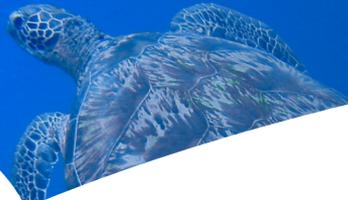


**NOAA
FISHERIES**



Novel approaches to determine population vital rates

Peter H. Dutton

Marine Turtle Genetics Program Leader,
Mammal & Turtle Research Division

NOAA Fisheries, Southwest Fisheries Science Center

Review of NOAA Fisheries' Science on Marine Mammals & Turtles
Southwest and Northwest Fisheries Science Centers

27-31 July 2015

La Jolla, CA

Unanswered questions?

- How many females laid all these nests?

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- How many males are there?

Unanswered questions?

- How many females laid all these nests?
- How many males are there?
- What is age of first reproduction?

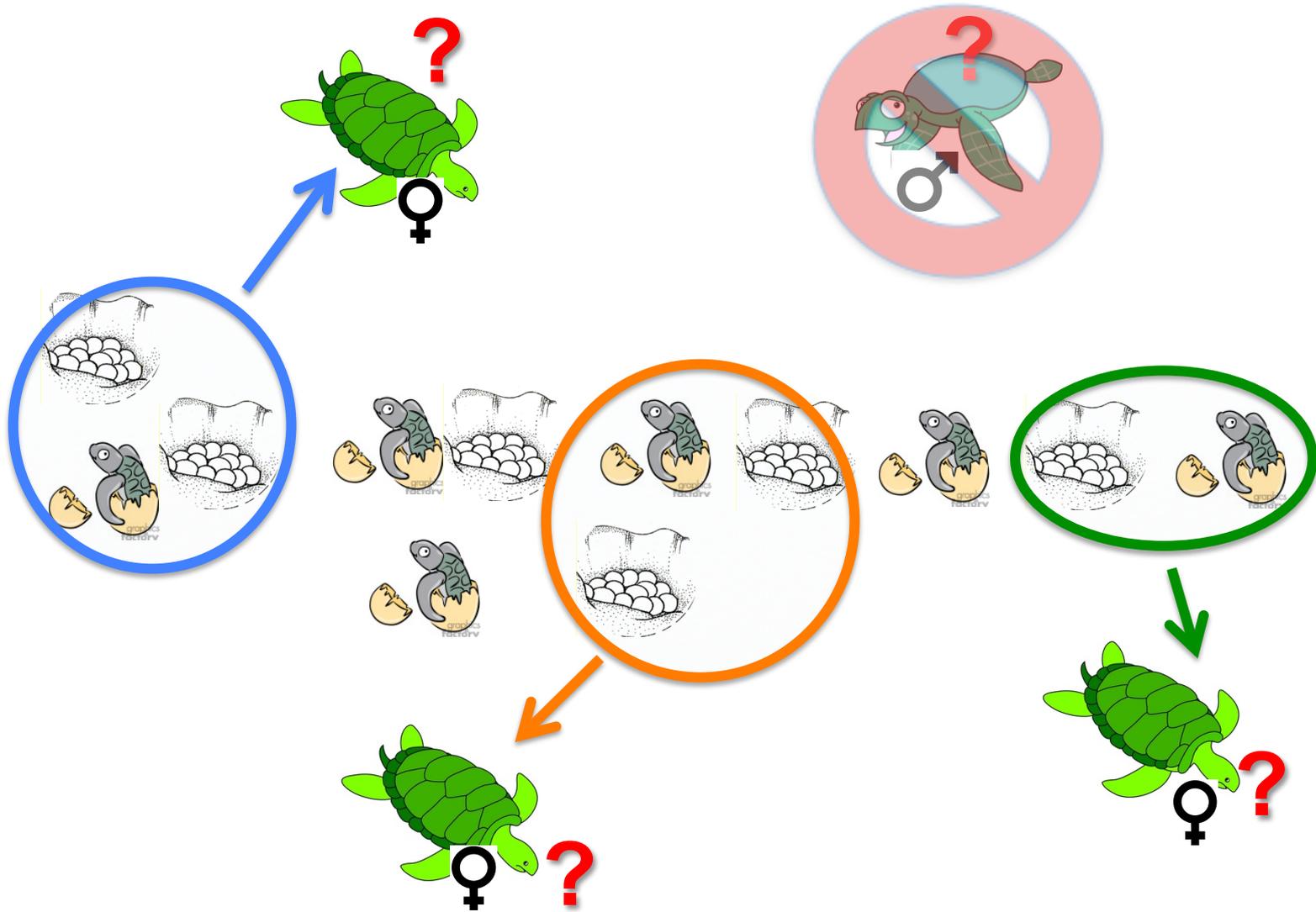
Unanswered questions?

- How many females laid all these nests?
- How many males are there?
- What is age of first reproduction?
- What is juvenile survivorship?

- Genetic “tag” (fingerprinting) as CMR tool
- Kinship analysis to infer unknown identities
e.g. of turtles that we can’t observe or tag

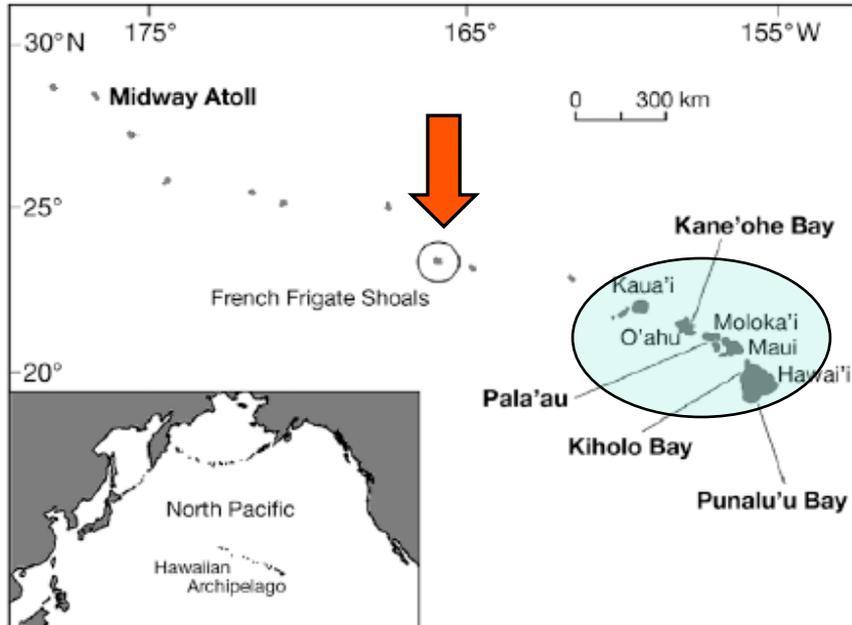
How many females laid all these nests?

Scenario 1: nesters NOT observed



Case Study #1

Hawaiian green turtles – Revisited!!



Stacy Hargrove



George Balazs-
PIFSC

Recent scattered nesting around Main Hawaiian Islands
Nesters almost all unobserved
Widespread nests sampled



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journal homepage: www.elsevier.com/locate/jembe



Insights on the demography of cryptic nesting by green turtles (*Chelonia mydas*) in the main Hawaiian Islands from genetic relatedness analysis

Amy Frey ^{a,*}, Peter H. Dutton ^a, George H. Balazs ^b

^a Protected Resources Division, Southwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, 8901 La Jolla Shores Dr., La Jolla, CA 92037, USA

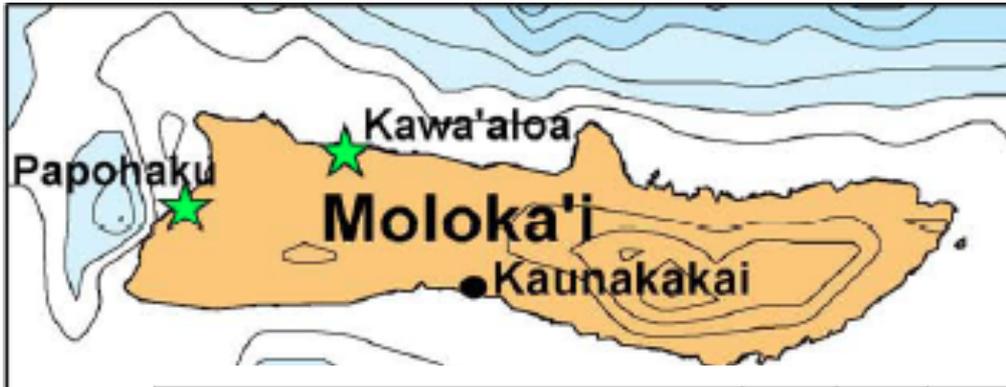
^b Pacific Islands Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, 2570 Dole Street, Honolulu, HI 96822, USA



Amy Frey

- Sample set: 181 salvaged embryos/hatchlings from 77 nests
- One sample per nest was sequenced (mtDNA)
- All samples were genotyped using 14 microsatellite loci
- Used Colony v2.1 (Jones, 2009) to reconstruct maternal genotypes and match to unknown nests
- Determined number of females laid nests

Genetic census of green turtle Molokai nests



Eight females laid 38 of the nests at Kawa'aloa

Female 14 laid the two nests on Papohaku in 2008

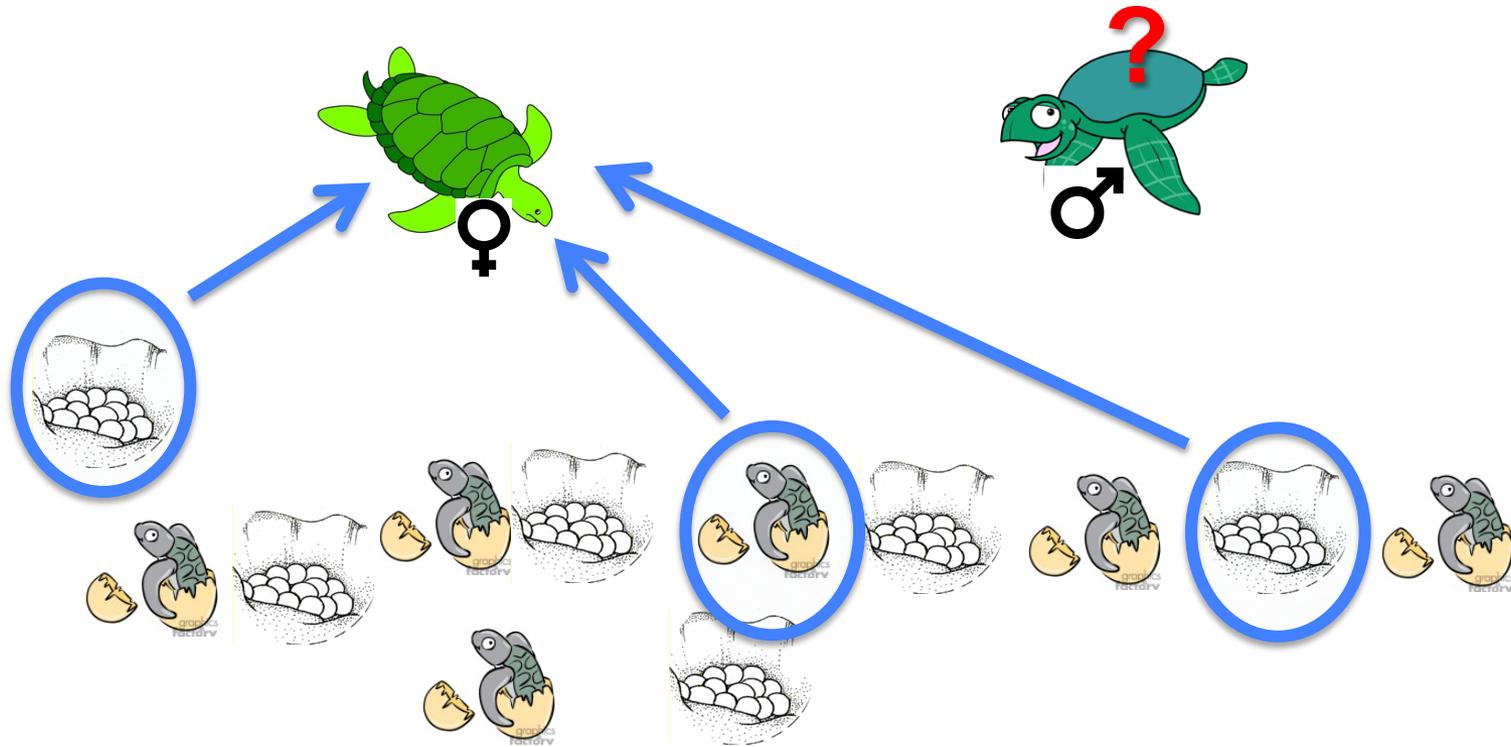
	'04	'06	'07	'08	'09	'10
Molokai-Papohaku				2*		
Molokai- Kawaaloo	2	4	10	3	11	8
No. Females	2	1	4	2*	5	3
Female 7	1	-	5	-	-	3
Female 8	1	4	-	-	3	-
Female 11	-	-	1	-	3	-
Female 12	-	-	3	-	1	-

} Nests/yr

Additional demographic inferences

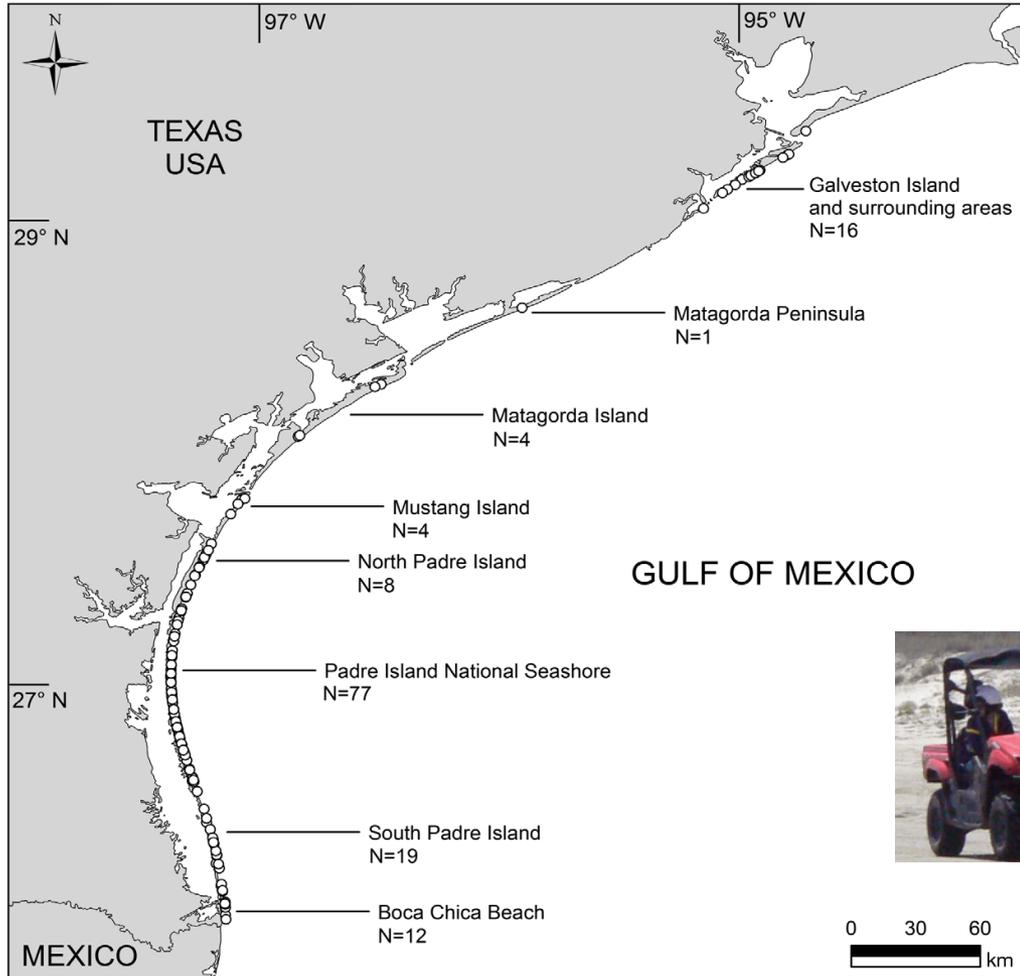
- Reconstructed MHI nester genotypes show high degree of relatedness
- Nests laid by relatively few, but related individuals (mtDNA+nDNA)
- MHI nesting “population” established from new founders derived from FFS genetic stock – possibly Sea Life Park

Scenario 2: Nesters observed/tagged

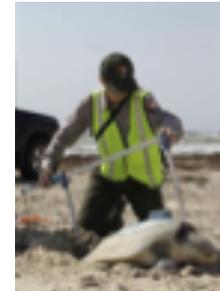


Nests unknown

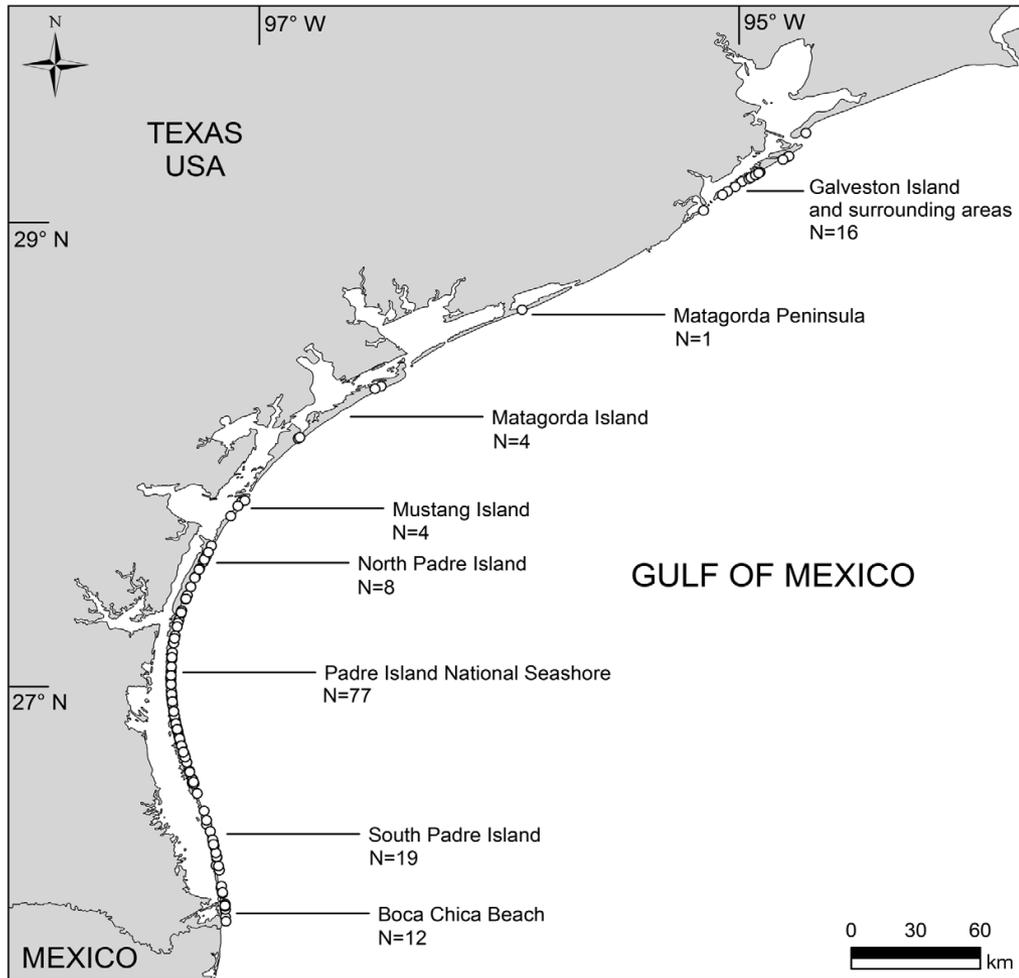
Case Study #2: Kemp's ridley Texas nesting census



Donna Shaver –
National Park Service



Case Study #2: Kemp's ridley Texas nesting census



2003 - 2006

salvaged embryos
from 141 nests

Sampled 159
females

Matched unknown
nests to “tagged”
females

Identified number of
“unknown” females

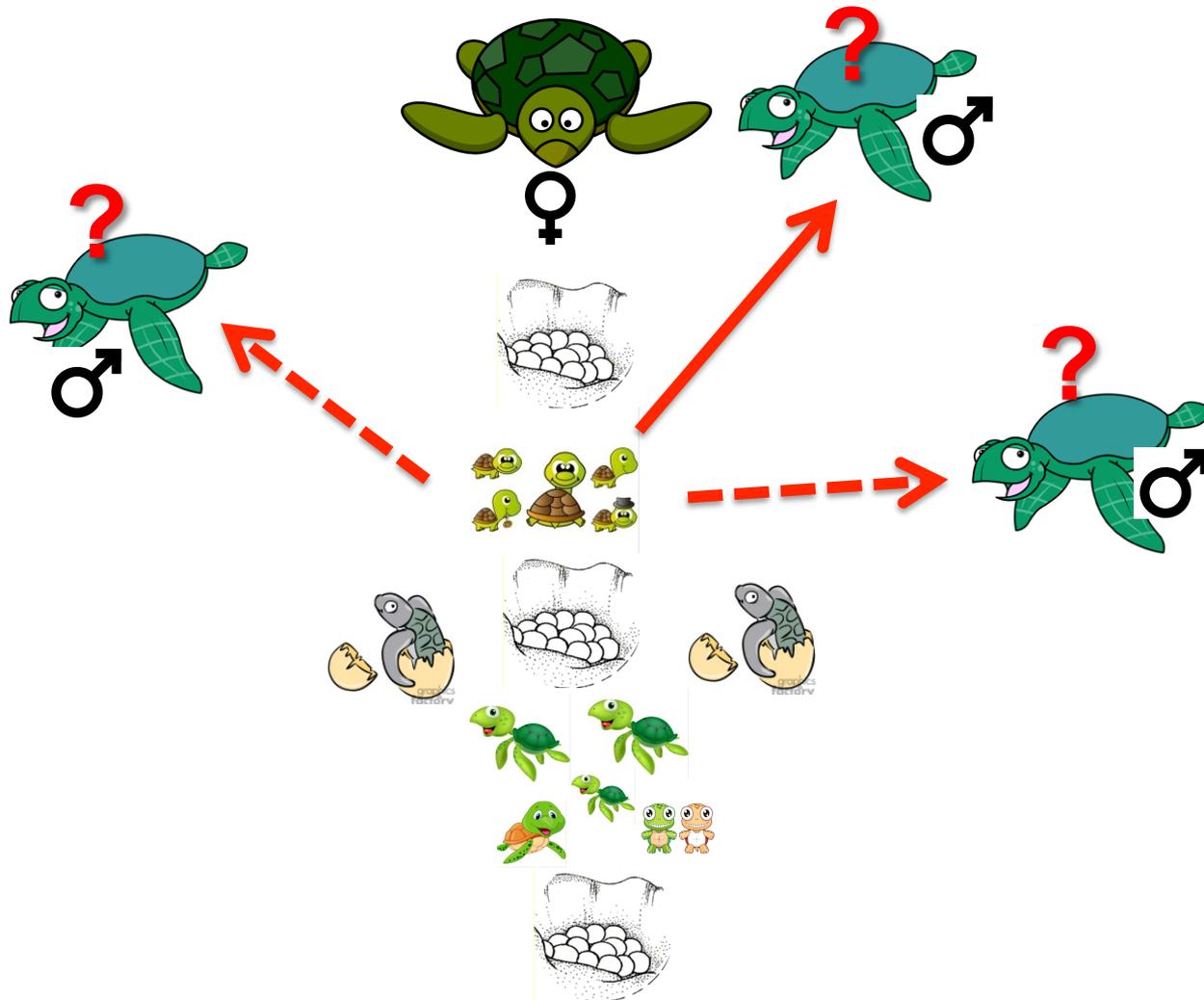
Kemp's ridley *Lepidochelys kempii* nesting abundance in Texas, USA: a novel approach using genetics to improve population census

Amy Frey^{1,*}, Peter H. Dutton¹, Donna J. Shaver², Jennifer Shelby Walker²,
Cynthia Rubio²

Year	Females observed (nests)	Females assigned using genetics (nests)	Females observed assigned using genetics	Total females (nests assigned)	Total observed nests	Estimated no. females (range)
2003	8(10)	6(7)	3	11(14)	19	7.6 (6.2–10.6)
2004	19(23)	12(16)	4	27(37)	42	16.8 (13.9–23.3)
2005	20(25)	13(19)	5	28(39)	50	20.0 (16.3–27.8)
2006	43(50)	28(48)	20	51(91)	102	40.8 (33.2–56.7)

How many males are there?

Scenario 3: Mother and nests known/sampled



Case Study #3: St. Croix leatherbacks

Population Vital Rates (demographic parameters)

1. Age to maturity (long-term CMR)
2. Survival rates (long-term CMR)
3. Breeding sex ratios (census males)
4. Mating systems (paternity/male reproductive success)



Kelly Stewart



Genetic tagging of hatchlings & nesters

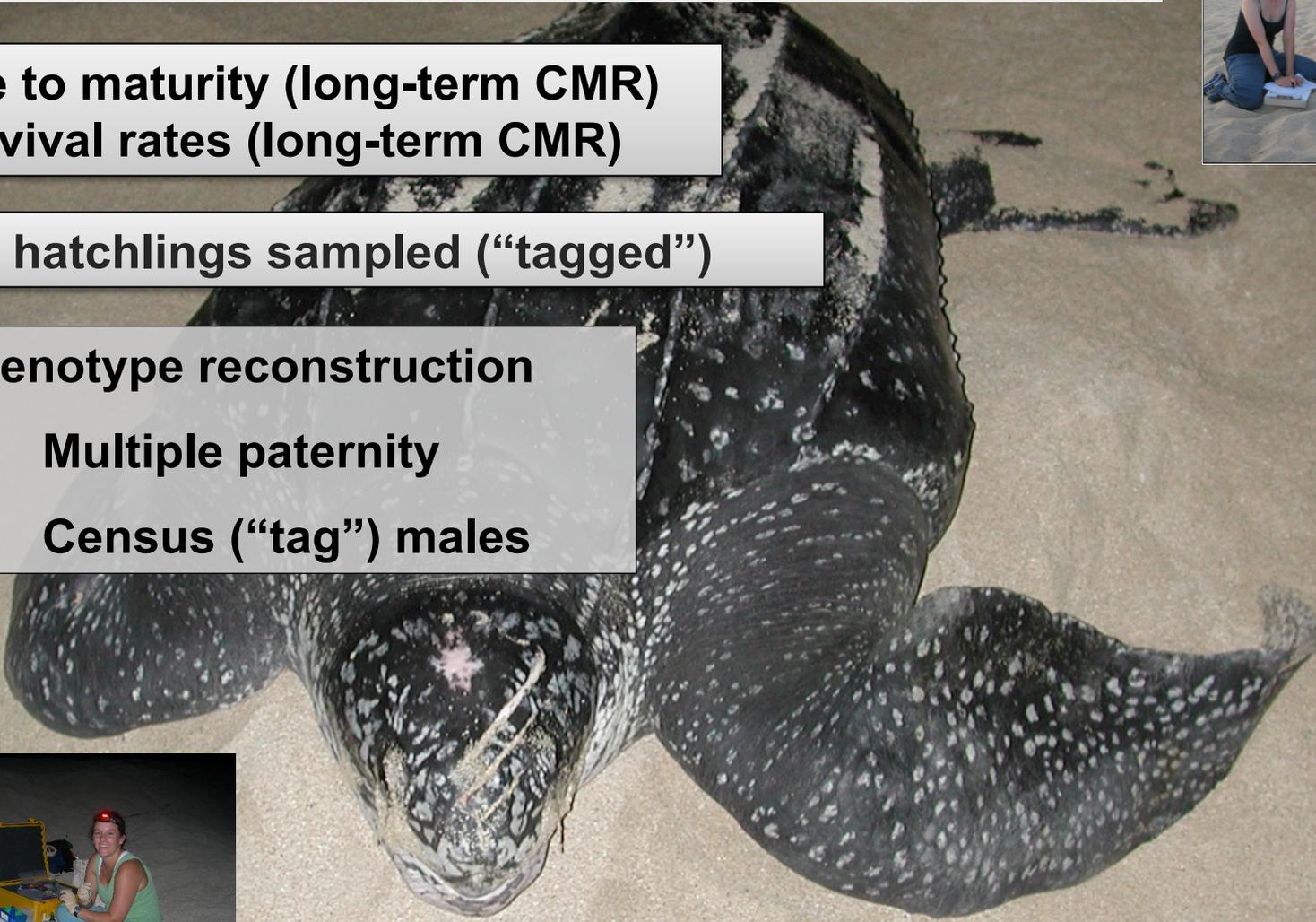
- Age to maturity (long-term CMR)
- Survival rates (long-term CMR)

34,161 hatchlings sampled (“tagged”)

Use genotype reconstruction

Multiple paternity

Census (“tag”) males



Methods *(Dutton & Stewart 2013:MTN 138)*

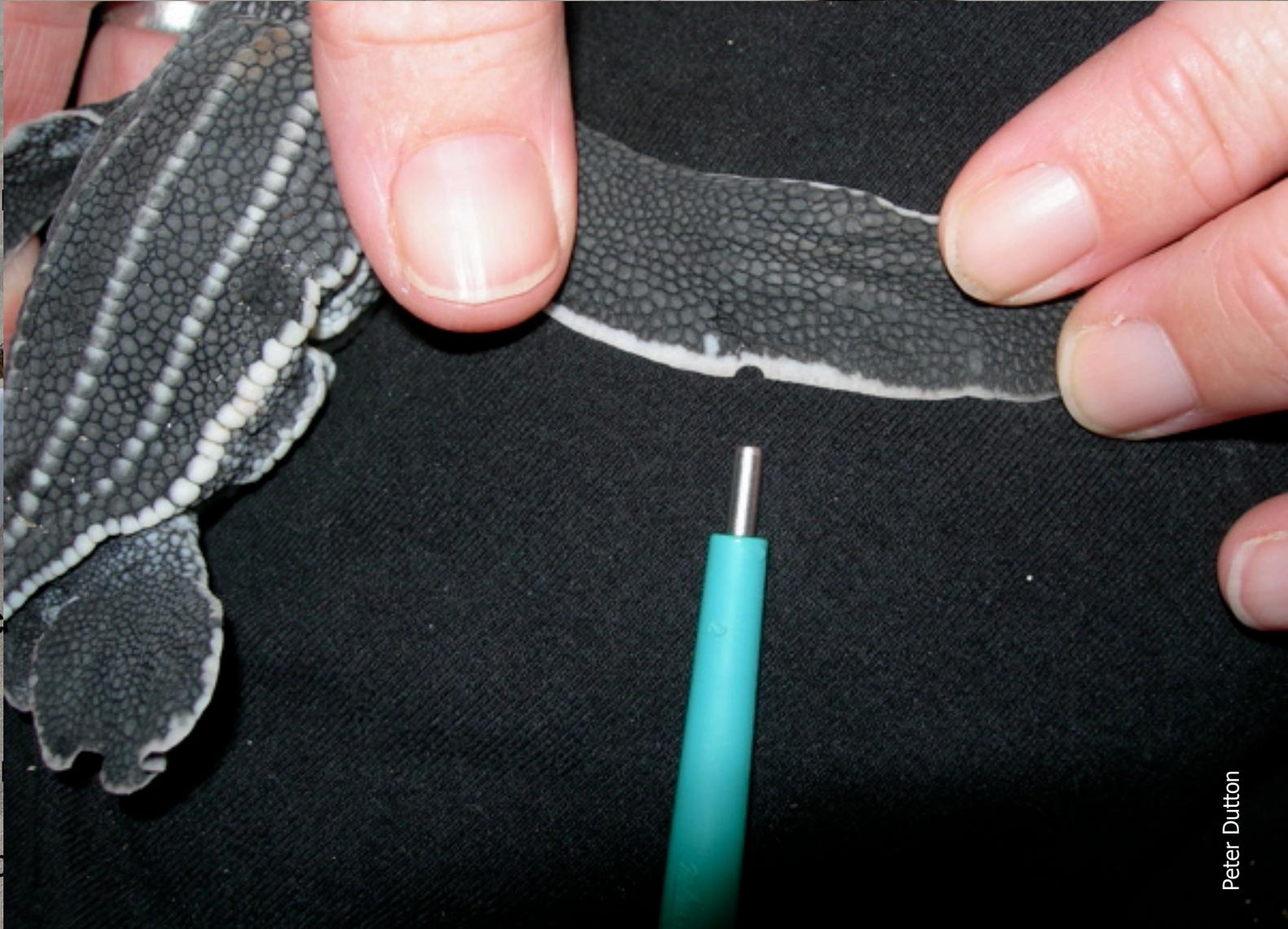
Hatchling

Disinfect

Sample storage

Sample

Steve Brewer



Genotype reconstruction

Female TTZ405, nest hatched July 11, 2010

	D1		5H7		5C8	
Maternal	219	259	224	232	288	288
Hatchling ID						
96401	219	231	232	236	288	292
96402	219	231	232	236	288	292
96403	231	259	232	236	288	292
96404	231	259	208	232	288	292
96405	231	259	208	232	288	292
96406	247	259	232	236	288	292
96407	219	231	208	232	288	292
96408	219	247	208	224	288	292
96409	219	247	224	236	288	292
96410	247	259	208	232	288	292
Paternal	231	247	208	236	292	292

- Account for maternal alleles in hatchling genotypes.
- Identify paternal alleles.
- Reconstruct genotype of male (without sampling him!).

Breeding Sex Ratios in Adult Leatherback Turtles (*Dermochelys coriacea*) May Compensate for Female-Biased Hatchling Sex Ratios

Kelly R. Stewart^{1,2*}, Peter H. Dutton¹

¹ Marine Mammal and Turtle Division, Southwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, La Jolla, California, United States of America, ² The Ocean Foundation, Washington D. C., United States of America



- Fingerprinted 662 hatchlings from 38 nests laid by 55 females
- Identified (“tagged”) 47 breeding males
- Breeding sex ratio estimate (~ 1:1)



Multiple year analysis (*Stewart & Dutton in prep*)

Year	2009	2010	2011
Females	45	46	28
Males	41	47	27
Males: Females	1.1: 1.0	0.98: 1.0	1.04: 1.0
Multiple Paternity	47.7%	17.4%	40.5%

- 1) BSR is consistently approx 1:1.
- 2) We identified (“tagged”) 115 individual males some males mated with 3 females in season.
- 3) Males skipped mating the next year, but returned in year 3, similar to females (CMR males)

Genetic tagging



1. Males can now be identified without sampling them
2. Adult sex ratios can be determined
3. Male reproductive success can be calculated

Future opportunities & challenges

- Methods (both field and lab) now proven
 - Technologies will continue to rapidly develop
 - Genomics/Next Gen
 - DNA Chips
- Long-term commitment required
 - Need to start sampling hatchlings now (Mark)
 - Need to sample adults/strandings/juveniles (Recapture)
5 – 30 years?

Future opportunities & challenges

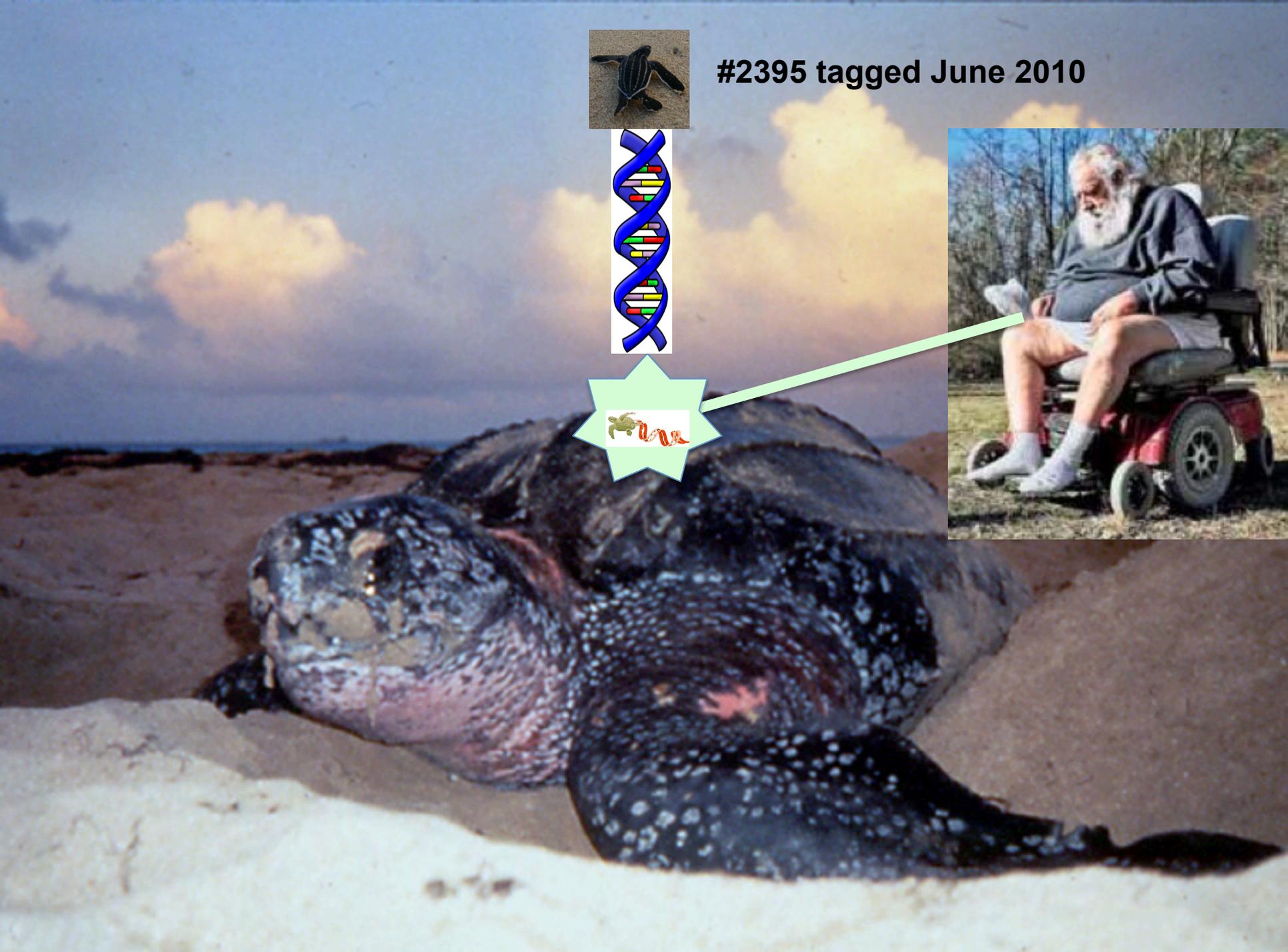
- Sample storage and collection management
 - Thousands of samples per project/season
- Bioinformatic systems need to be developed
 - E.g. “tagging database” : information sharing
 - “FBI” fingerprint database (e.g. GenBank)

Future opportunities & challenges

- Mass tagging hatchlings may not be compatible with conservation priorities
- Most suited to projects where nest management and saturation tagging is priority



#2395 tagged June 2010



Questions?

