean (seInd)	Australia	Indonesia		FitzSimmons <i>et al.</i> , 1996; Pacioni <i>et al.</i> , 2012; Limpus <i>et al.</i> , database ¹
northwest Indian Ocean (nwInd)	Oman	Bahrain, Iran, Pakistan, Qatar, Saudi Arabia, Somalia, United Arab Emirates, Yemen		Baldwin <i>et al.</i> , 2003; Limpus, 2008a; Rees <i>et al.</i> 2010; Hamann <i>et al.</i> 2013; Shamblyn <i>et al.</i> , 2014
southwest Indian Ocean (swInd)	South Africa	France, Kenya, Madagascar, Mozambique, Seychelles, Somalia, Tanzania		Baldwin <i>et al.</i> , 2003; Lushci <i>et al.</i> , 2006; Limpus, 2008a; Shamblyn <i>et al.</i> , 2014
<i>Chelonia mydas</i>				
western New Caledonia (wNC)	New Caledonia	Australia, Papua New Guinea		Deithmers <i>et al.</i> , 2006; Limpus, 2008b; Read <i>et al.</i> , 2014; Limpus <i>et al.</i> , database ¹
Coral Sea Platform (CS)	Australia	Papua New Guinea		Deithmers <i>et al.</i> , 2006, Limpus, 2008b; Limpus <i>et al.</i> , database ¹
Southern Great Barrier Reef (sGBR)	Australia	Fiji, New Caledonia, Papua New Guinea, Vanuatu		Limpus <i>et al.</i> , 1992; Norman <i>et al.</i> , 1994; FitzSimmons <i>et al.</i> , 1997a,b; Deithmers <i>et al.</i> , 2006; Limpus, 2008b; Read <i>et al.</i> , 2014; Limpus <i>et al.</i> , database ¹
Northern Great Barrier Reef (nGBR)	Australia	Indonesia, New Caledonia, Papua New Guinea, Vanuatu		Limpus <i>et al.</i> , 1992; Norman <i>et al.</i> , 1994; FitzSimmons <i>et al.</i> , 1997a,b; Deithmers <i>et al.</i> , 2006; Limpus, 2008b; Limpus <i>et al.</i> , database ¹
Gulf of Carpentaria (GoC)	Australia			Norman <i>et al.</i> , 1994; FitzSimmons <i>et al.</i> , 1997a,b; Deithmers <i>et al.</i> , 2006
Cobourg Peninsula (CP)	Australia			Jensen, 2010
Ashmore Reef (AR)	Australia			Deithmers <i>et al.</i> , 2006; Jensen, 2010
Scott-Browse (SB)	Australia			Deithmers <i>et al.</i> , 2006; Jensen, 2010
North West Shelf (NWS)	Australia	Indonesia		Norman <i>et al.</i> , 1994; FitzSimmons <i>et al.</i> , 1997a, b; Deithmers <i>et al.</i> , 2006, Limpus 2008b, Limpus <i>et al.</i> database ¹
Cocos (Keeling) Islands (CK)	Australia			Jensen, 2010
northern New Guinea (nNG)	Indonesia, Papua New Guinea	Australia, Japan, Malaysia		Norman <i>et al.</i> , 1994; Deithmers <i>et al.</i> , 2006; Velez-Zuazo <i>et al.</i> , 2006; Limpus, 2008b; Nishizawa <i>et al.</i> , 2013; Limpus <i>et al.</i> , database ¹

Micronesia (FSM)	Micronesia	Indonesia, Japan, Marshall Islands, Palau, Philippines	deVeyra, 1994; Norman <i>et al.</i> , 1994; Dethmers <i>et al.</i> , 2006; Nishizawa <i>et al.</i> , 2013; Limpus <i>et al.</i> , database
Aru (Aru)	Indonesia		Dethmers <i>et al.</i> , 2006
West Java (wJ)	Indonesia	Australia	Norman <i>et al.</i> , 1994; Dethmers <i>et al.</i> , 2006; Limpus, 2008b; Limpus <i>et al.</i> , database ¹
east Borneo (eB)2	Indonesia	Malaysia, Philippines	Sagun, 2003; Dethmers <i>et al.</i> , 2006; Mahardika <i>et al.</i> , 2007; Adnyana <i>et al.</i> , 2008; Arshaad <i>et al.</i> , 2008
West Borneo (wB)	Malaysia	Philippines	Norman <i>et al.</i> , 1994; Bali <i>et al.</i> , 2002; Dethmers <i>et al.</i> , 2006; Arshaad <i>et al.</i> , 2008
Sulu Sea (SS)	Philippines, Malaysia	Indonesia, Palau, Papua New Guinea	De Silva, 1982; Dethmers <i>et al.</i> , 2006; de Veyra, 1994; Sagun, 2004; Arshaad <i>et al.</i> , 2008; Isnain, 2009; Limpus <i>et al.</i> , database ¹
southwest Japan (swJ)*	Japan	Philippines	Sagun, 2003; Cheng <i>et al.</i> , 2008; Nishizawa <i>et al.</i> , 2011
east Taiwan (eT)	Taiwan		Cheng <i>et al.</i> , 2008; Nishizawa <i>et al.</i> , 2011
west Taiwan (wT)	Taiwan		Cheng <i>et al.</i> , 2008; Nishizawa <i>et al.</i> , 2011
Vietnam (V)	Vietnam	Indonesia, Malaysia, Philippines	Arshaad & Kadir, 2009; Dung, 2009
east Peninsular Malaysia (ePM)	Malaysia	Indonesia, Philippines, Singapore, Vietnam	Dethmers <i>et al.</i> , 2006; Arshaad <i>et al.</i> , 2008; van de Merwe <i>et al.</i> , 2009; Lau <i>et al.</i> , 2009; Limpus <i>et al.</i> , database ¹
Gulf of Thailand (GT)	Thailand	Cambodia, Malaysia, Philippines, Singapore, Vietnam	Kittiwattanawong <i>et al.</i> , 2002, 2003; Arshaad & Kadir, 2009; Kittiwattanawong & Manansap, 2009; Limpus <i>et al.</i> , database ¹
Adaman Sea (AS)	Thailand	India	Kittiwattanawong <i>et al.</i> , 2002, 2003; Arshaad & Kadir 2009; Kittiwattanawong & Manansap, 2009; Limpus <i>et al.</i> , database ¹
Myanmar (M)	Myanmar		Arshaad & Kadir, 2009
east Arabian Peninsula (eAP)	Saudi Arabia, Oman	Eritrea, Maldives, United Arab Emirates, Yemen	Ross, 1984; Miller, 1989; Gasperetti <i>et al.</i> , 1990; Bowen <i>et al.</i> , 1992; Broderick, 1998; Limpus <i>et al.</i> , database ¹
north Mozambique Channel (nMC)*	Seychelles, Comoros, France3, Madagascar	Mozambique, Tanzania, Somalia	Le Gall & Hughes, 1987; Mortimer & Broderick, 1999; Formia <i>et al.</i> , 2001; Bourjea <i>et al.</i> , 2007; Limpus <i>et al.</i> , database ¹
south Mozambique Channel (i.e., Europa) (sMC)	France3	Comoros, Madagascar, Mozambique, Seychelles	Le Gall & Hughes, 1987; Bourjea <i>et al.</i> , 2007
Central Mozambique Channel (i.e., Juan de Novo) (cMC)	France3	Comoros, Madagascar, Mozambique, Seychelles	Bourjea <i>et al.</i> , 2007
<i>Dermochelys coriacea</i>			
western Pacific Ocean (wPac)	Indonesia (Papua), Papua New Guinea, New Ireland, New Britain, Solomon Islands, Vanuatu	Australia, Federated States of Micronesia, Japan, Korea, Malaysia, Marshall Islands, New Caledonia, New Zealand, Palau, Philippines, United States of America	Dutton <i>et al.</i> , 1999, 2007; Adnyana, 2009; Limpus, 2009b; Minami <i>et al.</i> , 2009; Benson <i>et al.</i> , 2011; Limpus <i>et al.</i> , database ¹

southwest Indian Ocean (swInd)	South Africa India ⁴ , Malaysia, Sri Lanka	Mozambique, Namibia Australia, France ³ , Indonesia, Madagascar, Seychelles, United Kingdom ⁵	Dutton <i>et al.</i> , 1999; Luschi <i>et al.</i> , 2006 Dutton <i>et al.</i> , 1999; Shanker <i>et al.</i> , 2011; Shanker, pers. comm.
<i>Eretmochelys imbricate</i>			
Solomon Islands (Sol)	Solomon Islands	Australia, Papua New Guinea	Limpus, 2009a; Limpus <i>et al.</i> , database ¹
north Queensland (nQld)	Australia	Indonesia, Papua New Guinea	Limpus, 2009a; FitzSimmons, 2010; Limpus <i>et al.</i> , database ¹
northeast Arnhemland (neAl)	Australia	Indonesia, Philippines	Limpus, 2009a; FitzSimmons, 2010
Sulu Sea (SS)	Malaysia	Indonesia, Singapore	De Silva, 1982; Adnyana <i>et al.</i> , 2008; Arshaad & Kadir, 2009; Isnain, 2009
western Peninsular Malaysia (wPM)	Malaysia		Lau <i>et al.</i> , 2009
Gulf of Thailand (GoT)	Thailand		Arshaad & Kadir, 2009
eastern Indian Ocean (eIO)	Australia		FitzSimmons, 2010
western/central Indian Ocean (wIO)	Seychelles, Chagos		Mortimer & Broderick, 1999; FitzSimmons, 2010
Arabian/PersianGulf* (AG)	Iran, Saudi Arabia		FitzSimmons, 2010; Tabib <i>et al.</i> , 2011, 2014
<i>Lepidochelys olivacea</i>			
western Cape York (wCYP)	Australia	Indonesia	Jensen <i>et al.</i> , 2013; Limpus <i>et al.</i> , database ¹
Northern Territory (wNT)	Australia	Indonesia	Jensen <i>et al.</i> , 2013; Whiting <i>et al.</i> , 2007
Peninsular Malaysia (PM)	Malaysia		Bowen <i>et al.</i> , 1998
Andaman Sea (AS)	India ⁴		Shanker <i>et al.</i> , 2011
Sri Lanka (SL)	Sri Lanka		Bowen <i>et al.</i> , 1998; Shanker <i>et al.</i> , 2004
eastern India (eI)	India	Sri Lanka	Kapurusinghe & Cooray, 2002; Shanker <i>et al.</i> , 2004; Frazier, 2007
<i>Natator depressus</i>			
eastern Australia (eAust)*	Australia		Pittard, 2010
Aratura Sea (AS)*	Australia	Papua New Guinea, Indonesia	Limpus, 2007; Pittard, 2010; Limpus <i>et al.</i> , database ¹
Joseph Bonaparte Gulf (BG)	Australia		Pittard, 2010
southwest Kimberley (swKim)	Australia		Pittard, 2010
Pilbara Coast (PI)	Australia		Pittard, 2010

¹This is a global database focused on the Indo-Pacific that is curated by C. J. Limpus. It includes records of nesting locations, tag recoveries and satellite telemetry data based on published literature, reports, conference and workshop presentations, government and personal databases and pers. comm. information from people throughout the region.

²see Dethmers *et al.* (2006), Mahardika *et al.* (2007) and Arshaad & Kadir (2009) for different interpretations of stock boundaries.

³Western Indian Ocean islands

⁴Andaman and/or Nicobar Islands

⁵British Indian Ocean Territory; Chagos Archipelago

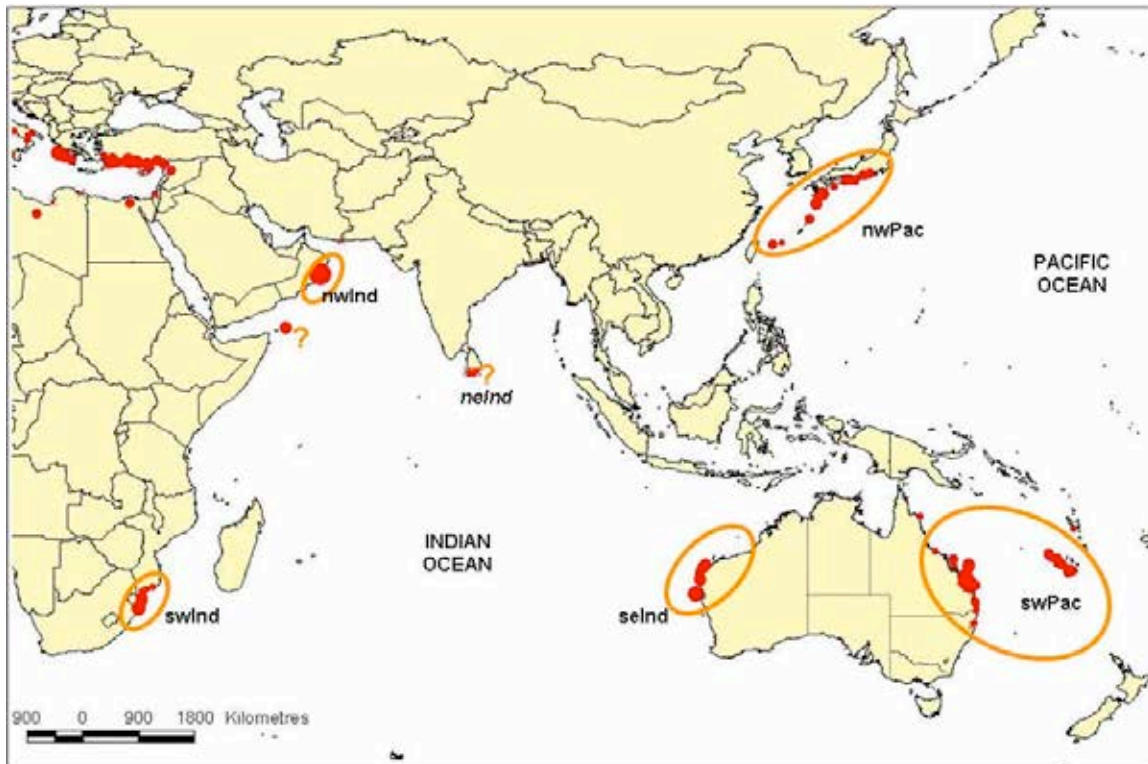


Figure 1. Location of *Caretta caretta* rookeries throughout the Indo-Pacific showing the relative size of rookeries and the grouping of rookeries into identified genetic stocks.

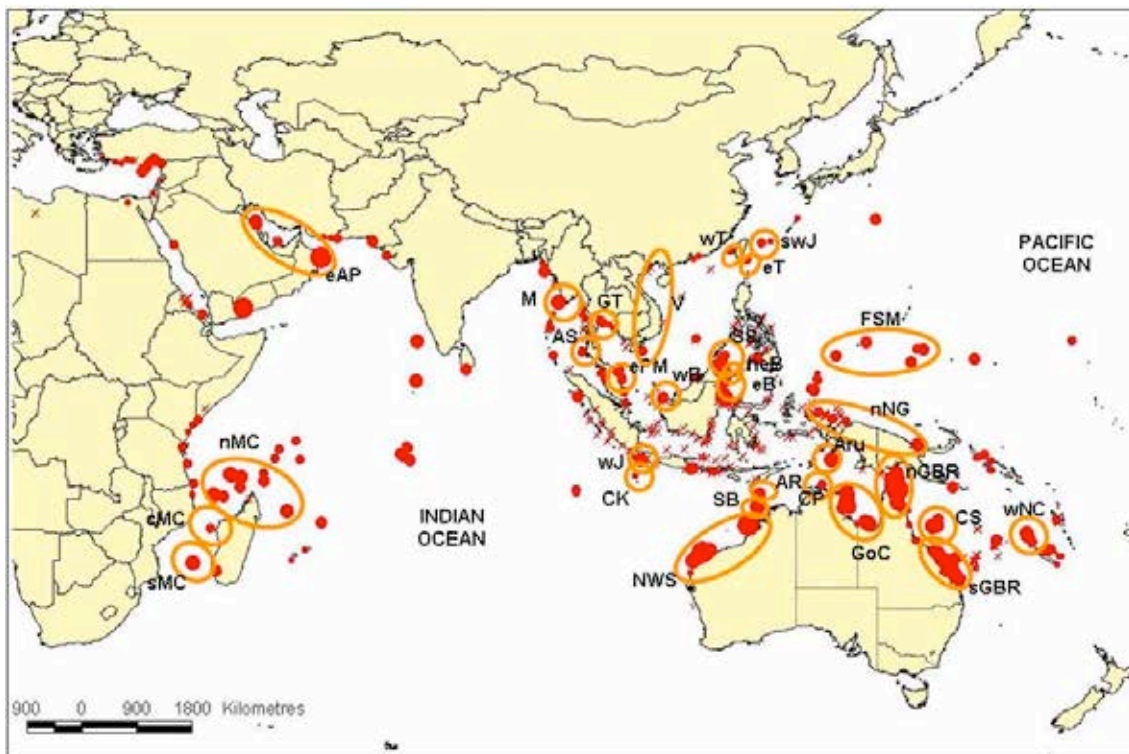


Figure 2. Location of *Chelonia mydas* rookeries throughout the Indo-Pacific showing the relative size of rookeries and the grouping of rookeries into identified genetic stocks.

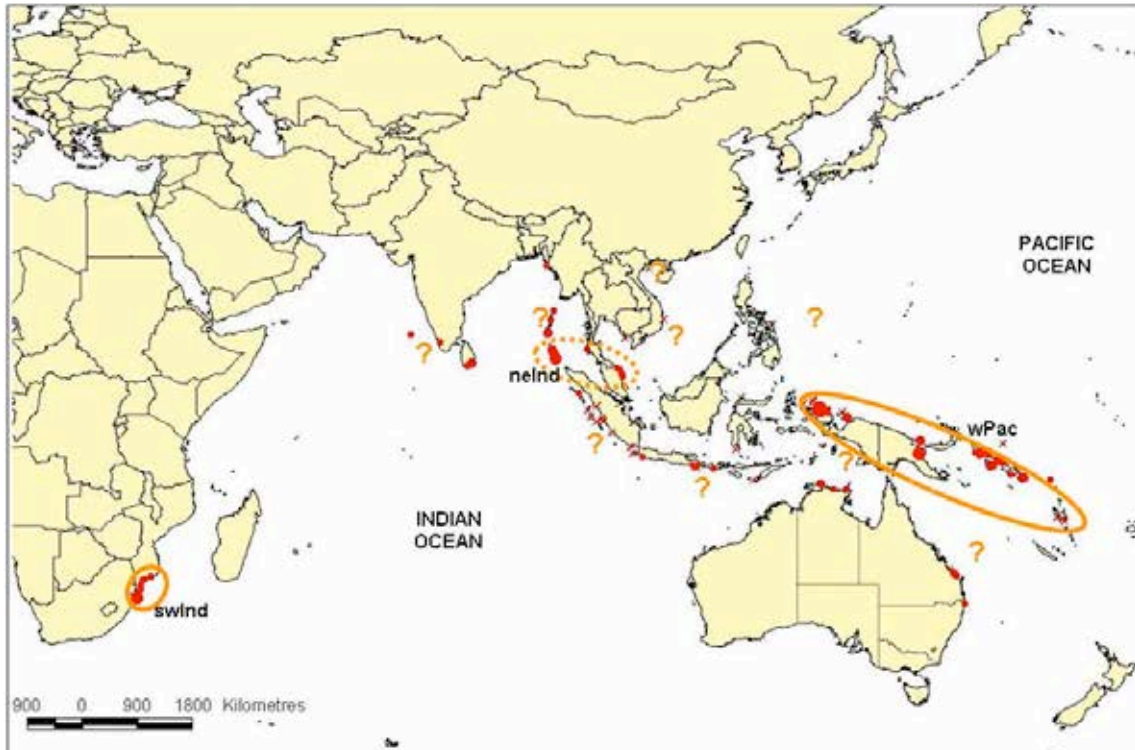


Figure 3. Location of *Dermochelys coriacea* rookeries throughout the Indo-Pacific showing the relative size of rookeries and the grouping of rookeries into identified genetic stocks.

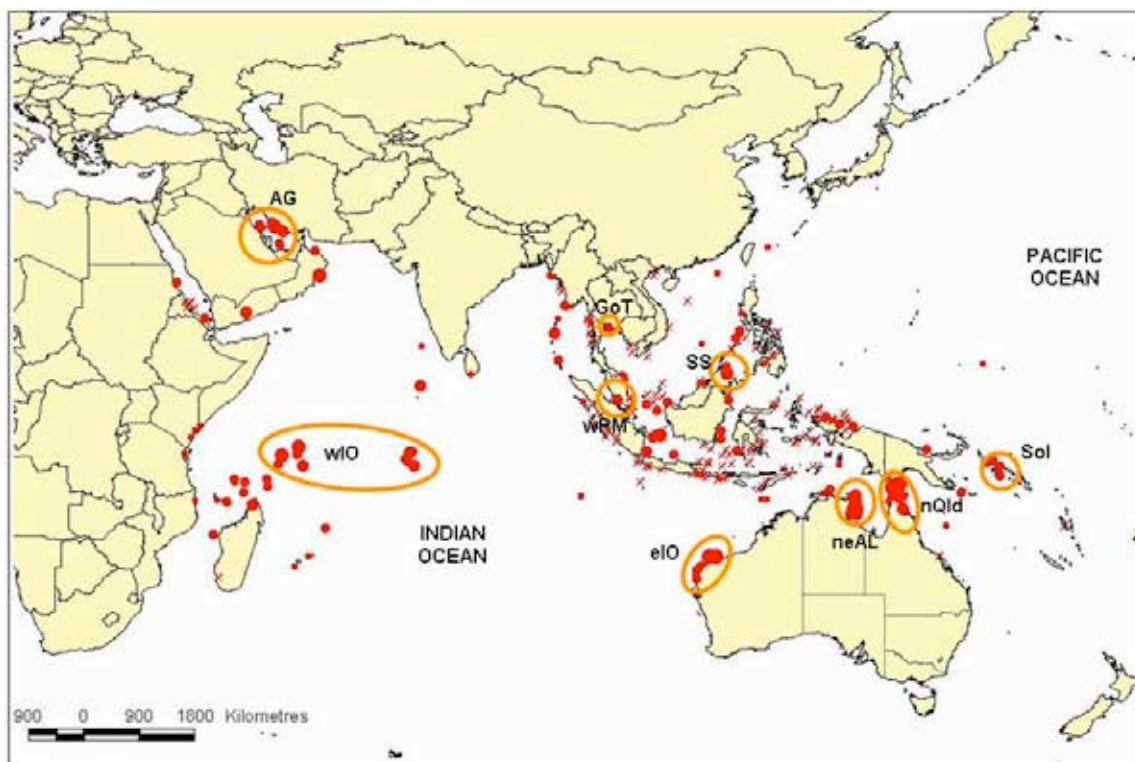


Figure 4. Location of *Eretmochelys imbricata* rookeries throughout the Indo-Pacific showing the relative size of rookeries and the grouping of rookeries into identified genetic stocks.

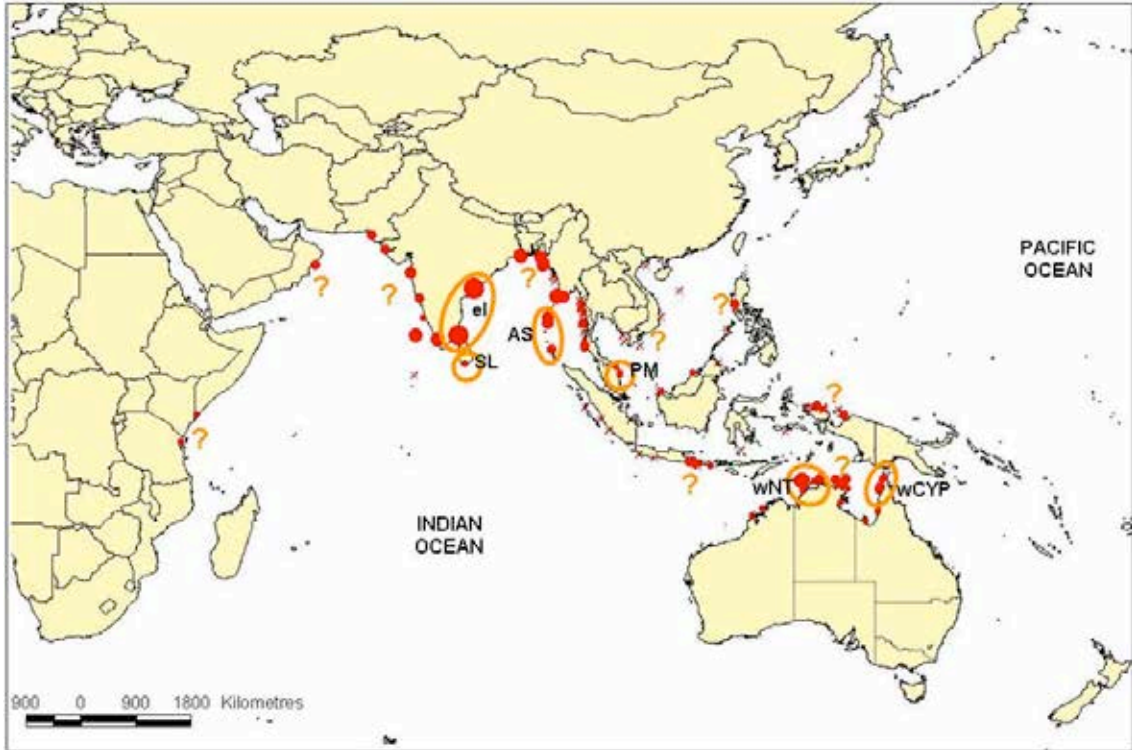


Figure 5. Location of *Lepidochelys olivacea* rookeries throughout the Indo-Pacific showing the relative size of rookeries and the grouping of rookeries into identified genetic stocks.

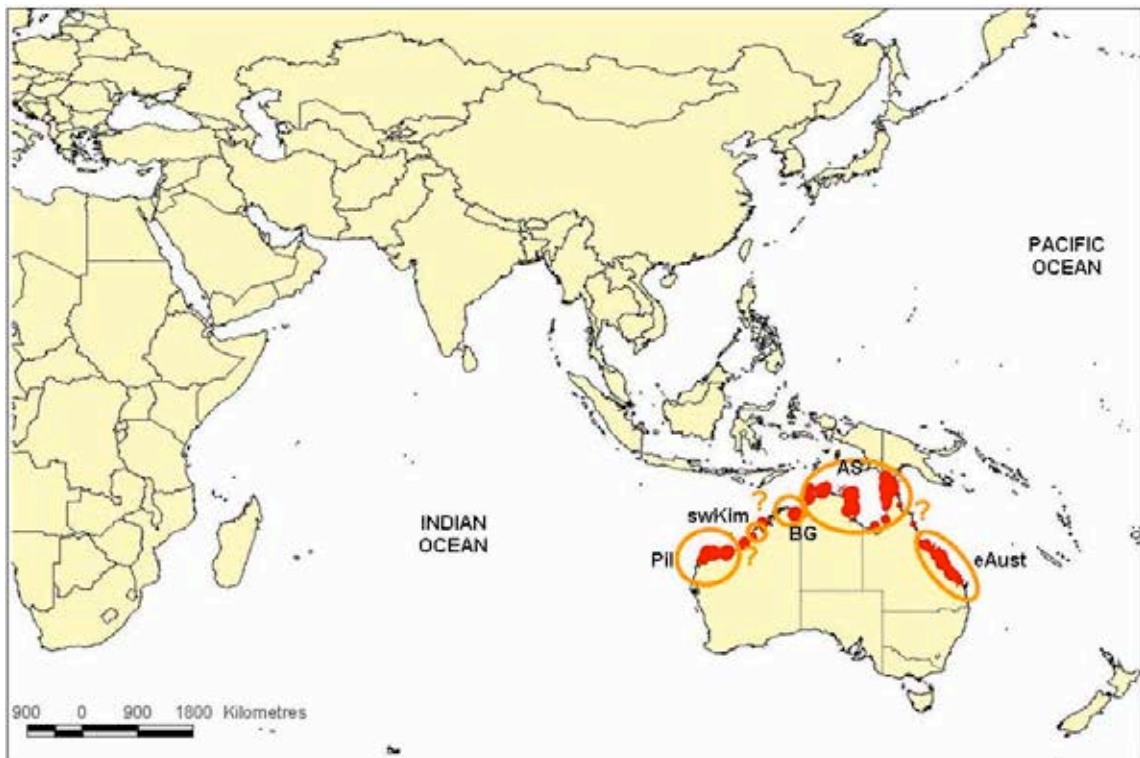


Figure 6. Location of *Natator depressus* rookeries throughout the Indo-Pacific showing the relative size of rookeries and the grouping of rookeries into identified genetic stocks.

A SUMMARY OF SEA TURTLE GENETIC STUDIES IN THE INDIAN OCEAN AND SOUTHEAST

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Our summary has compiled available information about genetics of nesting and in-water sea turtle populations in the Indian Ocean and Southeast Asia so that others interested in this field of research might easily identify areas requiring further investigation. We have also identified studies with contradictory results that would benefit from additional investigation. Study outcomes have been presented without distinguishing among samples from different tissues or fluids, which included blood, skin, muscle, liver, eggshell, and egg albumen, as it was not anticipated that this would be an influential factor on the results.

GENETIC STRUCTURE OF NESTING SEA TURTLE POPULATIONS IN THE INDIAN OCEAN AND SOUTHEAST ASIA

Understanding the genetic structure of nesting populations is important to identify populations of conservation importance, determine population connectivity, and define management units within species (reviewed by Jensen *et al.*, 2013a). Haplotypes known for nesting populations of green (Table 1 and 2), olive ridley (Table 3), hawksbill (Table 4 and 5), loggerhead (Table 6), leatherback (Table 7), and flatback (Table 8) sea turtles are presented below. Earlier studies utilised short (~380bp) mtDNA sequences but new mtDNA D-loop primers yield long (~800bp) sequences which improve resolution of stock structure and identify additional management units; it is recommended all

future mtDNA studies utilise the longer sequences (see Abreu-Grobois *et al.*, 2006; Shamblin *et al.*, 2012). Studies such as Dutton *et al.* (2013) and Jensen *et al.* (2013b) have re-analysed shorter sequences and published additional haplotypes. New sequences should be designated a number according to guidelines at SWFC (2014) and ACCSTR (2014) and submitted to GenBank (www.ncbi.nlm.nih.gov). The forthcoming manuscripts about green sea turtle haplotypes by Jensen *et al.* (see table 1) and hawksbill sea turtle haplotypes by FitzSimmons *et al.* (see Table 4) should resolve problems in understanding haplotypes for these species and understanding the relationship between previous sequence designations. It is hoped that future work can utilise longer sequences and potentially re-analyse samples collected previously, especially those still to be allocated a sequence number.

There is a lack of samples both by region (northwest Indian Ocean, eastern Africa, Bangladesh, Sri Lanka) and species (leatherback, loggerhead, olive ridley and flatback sea turtles) which could be addressed by collaboration between researchers in the appropriate region and those at labs with the capacity to conduct molecular genetics. As FitzSimmons (2014) explains in the preceding paper of this issue of IOTN, greater resolution of population stock structure in the Indian Ocean will inform more effective management plans and conservation efforts of the genetically diverse sea turtle populations in the Indian Ocean and Southeast Asia.

Country, Location and Reference	n	Aa	A1 (Cmp76)	A2 (Cmp47)	A3 (Cmp20)	B4 (Cmp81)	C1 (Cmp83)	C2 (Cmp86)	C3 (Cmp49)	C4 (Cmp87)	C8 (Cmp89)	C9 (Cmp90)	C14 (Cmp91)	Caru(Cmp91)	CM8	CMKW1	CMKW2	CMKW3	CMKW4	CMKW5	CMOM1 (Cmp73)	CMOM2 (Cmp72)	CMOM3 (Cmp62)	CMOM4 (Cmp71)	D2 (Cmp57)	Glo33	H1 (Cmp62)	H2 (Cmp63)	H3 (Cmp64)	IND1 (Cmp49)	IND2 (Cmp57)	IND3 (Cmp75)	L1 (Cmp71)	L2 (Cmp72)	L3	May23	NRC	z	TBA														
Madagascar, Nosy Iranja ⁶	13								X																																												
Mozambique Channel, Europa Island ⁶	33							X							X																																						
Mozambique Channel, Juan de Nova Island ⁶	20								X																																												
Mozambique Channel, Mayotte ⁶	41		X	X				X																																													
Mozambique Channel, Gloriseuses ⁶	39		X						X																																												
Oman ⁸	?																				X																																
Reunion ¹	55	X							X																																												
Seychelles, Aldabra ¹	26	X							X																																												
Seychelles, Aldabra ⁶	26	X	X						X																																												
Seychelles, Cosmoledo ¹	33	X	X						X																																												
Seychelles, Cosmoledo ⁶	31	X	X						X																																												
Seychelles, Farquhar ¹	9	X							X																																												
Seychelles, Farquhar ⁶	7	X	X						X																																												
Seychelles, Granitics ¹	2								X																																												

*See green turtle mtDNA sequences maintained by SWFSC (2014). ¹Broderick *et al.* (1998). Unknown length segment from mtDNA control region. Primers TCR5, TCR6GC; ²Moritz *et al.* (2002). 384bp sequence of mtDNA control region. Primers not named; ³Dethmers *et al.* (2006). 384bp sequence from mtDNA control region. Primers TCR5, TCR6GC; ⁴Mortimer & Broderick (1999). Segment of mtDNA control region. Primers TCR5, TCR6GC; ⁵Formia *et al.* (2006). 488bp sequence from mtDNA control region. Primers LTCM1, HDCM1, LTCM1-HDCM1.1, LTCM1.1-HDCM1; ⁶Bourjea *et al.* (2007). 396bp sequence from mtDNA control region. Primers TCR-5, TCR-6; ⁷Al-Mohanna *et al.* (2013). ~400bp sequence from mtDNA control region. Primers HDCM-1, TCR-5. ⁸Alansari (Unpubl). Unknown length segment from mitochondrial D-loop. Primers not described.

Table 2 .Known Haplotypes of Nesting Green Sea Turtles (*Chelonia mydas*) in Southeast Asia. Jensen *et al.* (In Prep) will standardize all of the haplotype names and show the relationship among past names.

Country, Location and Reference	n	Original Haplotype (Current Sequence Designation)																																					
		A1 (CMP76)	A2 (CMP47)	A3 (CMP20)	A6 (CMP67)	B1 (CMP44)	B3 (CMP80)	B4 (CMP81)	B5 (CMP82)	B6	C3 (CMP49)	C4 (CMP87)	C5 (CMP40)	C7 (CMP88)	C14 (CMP91)	Caru (CMP91)	CMP18	D2 (CMP57)	G2	G3	G4	G5	G7	G11	G12	G13	G14	G15	J14212	M1	M2	M3	P1	P2	R1	T1	T2	T3	
Brunei, Brunei Beach ¹	4										X	X					X																						
Indonesia, Derawan Island ¹	22		X							X		X					X															X							
Indonesia, Eru ^{1,3}	28		X										X																										
Indonesia, Eru ²	28		X												X																								
Indonesia, Pangumbahan ¹	23									X																													
Indonesia, Pangumbahan ^{2,3}	23									X		X																											
Indonesia, Panjang Is ¹	16		X							X	X	X	X					X																	X				
Indonesia, Sangalaki Is ¹	38				X					X	X	X	X					X																		X			
Indonesia, Sangalaki ²	29									X	X	X	X					X																		X			
Indonesia, Sangalaki Is ³	29				X					X	X	X	X					X																					
Malaysia, Mal. Turtle Islands ³	28									X								X																					
Malaysia, Pahang ¹	12									X																													
Malaysia, Paka ^{1,3}	15									X																													
Malaysia, Palau Redang ²	27									X	X	X	X					X																					
Malaysia, Perak ¹	15									X																													
Malaysia, Redang Is ¹	31									X								X																					
Malaysia, Redang Is ³	12									X	X	X	X					X																					
Malaysia, Sabah Turtle Islands ¹	58									X								X																					
Malaysia, Sarawak ¹	62									X	X	X	X					X																					
Malaysia, Sarawak Turtle Islands ^{2,3}	22									X	X	X	X					X																					

Country, Location and Reference	n	A1 (Cmp76)	A2 (Cmp47)	A3 (Cmp20)	A6 (Cmp67)	B1 (Cmp44)	B3 (Cmp80)	B4 (Cmp81)	B5 (Cmp82)	B6	C3 (Cmp49)	C4 (Cmp87)	C5 (Cmp40)	C7 (Cmp88)	C14 (Cmp91)	Caru (Cmp91)	Cmp18	D2 (Cmp57)	G2	G3	G4	G5	G7	G11	G12	G13	G14	G15	J14212	M1	M2	M3	P1	P2	R1	T1	T2	T3			
Malaysia, Sipadan Is ¹	40										X		X		X			X																							
Malaysia, Sipidan ²	30										X		X		X			X																							
Malaysia, Sipidan Is ³	30										X		X		X			X																							
Malaysia & Philippines, Turtle Islands ²	67										X		X		X			X																							
Myanmar, Coco Is ¹	30		X								X		X		X			X											X	X	X										
Myanmar, Tameahla Is ¹	30										X		X		X			X											X												
Philippines, APO Reef NP ¹	4										X																														
Philippines, Panikian Is ¹	9			X																																					
Philippines, Phil. Turtle Islands ^{3,13}	62										X		X					X																							
Thailand, Huyong Is ¹	19								X		X																												X		
Thailand, Huyong Is ⁴	19	X			X	X																																			
Thailand, Kham Is ¹	30				X				X		X		X					X																					X	X	
Thailand, Kham Is ⁴	30	X	X	X	X	X	X	X	X	X																															
Vietnam, Con Dao Is ¹	42										X		X															X													
Vietnam, Minh Chau ¹	11									X																															

¹See green turtle mtDNA sequences maintained by SWFSC (2014). ²Arshaad & Kadir (2008). 389bp sequence of mtDNA control region. Primers TCR5, TCR1; ³Moritz *et al.* (2002). 384bp sequence of mtDNA control region. Primers not described; ⁴Dethmers *et al.* (2006). 384bp sequence from mtDNA control region. Primers TCR5, TCR1GC; ⁵Kitiwattanaong *et al.* (2003). 438bp sequence from mtDNA control region. Primers Green15552F, Green15579F, Green16300R, Green16087R. See also Joseph (2013, 2014) for descriptions of additional studies in Malaysia.

Table 3. Known Haplotypes of Nesting Olive Ridley Sea Turtles (*Lepidochelys olivacea*) in the Indian Ocean and Southeast Asia. Some longer haplotypes (Lo#) overlap with shorter sequences (H, J). Samples are required for nesting populations in the northwest Indian Ocean (Oman), northeast Indian ocean (Bangladesh, Myanmar and Thailand), in the South China, Arafura and Timor Sea.

Country, Location and Reference	n	Published Haplotype (Shorter Sequence)																					
		G	H	I	J	K	K1	K2	K3	K4	K5	N	New3	New6	Lo1 (J)	Lo2 (G)	Lo3	Lo4 (H)	Lo5	Lo15 (J)	Lo21	Lo27	
Australia, Flinders Beach ¹	9														X	X	X				X		X
Australia, McClure Islands ¹	11														X	X					X		
Australia, McClure Islands ²	8	X			X																		
Australia, Tiwi Islands ¹	64														X	X	X	X	X			X	
India, Andaman & Nicobar Islands ²	?				X	X	X		X	X	X												
India, Goa, Kerala, Lakshadweep, Orissa & Tamil Nadu ²	?	X			X	X	X	X	X	X	X		X	X									
India, Orissa ³	81				X	X	X	X	X	X	X	X											
Malaysia, Kijal and Paka ⁴	5				X																		
Sri Lanka, SW coast ¹	17	X	X	X	X																		

¹Jensen *et al.* (2013b). ~880bp fragment of mtDNA control region. Primers LTEi9, H950. ²Shanker *et al.* (2011). 350bp sequence from mitochondrial d-loop region. Primers HDCM1, LDCM1, LTCM1, TCR1-TCR6; ³Shanker *et al.* (2004). 400bp sequence from mtDNA control region. Primers HDCM1, TCR5; ⁴Bowen *et al.* (1998). 470bp sequence from mtDNA control region. Primers LTCM1, HDCM1.

Table 4. Known Haplotypes of Nesting Hawksbill Sea Turtles (*Eretmochelys imbricata*) in Southeast Asia. FitzSimmons *et al.* (In Prep) will describe new haplotypes, standardise all of the haplotype names, and show the relationship among past names.

Country, Location and Reference	n	Haplotype															
		E11	E12	E13	E14	E15	E16	E17	E18	E19	E110	E111	E112	E113	E114	E115	14
Brunei, Brunei Beach ¹	4				X					X	X						
Indonesia, Kimar Belitang ¹	9									X	X						
Indonesia, Seribu Islands ²	9																X
Malaysia, Melaka ¹	29									X							
Malaysia, Sabah Turtle Islands ¹	20		X							X	X			X	X		
Myanmar, Coco Island ¹	4	X								X						X	
Philippines, APO Reef NP ¹	4					X	X	X									
Philippines, Bataan ¹	1										X						
Philippines, Davao Gulf ^{1*}	2								X				X				
Philippines, Misamis Oriental ¹	1			X													
Thailand, Khram Island ¹	14									X		X	X				

¹Arshaad & Kadir (2008). 740bp sequence of mtDNA control region. Primers LTE19, H950; ²Okayama *et al.* (1999). Fragment of unknown length from control region of DNA. Primers L15921, TCR1; ^{*}Written as Davao Gulf in Arshaad & Kadir (2008). See also Vargas *et al.* (2013) for haplotypes EIIP-33 and EiATL from Indo-Pacific turtles.

Table 5. Known Haplotypes of Nesting Hawksbill Sea Turtles (*Eretmochelys imbricata*) in the Indian Ocean. FitzSimmons *et al.* (In Prep) will standardise all of the haplotype names and show the relationship among past names. Further samples is required in the southwest Indian Ocean and northwest Indian Ocean (including Yemen and Oman), and northeast Indian Ocean (Andaman and Nicobar Islands).

Country, Location and Reference	n	Haplotype																										
		AAAAA	BAAAA	CAAAA	ABAAA	A1	A6	A7	B3	B9	E1	E2	E3	E5	Iran1	Iran2	Iran3	Iran4	Iran5	Iran6	Iran7	PG7.1	PG7.2	PG7.3	PG7.4	PG7.5	T8A	
Arabian Peninsula ^{1,2}	14					X																						
Australia, Western Australia ²	31						X																					
Chagos Islands, Diego Garcia ^{1,2}	3								X																			
Chagos Islands, Peros Banhos ^{1,2}	5							X	X	X																		
Chagos Islands, Salomon Atoll ^{1,2}	1							X																				
Iran, Kish and Qeshm Islands ³	30									X	X				X	X	X	X	X	X								
Iran, Kish and Qeshm Islands ⁴	45										X	X			X	X	X	X	X	X								
Iran, Hendoroubi, Nakhiloo, Ommolkaram & Sheedver ⁵	-														X	X	X	X	X	X								
Iran, Kish, Nakhiloo & Qeshm Islands ^{6,7}	69	X	X	X	X	X															X	X	X	X	X			
Seychelles, Aldabra ¹	2								X																			
Seychelles, Amirantes ¹	24							X	X	X																		X
Seychelles, Cosmoledo ¹	2							X																				
Seychelles, Farquhar ¹	1								X																			
Seychelles, Granitics ¹	32							X	X	X																		
Seychelles, Platte Island ¹	25							X	X	X																	X	
Seychelles, Undescribed location ²	73							X	X	X																	X	

¹Broderick *et al.* (1998). Segment of mtDNA control region. Primers TCR5, TCR1GC; ²Mortimer & Broderick (1999). Segment of mtDNA control region. Primers TCR5, TCR1GC; ³Tabib *et al.* (2011). 890bp sequence from mtDNA control region. Primers H950, LCM15382; ⁴Tabib *et al.* (2014). 890bp sequence from mtDNA control region. Primers H950, LCM15382; ⁵Mobaraki *et al.* (2014). Sample size unknown; six additional haplotypes not named in conference abstract; ⁶Nezhad *et al.* (2012) and ⁷Nezhad *et al.* (2013) Unknown length sequence from mtDNA control region. Primers H950, LCM15382. *Referred to as loggerhead turtles in Methods but hawksbills otherwise throughout the paper. See also Vargas *et al.* (2013) for haplotypes E1IP-33 and E1ATL from Indo-Pacific turtles.

Table 6. Known Haplotypes of Nesting Loggerhead Sea Turtles (*Caretta caretta*) in the Indian Ocean. Haplotypes for the the major regional rookery in Yemen are currently unknown.

Country, Location and Reference	n	Haplotype			
		D	L	CC-A116	CC-A2.1
Oman, Masirah Island ^{1,2}	8		X	X	
South Africa, Tongaland ^{1,2}	15	X			X

¹Bowen *et al.* (1994). Unknown fragment length from closed-circular mtDNA; ²Shamblin *et al.* (2014). ~800bp from mtDNA control region. Primers LCM15382, H950g. See also Pacioni *et al.* (2013) for descriptions of studies in Western Australia.

Table 7. Known Haplotypes of Nesting Leatherback Sea Turtles (*Dermochelys coriacea*) in the Indian Ocean and Southeast Asia. Greater sampling in the northeast Indian Ocean would improve understanding of the number and range of management units.

Country, Location and Reference	n	Published Haplotype (Shorter Sequence)						
		A	D	E	H	I	Dc1.1*	Dc1.4*
India, Great Nicobar Is ¹	114	X	X	X			X	
Indonesia, Papua, Jamursba-Medi ²	31	X	X	X			X	
Indonesia, Papua, War Mon ²	9						X	
Malaysia, Terengganu ³	9	X	X	X	X			
Papua New Guinea ²	18	X	X	X			X	
South Africa, Tongaland ³	8	X						
South Africa, Natal ⁴	41						X	X

¹Shanker *et al.* (2011). 350bp fragment of control region of mtDNA. Primers HDCM1, LDCM1, LTCM1, TCR1-TCR6; ²Dutton *et al.* (2007). 496bp fragment of control region of mtDNA. Primers LTCM2, HDCM2; ³Dutton *et al.* (1999). 496bp fragment of control region of mtDNA. Primers LCM15382, HDCM1; ⁴Dutton *et al.* (2013). 832bp sequence from D-loop of mtDNA. Primers LCM15382, H950g; *Haplotype A in Dutton *et al.* (1999).

Table 8. Known Haplotypes of Nesting Flatback Sea Turtles (*Natator depressus*) in the Indian Ocean.

Country, Location and Reference	n	Haplotype										
		Nd1	Nd2	Nd3	Nd4	Nd6	Nd7	Nd8	Nd9	Nd10	Nd11	Nd12
Australia, Bare Sand Is	16	X					X			X		
Australia, Barrow Is	29	X	X	X	X							
Australia, Cape Domett	35	X	X	X								
Australia, Cape Thouin	25	X	X	X	X							
Australia, Eco Beach	28	X	X	X								X
Australia, Field Is	38	X	X				X	X	X	X		
Australia, West Island	31	X				X	X			X	X	X

All haplotypes from FitzSimmons *et al.* (unpubl.) in Pittard (2010).

GENETIC STRUCTURE OF FEEDING GROUND SEA TURTLE POPULATIONS IN THE INDIAN OCEAN AND SOUTHEAST ASIA

Haplotypes known for feeding ground populations of loggerhead (Table 9), green (Table 10 and 11) and hawksbill (Table 12 and 13) sea turtles are presented below. There are no known haplotypes of foraging olive ridley, leatherback or flatback sea turtles in the Indian Ocean. As for nesting populations, new mtDNA D-loop primers yield long (~800bp) sequences should be utilised in future studies and new sequences should be submitted to GenBank (www.ncbi.nlm.nih.gov) and numbered according to sequences at SWFC (2014) and ACCSTR (2014).

Table 9. Known Haplotypes of Foraging Loggerhead Sea Turtles (*Caretta caretta*) in the Indian Ocean

Country, Location and Reference	n	Haplotype
		C (C-A11)
Kuwait, southern Kuwait Bay	1	X

Al-Mohanna & George (2010). 306bp sequence from D-loop of mtDNA. Primers HDCM-1, TCR-5. See also Pacioni *et al.* (2013) for descriptions of studies in Western Australia.

Table 10. Known Haplotypes of Foraging Green Sea Turtles (*Chelonia mydas*) in Southeast Asia. Jensen *et al.* (In Prep) will standardise all of the haplotype names and show the relationship among past names.

Country, Location and Reference	n	Haplotype										
		A2	A3	Caru	C3	C4	C5	C8	C14	D2	E2	L1
Brunei, Lawas ¹	28		X		X	X	X		X	X		X
Malaysia, Tun Sakaran MP & Sabah, Sipadan Is ²	65	X	X	X	X		X				X	X
Sabah, Sipadan Is ^{3,4}	33	X	X	X	X		X			X	X	
Sabah, Mantanani and Mengalum Islands ^{5,6}	20			X	X	X		X		X	X	

¹Arshaad *et al.* (2013). Undescribed length sequence from mtDNA control region. Primers H950, LTEi9; ²Kuen & Joseph (2013). Segment of mtDNA not described. Primers TC5, TC6; ³Joseph & Kuen (2012), ⁴Joseph & Kuen (2014). 380bp segment of mtDNA control region. Primers not described; ⁵Kuen & Joseph (2011) and ⁶Kuen & Joseph (2014). Segment of mtDNA control region. Primers TCR5, TCR6.

Table 11. Known Haplotypes of Foraging Green Sea Turtles (*Chelonia mydas*) in the Indian Ocean. Jensen *et al.* (In Prep) will standardise all of the haplotype names and show the relationship among past names.

Country, Location and Reference	Haplotype																																						
	u	Aa	Ac	A1	A2	A3	A7	B1	B3	B6	B7	C1	C3	C4	C5	C7	C8	C9	C14	C15	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	D2	D5	K1	x	z	TBA			
Australia, Aru Is ¹	40			X	X	X	X					X	X	X	X				X											X									
Australia, Ashmore Reef	65			X	X	X	X	X	X			X	X	X	X				X										X				X						
Australia, Coubour Peninsula ¹	91			X	X	X	X	X	X	X		X	X	X	X				X			X	X							X			X						
Australia, Field Island ¹	62			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X							X	X						X						
Australia, Fog Bay ¹	67			X							X	X	X	X	X	X	X	X	X								X	X											
Australia, Sir Edward Pellew Islands ¹	102			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X																				
Chagos Islands, Diego Garcia ²	1											X																											
Cocos Keeling Islands ^{1,2}	36											X	X	X	X																								
Seychelles, Aldabra ²	75	X	X	X									X																						X	X			
Seychelles, Amirantes ²	48	X										X	X	X																					X				
Seychelles, Farquhar ²	8	X	X	X								X	X	X																									
Seychelles, Providence ²	25	X	X	X								X	X	X																									

¹Dethmers *et al.* (2010). 385bp segment of mtDNA control region. Primers TCR5, TCR6; ²Broderick *et al.* (1998). Segment of mtDNA control region. Primers TCR5, TCR1GC.

Table 12. Known Haplotypes of Foraging Hawksbill Sea Turtles (*Eretmochelys imbricata*) in the Indian Ocean.

Country, Location and Reference	n	Haplotype																
		A1	B3	B9	B10	E1	E2	E3	E4	U	W	X	Y	Z	3	23	24	TBA
Chagos Islands, Chagos Bank ¹	1					X												
Chagos Islands, Diego Garcia ¹	40	X		X		X	X						X					
Chagos Islands, Peros Banhos ¹	4			X		X	X											
Chagos Islands, Salomon Atoll ¹	6	X		X		X	X					X						X
Chagos Islands ²	50	X	X		X	X	X		X									
Maldives ³	1														X			
Seychelles, Undescribed location ³	7														X	X	X	
Seychelles, Aldabra ¹	104	X		X		X	X			X	X		X					X
Seychelles, Amirantes ¹	15	X		X		X	X			X			X	X				X
Seychelles, Granitics ¹	17																	X
Seychelles, Platte Island ¹	1					X	X											X
Seychelles, Providence ¹	21	X		X		X							X					X
Seychelles, Undescribed location ²	191	X	X	X	X	X	X	X	X		X							

¹Broderick *et al.* (1998). Segment of mtDNA control region. Primers TCR5, TCR1GC; ²Mortimer & Broderick (1999). Segment of mtDNA control region. Primers TCR5, TCR1GC; ³Okayama *et al.* (1999). Unknown length sequence from mitochondrial control region. Primers L15926, TCR6.

Table 13. Known Haplotypes of Foraging Hawksbill Sea Turtles (*Eretmochelys imbricata*) in Southeast Asia.

Fitzsimmons *et al.* (In Prep) will describe new haplotypes, standardise all of the haplotype names, and show the relationship among past names.

Country, Location and Reference	n	Haplotype		
		T	H1	H4
Malaysia, Tun Sakaran MP and Sabah, Sipadan Is ¹	4		X	X
Philippines ²	2	X		

¹Kuen & Joesph (2013). Primers TC5 and TC6; ²Okayama *et al.* (1999). Fragment of unknown length from control region of DNA. Primers L15921, TCR1.

GENETIC DIVERSITY AMONG SEA TURTLE NESTING BEACHES IN THE INDIAN OCEAN AND SOUTHEAST ASIA

Genetic diversity has been described among nesting olive ridley sea turtles in India (Shanker *et al.*, 2011) and Australia (Jensen *et al.*, 2013b); hawksbill turtle populations in the Persian Gulf (Mostafavi *et al.*, 2011; Zolgharnein *et al.*, 2011; Tabib *et al.*, 2011, 2014; Nezhad *et al.*, 2012, 2013); and, green turtle populations in Thailand (Kittiwattanawong *et al.*, 2003), Malaysia (Joseph, 2013, 2014), Sri Lanka (Ekanayake *et al.* (2012), and the Mozambique channel (Bourjea *et al.*, 2007). The population genetics of hawksbill turtles in the Persian Gulf have been summarized in Table 14 due to contradictory results that may be the result of different methodologies among studies. The importance of understanding genetic diversity among nesting populations has been reviewed by FitzSimmons and Limpus (2014).

OTHER MOLECULAR GENETICS STUDIES IN THE INDIAN OCEAN AND SOUTHEAST ASIA

The use of microsatellite markers to understand paternity and mating systems in sea turtles is reviewed by Jensen *et al.* (2013a), and studies on paternity of sea turtle nesting populations in the region are summarised in Table 15.

DNA barcoding can be used for species identification, such as during forensic investigation of the species of turtle eggs or meat for commercial sale. Elmeer *et al.* (2011) has sequenced the cytochrome c oxidase subunit I (COI or cox1) gene from mitochondrial DNA of green turtles in Qatar for use in DNA barcoding. In a different type of forensic DNA analysis, 57 items made from tortoiseshell that had been confiscated by the US Fish and Wildlife Service identified 16 haplotypes, 94% of which were of Indo-Pacific origin (Shattuck, 2011).

Table 14 .Genetic Diversity Among Sea Turtle Nesting Beaches in the Persian Gulf.

Country, Location and Reference	Species	n	Genetic Marker	Results
Iran, Hormoz & Shidvar Islands ¹	<i>Eretmochelys imbricata</i>	60	8 microsatellite loci	Hormoz Is: Av HO=0.39, Av. HE=0.77; Shidvar Is: Av HO=0.53, Av. HE=0.77; All loci in two regions have differentiations from Hardy-Weiberg equilibrium. Fst=0.048 P<0.01; DTN=0.27. Populations at the two islands are significantly different.
Iran, Kish & Qeshm Islands ²	<i>Eretmochelys imbricata</i>	30	5 haplotypes	Kish Is: h=0.64, π=0.002; Qeshm Is: h=0.77, π=0.001; Overall: h=0.69, π=1.56. Results indicate low genetic diversity in this area and high rates of migration between the populations of these two islands.
Iran, Kish & Qeshm Islands ³	<i>Eretmochelys imbricata</i>	45	7 haplotypes	Kish Is: h=0.111, π=0.0002; Qeshm Is: h=0.313, π=0.0006; Overall: h=0.212, π=0.00038. Fst=0.999±0.0002; Nm=0.000. Results suggest low genetic diversity in this area but a significant difference between the nesting populations of Kish and Qeshm Islands.
Iran, Kish & Qeshm Islands ⁴	<i>Eretmochelys imbricata</i>	64	5 microsatellite loci	Average Ho=0.570, Av. HE=0.616. Eight out of 10 tests differed significantly from Hardy-Weinberg Equilibrium P<0.05. FST=0.167 P<0.01; RST= 0.634; Nm=1.26; Genetic distance=0.33; Genetic similarity=0.78. The turtle populations of Kish and Qeshm Islands are significantly different.
Iran, Kish, Qeshm & Nakhiloo Islands ^{5,6}	<i>Eretmochelys imbricata</i>	69	4 haplotypes	Significant genetic variation among turtles nesting at these islands was not detected P>0.05.

¹Mostafavi *et al.* (2011); ²Tabib *et al.* (2011); ³Tabib *et al.* (2014); ⁴Zolgharnein *et al.* (2011); ⁵Nezhad *et al.* (2012); ⁶Nezhad *et al.* (2013).

Table 15 . Studies on Paternity of Green and Hawksbill Turtle Nests in the Indian Ocean and Southeast Asia.

Country, Location and Reference	Species	Total # Females Examined	Total # Clutches Examined	# Single Clutches	# Successive Clutches	# Hatchlings Examined from Each Clutch	Results
Seychelles, Cousine Island ¹	<i>Eretmochelys imbricata</i>	43	51	42	<ul style="list-style-type: none"> -2 clutches from 7 females -3 clutches from 5 females -4 clutches from 1 female 	3-20	<ul style="list-style-type: none"> -Single paternity (90.7% of females) more common than multiple paternity (9.3% of females). -Two fathers in 100.0% of clutches with multiple paternity. -No males appeared to have fertilized >1 female. -Evidence that females predominantly monogamous and store sperm within a nesting season
Sri Lanka, Kosgodia ²	<i>Chelonia mydas</i>	19	24	17	<ul style="list-style-type: none"> -3 clutches from 1 female -4 clutches from 1 female 	10	<ul style="list-style-type: none"> -Single paternity (53% of females) more common than multiple paternity (47% of females). -Two fathers in 12.5% of clutches with multiple paternity. -Three fathers in 37.5% of clutches with multiple paternity. -No males appeared to have fertilized >1 female. -Evidence of male/s siring first clutch also siring successive clutches, therefore, females mate with same male multiple times during a nesting season and/or sperm storage.

¹Phillips *et al.* (2013). 33 variable microsatellite loci examined using two leatherback primers (D1 and D110) and four adapted hawksbill primers (Eim11, Eim38, Eim41, HKB31); ²Ekanayake *et al.* (2013). 1 microsatellite loci using four green turtle primers (Cm3, Cm58, Cm72, Cm84) and two loggerhead turtle primers (Cc7, Cc17).

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A SUMMARY OF THE INDIAN OCEAN AND SOUTH EAST ASIA REGIONAL MEETING AT NEW ORLEANS , USA

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This year, the Indian Ocean and South East Asia Regional Meeting (IOSEA) was held on 13th April in New Orleans, USA, prior to the 34th International Sea Turtle Symposium. Approximately 20 participants from 15 countries, including Australia, Bangladesh, France, Japan, Malaysia, Mozambique, Philippines, Seychelles, Sri Lanka, Tanzania, United Arab Emirates, United Kingdom and United States, attended. Lalith Ekanayake (co-organiser of the meeting) gave a brief introduction to the meeting, its history, and welcomed new participants before introducing seven presentations.

Jeanne Mortimer described the status of sea turtle research and conservation in the Seychelles and Chagos Islands. She explained new initiatives for the outer island, progress of the satellite tagging programme and genetic studies, and the sand temperature monitoring programme. Peter Richardson discussed the IOSEA Western Indian Ocean Marine Turtle Task Force and 8th WIOMSA Scientific Symposium held in Mozambique in November 2013. Jeff Miller summarised the current research on sea turtles in Saudi Arabia. Teri Shore discussed threats from industrialisation of the Great Barrier Reef and potential harm to sea turtle nesting

beaches and marine habitat in the area. Andrea Phillott (co-organiser of the meeting) described her current research on hatchery management practices in the Indian Ocean and Southeast Asia region. Hiroyuki Suganuma discussed broad aspects of sea turtle conservation and management issues in Japan, including protection of nests from monitor lizards.

During the general discussion, participants raised topics of general interest. Lalith Ekanayake described the recent theft of albino turtles from a turtle hatchery in Sri Lanka. Nick Pilcher raised a question about turtle by-catch and pointed out that there are very few studies on turtle by-catch in the region. He suggested regional participants consider focusing on small scale fishery by-catch of sea turtles and explained about the CMS dugong survey methodology and concurrent collection of turtle by-catch data within the same survey. Mark Guinea raised the potential impact of port development in Asian countries.

The next meeting will be held in Turkey before the 35th International Sea Turtle Symposium. We hope more regional participants will be able to attend as the venue is closer and travel will be cheaper.

REPORTS



REPORT FROM THE 34TH ANNUAL SYMPOSIUM ON SEA TURTLE BIOLOGY AND CONSERVATION, NEW ORLEANS, 10-17 APRIL 2014

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The 34th Annual Symposium on Sea Turtle Biology and Conservation was held in the City of New Orleans, USA on 10-17 April 2014. The theme of the symposium was “Cultures,” which honored the interactions between various cultures with sea turtle populations across time and geography. The symposium was held in conjunction with the Southeast Regional Sea Turtle Network. The structure of the symposium was similar to past symposia, with pre-symposium workshops and regional meetings, plus 3.5 days of symposium meetings. Overall, the meeting was a success from basically every perspective; details are offered below.

A total of 785 people from 73 countries registered for the Symposium. The venue for the symposium was the Marriott Hotel on Canal Street, New Orleans. A total of 176 oral papers and 273 posters were originally submitted to organizers. These original submissions included the highest number of oral presentations on in-water biology science ever submitted to a symposium, with a total of 35, or approximately 20% of all oral presentations originally submitted. Due to normal attrition associated with every symposium, in the end the symposium included a total of 158 oral presentations in general sessions and a total of 235 posters. Of the oral presentations, 32 (20%) corresponded to in-water biology research, more than any other category presented in this symposium.

Pre-symposium Workshops. Five workshops were offered the weekend before the symposium started. These were the Sea Turtle Rehabilitation and Health Workshop (with a total of 237 registered participants), the Educators Outreach Workshop (with 18 local, national and international participants), the Digital Marketing Workshop (with 83 participants), the GIS Workshop with 197 participants, and the Temperature-dependent Sex Determination Workshop (with 151 participants).

Pre-symposium Meetings. A total of eight Special Interest and Regional meetings were held the weekend prior to the main symposium presentations. These were the Terrapin, Tortoise & Freshwater Meeting, the RETOMALA, the

Africa Regional, the Mediterranean Regional, the East Asia Regional, Indian Ocean and Southeast Asia Regional, the Pacific Islands Region-Oceania, Eastern Pacific Hawksbill Initiative and the Marine Turtle Specialist Group. These meetings were successful and contributed to bring attendees early to the symposium.

Key Note Speakers. Three key note speakers delivered three 30-minute addresses to symposium participants. Jack Frazier’s presentation gave the audience a comprehensive overview of the topic Sea Turtles and Cultures, which nicely served to frame the theme of the symposium. Duncan MacKenzie immediately followed Jack’s presentation, speaking to the audience about the pros and cons of using sea turtles as animal models to conduct physiological studies. On the last day of the symposium, and after stripping down to his swimsuit, David Owens delivered an enthusiastic, informative and entertaining speech about the history of sea turtle research and the historical involvement of women in this research. All three addresses were excellent and very well received by the audience.

Symposium Sessions. This symposium included traditional sessions held at previous symposia, such as Anatomy, Physiology and Health; In-Water Biology Session (Ecology, Telemetry, Foraging, Behavior); Nesting Biology (Ecology, Behavior, and Reproductive Success), Population Biology and Monitoring (Status, Modeling, Demography, Genetics, Nesting Trends, In-Water Trends), Fisheries and Threats Session; Conservation, Management and Policy; Education, Outreach And Advocacy; and Social, Economic and Cultural Studies.

Two special sessions were also held during the symposium: Biology and Conservation of the Sea Turtles of the Gulf of Mexico and Collaborative Fisheries Research. As the title implies, the first session focused on work conducted in the Gulf of Mexico and was held the first day of the symposium. This session included papers from the entire Gulf (Mexican and US waters), and offered an emphasis on in-water work. The second special session on collaborative fisheries

focused on work being done by scientists in collaboration with fishermen to collect fisheries-specific information and promote effective conservation and management practices among fishermen.

Archie Carr Student Awards. There were 54 oral presentations and 92 poster presentations submitted by students for consideration in the Archie Carr Awards for Best Student Presentations. The winner for Best Biology Poster was Eric Parks and Runners-Up were Celine Mollet Saint Benoit and Cristian Ramirez-Gallego. Best Conservation Poster went to Meghan Gahm, and the Runner-Up was Kimberly Riskas. The Best Biology Oral was won by Cali Turner Tomaszewicz, and Runners-Up were Melanie Lopez-Castro and Nathan Robinson. The Best Conservation Oral winner was Jose Luis Crespo-Picazo, and Aliko Panagopoulou was Runner-Up. The judges who served in this competition were: Larisa Avens, Ana Barragan, Cathi Campbell, Wendy Dow Piniak, Mariana Fuentes, Marc Girondot, Caroline Good, Emma Harrison, Jen Keller, Cynthia Lagueux, Ann Marie Lauritsen, Kate Mansfield, Zoe Meletis, Dave Owens, Erin Seney and Brian Shamblin.

Business Meeting. Important issues were addressed during the plenary business meeting conducted the last day of the New Orleans symposium. One of the most important issues was the approval of the overhauled Constitution and Bylaws of the Society, which was approved by the membership promptly. Other issues discussed were the travel committee report, the Treasurer's report and the Resolutions submitted, among others.

Board Meeting. The Board meeting held during the New Orleans symposium was fruitful and lasted until midnight of the first day of the symposium. The Board received and discussed reports from the Nominations Committee, Student Committee, Travel Committee, Students Awards Committee, Awards Committee, as well as reports from the Treasurer and the Bylaws and Constitution Committee. The issue of Annual vs. Biennial symposia was discussed only briefly and was left for the annual Board retreat meeting in August to allow Board members to gather more information and be better prepared to discuss this issue in depth.

Social Events. Welcome Social, Live and Silent Auctions, Farewell party, Student Awards were some of the social events held during the symposium. Among those events, a Speed Chatting with Experts event was held the night of the first day of the meeting, with the following lineup: Nancy Mettee - Turtle Rehab and First aid in the Field; Roldán Valverde- Arribadas and Turtles of the Gulf of Mexico; Brad Nahill - Volunteering and Tourism; David Godfrey - NGO funding and Non-profit management issues; Anne

& Peter Meylan - In-water Turtle Research; T. Todd Jones - Physiological Ecology; Erin Seney - Consulting, fieldwork, and policy; Pamela Plotkin - Conservation Science; Robert Hardy - Satellite Tracking; Michael Jensen - Genetics; Jack Frazier - 'Hall of Fame.' Of all social events, the Welcome Social held the night before the first day of the symposium was probably the most popular. This included a surprise Mardi Gras-style parade with a second line Jazz band guiding symposium attendees over the streets of New Orleans.

Travel grants. A total of 119 registrants received a travel grant to the New Orleans symposium (12 from Africa, 13 from US/Canada, 5 from English-speaking Caribbean, 4 from South Asia, 8 from Asia Pacific, 16 from South America, 6 from Europe, 23 from Mexico-Central America, and 32 others). This level of travel grant awards represents about 15% of the total registered participants. Travel grants took the form of room grants, which was highly advantageous for the awardees and for the Society. Room awards contributed a total of about 561 room nights, which made a significant contribution to our hotel's room block. Because rooms were awarded to a group and not to individuals the organizing committee was able to serve more people in a more effective way. Also, this strategy saved our Treasurer the time and effort to write checks and keep track of the awards, and gave the Society better control over how the grants are assigned and used, thus increasing efficiency and effectiveness of the awards.

Awards. During the symposium, a series of awards were made to prominent members of our sea turtle society. Anne Meylan, Frank Paladino and Jim Richardson were awarded the Lifetime Achievement Award for their extensive and significant contributions to the promotion of sea turtle biology and conservation. Congratulations to the awardees. Resolutions. An important component of the every symposium is the issuing of Resolutions, documents that allow the Society at large to pronounce itself with regard to issues pertaining to sea turtle conservation around the world. Two highly important resolutions were passed during the New Orleans symposium: The first resolution was relayed to the Australian Minister of the Environment, the Hon Greg Hunt, regarding the protection of sea turtle populations in the Great Barrier Reef region. The second resolution was sent to the President of Mexico, Enrique Peña Nieto, and pertained to the protection of loggerheads in Baja California, Mexico. Receipt of the letters was acknowledged and press notices regarding these letters appeared in Australian and Mexican newspapers.

Finances. Society's finances were a major concern going into the New Orleans symposium. Indeed, during the plenary business meeting we learnt that the Society's

finances were in worse shape than originally thought. Fortunately, thoughtful planning by the Society's Board and effective execution by the organizing committee resulted in a successful symposium, both scientifically and financially. After paying for all our obligations incurred prior and during the symposium, our revenues were sufficient to overcome past debts and leave us in a solvent situation. Hopefully, the model developed for the New Orleans symposium will be adopted for future symposia.

The financial success achieved in New Orleans was due to a series of measures taken. For instance, historical but expensive items, such as simultaneous translation and exceedingly high travel grant levels were significantly reduced or eliminated. Also, the New Orleans symposium was held as a joint meeting with the Southeast Regional Sea Turtle Network, which eliminated any competition for resources. Additionally, important sponsorship was secured from major donors, such as Shell and the National Federation of Wildlife and Fisheries, as well as the Marine Turtle Conservation Act of the USFWS, and the National Atmospheric Aeronautic Administration. Also importantly, organizers were able to secure sponsorship from the Virginia Institute of Marine Science to cover all meeting expenses for one entire day of the Symposium (CFR session), which significantly reduced our costs. Significantly, the organizing committee was able to partner with Southeastern Louisiana University, which allowed us to receive tax-exempt status in Louisiana, among other measures. Finally, significant assistance from The Zenith Group, our contracted meeting provider, made it possible for us to realize significant savings on hotel expenses.

Memorial Tribute. During the closing ceremonies of the symposium, a simple memorial tribute was conducted to honor the lives of three colleagues who lost their lives since the last symposium. They are Jairo Mora (Costa Rica), Creusa "Tetha" Hitipieuw (Malaysia), George Petro (Vanuatu). Heartfelt words were pronounced by Didiher Chacón, Peter Dutton and Ken MacKay, respectively.

Acknowledgments. Organising the New Orleans symposium took a significant number of hours and effort. The successful organisation strongly benefits from the

selfless work of a large number of volunteers. To them, my personal thanks. However, among all the people that contributed one way or another to the success of the symposium, I would like to recognise the following five individuals: the symposium Registrar Rick Herren, who handled all registrations issues with utmost efficiency and dedication; program officers Elena Finkbeiner and Ingrid Yañez, who tirelessly and selflessly helped me secure adequate funding for the symposium; and Program Chairs Kelly Stewart and Michael Jensen, who did a professional and superb job ensuring the soundness of the program and the entire abstract selection process. To the five of them, my deep and personal thanks.

Funding. Generous funding by many entities made it possible for the New Orleans symposium to be a success. The organizing committee deeply thanks the donors below for their generosity. At the Platinum level (\$25,000 and above): National Fish and Wildlife Foundation, as well as an anonymous donor. At the Gold level (\$10,000 - \$24,999): Shell, Wildlife without Borders of the USFWS, NOAA, Shared Heart Foundation, Texas Sea Grant and Southeastern Louisiana University. At the Silver level (\$1,000 - \$9,999): Virginia Sea Grant, World Wildlife Fund, Virginia Institute of Marine Science, Entergy, Western Pacific Regional Fishery Management Council, The Ocean Foundation, International Seafood Sustainability Foundation, Disney's Animal Science and the Environment, Southeastern Regional Sea Turtle Network, Loggerhead Marinelife Center, Wildlife Computers, Environmental Business Specialists, Sea Turtle Conservancy, Florida Sea Turtle License Plate, Sirtrack, Ocean Conservancy, WIDECASST, Audubon Nature Institute, Abita Brewery, LivBlue, Virginia Institute of Marine Science, Vaughan W. Brown Charitable Trust, Anonymous and the National Park Service. At the Bronze level (\$500 - \$999): CLS America, Ecological Associates Inc., Desert Star Systems, New England Biolabs, All Creatures Wildlife Solutions and Eastman Environmental. At the Inconel level (\$10 - \$499): Georgia Sea Turtle Center, PersonalLoans.com, Marinelife Alliance, Coastal Wildlife Club, Inc., Janet Hochella, Kiki Jenkins, Mission: Clean Beaches, Sandy Sly, Usagi Family, Debbie Sobel, ProFaunaBaja - ASUPMATOMA, Marydele Donnelly and Wilma Katz.

RESOURCE OF INTEREST

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INDIAN OCEAN-SOUTHEAST ASIA MARINE TURTLE MEMORANDUM of UNDERSTANDING GENETICS DIRECTORY (<http://www.ioseaturtles.org/geneticsdb.php>)

The genetics directory was established in May 2008, and provides basic information about sea turtle genetics studies around the Indian Ocean and Southeast Asia. Viewers can search the directory by Country, Project Name, Date, and keywords; search results show the project title, investigator contact information, a brief summary/ results to date, and future planned activities. Currently

under-utilised, the genetics directory has the potential to increase collaboration among researchers in the region if information about ongoing genetics research is submitted and updated by investigators. Those able to collect samples, but without the capacity to conduct molecular bench work, could then collaborate with researchers at established genetics labs. Links to resources such as collection protocols, CITES Information, GENBank, and mtDNA sequences at SWFSC and ACCSTR would also ensure facilitate the co-ordinated submission and designation of sequence numbers, and provide assistance to regional biologists entering this field of research.

PHOTO OF INTEREST



First Satellite Tagged Turtle in Sumatra

Green sea turtle '*Maia*' is the first turtle from Sumatra to carry a satellite tag. Released on 14th June 2010, Maia was followed from Pulau Banyak, Aceh, Sumatra, Indonesia ; her track can be seen at <http://www.seaturtle.org/tracking/index.shtml?keyword=Maia>. As reviewed by FitzSimmons and Limpus in this issue of IOTN, satellite telemetry complements molecular genetic studies to establish the habitat range of genetic stocks.

Photo Credit: David Robinson

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Two authors to be separated by ‘&’ symbol, e.g., as Rai & Sahu, 2001

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Silas, E.G., M. Rajagopalan, A.B. Fernando & S.S. Dan. 1985. Marine turtle conservation and management: A survey of the situation in Orissa 1981/82 & 1982/83. *Marine Fisheries Information Service Technical & Extension Service* 50: 13-23.

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