NOAA Coral Reef Conservation Program
FY2009 Progress Report

Performance Evaluation of Marine Zoning in the Florida Keys National Marine Sanctuary

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Abstract
This multi-year project has used a multi-tiered approach to evaluate Marine Protected Areas in the Florida Keys National Marine Sanctuary. During the Federal Fiscal Year 09 (Oct. 08- Sept. 09), spatial and temporal rates of movement of acoustically tagged snappers and groupers were measured in the Tortugas region, including annual spawning migratory movements between Riley's Hump, the Tortugas Ecological Reserves and the Dry Tortugas National Park, including the Research Natural Area. In addition, the abundance and size-structure of spiny lobsters in and adjacent to the Western Sambo Ecological Reserve were surveyed. Results will be used to assess the importance of habitat linkages between adjacent marine protected areas and provide information for an ecosystem-based approach to management of marine resources.

Background
This multi-year project uses a multi-tiered approach to evaluate Marine Protected Areas (MPAs) in the Florida Keys National Marine Sanctuary (FKNMS). The FKNMS MPAs were established to resolve user conflicts, to protect critical coral reef ecosystems from exploitation, and to insure the sustainability of valuable marine resources. In past years, our research focused on the efficacy of one of the largest ecological reserves in the FKNMS, the Western Sambo Ecological Reserve (WSER). We continue to evaluate the efficacy of this reserve design relative to habitat use, population structure and animal movement, recognizing the potential need to alter MPA boundaries to include additional habitat for spawning of indicator species such as lobsters, snappers and groupers. In addition, the present project builds on past research and monitoring in the FKNMS by the Florida Fish and Wildlife Conservation Commission and focuses on connectivity between the network of marine reserves in the Dry Tortugas region, including the connections between populations of fish in the Dry Tortugas National Park (DRTO), the DRTO Research Natural Area (RNA, a type of marine reserve), the Tortugas North Ecological Reserve (TNER) and spawning habitat at Riley's Hump (RH), located within the Tortugas South Ecological Reserve (TSER). The following submission summarizes annual progress on the *Performance Evaluation of Marine Zoning in the Florida Keys National Marine Sanctuary* project (ID: 10007 – 2009) for October 2008 to October 2009 in three parts: 1) Dry Tortugas Finfish project; 2) Dry Tortugas Lobster project and 3) WSER Lobster project.

DRY TORTUGAS FINFISH
Introduction
The TSER, TNER and RNA create a network of no-take reserves that protect 600 km^2 of coral reef habitat, adjacent to and within the DRTO, 70 miles west of Key West, FL (Figure 1). The Dry Tortugas coral reef ecosystem is unique in terms of the variety and complexity of available habitat, the diversity of biological resources, and the presence of key spawning locations that hypothetically supply larval/juvenile recruits to the Florida Keys and south Florida (Domeier, 2004; Burton et al., 2005; Ault et al., 2006). The TSER and TNER were established in the Tortugas region in 2001 and the no-take RNA was established within the DRTO in 2007. The established marine reserves and adjacent open fished areas of the Tortugas region provide an excellent system for empirical studies on habitat utilization, spillover, broad scale movements, residence times on aggregation sites, and the efficacy of a network of MPAs in protecting marine resources and conserving marine biodiversity.

This network is designed to enhance biodiversity and sustainability throughout the Tortugas and the Florida Keys coral reef ecosystem by creating refuge for various life history stages of numerous exploited fishery resources, including snappers and groupers. The purpose of our CRCP telemetry project was to determine regional connectivity and test the hypothesis that fish move from foraging grounds (RNA, TNER, and DRTO) to spawning sites in the TSER. Data will be used to assess the size, shape and site selection of the Tortugas marine reserves and their efficacy as an ecosystem-based management tool. For example, changes in reserve boundaries may be implemented to enhance or reduce spillover of key species, based on observed home ranges and movement patterns of snappers and groupers during the spawning season.

In addition, we began the effort to determine residence times and behavior of snappers and groupers in spawning aggregation areas. Snappers and groupers migrate long distances to specific sites to form spawning aggregations of 100 – 1000s of individuals at specific times of the year. Unfortunately, traditional fishery management strategies have not always accounted for the vulnerable nature of spawning events and these prime fishery targets are rapidly overfished. Recent changes in fishery regulations have placed greater emphasis on marine protected areas (MPAs) to preserve reef habitat, enhance reef fish production, conserve functional ecosystem processes, and protect a certain proportion of the population. After years of overexploitation, the TSER was established to protect the most important known multi-species aggregation site in the southeastern United States (Lindeman et al., 2000). Re-formation of the mutton snapper spawning aggregation has been documented since closure of the TSER to fishing, but little is known about adult reef fish movements in the region or the characterization of transient reef fish spawning aggregations at Riley's Hump.

Materials and Methods

Finfish – Acoustic Array

The acoustic receiver array was first deployed in three phases between May and July 2008. The array covers approximately 800 km^2 and is designed to capture small scale movement and long range migrations of fishes in water 5 – 50 meters deep. In the first phase, 33 VR2 receivers were placed within the DRTO, including within and outside the borders of the RNA. This work was funded by our USGS research grant: *Efficacy of a newly-established RNA for protecting coral reef fishes within DRTO*, but is complementary to the objectives of our CRCP grant. The second phase was completed in June 2008, with an additional 23 acoustic receivers placed throughout DRTO, the TNER and open use areas of the FKNMS. The final nine receivers were set up during July 2008 at RH in the TSER. The coverage of our array is complemented by two collaborative acoustic projects: Mote Marine Laboratory's Nurse shark project (PI: Wes Pratt) and a USGS sea turtle study (PI: Kristen Hart).

The receivers were secured to a PVC stand attached to a concrete platform that functioned as ballast and provided stability. The VR2 receivers were positioned "tip up" approximately 1 meter above the seafloor inside a PVC pipe sleeve (63.5 or 76.2 mm) and secured by a tie wrap. Each receiver tip was protected by a coat of antifouling paint. A 3 m subsurface buoy was attached to a stainless steel U-bolt at the base of each receiver stand with a 6.35 mm polypropylene line. Prior to deployment, each VR2 sonic receiver was initialized in the laboratory with a personal computer and VUE software provided by the manufacturer (VEMCO; AMIRIX Systems Inc.). Receiver sites were preselected based on reef fish population structure,

habitat type, rugosity, depth and reserve boundary locations. The VR2 receiver stand and a surface marker were dropped together from the research vessel when it was determined by a fathometer reading that the vessel was over sand substrate and site coordinates were immediately recorded upon deployment. A team of divers immediately confirmed the position and placement of the receiver stand on the seafloor. Receivers were serviced for maintenance twice per year in the field. Individual receivers were brought to the surface and data was uploaded to a personal computer using VUE software with an upload cable or by Bluetooth® technology. If the receiver required a battery replacement, the battery was replaced and the receiver was reinitialized. In addition, the subsurface buoy and line were scraped clean of fouling organisms.

Finfish – Acoustic Tagging

All fish captured at RH were surgically implanted with VEMCO V16-4H coded transmitter tags *in-situ* at 33 – 40 m. This avoided exposure of fish to barotrauma induced mortality associated with the capture of fish from relatively deep water. Fish were caught in fish traps baited with threadfin herring and sardines soaked 3 – 12 hrs. Traps were set on the south slope of RH in an area identified by Burton et al. (2005) as the focal point of the aggregation zone. Rather than hauling traps to the surface, fish were transferred from a trap to a catch bag by divers at depth. Each fish was positioned ventral side up in a V-cradle surgery station and a 2.5 cm incision was made along the midline, posterior to the pelvic girdle. Scales were removed on either side of the incision to expose the skin. The tag was implanted within the peritoneal cavity and the incision was closed with three hand tied sutures. Sterile synthetic absorbable braided sutures (VICRYL Plus; Ethicon, Inc.) with an antibacterial coating and a size 0 cutting needle were used. The entire underwater surgical procedure took approximately 3 – 6 minutes. Standard, fork and total lengths were recorded and the fish were immediately released.

Progress and Results

Finfish

During FY 2009, VR2 receivers were successfully uploaded, redeployed and are operational on or near their originally proposed locations (Figure 1). All receivers were serviced during May/June 2009 and October 2009. Sixty-five VR2 stations have recorded 856,000 detections since May 2008 (Table 1). Stations 20, 35, 35A, and 37B have large numbers of detections (> 50,000) because of one or two fish in residence near these inshore sites. The numerous detections at stations 2 and 48 are from multiple individual fish because of the proximity of these stations to spawning habitat along the southern slope of RH. Two stations (11 & 14) have yet to record detections and may be relocated. One receiver (site 67) in the TNER was not recovered in October 2009 due to poor underwater visibility. We expect to recover this receiver in May 2010. Two receivers malfunctioned in the RNA after the May 2009 upload (sites 20 & 69); consequently no data was collected May thru October 2009 at these sites. Both these receivers are part of our aging inventory of VR2s. We are in the process of phasing out old VR2s with new VR2Ws (Bluetooth®) programmed with Vemco's latest firmware. Receivers lost during Hurricane Ike in 2008 have not been recovered. Three of these sites (32, 34, 36) were searched during October 2009, but no evidence of the VR2s were found. It is not known if these receivers were swept away by storm surge or were simply buried by shifting sand. The portion of the RNA array along the southern RNA boundary was repositioned into deeper water in October

2008, along the reef line to the south of Bird Key. All VR2s in the array are currently in deeper water (>15 m) to avoid storm surge in the future.

Selected reef fish species were acoustically tagged inside the TSER during June 2009. Fifteen mutton snapper, *Lutjanus analis*, 4 black grouper, *Mycteroperca bonaci*, and 1 Nassau grouper, *Epinephulus striatus*, were acoustically tagged from the M/V Spree. This effort brings the cumulative number of acoustically tagged fish in the TSER to 23 mutton snapper, 4 black grouper, 2 Nassau grouper, and 3 red grouper (Table 2). Additionally, snapper and groupers were also tagged in the DRTO/RNA, potentially contributing to telemetry data collected at RH. Approximately 59 % of fish tagged within the TSER have been successfully tracked greater than 20 days since the inception of the study. The average tracking period for these fish is 99 days (+/- 102 sd). Preliminary results indicate a possible corridor exists for the seasonal movements of mutton snapper between the DRTO/RNA and the TSER, providing a link between marine protected areas (Figure 2). Individual mutton snapper were documented making repeated migratory round trips (up to 3 trips/fish) to spawning grounds during the spawning season (May to August). Individual fish stay on the spawning grounds for up to 10 days surrounding the full moon phase before returning to the DRTO/RNA. Limited movement has been detected to the east or directly north to the TNER, however one mutton snapper tagged at RH was detected near the TNER and later at Pulaski Shoals, a movement of 40 km in 2 days. Mutton snapper appear to emigrate from RH by the end of August, although possible residential mutton snapper have been observed there as late as October.

A relatively large (~ 4000) active swimming aggregation of *L. analis* was documented on 12th June 2009 between 1415 and 1715 hrs, 5 d after the full moon, along the south slope of RH (35 – 50 m). At 1615 hrs, approximately 60 fish separated into a tightening spiraling subgroup above the aggregation and released a cloud of gametes that were dispersed by tail thrusts as the fish separated and descended. This sequence was observed 20 m below the surface twice in 5 min, preceded by two similar events without a release of gametes. Additionally, conspecific groups of *Lutjanus cyanopterus*, *Lutjanus jocu*, and *Trachinotus falcatus* were nearby, and spawning coloration displays by *Caranx chrysos* and *Caranx hippos* were noted. The spawning of this species was previously described in Belize by Heyman (2008); however, this is the first time mutton snapper has been observed spawning in Florida. In addition, the number of snapper observed in the aggregation represents a significant increase in the size of the spawning population since first reported by Burton et al. (2005). These authors previously observed an increasing number of fish in annual surveys in successive years; from a solitary fish in 1999 to 300 fish in 2004. Together these findings provide clear empirical evidence that this marine protected area is contributing significantly to the preservation of coral reef resources in the Dry Tortugas.

Extensive nurse shark and sea turtle data have been collected by the array in addition to long range movement information on lemon sharks tagged near Jupiter, FL (S. Gruber, Bimini Biological Station). Furthermore, the presence of a solitary white shark near a snapper spawning aggregation was confirmed by a benthic video/acoustic recorder on Riley's Hump during June 2009.

Future Work

Finfish

Our Tortugas Regional Array covering TNER, TSER, RNA, DRTO and open use areas of the FKNMS is continuously collecting data. We will continue to coordinate and share data with other regional telemetry projects (Pratt-Mote; Hart-USGS). These concurrent studies provide additional receiver coverage along the north side and central portion of the RNA. Fishes that are tagged at the spawning aggregation site may be detected at stations established by these research groups and vice versa, providing invaluable data on the connectivity of this coral reef ecosystem.

All VR2s will be serviced and downloaded during May 2010 & October 2010. These data will include fish tagged in 2008, 2009 and fish to be tagged in 2010. In addition our VR28, a tracking 4-channel receiver that provides transmitter position and bearing, will be towed from a small boat and used to expand spatial coverage of the VR2s. Specific areas to be covered by the VR28 include the deep water TSER habitat (Miller's Ledge) and deeper water west of RH.

A cruise to RH will be scheduled for May 2010 (peak spawning period) to acoustically tag mutton snapper (n = 10) and black grouper (n = 10). Fish will be surgically implanted *in-situ* with V16 coded transmitters that use a single-frequency coding scheme. Ten of these transmitters will be equipped with a depth sensor and all transmitters will last the duration of the study. During the CRCP timeframe, we will continue to tag the snapper/grouper complex of fish on our RNA project (FWC/USGS), which focuses on immigration and emigration of targeted reef fishes in and near the RNA, potentially contributing to information collected at RH. Data downloaded will yield time, location and depth and will provide species-specific information on fish movement rates and spawning activities. This information will be analyzed to examine movement and core habitat utilization areas of snappers/groupers and determine long range movement between MPAs. All data collected will be entered into an FWC Access data base with statistical analyses using SPSS or SAS. Spatial and temporal data will be processed using Arcview GIS and Tracking Analysis software to examine movement patterns in association with habitats and MPA boundaries. An oral presentation on our research progress will be given at the National Park Service/Florida Fish and Wildlife Conservation Commission RNA Workshop on January 12th 2010. We expect sufficient data to be collected for the preparation of a peer-reviewed manuscript to commence by November 2010.

DRY TORTUGAS - LOBSTER

Lobster – Acoustic tagging

Twelve spiny lobsters were captured within the boundaries of the DRTO and Vemco acoustic tags were attached. All lobsters were tagged with V16 acoustic transmitters on Oct. 7- 8, 2009. One female was tagged near the south boundary of DTRO. The others were tagged in the vicinity of Fort Jefferson where the concentration of VR2 receivers is greatest. Lobsters were taken from their dens by SCUBA divers and placed in a live well on the research vessel. Acoustic tags were placed on the carapace of each lobster with the use of plumber's epoxy clay. Lobsters remained submerged through the entire process to minimize stress to the animal. Lobsters were measured and sexed and the reproductive status of each female was assessed.

Once tagged and all data collected, lobsters were returned to their original den. Size of tagged lobsters ranged from 74 mm to 156 mm carapace length. Results from this effort will be summarized in the FY 2010 final report.

WESTERN SAMBO ECOLOGICAL RESERVE - LOBSTER

Introduction

Lobsters were re-surveyed in WSER, Eastern Sambo Special Use Area (ESSUA), Middle Sambo, and Pelican Shoal during 2009. Both WSER and ESSUA are no-take reserves and Middle Sambo and Pelican Shoal are open fished zones. Additionally, this year we surveyed lobsters in the outlier reef just south of the WSER boundaries, where lobsters appear to release their eggs (R. Bertelsen, pers. comm.). We used size distribution surveys and 500 m^2 belt transect surveys of spiny lobsters inside marine reserve zones and their exploited reference areas in FKNMS during the closed fishing season to determine lobster size, sex, and abundance. Sampling was designed to test the hypothesis that no-take zones would sufficiently protect lobsters so that lobsters in these areas would become larger and more abundant than those in unprotected areas.

Methods

Lobster - Size distribution surveys

Three-hundred and ninety-nine lobsters were captured for size structure estimates (Table 3 and 4). We measured lobsters and examined them for molt condition, sex, reproductive status (females), and evidence of disease. We stratified sampling by habitat type because we expected each habitat to shelter a different size range of spiny lobsters (Hunt et al., 1991). Strata included fore/backreef, patch reef, and outlier reef. We attempted to capture at least 50 spiny lobsters per stratum inside and outside the reserves.

Lobster Monitoring - Area Surveys

To compare abundance, we searched for lobsters in reserves (WSER and ESSUA) and reference (Pelican Shoal and Middle Sambo) zones using area-based surveys. Divers counted all lobsters in 143 transects (500 m^2) on the fore/backreef, outlier reef (no reference site), and patch reefs of reserve and reference areas. Divers searched a 5 m wide area on each side of a 50 m tape and replicated this measure in each habitat.

Lobster Monitoring - Statistics

If data met the requirements, we used parametric tests (t tests and ANOVA); if not, we used non-parametric tests (Mann-Whitney and Kruskal-Wallis). Mean size of lobsters from the fore/backreef was compared using ANOVA with a Hochberg post hoc test. Males and females were separated to control for the different ratios of males to females in our samples, since males tend to be larger. The two patch reef sites were compared with an independent samples t-test (males) and Mann-Whitney Test (females). We did not include the outlier reef since it did not have a comparable reference site. Tests of sexual dimorphism (male - female size) for the fore/backreef within and outside the reserve were conducted using a multiple T-test assuming unequal variance due to the unequal sample sizes. Differences in lobster density between regions were evaluated using the Kruskal-Wallis Test and t-test. Again, we did not include the outlier

reef, since it did not have a reference site. Differences in lobster density between habitat types were evaluated using the Kruskal-Wallis Test and Mann-Whitney Test.

Results

Lobster - Inside and outside the Marine Reserves

There were significant differences in size of male lobsters from each of the fore/backreef regions (Pelican Shoal, WSER, Middle Sambo and ESSUA) (Table 4, ANOVA, d.f. = 3, F = 2.88, P = 0.040). Males from WSER were larger than those from Pelican Shoal. There were no differences in size between regions among female lobsters residing at the fore/backreef (Table 4, ANOVA, d.f. = 3, F = 1.48, P = 0.222). There were also no differences in size of females (Mann-Whitney test, $U = 149.5$, $P = 0.438$) or males (t test, d.f. = 50, $t = 1.238$, $P = 0.222$) from the patch reef regions. In general, the mean size of male and female lobsters increased from Pelican Shoal (outside WSER) through Middle Sambo (adjacent to WSER) to WSER itself (Table 4). Although the ESSUA is technically a lobster no-take zone, the small size of this reserve provides no practical protection for those resident lobsters, so the size of its lobsters is very similar to adjacent Middle Sambos and Pelican Shoal.

Lobster- habitat type

There were significant differences in size of females lobsters from each of the three habitats (Table 4, Kruskal-Wallis Test, $\chi^2 = 11.64$, d.f. = 2, $P = 0.003$). Females caught on the patch reefs were significantly smaller than those caught on the fore/backreef (Mann-Whitney test, $U = 1830.5$, $P = 0.002$) or the outlier reef (Mann-Whitney test, $U = 487.5$, $P = 0.003$).

Lobster - Sexual dimorphism

A comparison of mean carapace size (CL) between male and female lobsters is presented in Table 5. Significant difference in size between males and females should be an indicator of an effective marine protected area, since protected males are likely growing faster than protected females. Sexual dimorphism in size also generally increased from east to west. Size differences between male and female lobsters were greatest inside the WSER where the differences approached 10 mm CL in the patches and were nearly 7 mm CL in the fore/backreef. In the fished area, the size differences were the least at Pelican Shoal, 2 mm CL. Statistically significant differences in size were found at the WSER fore/backreef, Western Sambo outlier reef, and Middle Sambo. Even though Middle Sambo reef is a fished area, the significant difference in size between males and females and close proximity to WSER may indicate spillover. Although the ESSUA reef is within a marine reserve, its small size (<1 km^2) compared to typical lobster movement (>1 km/day) preclude it from affording protection for resident lobsters.

Lobster - Density

Lobster densities per 500 m^2 transect are reported in Table 7. There were no differences in density of lobsters between any of the fore/backreef locations (Pelican Shoal, WSER, Middle Sambo and Eastern Sambo) (Kruskal-Wallis test, $\chi^2 = 2.797$, d.f. = 3, $P = 0.424$) or patch reef locations (Pelican Shoal and WSER) (t test, d.f. = 41, $t = .930$, $P = 0.358$), but there were differences in density between the habitat types (Kruskal-Wallis test, $\chi^2 = 12.87$, d.f. = 2, $P = 0.002$). There were significantly fewer lobsters at the patch reefs than at the fore/backreef (Mann-Whitney test, $U = 1075.0$, $P = 0.000$).

Lobster – Outlier reef

The sex ratio at the outlier reef was more skewed than at other locations (Table 3). This result is consistent with FWC's observations of lobsters tagged with sonic tags. The outlier reef appears to be where a number of females go to release their eggs (R. Bertelsen pers. comm.). The influx of migrating females could account for the skewed sex ratio during the breeding season (Mar-Sept).

Future Work

Lobster

We will continue annual surveys of spiny lobster in and adjacent to the WSER and incorporate sonic tagging of spiny lobsters in the Tortugas region. We will continue to use a combination of belt-transects and the capture, measurement and release of at least 50 spiny lobsters per stratum to estimate abundance and size structure inside and outside the ERs. We will also focus more on the outlier reef.

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Projects

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Figure 1. The TSER, TNER, and RNA within the DRTO create a network of no-take reserves that protect 600 km^2 of coral reef habitat in the Dry Tortugas. Location of FWC VR2 receivers are indicated for FY 2009. The FWC array is complemented by two collaborative telemetry projects: the Mote Marine Laboratory nurse shark project (PI: Dr. Wes Pratt) and USGS sea turtle project (PI: Dr. Kristen Hart).

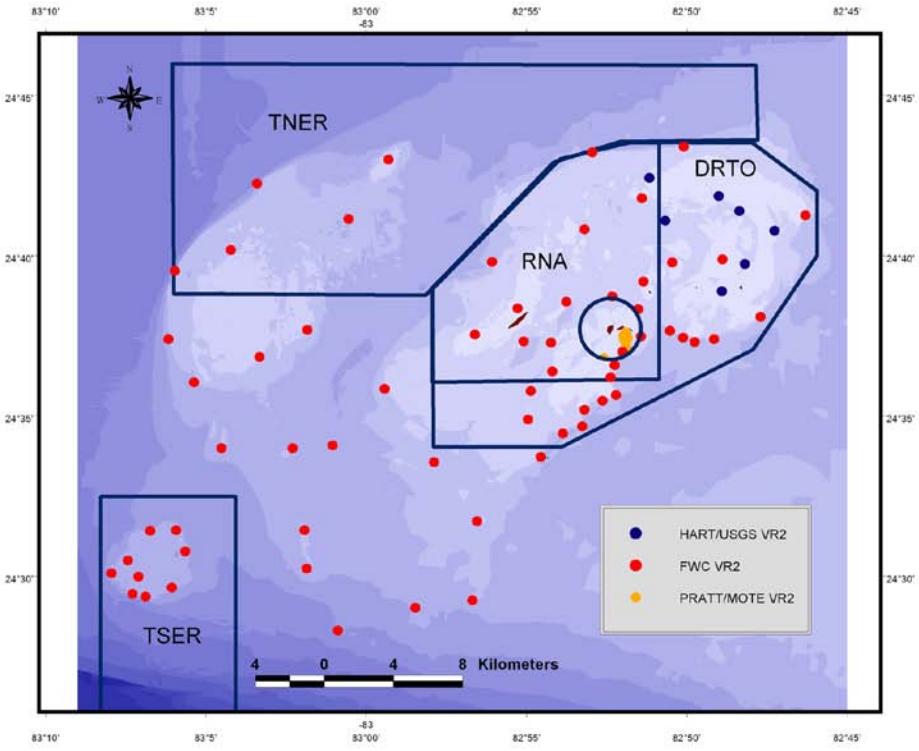

Figure 2. Tagging sites and preliminary spawning migratory movements of mutton snapper in the Dry Tortugas region.

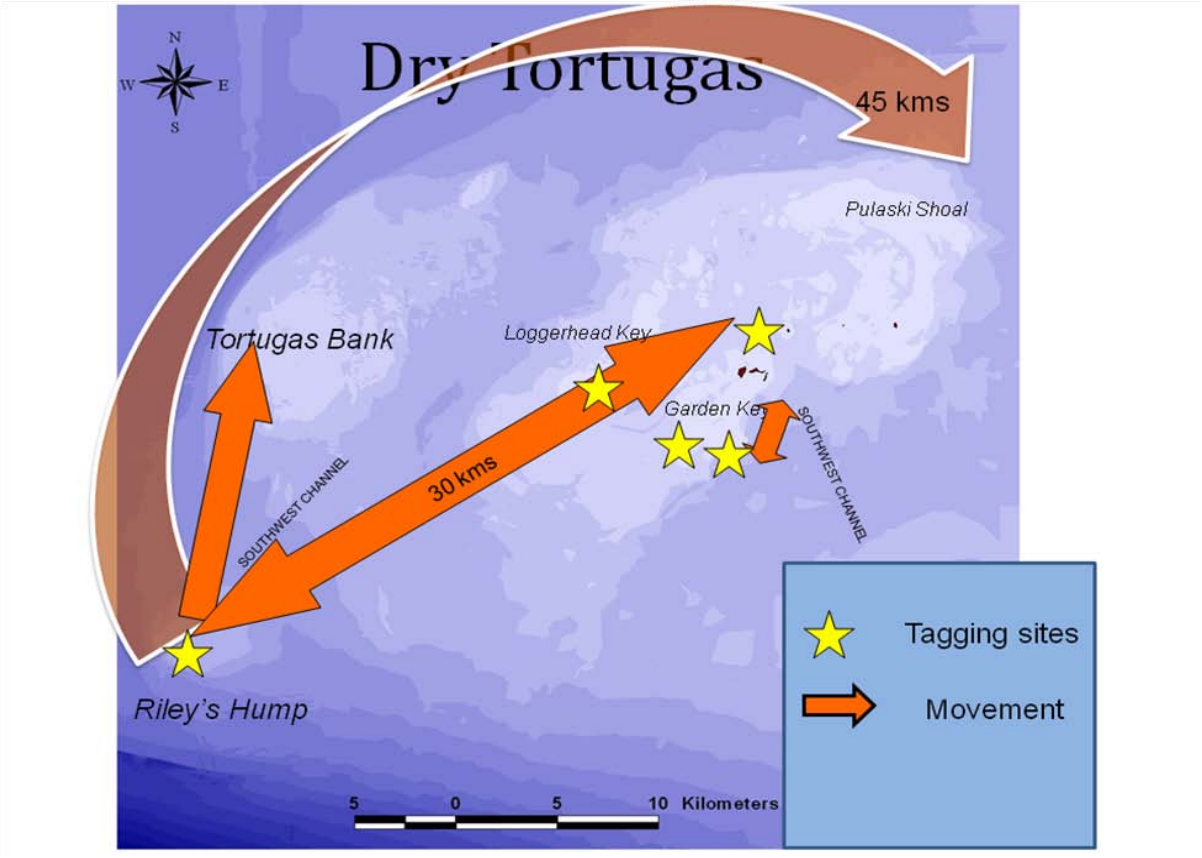

Table 1. Location of VR2 receiver stations in the Dry Tortugas region. The management zone and cumulative number of detections is included for each station. Tortugas South Ecological Reserve (TSER), Tortugas North Ecological Reserve (TNER), Dry Tortugas National Park (DRTO), Research Natural Area (RNA), Florida Keys National Marine Sanctuary (FKNMS) and open waters (OPEN).

STATION	LATD	LATM	LOND	LONM	DEPTH (M)	ZONE	Number of Detections
1	24	30.077	83	7.943	31.4	TSER	2650
2	24	29.435	83	7.291	32.6	TSER	104454
3	24	29.968	83	7.103	30.5	TSER	6236
4	24	29.631	83	6.065	34.4	TSER	23756
5	24	30.478	83	7.431	32.3	TSER	28
6	24	31.408	83	6.732	28.7	TSER	78
7	24	31.422	83	5.926	27.4	TSER	892
8	24	39.520	83	5.966	34.7	TNER	82
9	24	36.036	83	5.371	30.5	OPEN	20
10	24	36.824	83	3.325	20.7	FKNMS	5
11	24	37.673	83	1.838	17.4	FKNMS	0
12	24	42.994	82	59.301	18.3	TNER	39
14	24	30.222	83	1.852	28.3	OPEN	0
15	24	35.839	82	59.420	19.2	FKNMS	15
16	24	33.551	82	57.880	19.1	FKNMS	5
17A	24	33.710	82	54.547	22.9	FKNMS	149
18	24	31.424	83	1.927	25.6	FKNMS	22
19	24	28.997	82	58.463	31.1	OPEN	19
20	24	39.185	82	51.348	15.2	RNA	131354
21	24	38.648	82	51.336	12.2	RNA	343
22	24	38.316	82	51.514	14.6	RNA	285
25	24	36.991	82	52.000	22.6	RNA	10890
26	24	36.572	82	52.246	22.3	RNA	2132
27	24	36.198	82	52.366	24.4	RNA	7403
28	24	35.638	82	52.200	24.4	DRTO	2845
29	24	35.462	82	52.619	24.4	DRTO	31698
33	24	36.329	82	53.041	8.5	RNA	41
35	24	36.384	82	54.148	6.1	RNA	51407
37	24	37.647	82	53.980	19.2	RNA	16
38	24	37.807	82	53.355	16.8	RNA	24
39	24	37.810	82	52.679	12.8	RNA	268
40	24	38.234	82	52.086	13.7	RNA	562
41	24	39.778	82	50.450	16.2	DRTO	343
44	24	37.642	82	50.522	21.9	DRTO	4756
45	24	37.428	82	50.112	22.6	DRTO	2981
46	24	37.293	82	49.749	25.6	DRTO	254
47	24	37.387	82	49.150	22.6	DRTO	169
48	24	29.346	83	6.878	29.6	TSER	54772
49	24	30.762	83	5.647	25.6	TSER	3517
50	24	37.387	83	6.165	33.8	OPEN	41
51	24	33.984	83	4.512	26.5	OPEN	2

52	24	40.172	83	4.219	22.3	TNER	51
53	24	42.242	83	3.407	34.1	TNER	106
54	24	33.986	83	2.295	26.2	FKNMS	14
55	24	34.076	83	1.046	26.2	FKNMS	16
56	24	41.128	83	0.546	24.4	TNER	70
57	24	29.234	82	56.686	25.6	FKNMS	148
58	24	38.345	82	55.275	4.4	RNA	90
59	24	37.313	82	55.082	22.6	RNA	1979
60	24	40.814	82	53.187	15.5	RNA	20881
61	24	41.786	82	51.397	14.9	RNA	234
62	24	43.477	82	48.530	16.2	DRTO	16
62A	24	43.393	82	50.089	27.1	DRTO	* Not listed in VUE
63	24	39.872	82	48.885	13.1	DRTO	135
64	24	38.083	82	47.692	22.3	DRTO	560
65	24	41.251	82	46.291	22.6	DRTO	1364
66	24	31.710	82	56.535	18.3	FKNMS	58
67	24	43.217	82	52.946	29.6	RNA	30
68	24	37.533	82	56.605	6.1	RNA	3839
69	24	39.800	82	56.073	24.4	RNA	* Not listed in VUE
70	24	32.642	82	55.796	25.0	OPEN	* Not listed in VUE
24A	24	37.467	82	51.426	21.3	RNA	2731
30A	24	35.182	82	53.185	22.3	DRTO	1569
31A	24	34.662	82	53.257	22.3	DRTO	682
32A	24	34.441	82	53.863	23.8	DRTO	920
33A	24	34.878	82	54.950	17.7	DRTO	2
34A	24	35.764	82	54.858	18.3	DRTO	227
35A	24	36.377	82	54.195	14.3	RNA	90248
36A	24	37.274	82	54.230	13.4	RNA	138
37B	24	38.549	82	53.753	21.0	RNA	287668
40A	24	38.719	82	52.321	20.7	RNA	387
14A	24	28.287	83	0.885	44.2	OPEN	* Not listed in VUE

Table 2. All acoustically tagged fish captured and released in the Dry Tortugas between May 2008 - October 2009, including the date of last known detection and the number of days an individual fish was tracked (d). All fish tagged at Riley's Hump are indicated by the Tortugas South Ecological Reserve (TSER) zone.

Species	Date	Zone	Depth (m)	TL (mm)	Code	Tag type	Last detection	Tracking duration (d)
Epinephelus morio	7/3/2008	TSER	25.9	685.8	2153	V16-3H	no detections	0
Epinephelus morio	7/3/2008	TSER	26.8	584.2	2166	V16-4H	7/16/2008	13
Epinephelus morio	7/6/2008	TSER	37.5	406.4	2154	V16-3H	12/3/2008	147
Epinephelus striatus	7/5/2008	TSER	33.6	584.2	49585	V16-4H	8/20/2008	45
Epinephelus striatus	6/11/2009	TSER	32.0	660.4	52510	V16P-4H	10/2/2009	111
Haemulon plumieri	5/19/2008	DRTO	6.4	289.0	49601	V9-2L	no detections	0
Haemulon plumieri	5/27/2008	RNA	10.1	253.0	49595	V9-2L	no detections	0
Haemulon plumieri	5/27/2008	RNA	4.6	272.0	49602	V9-2L	no detections	0
Lutjanus analis	5/16/2008	DRTO	9.8	647.7	2170	V16-4H	9/3/2009	467
Lutjanus analis	5/17/2008	DRTO	8.5	609.6	2175	V16-4H	7/15/2009	418
Lutjanus analis	5/17/2008	DRTO	8.5	551.2	2176	V16-4H	7/15/2009	418
Lutjanus analis	5/22/2008	RNA	12.2	468.0	2174	V16-4H	no detections	0
Lutjanus analis	5/24/2008	DRTO	14.9	610.0	2185	V16-4H	8/8/2008	74
Lutjanus analis	5/26/2008	RNA	4.6	566.0	2168	V16-4H	8/23/2009	447
Lutjanus analis	5/30/2008	RNA	7.3	692.0	2167	V16-4H	7/15/2009	405
Lutjanus analis	5/30/2008	RNA	7.3	645.0	2177	V16-4H	7/15/2009	405
Lutjanus analis	7/1/2008	TSER	29.0	508.0	49589	V16-4H	8/13/2008	42
Lutjanus analis	7/1/2008	TSER	32.6	635.0	49590	V16-4H	8/22/2008	51
Lutjanus analis	7/1/2008	TSER	29.0	609.6	49591	V16-4H	9/5/2008	64
Lutjanus analis	7/2/2008	TSER	27.5	469.9	13675/ 55	V16P-4H	7/5/2008	3
Lutjanus analis	7/5/2008	TSER	36.6	457.2	13674/54	V16P-4H	7/25/2008	20
Lutjanus analis	7/5/2008	TSER	36.6	482.6	13677/ 57	V16P-4H	9/11/2009	426
Lutjanus analis	7/5/2008	TSER	33.6	482.6	13678/58	V16P-4H	5/5/2009	300
Lutjanus analis	7/5/2008	TSER	33.6	577.9	13679/ 59	V16P-4H	7/26/2008	21
Lutjanus analis	10/13/2008	RNA	4.3	603.3	2198	V16-4H	10/6/2009	353
Lutjanus analis	10/13/2008	RNA	4.3	590.6	2200	V16-4H	10/21/2008	8
Lutjanus analis	10/13/2008	RNA	4.3	571.5	2201	V16-4H	10/6/2009	353
Lutjanus analis	10/13/2008	RNA	4.3	590.6	49587	V16-4H	10/15/2008	2
Lutjanus analis	10/13/2008	RNA	4.3	717.6	49588	V16-4H	7/14/2009	271
Lutjanus analis	10/14/2008	DRTO	2.1	616.0	52502	V16-4H	6/11/2009	237
Lutjanus analis	10/15/2008	RNA	11.0	743.0	52503	V16-4H	10/20/2008	5
Lutjanus analis	10/15/2008	RNA	11.0	704.9	52504	V16-4H	10/6/2009	351
Lutjanus analis	10/15/2008	RNA	11.0	533.4	52505	V16-4H	10/6/2009	351
Lutjanus analis	5/9/2009	RNA	8.5	520.7	56742	V16-4H	9/11/2009	122
Lutjanus analis	5/12/2009	RNA	4.6	609.6	52507	V16-4H	7/14/2009	62
Lutjanus analis	5/12/2009	RNA	4.6	584.2	52508	V16-4H	no detections	0
Lutjanus analis	5/13/2009	RNA	9.5	647.7	52509	V16-4H	no detections	0
Lutjanus analis	6/9/2009	TSER	34.2	609.6	131/14805	V16P-4H	6/10/2009	1
Lutjanus analis	6/9/2009	TSER	32.0	635.0	13676/ 56	V16P-4H	6/28/2009	19
Lutjanus analis	6/9/2009	TSER	32.0	635.0	13680/ 60	V16P-4H	6/18/2009	9
Lutjanus analis	6/9/2009	TSER	32.0	711.2	13682/ 62	V16P-4H	7/2/2009	23
Lutjanus analis	6/9/2009	TSER	34.2	609.6	13683/ 63	V16P-4H	7/13/2009	34

Lutjanus analis	6/10/2009	TSER	32.0	609.6	52515	V16P-4H	7/12/2009	32
Lutjanus analis	6/11/2009	TSER	36.6	469.9	52511	V16P-4H	8/29/2009	78
Lutjanus analis	6/11/2009	TSER	32.0	660.4	52512	V16P-4H	6/13/2009	2
Lutjanus analis	6/11/2009	TSER	32.0	622.3	52513	V16P-4H	6/18/2009	7
Lutjanus analis	6/11/2009	TSER	34.2	736.6	52514	V16P-4H	9/11/2009	90
Lutjanus analis	6/11/2009	TSER	32.0	584.2	52516	V16P-4H	7/29/2009	48
Lutjanus analis	6/11/2009	TSER	32.0	673.1	13681/ 61	V16P-4H	6/15/2009	4
Lutjanus analis	6/12/2009	TSER	36.6	673.1	56746	V16P-4H	6/19/2009	7
Lutjanus analis	6/12/2009	TSER	32.0	723.9	56747	V16P-4H	6/19/2009	7
Lutjanus analis	6/12/2009	TSER	32.0	711.2	56748	V16P-4H	7/15/2009	33
Lutjanus analis	9/25/2009	RNA	12.5	762.0	56744	V16-4H	no detections	0
Lutjanus analis	9/27/2009	RNA	4.6	762.0	14806/132	V16P-4H	no detections	0
Lutjanus analis	9/28/2009	RNA	11.9	565.2	14802/128	V16P-4H	10/5/2009	7
Lutjanus analis	9/29/2009	RNA	4.3	736.6	14803/129	V16P-4H	no detections	0
Lutjanus analis	9/30/2009	RNA	5.8	622.3	14804/130	V16P-4H	10/5/2009	5
Mycteroperca bonaci	5/21/2008	RNA	10.7	609.0	2173	V16-4H	no detections	0
Mycteroperca bonaci	5/26/2008	RNA	6.1	438.0	2169	V16-4H	12/3/2008	187
Mycteroperca bonaci	5/29/2008	DRTO	10.1	618.0	2171	V16-4H	6/29/2009	390
Mycteroperca bonaci	5/29/2008	RNA	8.5	548.0	2172	V16-4H	8/31/2008	92
Mycteroperca bonaci	5/30/2008	DRTO	9.2	562.0	2184	V16-4H	8/19/2008	79
Mycteroperca bonaci	6/3/2008	DRTO	14.9	640.0	2165	V16-4H	6/6/2008	3
Mycteroperca bonaci	10/11/2008	RNA	7.3	431.8	49586	V16-4H	11/2/2008	21
Mycteroperca bonaci	10/14/2008	DRTO	1.5	666.8	52506	V16-4H	no detections	0
Mycteroperca bonaci	5/8/2009	DRTO	10.4	533.4	56751	V16-4H	no detections	0
Mycteroperca bonaci	5/9/2009	DRTO	10.4	381.0	56730	V9-2L	no detections	0
Mycteroperca bonaci	5/9/2009	DRTO	10.4	469.9	56731	V9-2L	no detections	0
Mycteroperca bonaci	5/10/2009	DRTO	14.0	520.7	56736	V16-4H	10/3/2009	143
Mycteroperca bonaci	6/10/2009	TSER	27.5	1069.0	21	V16P-5H-S256	10/2/2009	112
Mycteroperca bonaci	6/10/2009	TSER	33.6	921.0	23	V16P-5H-S256	10/2/2009	112
Mycteroperca bonaci	6/10/2009	TSER	33.6	921.0	28	V16P-5H-S256	6/11/2009	1
Mycteroperca bonaci	6/10/2009	TSER	34.2	975.0	29	V16P-5H-S256	10/2/2009	112
Mycteroperca bonaci	9/26/2009	RNA	12.8	457.2	56741	V16-4H	no detections	0
Ocyurus chrysurus	5/16/2008	DRTO	9.8	432.0	49599	V9-2L	6/17/2009	391
Ocyurus chrysurus	5/17/2008	DRTO	8.5	381.0	49597	V9-2L	5/23/2008	6
Ocyurus chrysurus	5/17/2008	DRTO	8.5	432.0	49598	V9-2L	2/28/2009	281
Ocyurus chrysurus	5/19/2008	DRTO	6.1	376.0	49596	V9-2L	no detections	0
Ocyurus chrysurus	5/19/2008	DRTO	6.1	401.0	49600	V9-2L	8/18/2008	89
Ocyurus chrysurus	10/10/2008	DRTO	10.4	438.2	52519	V9-2L	9/10/2009	330
Ocyurus chrysurus	10/10/2008	DRTO	10.4	406.4	52520	V9-2L	9/17/2009	337
Ocyurus chrysurus	10/10/2008	DRTO	10.4	444.5	52521	V9-2L	8/16/2009	306
Ocyurus chrysurus	10/11/2008	RNA	7.3	419.1	52517	V9-2L	no detections	0
Ocyurus chrysurus	10/11/2008	RNA	7.3	514.4	52518	V9-2L	6/27/2009	256
Ocyurus chrysurus	5/7/2009	DRTO	9.5	401.3	56732	V9-2L	8/20/2009	103

Ocyurus chrysurus	5/7/2009	DRTO	9.5	426.7	56733	V9-2L	10/6/2009	149
Ocyurus chrysurus	5/7/2009	DRTO	9.5	374.7	56734	V9-2L	6/6/2009	29
Ocyurus chrysurus	9/24/2009	DRTO	11.9	440.0	61844	V9-2x	10/7/2009	13
Ocyurus chrysurus	9/24/2009	DRTO	11.9	406.4	61845	V9-2x	10/7/2009	13
Ocyurus chrysurus	9/25/2009	RNA	12.5	508.0	61843	V92x	no detections	0
Ocyurus chrysurus	9/25/2009	RNA	12.5	406.4	61841	V92x	10/1/2009	6
Ocyurus chrysurus	9/25/2009	RNA	8.8	431.8	61842	V92x	no detections	0

Table 3. Number of lobsters collected for size distribution analysis by region and habitat (males/females).

		Habitat		
Region **(Bold = reserve)**	Fore/backreef	Outlier reef	Patch reef	Total
Pelican Shoal	56 (20/36)		41 (25/16)	97(45/52)
Eastern Sambo (SUA)	65 (27/38)			65 (27/38)
Middle Sambo	61 (28/33)			61 (28/33)
Western Sambo (ER)	67 (30/37)		49(27/22)	116(57/59)
Western Sambo		60 (18/42)		60 (18/42)
Total	249(105/144)	60 (18/42)	90(52/38)	399(175/224)

Table 4. Mean size of lobster by sex, habitat, and region.

Habitat	Region (**Bold = reserve**)	Males Mean ±SD	Females Mean ±SD	Overall Mean ±SD
Fore/backreef	Pelican Shoal	79.0±7.1	76.9±6.1	78.0±6.6
	Eastern Sambo SUA	82.6±11.2	78.4±7.3	80.5±9.2
	Middle Sambo	82.7±6.3	77.1±7.2	79.9±6.8
	Western Sambo ER	86.8±11.2	80.1±7.7	83.4±9.4
Patch reef	Pelican Shoal	73.1±15.7	68.3±10.3	70.7±13.0
	Western Sambo ER	79.4±20.4	69.9±17.9	74.7±19.1
Outlier reef	Western Sambo	83.9±5.9	78.8±5.5	81.3±5.7
	Overall	81.1±11.1	75.6±8.9	

Table 5. Results of multiple T-tests comparing mean size (CL) of male and female lobsters.

Location(**bold = reserve**)	t	df	Sig. (2 tailed)	Mean difference
Pelican Shoal fore/backreef	1.06	34.02	.269	2.00
Eastern Sambo SUA f/breef	1.67	41.31	.102	4.11
Middle Sambo fore/backreef	3.25	58.89	.002	5.62
Western Sambo ER f/breef	2.82	49.47	.007	6.78
Pelican Shoal patch	1.20	38.95	.239	4.87
Western Sambo ER patch	1.74	46.71	.089	9.50
Western Sambo outlier reef	3.13	30.29	.004	5.13

Table 6. Number of transect (500 m^2) surveys conducted by region (note: Patch reef transects were stratified equally into 10 top and 10 side transects).

	Habitat			
Region **(Bold = reserve)**	Fore/backreef	Outlier reef	Patch reef	Total
Pelican Shoal	20		20	40
Eastern Sambo (SUA)	20			20
Middle Sambo	20			20
Western Sambo (ER)	20		23	43
Western Sambo		20		20
Total	80	20	43	143

Table 7. Number of lobsters per 500 m^2.

		Habitat		
Region **(Bold = reserve)**	Fore/backreef Mean±SD	Outlier reef Mean±SD	Patch reef Mean±SD	Overall Mean±SD
Pelican Shoal	1.60±1.39		.75±1.02	1.18±1.21
Eastern Sambo (SUA)	3.30±3.70			3.30±3.70
Middle Sambo	3.55±3.62			3.55±3.62
Western Sambo (ER)	2.35±2.41		1.09±1.31	1.72±1.86
Western Sambo		1.65±1.69		1.65±1.69
Total	2.24±2.56	1.65±1.69	1.28±1.17	2.28±2.42