

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

ANDREA D. PHILLOTT# AND RUVANI N.N. GAMAGE

Biological Sciences, Asian University for Women, Chittagong, Bangladesh

#andrea.phillott@auw.edu.bd

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](http://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.

**Table 1. Known Haplotypes of Nesting Green Sea Turtles (*Chelonia mydas*) in the Indian Ocean.** JENSEN ET AL. (IN PRESS) WILL STANDARDISE ALL OF THE HAPLOTYPE NAMES AND SHOW THE RELATIONSHIP AMONG PAST NAMES. NO PUBLISHED HAPLOTYPES FOR THE EAST COAST OF AFRICA, OR CENTRAL INDIAN OCEAN (INCLUDING SRI LANKA, MALDIVES AND CHAGOS) COULD BE FOUND.

Country, Location and Reference	n	Original Haplotype (Current Sequence Designation)
Arabian Peninsula <sup>1</sup>	44	Aa
Australia, Ashmore Reef <sup>2,3</sup>	20	A1 (GMP76)
Australia, Bountiful Is <sup>2</sup>	20	A2 (GMP47)
Australia, Bountiful Is <sup>3</sup>	49	A3 (GMP20)
Australia, Groote Eylandt <sup>2</sup>	23	B4 (GMP81)
Australia, Groote Eylandt <sup>3</sup>	23	C1 (GMP83)
Australia, Lacepedes Islands <sup>2,3</sup>	30	C2 (GMP86)
Australia, Northwest Cape <sup>2</sup>	15	C3 (GMP49)
Australia, Northwest Cape <sup>3</sup>	15	C4 (GMP87)
Australia, Port Bradshaw <sup>2</sup>	43	C5 (GMP89)
Australia, Port Bradshaw <sup>3</sup>	60	C6 (GMP90)
Australia, Scott Reef <sup>2,3</sup>	19	C7 (GMP91)
Chagos Islands, Chagos Bank <sup>1</sup>	2	C8 (GMP93)
Chagos Islands, Danger & Nelson Islands <sup>4</sup>	2	C9 (GMP94)
Chagos Islands, Salomon Atoll <sup>1,4</sup>	1	C10 (GMP95)
Comoros, Moheli <sup>5</sup>	10	D2 (GMP57)
Comoros, Moheli <sup>6</sup>	34	D3 (GMP71)
French Esparses Islands, Tromelin Island <sup>6</sup>	44	D4 (GMP75)
Kuwait, Qaruh Is & Umm Al-Maradim Is <sup>7</sup>	95	E1 (GMP72)
		TBA

Country, Location and Reference	n	Aa	A1 (GMP76)	A2 (GMP47)	A3 (GMP20)	B4 (GMP81)	C1 (GMP83)	C2 (GMP86)	C3 (GMP49)	C4 (GMP87)	C8 (GMP89)	C9 (GMP90)	C14 (GMP91)	C40 (GMP91)	CMKWI	CMKW2	CMKW3	CMKW4	CMKW5	CMOM1 (GMP73)	CMOM2 (GMP72)	CMOM3 (GMP62)	CMOM4 (GMP71)	D2 (GMP57)	G1033	H1 (GMP62)	H2 (GMP63)	H3 (GMP64)	IND1 (GMP49)	IND2 (GMP57)	IND3 (GMP55)	L1 (GMP71)	L2 (GMP72)	L3	May23	NRC	TBA
Madagascar, Nosy Iranja <sup>a</sup>	13																																				
Mozambique Channel, Europa Island <sup>b</sup>	33																																				
Mozambique Channel, Juan de Nova Island <sup>c</sup>	20																																				
Mozambique Channel, Mayotte <sup>c</sup>	41																																				
Mozambique Channel, Gloriosae <sup>c</sup>	39																																				
Oman <sup>d</sup>	?																																				
Reunion <sup>e</sup>	55	X																																			
Seychelles, Aldabra <sup>f</sup>	26	X																																			
Seychelles, Aldabra <sup>g</sup>	26	X																																			
Seychelles, Cosmoledo <sup>g</sup>	33	X																																			
Seychelles, Cosmoledo <sup>g</sup>	31	X																																			
Seychelles, Farquhar <sup>g</sup>	9	X																																			
Seychelles, Farquhar <sup>g</sup>	7	X																																			
Seychelles, Granitic <sup>g</sup>	2																																				

\*See green turtle mtDNA sequences maintained by SWFSC (2014). <sup>b</sup>Broderick *et al.* (1998). Unknown length segment from mtDNA control region. Primers TCR5, TCR6GC; <sup>c</sup>Mortitz *et al.* (2002). 384bp sequence of mtDNA control region. Primers not named; <sup>d</sup>Dethmers *et al.* (2006). 384bp sequence from mtDNA control region. Primers TCR5, TCR6GC; <sup>e</sup>Mortimer & Broderick (1999). Segment of mtDNA control region. Primers LTCM1, HDCM1, LTCM1.1-HDCM1.1; <sup>f</sup>Bourjea *et al.* (2007). 396bp sequence from mtDNA control region. Primers TCR-5, TCR-6; <sup>g</sup>Al-Mohanna *et al.* (2013). ~4000bp sequence from mtDNA control region. Primers HDCM-1, TCR-5. <sup>h</sup>Alansari (Unpubl.). Unknown length segment from mtochondrial 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)
Brunei, Brunei Beach <sup>1</sup>	4	x x x x
Indonesia, Derawan Island <sup>1</sup>	22	x x x x
Indonesia, Enu <sup>1,3</sup>	28	x x
Indonesia, Enu <sup>2</sup>	28	x x
Indonesia, Pangumbahan <sup>1</sup>	23	x x x x
Indonesia, Pangumbahan <sup>2,3</sup>	23	x x x x
Indonesia, Parjang Is <sup>1</sup>	16	x x x x x
Indonesia, Sangalaki Is <sup>1</sup>	38	x x x x x x
Indonesia, Sangalaki <sup>2</sup>	29	x x x x x x
Indonesia, Sangalaki Is <sup>3</sup>	29	x x x x x x
Malaysia, Mal. Turtle Islands <sup>3</sup>	28	x x x x
Malaysia, Pahang <sup>1</sup>	12	x x x x
Malaysia, Paka <sup>1,3</sup>	15	x x x x
Malaysia, Palau Redang <sup>2</sup>	27	x x x x x
Malaysia, Perak <sup>1</sup>	15	x x x x x
Malaysia, Redang Is <sup>1</sup>	31	x x x x x x
Malaysia, Redang Is <sup>2</sup>	12	x x x x x x
Malaysia, Sabah Turtle Islands <sup>1</sup>	58	x x x x x x
Malaysia, Sarawak <sup>1</sup>	62	x x x x x x
Malaysia, Sarawak Turtle Islands <sup>2,3</sup>	22	x x x x x x

Country, Location and Reference	n	A1 (Cmp76)	A2 (Cmp47)	A3 (Cmp20)	B1 (Cmp44)	B3 (Cmp80)	B4 (Cmp81)	B5 (Cmp82)	B6	C3 (Cmp49)	C4 (Cmp87)	C5 (Cmp40)	C7 (Cmp88)	C14 (Cmp91)	Caru (Cmp91)	D2 (Cmp57)	G2	G3	G4	G5	G7	G11	G12	G13	G14	G15	J14212	M1	M2	M3	P1	P2	P3	T1	T2	T3				
Malaysia, Sipadan Is <sup>1</sup>	40								x	x	x	x	x	x	x																									
Malaysia, Sipidan <sup>2</sup>	30								x	x	x	x	x	x	x																									
Malaysia, Sipidan Is <sup>3</sup>	30								x	x	x	x	x	x	x																									
Malaysia & Philippines, Turtle Islands <sup>2</sup>	67								x	x	x	x	x	x	x																									
Myanmar, Coco Is <sup>1</sup>	30	x							x	x	x	x	x	x	x																									
Myanmar, Tameahla Is <sup>1</sup>	30								x	x	x	x	x	x	x																									
Philippines, APO Reef NP <sup>1</sup>	4								x																															
Philippines, Panikian Is <sup>1</sup>	9	x																																						
Philippines, Phil. Turtle Islands <sup>3</sup>	62								x	x	x	x	x	x	x																									
Thailand, Huyong Is <sup>1</sup>	19	x							x	x	x	x	x	x	x																									
Thailand, Huyong Is <sup>4</sup>	19								x	x	x	x	x	x	x																									
Thailand, Kham Is <sup>1</sup>	30	x	x	x	x	x	x	x	x	x	x	x	x	x	x																									
Thailand, Kham Is <sup>4</sup>	30	x	x	x	x	x	x	x	x	x	x	x	x	x	x																									
Vietnam, Con Dao Is <sup>1</sup>	42								x	x	x	x	x	x	x																									
Vietnam, Minh Chau <sup>1</sup>	11								x																															

\*See green turtle mtDNA sequences maintained by SWFSC (2014). <sup>1</sup>Arshad & Kadir (2008). 389bp sequence of mtDNA control region. Primers TCR5, TCR1; <sup>2</sup>Moritz *et al.* (2002). 384bp sequence of mtDNA control region. Primers not described; <sup>3</sup>Dethmers *et al.* (2006). 384bp sequence from mtDNA control region. Primers TCR5, TCR1GC; <sup>4</sup>Kittiwattanawong *et al.* (2003). 438bp sequence from mtDNA control region. Primers Green1555F, Green1557F, Green1630R, 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.

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

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

<b>Country, Location and Reference</b>	<b>n</b>	<b>Haplotype</b>															
		<b>E1</b>	<b>E2</b>	<b>E3</b>	<b>E4</b>	<b>E5</b>	<b>E6</b>	<b>E7</b>	<b>E8</b>	<b>E9</b>	<b>E10</b>	<b>E11</b>	<b>E12</b>	<b>E13</b>	<b>E14</b>	<b>E15</b>	<b>14</b>
Brunei, Brunei Beach <sup>1</sup>	4				X					X	X						
Indonesia, Kimar Belitung <sup>1</sup>	9									X	X						
Indonesia, Seribu Islands <sup>2</sup>	9																X
Malaysia, Melaka <sup>1</sup>	29																X
Malaysia, Sabah Turtle Islands <sup>1</sup>	20		X							X	X						X X
Myanmar, Coco Island <sup>1</sup>	4	X								X							X
Philippines, APO Reef NP <sup>1</sup>	4				X	X	X										
Philippines, Bataan <sup>1</sup>	1												X				
Philippines, Davao Gulf <sup>1*</sup>	2										X						X
Philippines, Misamis Oriental <sup>1</sup>	1				X												
Thailand, Khram Island <sup>1</sup>	14									X	X	X					

<sup>1</sup>Arshaad & Kadir (2008). 740bp sequence of mtDNA control region. Primers LTE19, H950; <sup>2</sup>Okayama *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 EIP-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												
		PG7.1	PG7.2	PG7.3	PG7.4	PG7.5	TBA	Iran7	Iran6	Iran5	Iran4	Iran3	Iran2	Iran1
Arabian Peninsula <sup>1,2</sup>	14						X							
Australia, Western Australia <sup>2</sup>	31						X	X						
Chagos Islands, Diego Garcia <sup>1,2</sup>	3						X							
Chagos Islands, Peros Banhos <sup>1,2</sup>	5						X	X	X					
Chagos Islands, Salomon Atoll <sup>1,2</sup>	1						X							
Iran, Kish and Qeshm Islands <sup>3</sup>	30													
Iran, Kish and Qeshm Islands <sup>4*</sup>	45													
Iran, Hendourati, Nakhlou, Ommolkaram & Sheedivider <sup>5</sup>	-													
Iran, Kish, Nakhlou & Qeshm Islands <sup>6,7</sup>	69	X	X	X	X	X								
Seychelles, Aldabra <sup>1</sup>	2						X							
Seychelles, Amirantes <sup>1</sup>	24						X	X	X					X
Seychelles, Cosmoledo <sup>1</sup>	2						X							
Seychelles, Farquhar <sup>1</sup>	1						X							
Seychelles, Granitics <sup>1</sup>	32						X	X	X	X				X
Seychelles, Platte Island <sup>1</sup>	25						X	X	X					
Seychelles, Undescribed location <sup>2</sup>	73						X	X	X	X	X			X

<sup>1</sup>Broderick *et al.* (1998). Segment of mtDNA control region. Primers TCR5, TCR1GC; <sup>2</sup>Mortimer & Broderick (1999). Segment of mtDNA control region. Primers TCR5, TCR1GC; <sup>3</sup>Tabib *et al.* (2011). 890bp sequence from mtDNA control region. Primers H950, LCM15382; <sup>4</sup>Tabib *et al.* (2014). 890bp sequence from mtDNA control region. Primers H950, LCM15382; <sup>5</sup>Mobaraki *et al.* (2014). Sample size unknown; six additional haplotypes not named in conference abstract; <sup>6</sup>Nezhad *et al.* (2012) and <sup>7</sup>Nezhad *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 EIIIP-33 and EIIATL from Indo-Pacific turtles.

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

Country, Location and Reference	Haplotype				
	n	D	F	CC-A11.6	CC-A2.1
Oman, Masirah Island <sup>1,2</sup>	8		X	X	
South Africa, Tongaland <sup>1,2</sup>	15	X			X

<sup>1</sup>Bowen *et al.* (1994). Unknown fragment length from closed-circular mtDNA; <sup>2</sup>Shamblin *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	Published Haplotype (Shorter Sequence)							
	n	A	D	E	H	-	Dct.1*	Dct.4*
India, Great Nicobar Is <sup>1</sup>	114	X	X	X			X	
Indonesia, Papua, Jamursba-Medi <sup>2</sup>	31	X	X	X			X	
Indonesia, Papua, War Mon <sup>2</sup>	9						X	
Malaysia, Terengganu <sup>3</sup>	9	X	X	X	X			
Papua New Guinea <sup>2</sup>	18	X	X	X				X
South Africa, Tongaland <sup>3</sup>	8	X						
South Africa, Natal <sup>4</sup>	41						X	X

<sup>1</sup>Shanker *et al.* (2011). 350bp fragment of control region of mtDNA. Primers HDCM1, LDCM1, LTCM1, TCR1-TCR6; <sup>2</sup>Dutton *et al.* (2007). 496bp fragment of control region of mtDNA. Primers LTCM2, HDCM2; <sup>3</sup>Dutton *et al.* (1999). 496bp fragment of control region of mtDNA. Primers LCM15382, HDCM1; <sup>4</sup>Dutton *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	Haplotype											
	n	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](http://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**

<b>Haplotype</b>		
<b>Country, Location and Reference</b>	<b>n</b>	<b>C (CceA11)</b>
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.

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

<sup>1</sup>Arshaad *et al.* (2013). Undescribed length sequence from mtDNA control region. Primers H950, LTEi9; <sup>2</sup>Kuen & Joseph (2013). Segment of mtDNA not described. Primers TC5, TC6; <sup>3</sup>Joseph & Kuen (2012), <sup>4</sup>Joseph & Kuen (2014). 380bp segment of mtDNA control region. Primers not described;

<sup>5</sup>Kuen & Joseph (2011) and <sup>6</sup>Kuen & 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	n	Aa	Ac	A1	A2	A3	A4	B1	B2	B3	B6	B7	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28	C29	C30	C31	C32	C33	C34	C35	C36	C37	C38	C39	C40	C41	C42	C43	C44	C45	C46	C47	C48	C49	C50	C51	C52	C53	C54	C55	C56	C57	C58	C59	C60	C61	C62	C63	C64	C65	C66	C67	C68	C69	C70	C71	C72	C73	C74	C75	C76	C77	C78	C79	C80	C81	C82	C83	C84	C85	C86	C87	C88	C89	C90	C91	C92	C93	C94	C95	C96	C97	C98	C99	C100	C101	C102	C103	C104	C105	C106	C107	C108	C109	C110	C111	C112	C113	C114	C115	C116	C117	C118	C119	C120	C121	C122	C123	C124	C125	C126	C127	C128	C129	C130	C131	C132	C133	C134	C135	C136	C137	C138	C139	C140	C141	C142	C143	C144	C145	C146	C147	C148	C149	C150	C151	C152	C153	C154	C155	C156	C157	C158	C159	C160	C161	C162	C163	C164	C165	C166	C167	C168	C169	C170	C171	C172	C173	C174	C175	C176	C177	C178	C179	C180	C181	C182	C183	C184	C185	C186	C187	C188	C189	C190	C191	C192	C193	C194	C195	C196	C197	C198	C199	C200	C201	C202	C203	C204	C205	C206	C207	C208	C209	C210	C211	C212	C213	C214	C215	C216	C217	C218	C219	C220	C221	C222	C223	C224	C225	C226	C227	C228	C229	C230	C231	C232	C233	C234	C235	C236	C237	C238	C239	C240	C241	C242	C243	C244	C245	C246	C247	C248	C249	C250	C251	C252	C253	C254	C255	C256	C257	C258	C259	C260	C261	C262	C263	C264	C265	C266	C267	C268	C269	C270	C271	C272	C273	C274	C275	C276	C277	C278	C279	C280	C281	C282	C283	C284	C285	C286	C287	C288	C289	C290	C291	C292	C293	C294	C295	C296	C297	C298	C299	C300	C301	C302	C303	C304	C305	C306	C307	C308	C309	C310	C311	C312	C313	C314	C315	C316	C317	C318	C319	C320	C321	C322	C323	C324	C325	C326	C327	C328	C329	C330	C331	C332	C333	C334	C335	C336	C337	C338	C339	C340	C341	C342	C343	C344	C345	C346	C347	C348	C349	C350	C351	C352	C353	C354	C355	C356	C357	C358	C359	C360	C361	C362	C363	C364	C365	C366	C367	C368	C369	C370	C371	C372	C373	C374	C375	C376	C377	C378	C379	C380	C381	C382	C383	C384	C385	C386	C387	C388	C389	C390	C391	C392	C393	C394	C395	C396	C397	C398	C399	C400	C401	C402	C403	C404	C405	C406	C407	C408	C409	C410	C411	C412	C413	C414	C415	C416	C417	C418	C419	C420	C421	C422	C423	C424	C425	C426	C427	C428	C429	C430	C431	C432	C433	C434	C435	C436	C437	C438	C439	C440	C441	C442	C443	C444	C445	C446	C447	C448	C449	C450	C451	C452	C453	C454	C455	C456	C457	C458	C459	C460	C461	C462	C463	C464	C465	C466	C467	C468	C469	C470	C471	C472	C473	C474	C475	C476	C477	C478	C479	C480	C481	C482	C483	C484	C485	C486	C487	C488	C489	C490	C491	C492	C493	C494	C495	C496	C497	C498	C499	C500	C501	C502	C503	C504	C505	C506	C507	C508	C509	C510	C511	C512	C513	C514	C515	C516	C517	C518	C519	C520	C521	C522	C523	C524	C525	C526	C527	C528	C529	C530	C531	C532	C533	C534	C535	C536	C537	C538	C539	C540	C541	C542	C543	C544	C545	C546	C547	C548	C549	C550	C551	C552	C553	C554	C555	C556	C557	C558	C559	C560	C561	C562	C563	C564	C565	C566	C567	C568	C569	C570	C571	C572	C573	C574	C575	C576	C577	C578	C579	C580	C581	C582	C583	C584	C585	C586	C587	C588	C589	C590	C591	C592	C593	C594	C595	C596	C597	C598	C599	C600	C601	C602	C603	C604	C605	C606	C607	C608	C609	C610	C611	C612	C613	C614	C615	C616	C617	C618	C619	C620	C621	C622	C623	C624	C625	C626	C627	C628	C629	C630	C631	C632	C633	C634	C635	C636	C637	C638	C639	C640	C641	C642	C643	C644	C645	C646	C647	C648	C649	C650	C651	C652	C653	C654	C655	C656	C657	C658	C659	C660	C661	C662	C663	C664	C665	C666	C667	C668	C669	C670	C671	C672	C673	C674	C675	C676	C677	C678	C679	C680	C681	C682	C683	C684	C685	C686	C687	C688	C689	C690	C691	C692	C693	C694	C695	C696	C697	C698	C699	C700	C701	C702	C703	C704	C705	C706	C707	C708	C709	C710	C711	C712	C713	C714	C715	C716	C717	C718	C719	C720	C721	C722	C723	C724	C725	C726	C727	C728	C729	C730	C731	C732	C733	C734	C735	C736	C737	C738	C739	C740	C741	C742	C743	C744	C745	C746	C747	C748	C749	C750	C751	C752	C753	C754	C755	C756	C757	C758	C759	C760	C761	C762	C763	C764	C765	C766	C767	C768	C769	C770	C771	C772	C773	C774	C775	C776	C777	C778	C779	C780	C781	C782	C783	C784	C785	C786	C787	C788	C789	C790	C791	C792	C793	C794	C795	C796	C797	C798	C799	C800	C801	C802	C803	C804	C805	C806	C807	C808	C809	C810	C811	C812	C813	C814	C815	C816	C817	C818	C819	C820	C821	C822	C823	C824	C825	C826	C827	C828	C829	C830	C831	C832	C833	C834	C835	C836	C837	C838	C839	C840	C841	C842	C843	C844	C845	C846	C847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933

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

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

<sup>1</sup>Broderick *et al.* (1998). Segment of mtDNA control region. Primers TCR5, TCR1GC; <sup>2</sup>Mortimer & Broderick (1999). Segment of mtDNA control region. Primers TCR5, TCR1GC; <sup>3</sup>Okayama *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.

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

<sup>1</sup>Kuen & Joesph (2013). Primers TC5 and TC6; <sup>2</sup>Okayama *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 <sup>1</sup>	<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 <sup>2</sup>	<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 <sup>3</sup>	<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 <sup>4</sup>	<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 <sup>5,6</sup>	<i>Eretmochelys imbricata</i>	69	4 haplotypes	Significant genetic variation among turtles nesting at these islands was not detected P>0.05.

<sup>1</sup>Mostafavi *et al.* (2011); <sup>2</sup>Tabib *et al.* (2011); <sup>3</sup>Tabib *et al.* (2014); <sup>4</sup>Zolgharnein *et al.* (2011); <sup>5</sup>Nezhad *et al.* (2012); <sup>6</sup>Nezhad *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 # Examined	Total # Females	Total # Clutches Examined	# Single Clutches	# Successive Clutches	# Hatchlings Examined from Each Clutch	Results
•Single paternity (90.7% of females) more common than multiple paternity (9.3% of females).								
Seychelles, Cousine Island <sup>1</sup>	<i>Eretmochelys imbricata</i>	43	51	42	from 7 females •2 clutches from 5 females •3 clutches from 1 females •4 clutches	3-20	•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	
•Single paternity (53% of females) more common than multiple paternity (47% of females).								
Sri Lanka, Kosgoda <sup>2</sup>	<i>Chelonia mydas</i>	19	24	17	from 1 female •3 clutches from 1 females •4 clutches	10	•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.	

<sup>1</sup>Phillips *et al.* (2013), 33 variable microsatellite loci examined using two leatherback primers (D1 and D110) and four adapted hawksbill primers (Eim11, Eim38, Eim41, HKB3); <sup>2</sup>Ekanayake *et al.* (2013). 1 microsatellite loci using four green turtle primers (Cm3, Cm58, Cm72, Cm84) and two loggerhead turtle primers (Cc7, Cc117).

**Literature cited:**

- Abreu-Grobois A, J. Horrocks, A. Formia, P. Dutton, R. LeRoux, X. Velez-Zuazo, L. Soares & P. Meylan. 2006. New mtDNA d-loop primers which work for a variety of marine turtle species may increase the resolution of mixed stock analyses. In: Frick M, Panagopoulou A, Rees AF, Williams K (eds). Book of abstracts from the 26th annual symposium on sea turtle biology and conservation. International Sea Turtle Society, Athens. Pp. 179.
- ACCSTR. 2014. mtDNA Sequences. Accessed at <http://accstr.ufl.edu/resources/mtdna-sequences/> on 26th July 2014.
- Al-Mohanna S.Y., A.S.Y. Al-Zaidan & P. George. 2013. Green turtles (*Chelonia mydas*) of the north-western Arabian Gulf, Kuwait: The need for conservation. *Aquatic Conservation: Marine and Freshwater Ecosystems* 24: 166-178.
- Al-Mohanna S.Y. & P. George. 2010. Assessment of the origin of a loggerhead turtle, *Caretta caretta*, found in Kuwait waters, using mitochondrial DNA. *Zoology in the Middle East* 49: 39-44.
- Alansari A.S. Unpubl. Genetic Diversity of Green Turtles in Oman. [http://lifesciencedb.jp/ddbj/ff\\_list.cgi?max\\_num=all&project\\_id=483585&type=plain](http://lifesciencedb.jp/ddbj/ff_list.cgi?max_num=all&project_id=483585&type=plain). Accessed on 6th August 2014.
- Arshaad W.M. & S.A.S.A. Kadir. 2008. Regional analysis on stock identification of green and hawksbill turtles in the Southeast Asian region. The Third Technical Consultation Meeting Research for Stock Enhancement of Sea Turtles (Japanese Trust Fund IV Program), 15-17 October 2008.
- Arshaad W.M., N. Azliana, S.A.S.A. Kadir, & M. Katoh. 2013. Identification of natal origin sea turtles at Brunei Bay/Lawas foraging habitats. Regional Meeting on Conservation and Management of Sea Turtle Foraging Habitats in Southeast Asian Waters, 22-24 October 2013, AnCasa Hotel and Spa Kula Lumpur.
- Bourjea J., S. Lapegue, L. Gagnevin, D. Broderick, J.A. Mortimer, S. Ciccone, D. Roos, C. Taquet & H. Grizel. 2007. Phylogeography of the green turtle, *Chelonia mydas*, in the Southwest Indian Ocean. *Molecular Ecology* 11: 1-21.
- Bowen B.W., A.M. Clark, F.A. Abreu-Grobois, A. Chaves, H.A. Reichart & R.J. Ferl. 1998. Global phylogeography of the ridley sea turtles (*Lepidochelys* spp.) as inferred from mitochondrial DNA sequences. *Genetica* 101: 179-189.
- Broderick D., H. Johanson, S. Lavery, J.A. Mortimer, J. Miller & C. Moritz. 1998. Genetic Assessment of Western and Central Indian Ocean Marine Turtle Stocks: Final Report to the Department of Environment, Republic of Seychelles Government. Department of Zoology, University of Queensland, Australia.
- Dethmers K.E., D. Broderick, C. Moritz, N.N. FitzSimmons, C.J. Limpus, S. Lavery, S. Whiting, M. Guinea, R.I.T. Prince & R. Kennett. 2006. The genetic structure of Australasian green turtles (*Chelonia mydas*): exploring the geographical scale of genetic exchange. *Molecular Ecology* 15: 3931-3941.
- Dethmers K.E.M., M.P. Jensen, N.N. FitzSimmons, D. Broderick, C.J. Limpus & C. Moritz. 2010. Migration of green turtles from Australasian feeding grounds inferred from genetic analyses. *Marine and Freshwater Research* 61: 1376-1387.
- Dutton P.H., B.W. Bowen, D.W. Owens, A. Barragan & S.K. Davis. 1999. Global phylogeography of the leatherback turtle (*Dermochelys coriacea*). *Journal of Zoology, London* 248: 397-409.
- Dutton P.H., C. Hitipeuw, M. Zein, S.R. Benson, G. Petro, J. Pita, V. Rei, Al. Ambio & J. Bakarbessy. 2007. Status and genetic structure of nesting populations of leatherback turtles (*Dermochelys coriacea*) in the western Pacific. *Chelonian Conservation and Biology* 6: 47-53.
- Dutton P.H., S.E. Roden, K.R. Stewart, E. LaCasella, M. Tiwari, A. Formia, J.C. Thomé, S.R. Livingstone, S. Eckert, D. Chacon-Chaverri, P. Rivalan & P. Allman. 2013. Population stock structure of leatherback turtles (*Dermochelys coriacea*) in the Atlantic revealed using mtDNA and microsatellite markers. *Conservation Genetics* 14: 625-636.
- Ekanayake, E.M.L., T. Kapurusinghe, M.M. Saman, D.S. Rathnayakumara, P.Samaraweera, K.B. Ranawana & R.S. Rajakaruna. 2012. Genetic diversity of green turtle population nesting at Kosgoda turtle rookery, Sri Lanka. Proceedings of the Jaffna International Research Conference 176.
- Ekanayake, E.M.L., T. Kapurusinghe, M.M. Saman, D.S. Rathnayakumara, P.Samaraweera, K.B. Ranawana & R.S. Rajakaruna. 2013. Paternity of green turtle (*Chelonia mydas*) clutches laid at Kosgoda, Sri Lanka. *Herpetological Conservation and Biology* 8: 27-36.
- Elmeer K., P. McCormick & A. Almalki. 2011. Sequencing of

- cytochrome C oxidase subunit I gene of mitochondrial DNA from *Chelonia mydas* in Qatar. *Journal of American Science* 7: 783-788.
- FitzSimmons N.N. & C.J. Limpus. 2014. Marine turtle genetic stocks of the Indo-Pacific: Identifying boundaries and knowledge gaps. *Indian Ocean Turtle Newsletter* 20: 2-18.
- Formia A., B.J. Godley, J.-F. Dantaine & M.W. Bruford. 2006. Mitochondrial DNA diversity and phylogeography of endangered green turtle (*Chelonia mydas*) populations in Africa. *Conservation Genetics* 7: 353-369.
- Jensen M.P., N.N. FitzSimmons & P.H. Dutton. 2013a. Molecular genetics of sea turtles. In: *The Biology of Sea Turtles Volume III* (eds. Wyneken, J., K.J. Lohmann & J.A. Musick). CRC Press: Boca Raton LA, USA.
- Jensen M.P., C.J. Limpus, S.D. Whiting, M. Guinea., R.I.T. Prince, K.E.M. Dethmers, I.B.W. Adnyana, R. Kennett & N.N. FitzSimmons. 2013b. Defining olive ridley turtle *Lepidochelys olivacea* management units in Australia and assessing the potential impacts of mortality in ghost nets. *Endangered Species Research* 21: 241-253.
- Joseph J. 2013. Population genetics of green turtles (*Chelonia mydas*) in Malaysia based on mitochondrial DNA sequences. In: Proceedings of the Thirtieth Annual Symposium on Sea Turtle Biology and Conservation (comps. Blumenthal, J., A. Panagopoulou & A.F. Rees). NOAA Technical Memorandum NMFS-SEFSC-640: 177p.
- Joseph J. 2013. Population genetics of green turtles (*Chelonia mydas*) in Malaysia based on mitochondrial DNA sequences. In: Proceedings of the Thirtieth Annual Symposium on Sea Turtle Biology and Conservation (comps. Blumenthal, J., A. Panagopoulou & A.F. Rees). NOAA Technical Memorandum NMFS-SEFSC-640: 177p.
- Joseph J. 2014. Population genetics of green turtles (*Chelonia mydas*) in Malaysia based on mitochondrial DNA sequences. [http://iconferences.seaturtle.org/preview.shtml?event\\_id=17&abstract\\_id=3500](http://iconferences.seaturtle.org/preview.shtml?event_id=17&abstract_id=3500). Accessed on 16th June 2014.
- Joseph J. and C.Y. Kuen. 2012. Determination of natal origins of Juvenile green turtles foraging at Sipadann waters, Sabah, Malaysia. In: Proceedings of the Thirty-first Annual Symposium on Sea Turtle Biology and Conservation (comps. Jones, T.T. & B.P. Wallace). NOAA Technical Memorandum NOAA NMFS-SEFSC-631: 322p.
- Joseph J. and C.Y. Kuen. 2014. Determination of natal origins of juvenile green turtles foraging at Sipadann waters, Sabah, Malaysia. [http://iconferences.seaturtle.org/preview.shtml?event\\_id=18&abstract\\_id=3942](http://iconferences.seaturtle.org/preview.shtml?event_id=18&abstract_id=3942). Accessed on 16th June 2014.
- Kittiwattanawong K., S. Mananasup, M. Kinoshita & K. Nakayama. 2003. No genetic divergence between green turtle *Chelonia mydas* nesting populations from the Andaman Sea and the Gulf of Thailand. In: Proceedings of the 4th SEASTAR2000 Workshop: 15-19.
- Kuen C.Y. & J. Joseph. 2012. Genetics investigation of green turtle (*Chelonia mydas*) carcasses from the 2007 poaching incident in Sabah waters. In: Proceedings of the Thirty-first Annual Symposium on Sea Turtle Biology and Conservation (comps. Jones, T.T. & B.P. Wallace). NOAA Technical Memorandum NOAA NMFS-SEFSC-631: 322p.
- Kuen C.Y. & J. Joseph. 2014. Genetics investigation of green turtle (*Chelonia mydas*) carcasses from the 2007 poaching incident in Sabah waters. [http://iconferences.seaturtle.org/preview.shtml?event\\_id=18&abstract\\_id=3930](http://iconferences.seaturtle.org/preview.shtml?event_id=18&abstract_id=3930). Accessed on 16th June 2014.
- Kuen C.Y. & J. Joseph. 2011. Harvesting of sea turtles at feeding grounds in Malaysia: whose turtles' stock will be affected? In: Proceedings of Universiti Malaysia Terengganu 10th International Annual Symposium on Sustainability Science and Management (UMTAS) 2011, Kuala Terengganu, Malaysia 1: 511-515.
- Kuen C.Y. & J. Joseph. 2013. Using DNA to determine the origin of green and hawksbill turtles from the feeding grounds of Malaysian waters. In: Proceedings of the Thirtieth Annual Symposium on Sea Turtle Biology and Conservation (comps. Blumenthal, J., A. Panagopoulou & A.F. Rees). NOAA Technical Memorandum NMFS-SEFSC-640: 177p.
- Mobaraki A., N. FitzSimmons & M. Jensen. 2014. Reproduction and genetic study of hawksbill sea turtles in Iran. In: 34th Annual Symposium on Sea Turtle Biology and Conservation, New Orleans, Louisiana, USA, 10-17 April 2014. [http://iconferences.seaturtle.org/preview.shtml?event\\_id=17&abstract\\_id=3359](http://iconferences.seaturtle.org/preview.shtml?event_id=17&abstract_id=3359). Accessed on 16th June 2014.

- Moritz C., D. Broderick, K. Dethmers, N. FitzSimmons & C. Limpus. 2002. Population genetics of Southeast Asian and western Pacific green turtles, *Chelonia mydas*. Final Report to UNEP/CMS. <http://www.environment.gov.au/resource/population-genetics-Southeast-asian-and-western-pacific-green-turtles-chelonia-mydas>. Accessed on 6th June 2014.
- Mortimer J. A. & D. Broderick. 1999. Population genetic structure and developmental migrations of sea turtles in the Chagos Archipelago and adjacent regions inferred from mtDNA sequence variation. *Ecology of the Chagos Archipelago*, Linnean Society Occasional Publications.
- Mostafavi P.G., S. Shahnavaz, M. Noroozi, M.R. Fatemi, M.H. Shahhosseiny & A. Mahvari. 2011. Population genetic of *Eretmochelys imbricata* in two islands in the northern part of the Persian Gulf using microsatellite markers. *International Journal of Marine Science and Engineering* 1:69-73.
- Nezhad S.R.K., E. Modheji & H. Zolgharnein. 2012. Polymorphism analysis of mitochondrial DNA control region of hawksbill turtles (*Eretmochelys imbricata*) in the Persian Gulf. *Journal of Fisheries and Aquatic Sciences* 7: 339-345.
- Nezhad S.R.K., E. Modheji & H. Zolgharnein. 2013. Polymorphism analysis of mitochondrial DNA control region of hawksbill turtles (*Eretmochelys imbricata*) in the Persian Gulf. *Indian Journal of Geo Marine Sciences* 42: 300-303.
- Okayama T., R. Doaz-Fernandez, Y. Baba, M. Halim, O. Abe, N. Azeno & H. Koike. 1999. Genetic diversity of the hawksbill turtle in the Indo-Pacific and Caribbean Regions. *Chelonian Conservation and Biology* 3: 312-317.
- Pacioni C., S. Trocini, M. Heithaus, D. Burkholder, J. Thomson, K. Warren & M. Krützen. 2013. Preliminary assessment of the genetic profile of the Western Australian loggerhead turtle population using mitochondrial DNA. In: Proceedings of the First Western Australian Marine Turtle Symposium (comps. Prince, R.I.T., S. Whiting, H. Raudino, A. Vitenbergs & K. Pendoley). 28–29th August 2012. Science Division, Department of Parks and Wildlife, Perth, Western Australia. Pp. 65.
- Phillips K.P., T.H. Jorgensen, K.G. Jolliffe, S-M. Jolliffe, J. Henwood & D.S. Richardson. 2013. Reconstructing paternal genotypes to infer patterns of sperm storage and sexual selection in the hawksbill turtle. *Molecular Ecology* 22: 2301-2312.
- Pittard S.D. 2010. Genetic Population Structure of the Flatback Turtle (*Natator depressus*): A Nuclear and Mitochondrial DNA Analysis. Unpublished PhD Thesis submitted to University of Canberra. Pp. 116.
- Roberts M. A., T.S. Schwartz & S.A. Karl. 2004. Global population genetic structure and male-mediated gene flow in the green sea turtle (*Chelonia mydas*): Analysis of microsatellite loci. *Genetics Society of America* 111: 1857-1870.
- SFWSFC. 2014. Green turtle mtDNA sequences. <https://swfsc.noaa.gov/textblock.aspx?Division=PRD&ParentMenuId=212&id=11212>. Accessed on 26th July 2014.
- Shamblin B.M., A.B. Bolten, K.A. Bjorndal, P.H. Dutton, J.T. Nielsen, F.A. Abreu-Grobois, K.J. Reich, B.E. Witherington, D.A. Bagley, L.M. Ehrhart, A.D. Tucker, D.S. Addison, A. Arenas, C. Johnson, R.R. Carthy, M.M. Lamont, M.G. Dodd, M.S. Gaines, E. LaCasella & C.J. Nairn. 2012. Expanded mitochondrial control region sequences increase resolution of stock structure among North Atlantic loggerhead turtle rookeries. *Marine Ecology Progress Series* 469: 145-160.
- Shamblin B.M., A.B. Bolten, F.A. Abreu-Grobois, K.A. Bjorndal, L. Cardona, C. Carreras, M. Clusa, C. Monzón-Argüello, C.J. Nairn, J.T. Nielsen, R. Nel, L.S. Soares, K.R. Stewart, S.T. Vilaça, O. Türkozan, C. Yilmaz & P.H. Dutton. 2014. Geographic patterns of genetic variation in a broadly distributed marine vertebrate: New insights into loggerhead turtle stock structure from expanded mitochondrial DNA sequences. *PLoS ONE* 9: e85956.
- Shanker K., B.C. Choudhury & R.K. Aggarwal. 2011. Conservation genetics of Marine Turtles on the Mainland Coast of India and Offshore Islands. Final Project Report. Wildlife Institute of India, Dehradun and Centre for Cellular and Molecular Biology, Hyderabad.
- Shanker K., J. Ramadevi, B.C. Choudhury, L. Singh & R.K. Aggarwal. 2004. Phylogeography of olive ridley turtles (*Lepidochelys olivacea*) on the east coast of India: implications for conservation theory. *Molecular Ecology* 13: 1899-1909.
- Shattuck E.G. 2011. Geographic origins of illegally harvested hawksbill sea turtle products. Unpublished Master of Science

Thesis submitted to Michigan State University. <http://etd.lib.msu.edu/islandora/object/etd%3A346/dastream/OBJ/view>. Accessed on 6th June 2014.

Tabib M., H. Zolgharnein, M. Mohammadi, M.A. Salari-Aliabadi, A. Qasemi, S. Roshani, H. Rajabi-Maham & F. Frootan. 2011. mtDNA variation of the critically endangered hawksbill turtle (*Eretmochelys imbricata*) nesting on Iranian islands of the Persian Gulf. *Genetics and Molecular Research* 10: 1499-1503.

Tabib M., F. Frootan & M.A. Hesni. 2014. Genetic diversity and phylogeography of hawksbill turtle in the Persian Gulf. *Journal of Biodiversity and Environmental Sciences* 4: 51-57.

Vargas S.M., M.P. Jensen, A. Mobaraki, F.R Santos, D. Broderick, J. Mortimer, C. Limpus, S. Whiting & N.N. FitzSimmons. 2013. Phylogeography of the hawksbill turtle (*Eretmochelys imbricata*) from the Indo-Pacific Region. In: *Proceedings of the Thirtieth Annual Symposium on Sea Turtle Biology and Conservation* (Blumenthal, J., A. Panagopoulou & A.F. Rees). NOAA Technical Memorandum NMFS-SEFSC-640: 177p.

Zolgharnein H., M. Salari-Aliabadi, A.M. Forougmand & S. Roshani. 2011. Genetic population structure of hawksbill turtle (*Eretmochelys imbricata*) using microsatellite analysis. *Iranian Journal of Biotechnology* 9: 56-62.

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

LALITH EKANAYAKE

Chairman, Bio Conservation Society, Sri Lanka

[bccsl@yahoo.com](mailto:bcssl@yahoo.com)

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 Lankan. 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.