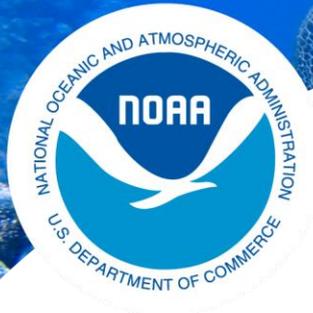




Delineating Stock Boundaries: Pacific Green Turtles



NOAA
FISHERIES

Michael P Jensen

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NOAA Fisheries, Southwest Fisheries Science Center

Review of NOAA Fisheries' Science on Marine Mammals & Turtles

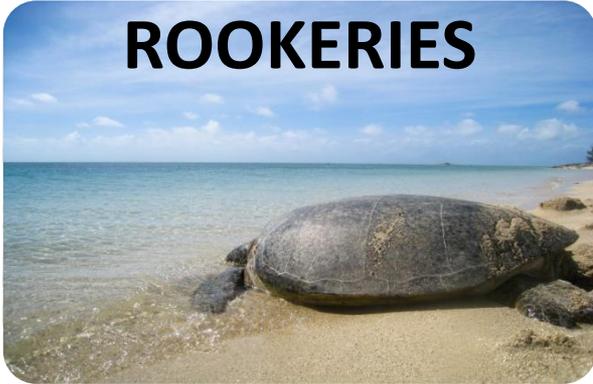
Southwest and Northwest Fisheries Science Centers

27-31 July 2015

La Jolla, CA

DEFINING BOUNDRIES OF TURTLE STOCKS

ROOKERIES



IDENTIFYING UNITS TO CONSERVE

- Identify Management Units (MUs) - mtDNA
- Identify broader regional groupings (e.g. DPS).

FORAGING

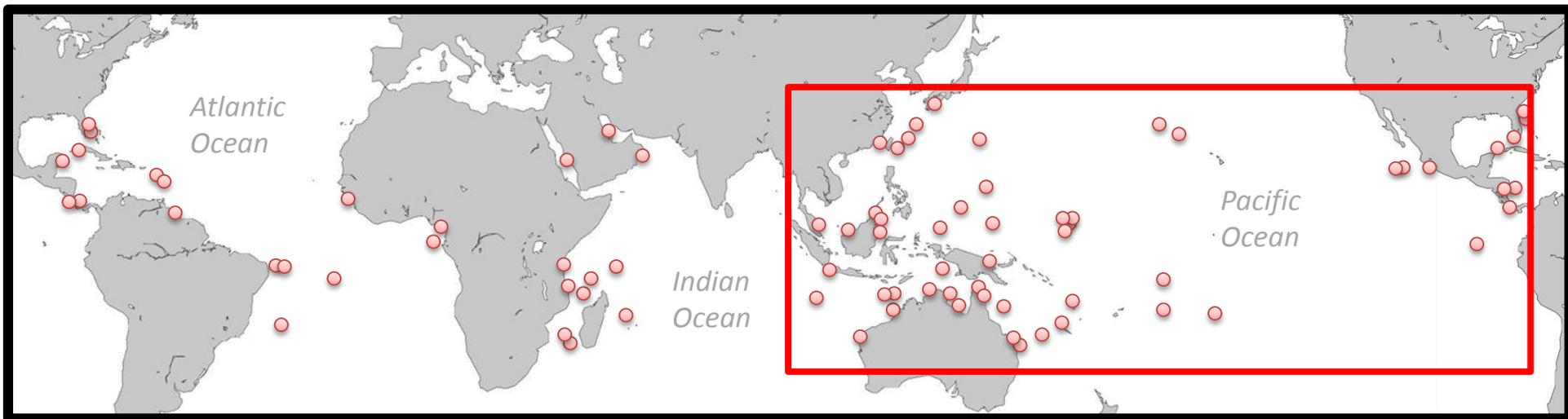


CONNECTIVITY BETWEEN FORAGING AND NESTING AREAS

- Identify the source populations of turtles sampled away from the nesting sites.
- Define boundaries of Management Units

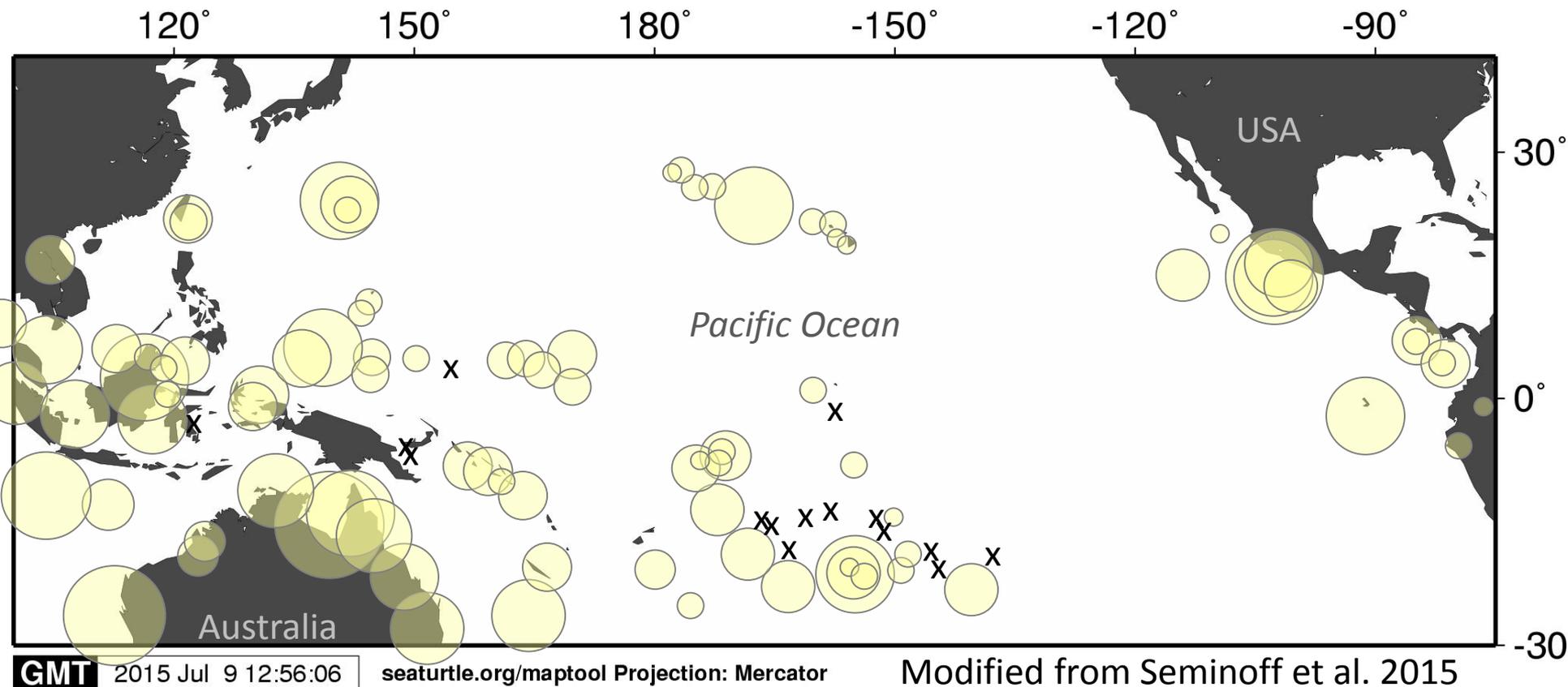
NMFS-SWFSC coordinating Global green turtle stock structure (mtDNA) survey:

- Approx. 4,400 rookery samples from 121 rookeries with mtDNA sequences completed.
- International collaboration needed to address information gaps.



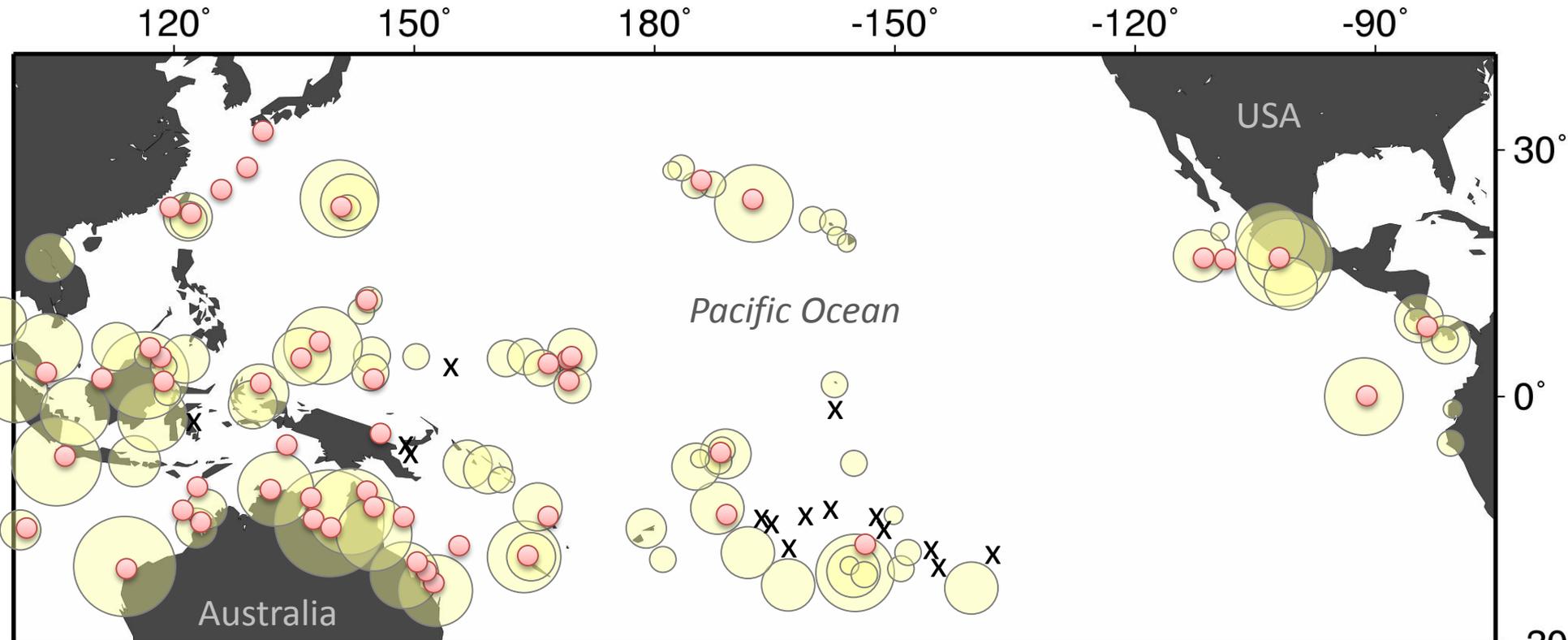
Distribution of green turtle nesting beaches across the Pacific Ocean

- Most abundant species of marine turtles
- Widely distributed globally



Genetic sampling of green turtle nesting beaches across the Pacific Ocean

- >60 green turtle rookeries sampled (>2000 samples)
- 41 genetic stocks or Management Units
- Structure generally exists on a scale of >500 km
- Gaps still exists



Genetic sampling of green turtle foraging areas across the Pacific Ocean

- First study to use mixed stock analysis on green turtles in the Pacific was from Hawaii (Dutton et al. 2008).
- Found that 100% of turtles foraging in Hawaii were from the French Frigate Shoals with no outside contribution.



Composition of Hawaiian green turtle foraging aggregations: mtDNA evidence for a distinct regional population

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ABSTRACT. To examine the stock composition of Hawaiian foraging populations and evaluate current life-history hypotheses, mtDNA control region sequences from immature and adult green turtles that forage around the Hawaiian Islands were compared to potential source nesting populations across the Pacific. We examined the stock composition of the feeding ground (FG) populations at 5 index sites across the Hawaiian Archipelago, as well as animals stranded in areas outside these index sites. Six haplotypes, based on mtDNA sequences, were observed among the 788 green turtles sampled around the Hawaiian Islands. Stock mixture analysis shows that the Hawaiian FG populations comprise one genetic stock derived from the nesting population at French Frigate Shoals (FFS), based on a mean estimate of 99.9% from FFS as opposed to other potential source stocks. We identified only 3 turtles with haplotypes not found at FFS, indicating that Hawaiian FGs might occasionally, albeit rarely, be visited by animals from rookeries outside the Hawaiian Archipelago, both in the eastern and western Pacific. These findings lead us to conclude that the numerous foraging aggregations around the Hawaiian Islands can be considered part of a distinct regional population for management. The finding that FGs scattered across a distance of over 2400 km belong to one genetic stock is unique among sea turtles, and allows Hawaiian green turtles to be assessed separately from other Pacific stocks with respect to risk. We explore the unique population ecology of Hawaiian green turtles with reference to the complex life history of this marine megaherbivore.

KEY WORDS: Population genetics · Control region · Mitochondrial DNA · mtDNA · Sea turtles

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INTRODUCTION

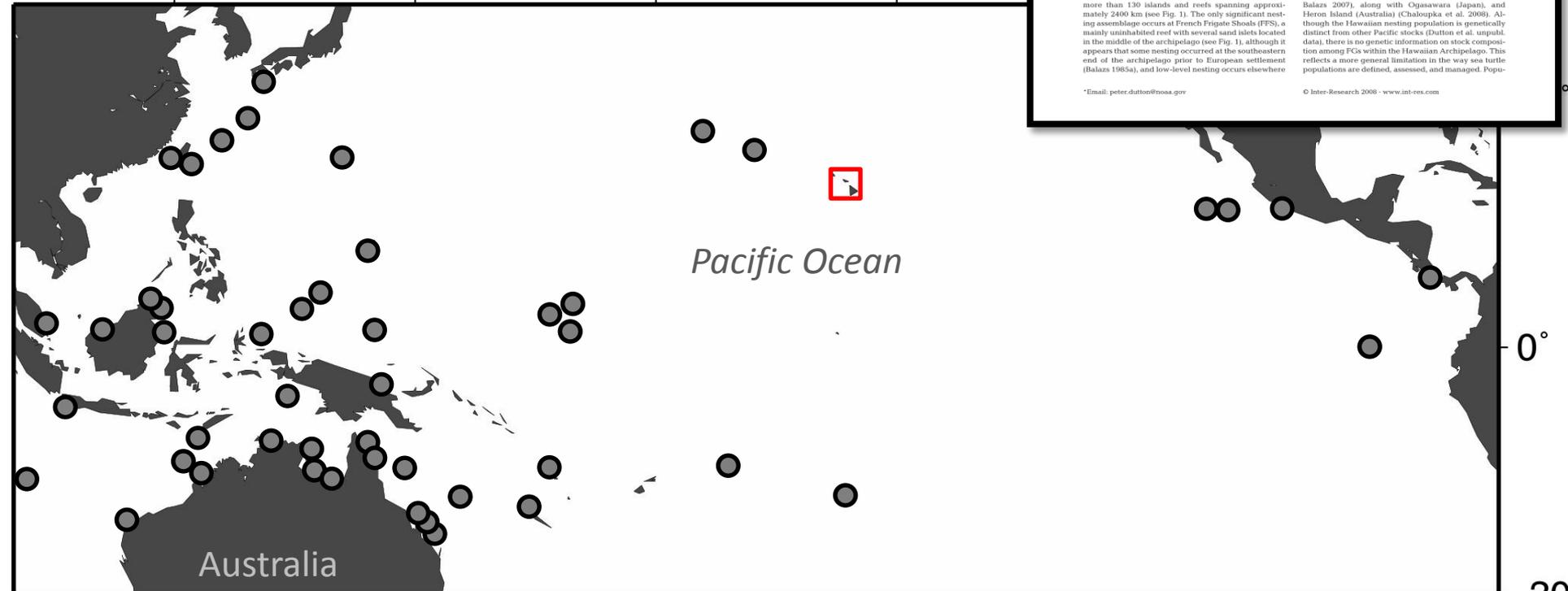
The green turtle *Chelonia mydas* occurs throughout the many coral reef and coastal foraging grounds (FG) within the Hawaiian Archipelago, which consists of more than 130 islands and reefs spanning approximately 2400 km (see Fig. 1). The only significant nesting assemblage occurs at French Frigate Shoals (FFS), a mainly uninhabited reef with several sand islets located in the middle of the archipelago (see Fig. 1), although it appears that some nesting occurred at the southeastern end of the archipelago prior to European settlement (Balazs 1965a), and low-level nesting occurs elsewhere

in the northwestern Hawaiian Islands. The FFS nesting population of threatened green turtles has been monitored since 1973 and is one of the few populations in the Pacific that appears to be increasing in numbers (Balazs & Chaloupka 2004a, 2006; Hays 2004; Chaloupka & Balazs 2007), along with Ogasawara (Japan), and Heron Island (Australia) (Chaloupka et al. 2008). Although the Hawaiian nesting population is genetically distinct from other Pacific stocks (Dutton et al. unpubl. data), there is no genetic information on stock composition among FGs within the Hawaiian Archipelago. This reflects a more general limitation in the way sea turtle populations are defined, assessed, and managed. Popu-

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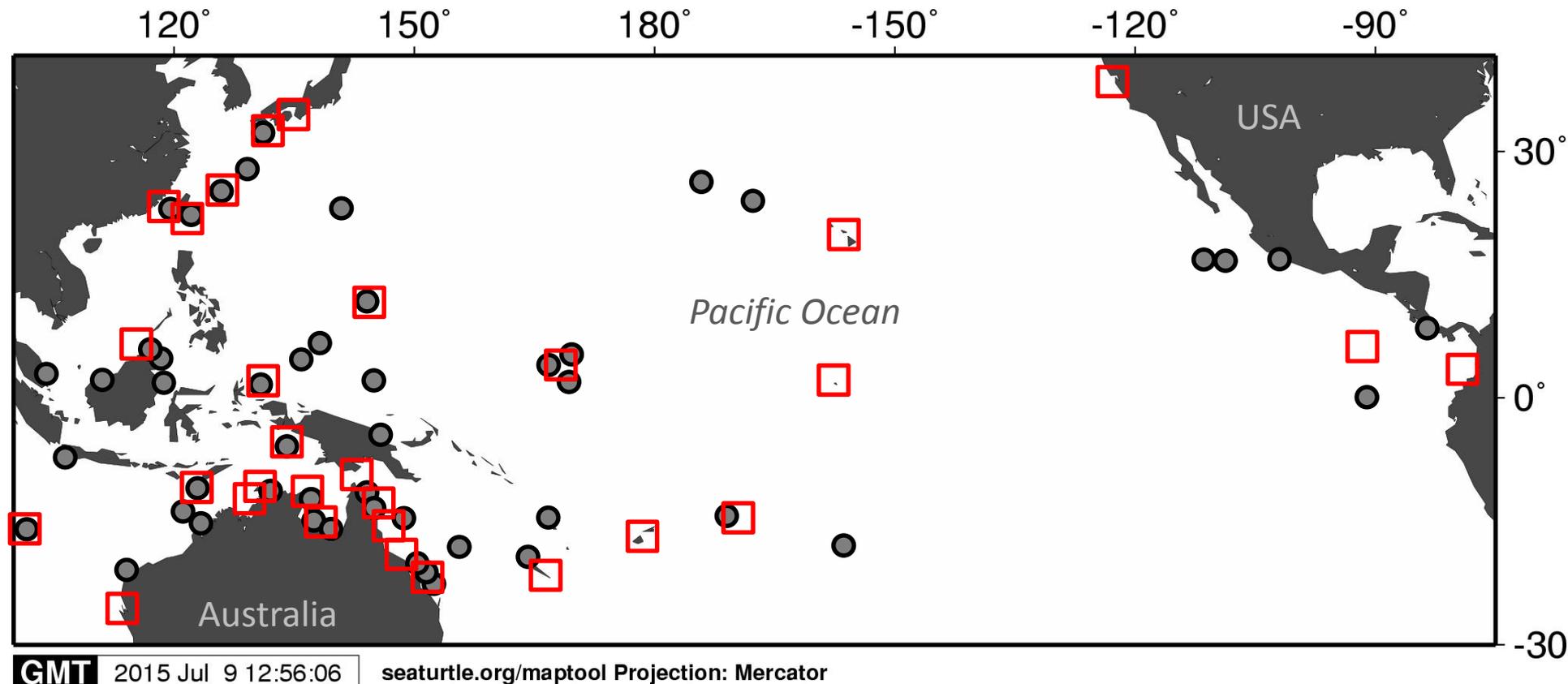
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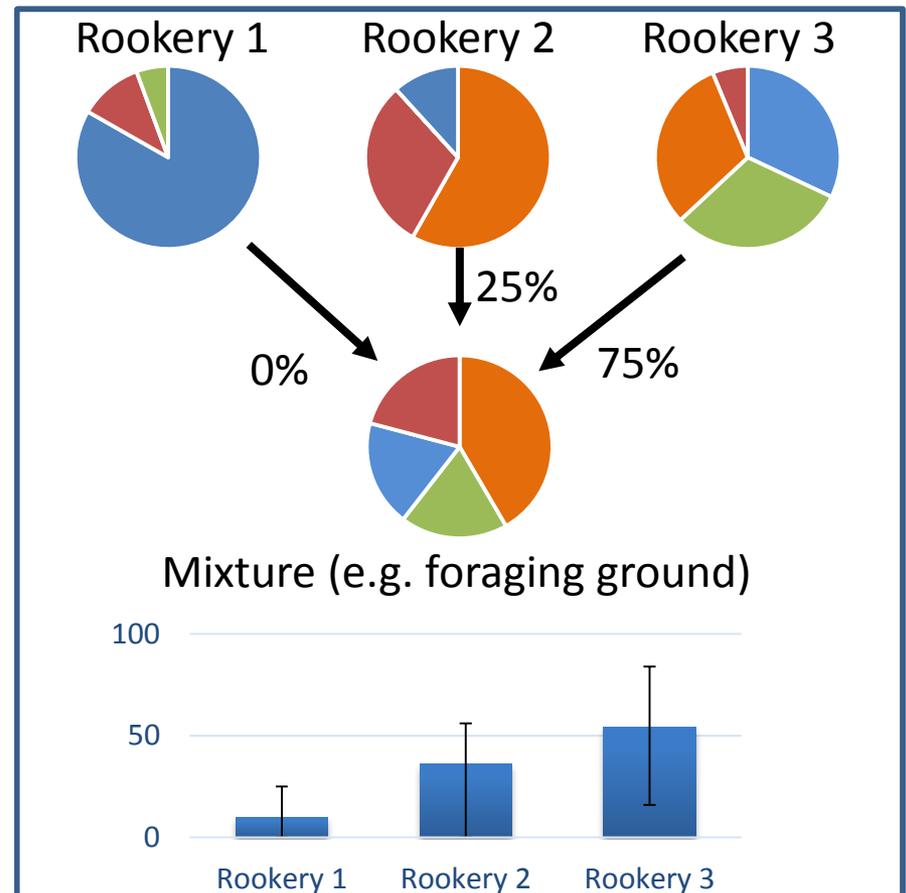
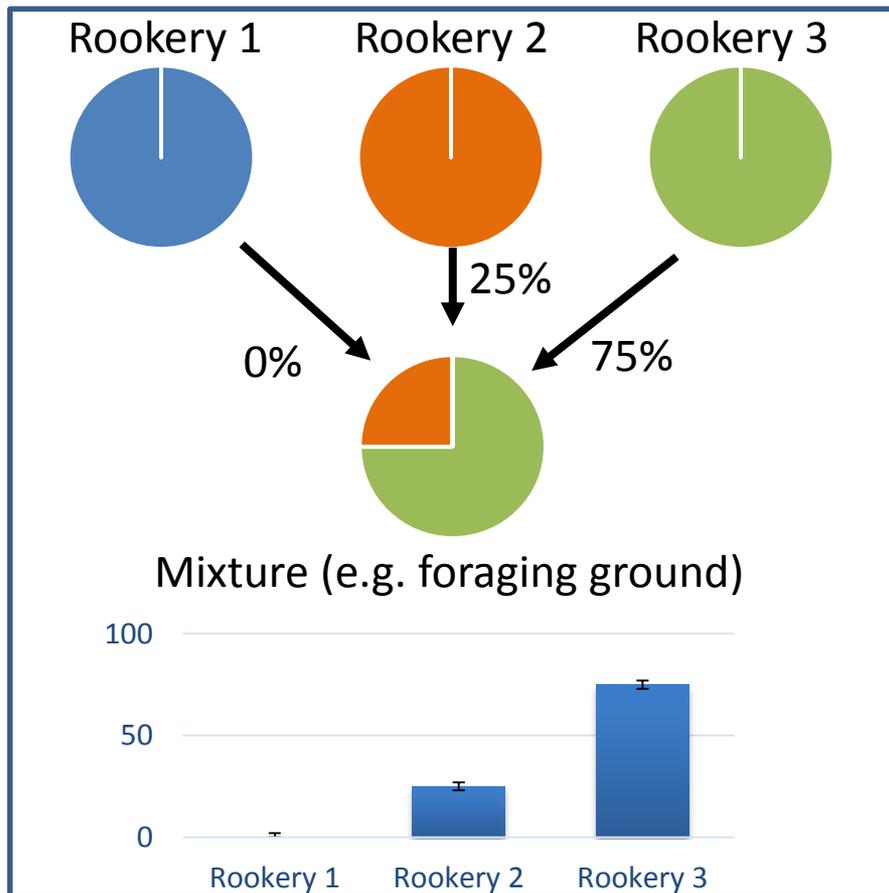
Genetic sampling of green turtle foraging areas across the Pacific Ocean

- 31 foraging areas sampled across the Pacific Ocean
- >4000 samples from foraging green turtles



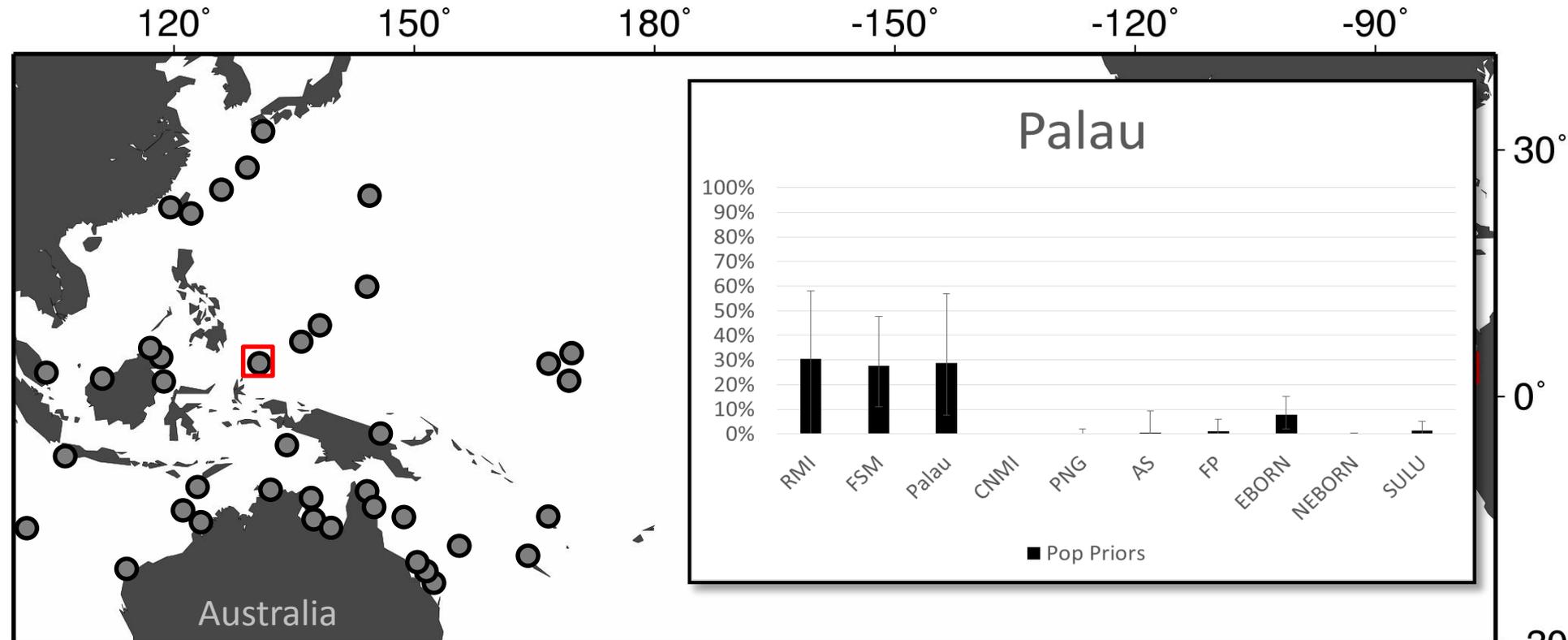
Mixed Stock Analysis using mtDNA

- Bayesian analysis to estimate the contribution of known source pops to a mixed aggregation
- sensitive to genetic structure and coverage of source rookeries



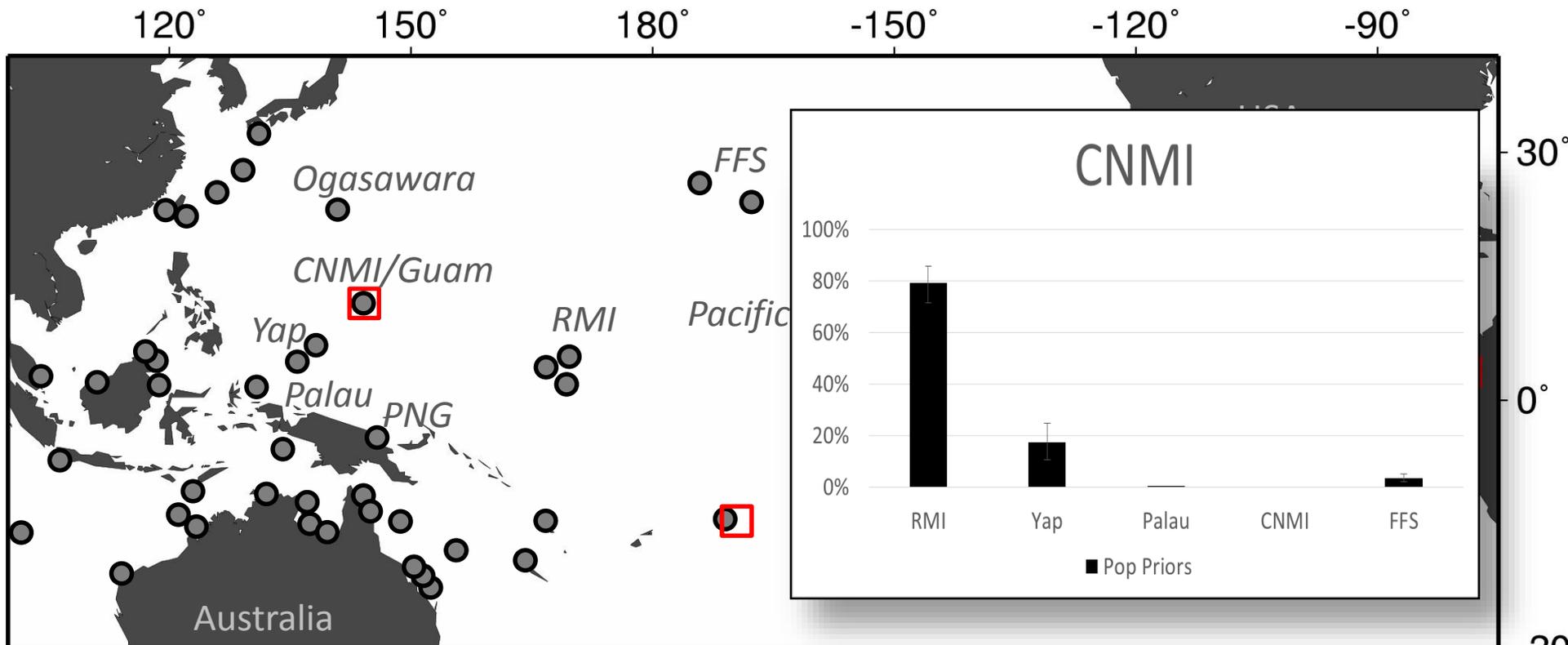
Helen Reef, Palau

- Green turtles foraging at Helen Reef originate from multiple regional rookeries



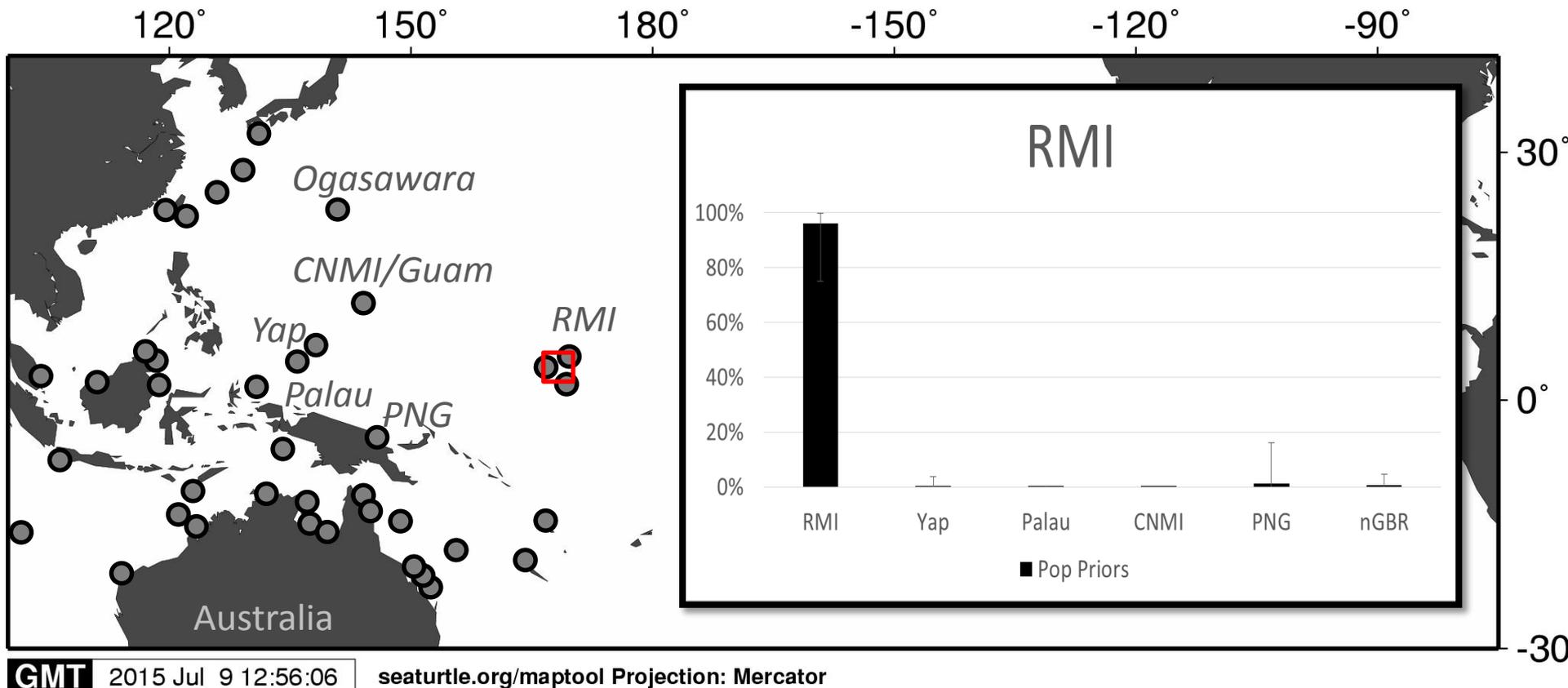
The Mariana Islands

- Most turtles (80%) are from the Marshall Islands 3000 km away
- 11 turtles (3%) were estimated to originate from the French Frigate Shoals >4000km



The Marshall Islands

- Most turtles originate from the Marshall Island rookery
- But Marshall Island green turtles also forage at distant FGs

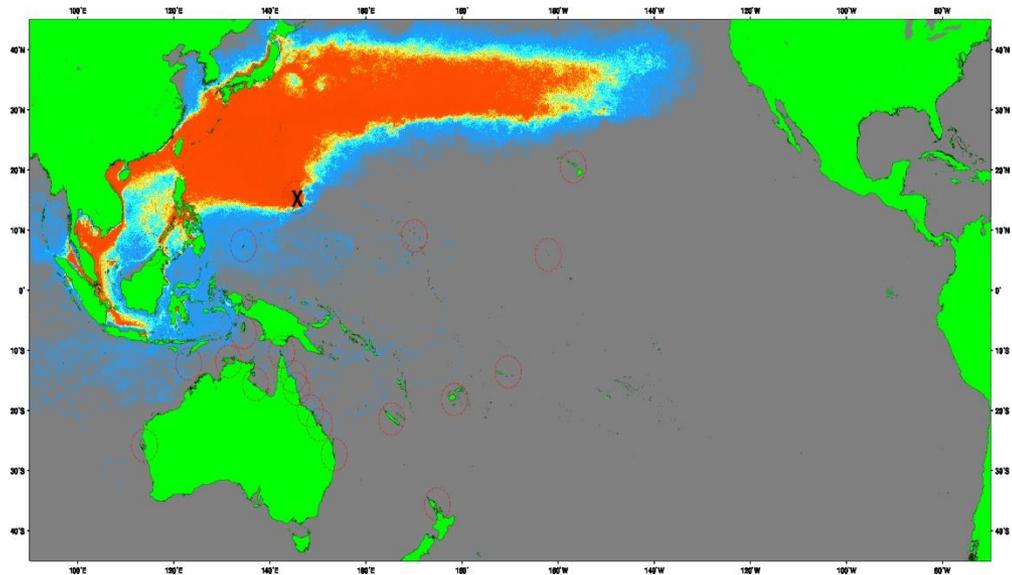


The effects of ocean current on connectivity of green turtle habitat

- In collaboration with Donald Kobayashi
Pacific Islands Fisheries Science Center

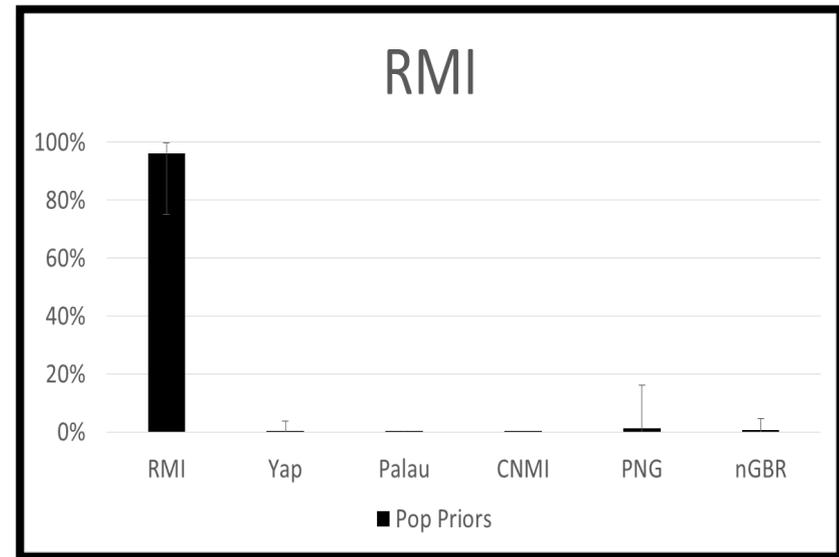
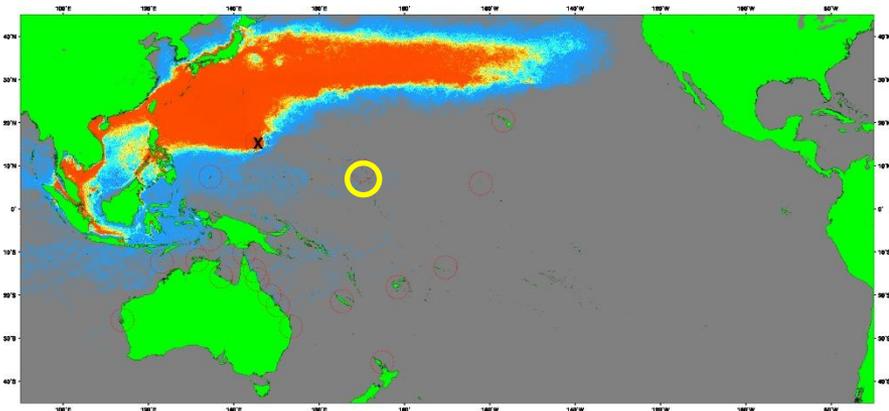
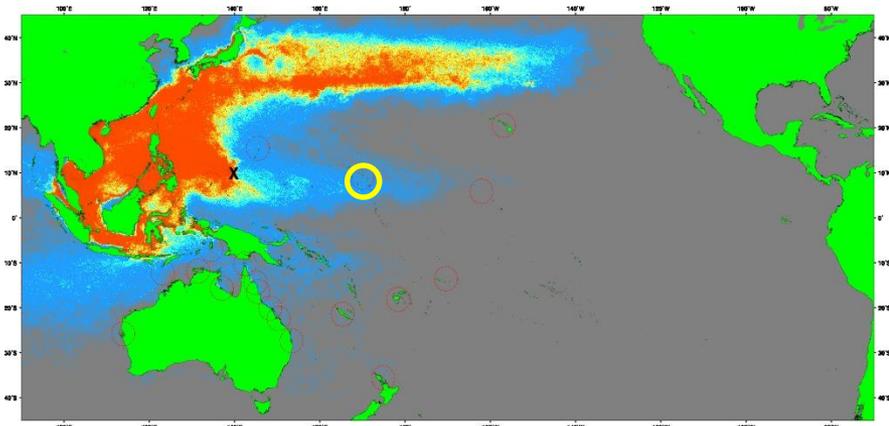


- Modelling hatchling dispersal to better understand recruitment patterns and improve mixed stock analysis. (Jensen, Dutton, Kobayashi).
- Release particles “virtual hatchlings” from rookeries and simulate passive drift for 3 years.
- Look at connectivity between release sites (rookeries) and foraging sites.
- Better understanding of hatchling dispersal routes.



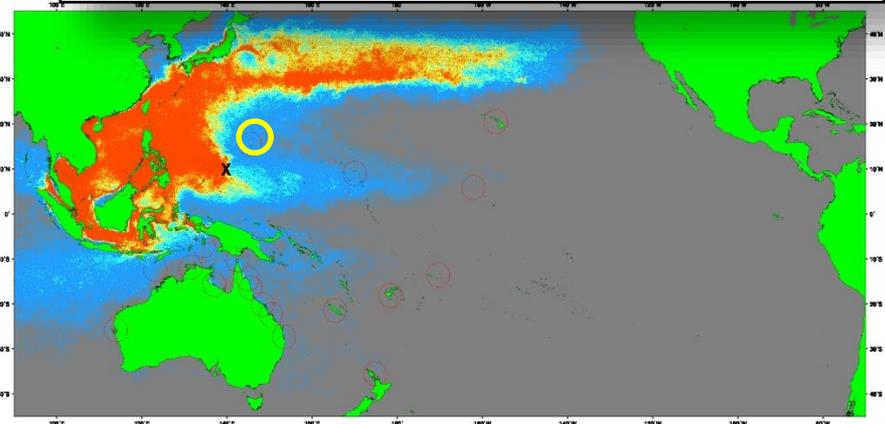
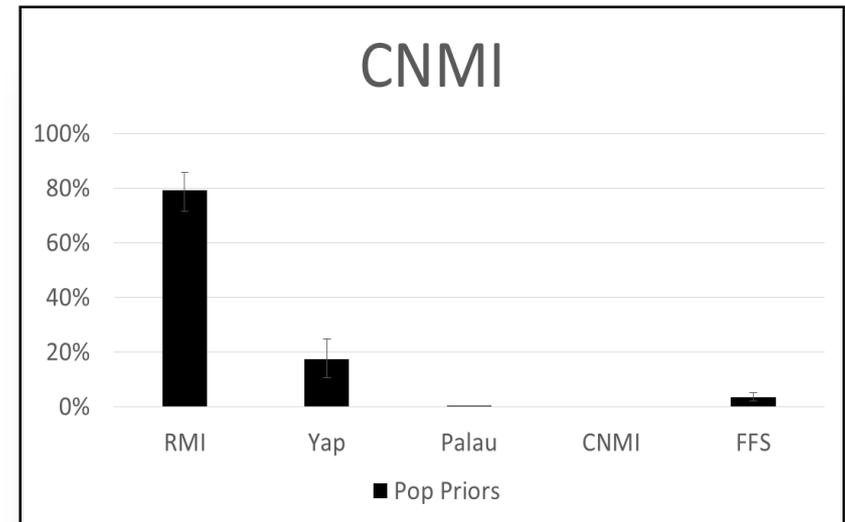
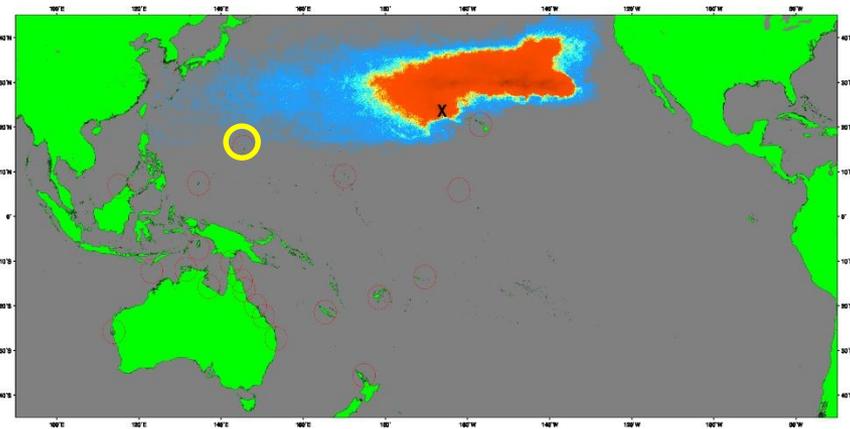
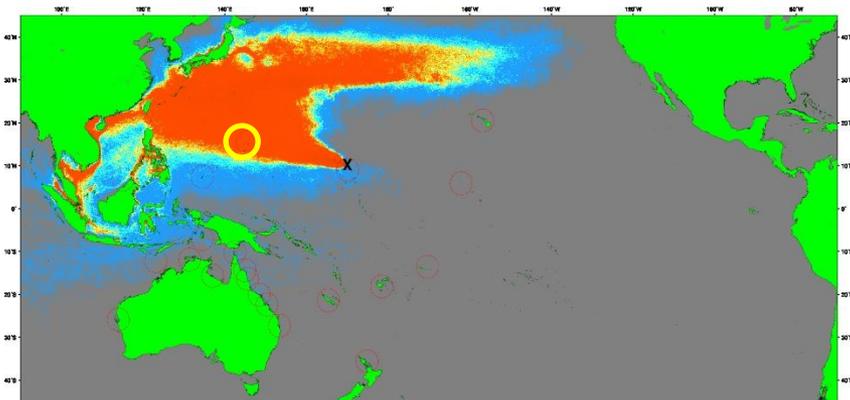
The Marshall Islands

- Most turtles originate from the Marshall Island rookery
- No contribution from other regional rookeries.



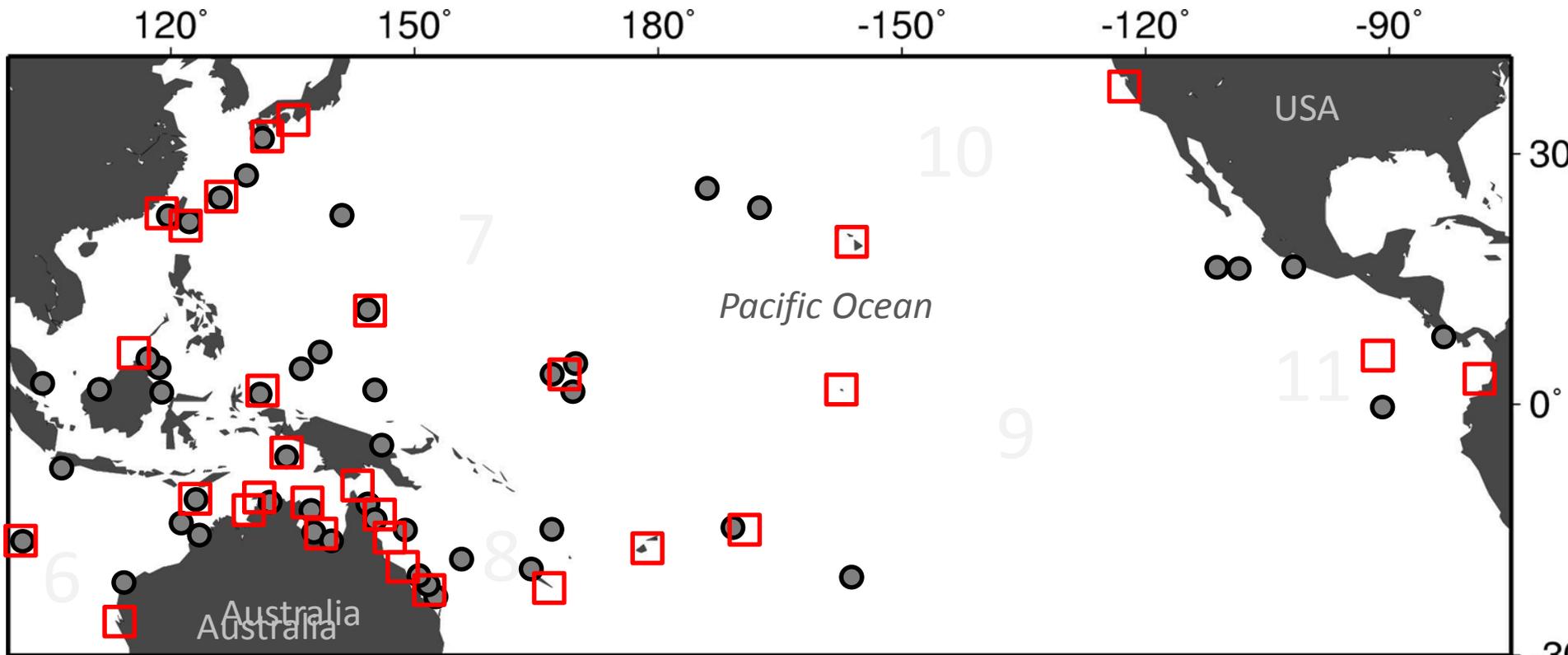
The Mariana Islands

- Most turtles (80%) are from the Marshall Islands 3000 km away
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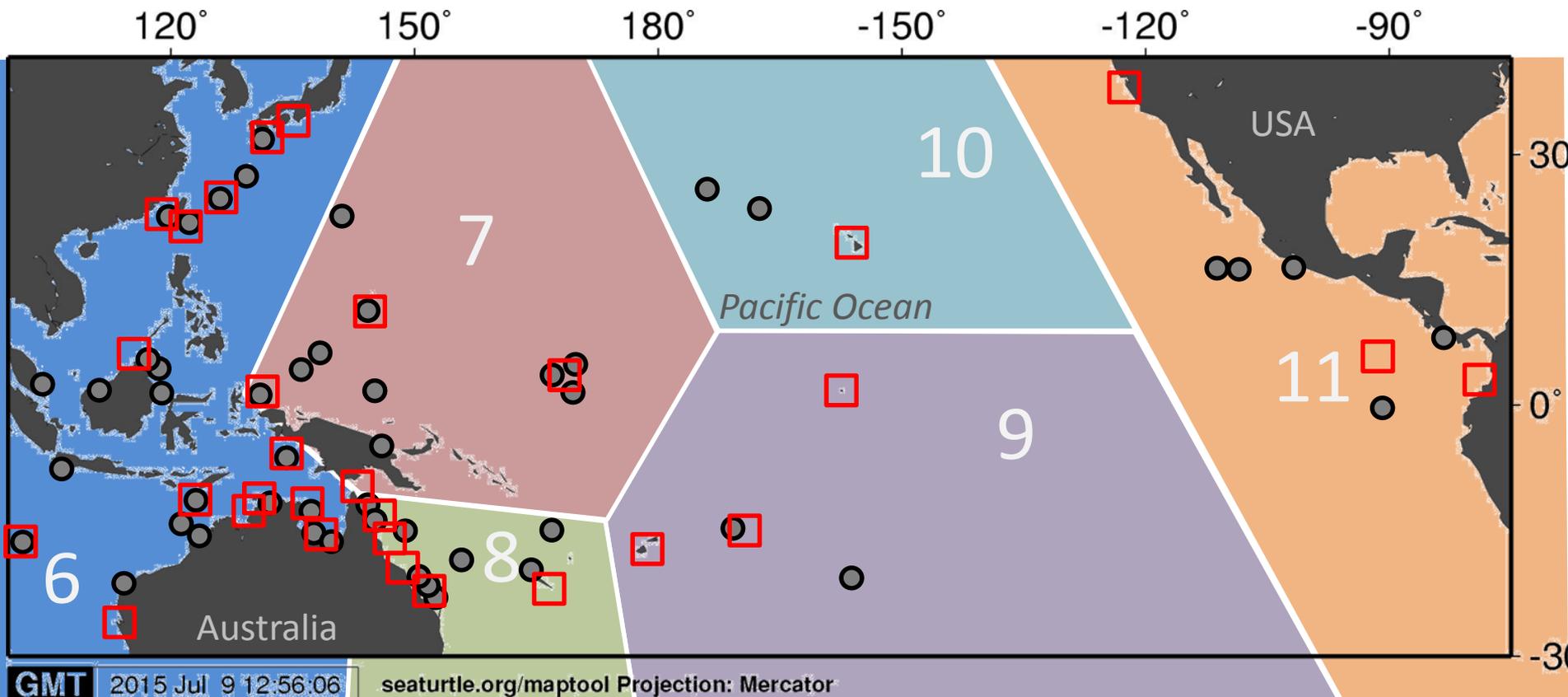
MSA for individual foraging areas

- We now have specific information on connectivity between rookeries and 30 feeding grounds across the Pacific.
- Detailed information of connectivity that show highly variable patterns influenced by rookery size, distance and ocean currents.
- Provide important information for management.



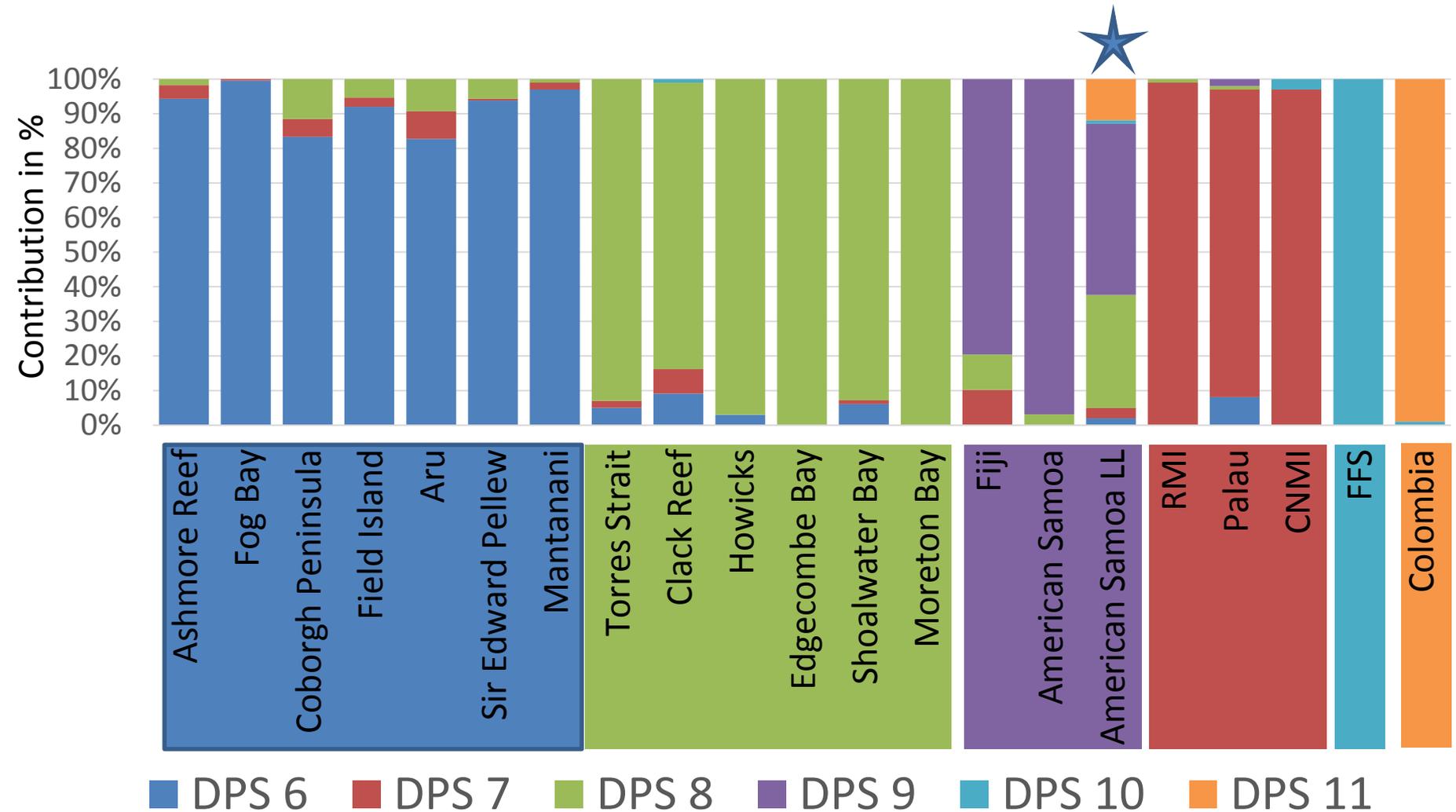
Boundaries of green turtle stocks in relation to DPSs

- Connectivity between rookeries and FGs within and across proposed DPSs.
- We can look at which DPS are impacted by impacts on foraging areas or in fisheries.



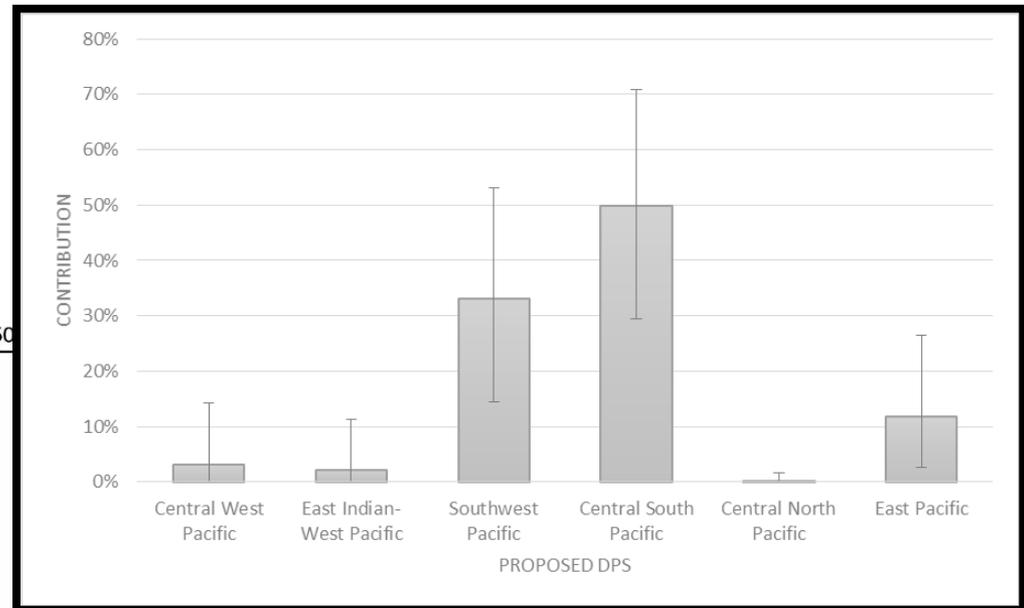
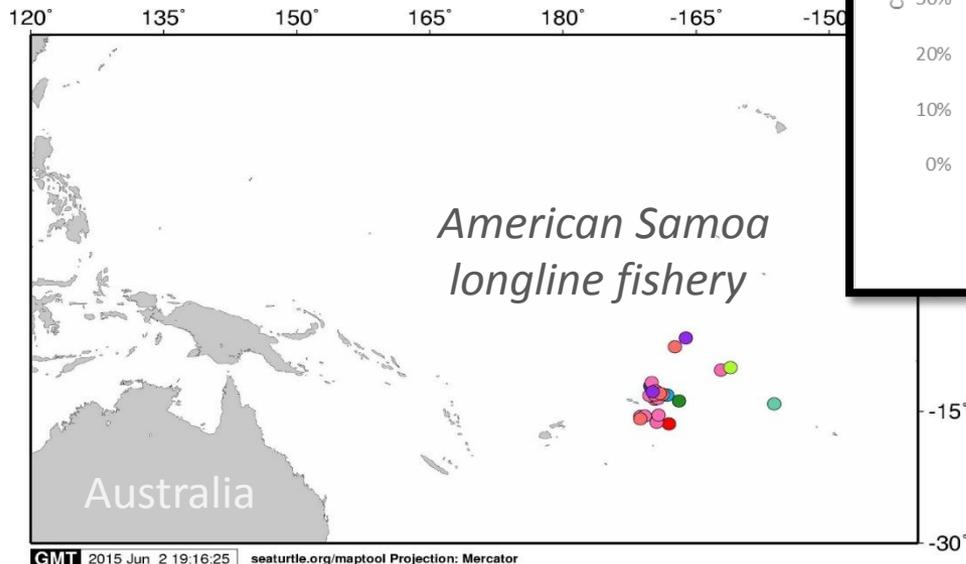
Boundaries of green turtle stocks

-MSA 20 foraging areas across the Pacific Ocean



American Samoa Longline Fishery

- Impacting green turtle rookeries from multiple DPSs
- Highly predictable by ocean current simulations



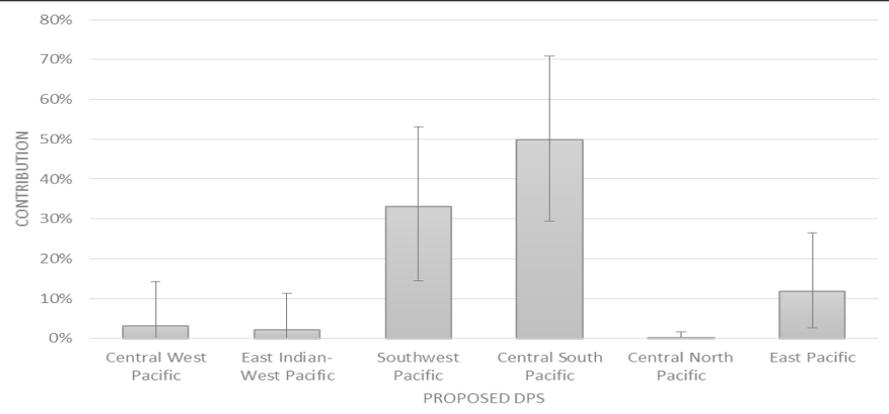
American Samoa

Southern GBR

French Polynesia

Northern GBR

Galapagos



A wealth of cool information

Ocean current simulation shows great promise as an additional tool to look at things like;

- Assess the connectivity of yet unsampled rookeries
- Improve msa models by using ocean modeling data as prior information

Mixed Stock Analysis gives insight into detailed population dynamics;

- Recruitment patterns for different age-classes (Jensen et al. in press).
- Combining hormone assays to look recruitment patterns for male and female green turtles (Jensen and Allen in prep).

Thanks for listening!

Acknowledgments

