Project Period	12/01/2017 - 12/01/2018
Project Location Description (from Proposal)	Marine protected areas across Mexico, Belize, Guatemala, and Honduras including Isla Mujeres, Punta Cancun y Punta Nizuc, Xcalak, Banco Chinchorro, Half Moon Caye, Port Honduras, South Water Caye, Punta de Manabique, Cayos Cochinos, Sandy Bay - West End, and Turtle Harbour - Rock Harbour.
Project Summary (from Proposal)	Support coral reef regional planning across 12 priority reefs in Mexico, Belize, Guatemala, and Honduras by building local capacity to interpret ecological and genetic data and using available models to manage important reef fish stocks beyond protected area boarders. Project will provide training for at least two management organizations in each of the four countries to develop targeted conservation strategies and monitor changes in coral reef ecosystems resulting from management.

Project Status and Accomplishments

A fundamental challenge facing conservation scientists and resource managers is developing and maintaining
effective marine protected area networks. This project enhanced protected areas management along the Mesoamerican reef by 1) assessing spatial patterns of reef fish population connectivity using genetic analysis
coupled with biophysical modeling; 2) integrating spatial patterns of connectivity with ecological, environmental, and
fisheries catch data to evaluate the effectiveness of protected areas networks for reef fish management; and 3) building
local capacity to interpret and use scientific data in protected area management planning. The project supported coral reef regional planning across 12 priority reefs in Mexico, Belize, Guatemala, and Honduras by building local capacity to interpret ecological and genetic data and by developing a tool to evaluate and predict marine protected area effectiveness.

The most significant achievements of this project are as follows:

1. Collated and genotyped 556 stoplight parrotfish (Sparisoma viride), spiny lobster (Panulirus argus) and red mangrove (Rhizophora mangle) samples from 21 sites for genetic connectivity analysis.
2. Developed ecological models and an open access evaluation tool to assess trends in fish biomass and benthic cover, identified main drivers for ecological change in fish and benthic communities by integrating ecological, fisheries, environmental, and population connectivity data, predicted potential total fish biomass and biomass of commercially and ecologically important reef fishes in a given reef (in or out MPAs) based on a core set of explanatory variables, and provided management recommendations to decision makers and set expectations for protected area performance based on the above analyses.
3. Led a workshop on Caye Caulker, Belize, from the 23rd to 25th October 2018, as part of a combined effort with the Healthy Reefs for Healthy People Initiative’s 6th annual regional partner meeting. These events were combined to provide the greatest access to a wide audience of stakeholders from across the Mesoamerican reef region. A total of 55 participants from 42 institutions from across the four countries attended the three-day event, with representatives from government and non-government organizations

Lessons Learned

We met our goals to assess genetic connectivity, develop a tool to evaluate and predict protected area effectiveness, and share our results with local stakeholders. Due to delays in the research permitting process we were not able to obtain genetic samples from Guatemala. In addition, we were not able to complete draft manuscripts for submission to scientific journals. The permitting process is often a cause for project delays in the Caribbean. However, in the future, we will collaborate with additional partners to expedite the process.

The feedback from the joint conference was extremely positive. Resource managers from governments and NGOs were excited about applying the protected area evaluation tool in their MPAs and other management areas. Conference participants provided valuable feedback allowing us to evolve the tool based on manager needs. The revised tool will be finalized and published in the public domain in the coming months.

Activities and Outcomes

Funding Strategy: Planning, Research, Monitoring
Metric: Coral - Research - # research studies completed
Required: Recommended
Description: Enter the number of research studies completed

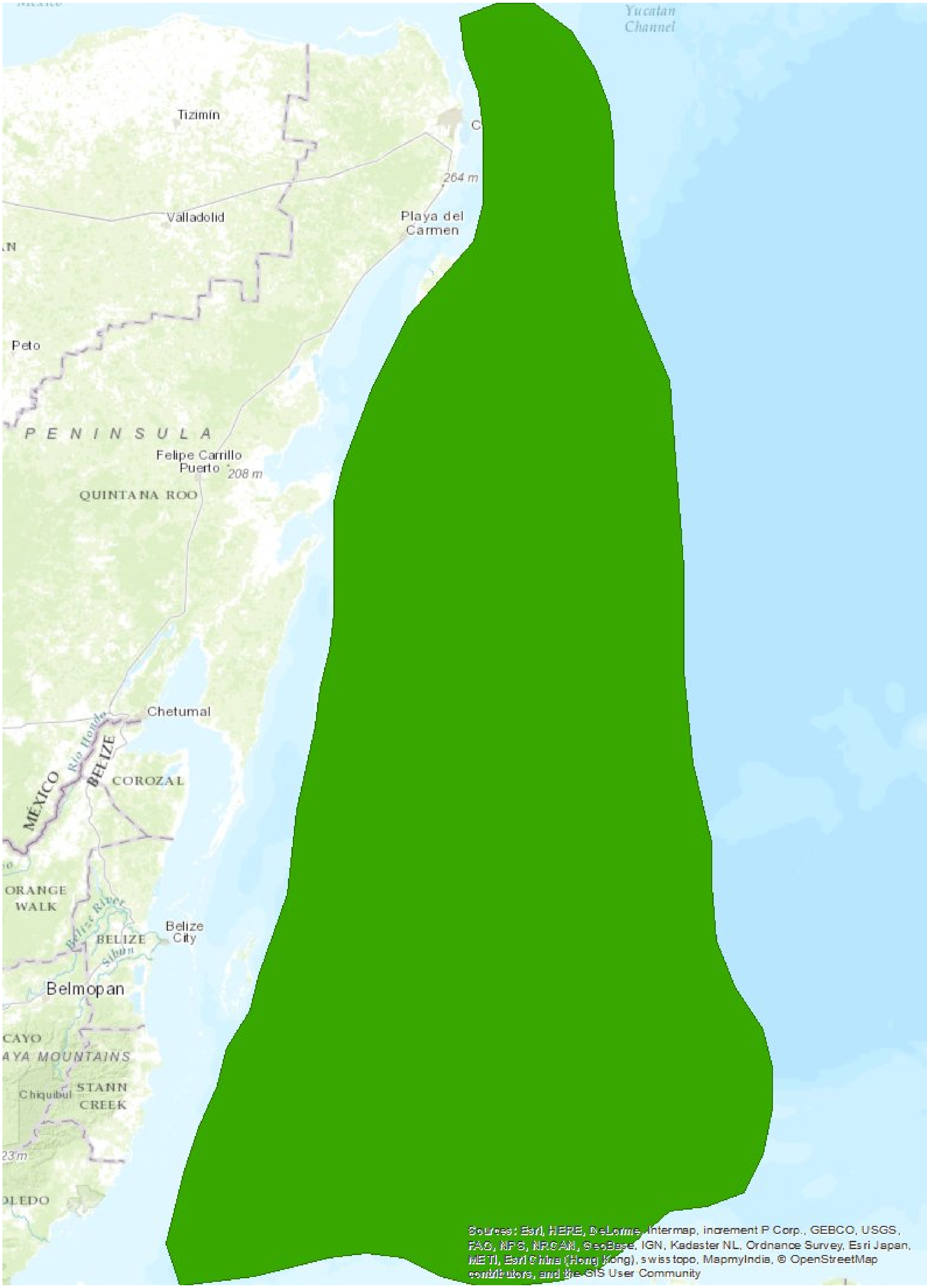
Starting Value	0.00 # research studies completed
Value To Date	4.00 # research studies completed
Target value	4.00 # research studies completed

Note:

Funding Strategy: Capacity, Outreach, Incentives
Metric: Coral - Building institutional capacity - # FTE with sufficient training
Required: Recommended
Description: Enter the number of staff or full-time equivalents with sufficient training and skills engaged in conservation activities

Starting Value	0.00 # FTE with sufficient training
Value To Date	55.00 # FTE with sufficient training
Target value	30.00 # FTE with sufficient training

Note:


Yucatan Channel
Tizimin
Valladolid
Playa del Carmen
264 m
Peto
PENINSULA
Felipe Carrillo Puerto
208 m
QUINTANA ROO
Chetumal
Rio Hondo
MÉXICO
BELIZE
COROZAL
ORANGE WALK
Belize River
Belize City
BELIZE
Sibun
Belmopan
CAYO
STANN CREEK
Chiquibul
Sources: Esri, HERE, DeLorme, Intermap, increment P Corp., GEBCO, USGS, FAO, NPS, NRCAN, GeoBase, IGN, Kadaster NL, Ordnance Survey, Esri Japan, METI, Esri China (Hong Kong), swisstopo, MapmyIndia, © OpenStreetMap contributors, and the GIS User Community

Rare's Final Programmatic Report Narrative

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2. Project Activities & Outcomes

Activities

- *Describe the primary activities conducted during this grant and explain any discrepancies between the activities conducted from those that were proposed.*

1. **Assess genetic population connectivity and larval dispersal of ecologically and commercially important species.**

   1.1. <u>Genomic analyses were conducted for stoplight parrotfish (*Sparisoma viride*) and spiny lobster (*Panulirus argus*).</u> Unfortunately, due to permitting issues in Honduras we were unable to receive samples of yellowtail snapper (*Ocyurus chrysurus*) and therefore could not conduct the genomic analyses required. As a substitute we have conducted genomic analyses on the red mangrove (*Rhizophora mangle*) a critical habitat for both commercially and ecologically important fish species. We successfully collated samples from three of the four countries of the MAR (Figure 1). Due to long processing times of research permits, we were unable to receive any samples from Guatemala within the project time frame.

   We successfully extracted DNA and genotyped 556 samples, from 21 of sites throughout the MAR, the breakdown of which is presented in Table 1.

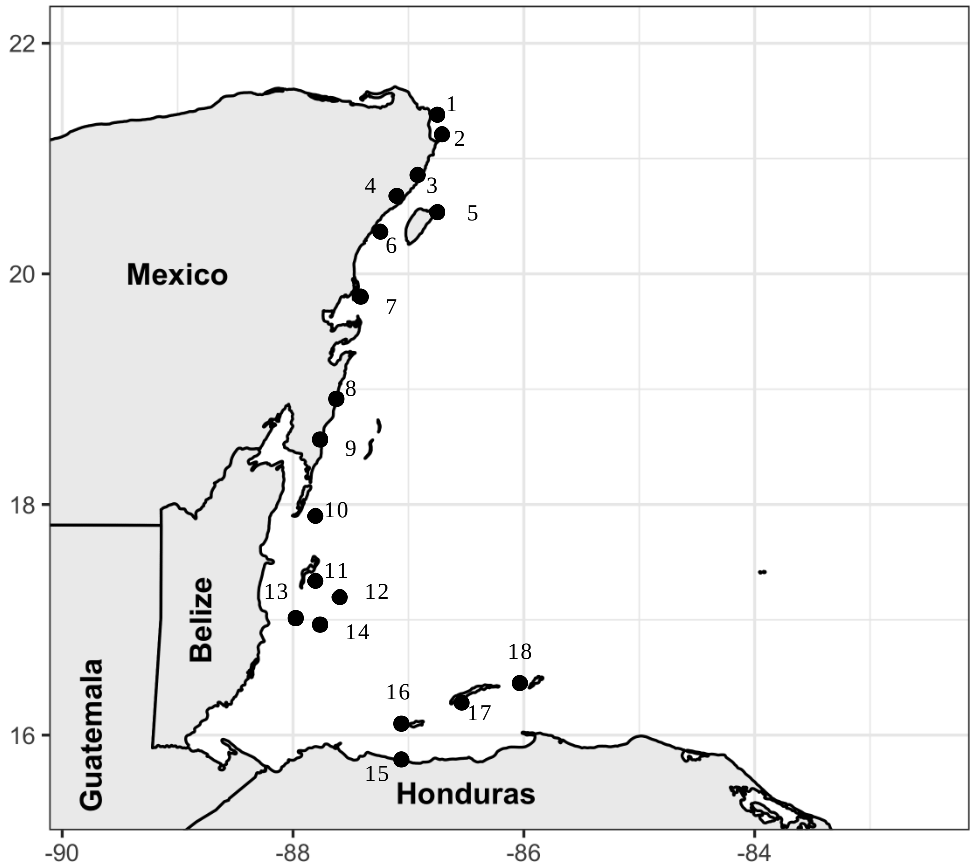


Figure 1. Map of sampling sites throughout the Mesoamerican reef system (1 - Isla de Mujeres; 2 - El Faro norte; 3 - Tanchate; 4 - Puerto Morelos; 5 - Cozumel; 6 - Akumal; 7 - Punta Allen/Sian Ka'an; 8 - Mahaual; 9 -Xcalak; 10 - Hol Chan; 11 - Calabash; 12 - Half Moon Bay; 13 - Carrie Bow Cay; 14 - Glovers Reef; 15 – Salado Barra; 16 - Utila, 17 - Roatan; and 18 - Guanaja). Note: Not all species were collected at all sites and some points may reflect multiple sampling locations.

Table 1. Successfully genotyped individuals of stoplight parrotfish, spiny lobster and red mangrove from the Mesoamerican reef ecoregion

Stoplight parrotfish (*Sparisoma viride*)

	Mexico	Belize	Honduras	*Total*
Number of sites	9	5	3	17
Number of individuals	202	57	91	350

Spiny lobster (*Panulirus argus*)

	Mexico	Belize	Honduras	*Total*
Number of sites	1	1	1	3
Number of individuals	32	38	8	78

Red mangrove (*Rhizophora mangle*)

	Mexico	Belize	Honduras	*Total*
Number of sites	-	1	4	5
Number of individuals	-	27	133	160

1.2 Connected genetic data with biophysical model: To investigate the larval connectivity patterns of the species of interest in the MAR, we developed a larval dispersal model using the Connectivity Modeling System (CMS; Paris et al., 2013). The CMS is a Lagrangian stochastic model using a 4th order Runga-Kutta integration scheme. It allows the coupling between hydrodynamic outputs, habitat, and biological factors. In the model, each particle represents a virtual larva and is characterized by its longitude, latitude, and depth. Using hydrodynamic outputs from the two models described in the previous paragraphs, particles were tracked at each time step of the model (*i.e.* 3600 seconds in our study). Habitat and larval biological characteristics of each species were incorporated in the model using the information gathered from the literature (see below).Consistent with the genetic results, we found substantial larval dispersal across the MAR. We were able to identify key source, sink, and larval retention areas across the region (see figures below). This data is used to evaluate marine protected area performance and identify optimal locations for new no-take areas.

Connectivity matrices

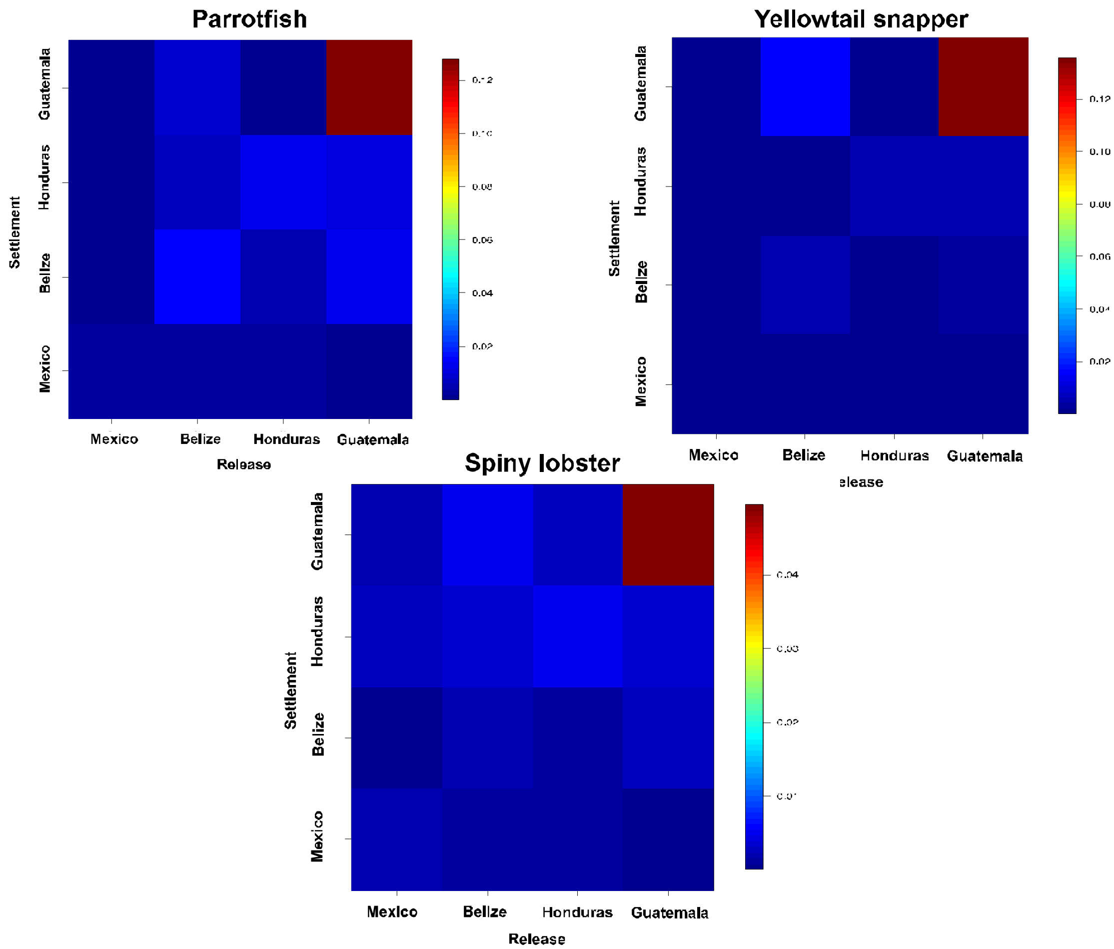


Figure 2: Connectivity matrix representing the larval transport success from release areas to settlement areas for parrotfish, yellowtail snapper, and spiny lobster. Areas were grouped per nation: Mexico, Belize, Honduras, Guatemala.

Local retention

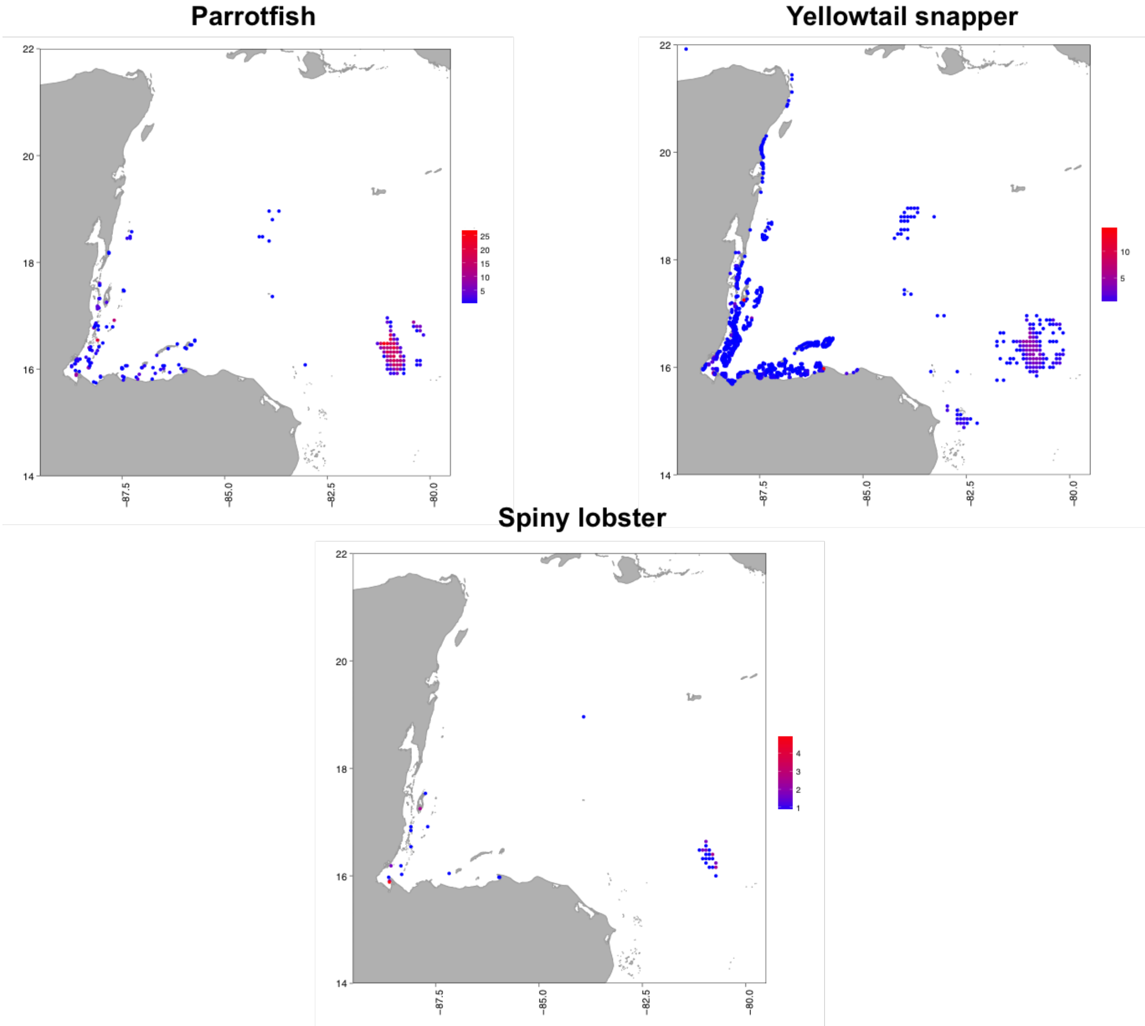


Figure 3: Proportion of larvae locally retained in each habitat area for parrotfish, yellowtail, and spiny lobster. Areas with null local retention are not showed for ease of representation.

Larval sources and sinks

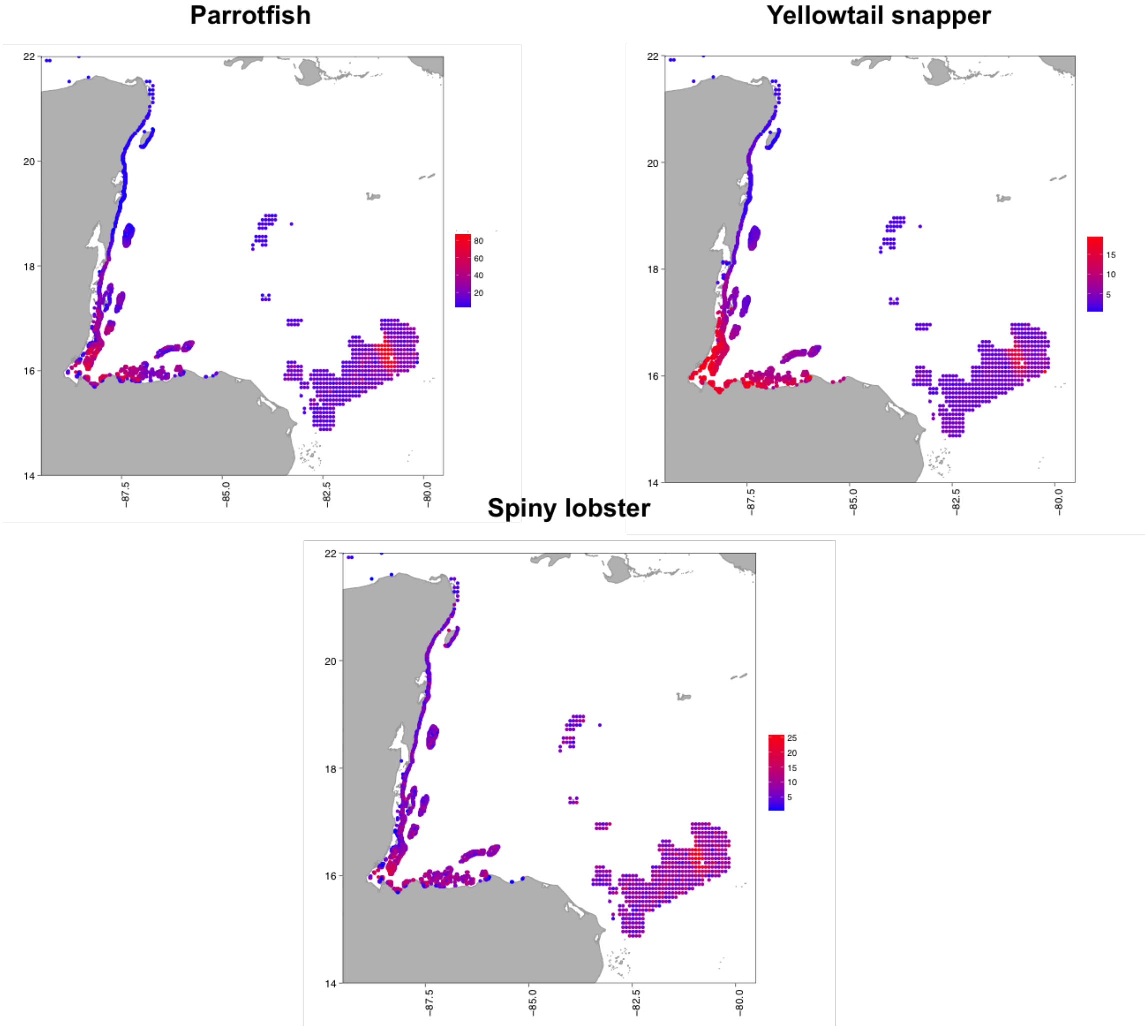


Figure 4: Proportion of settled larvae per release area, e.g. sources. Areas with null transport success retention are not showed for ease of representation.

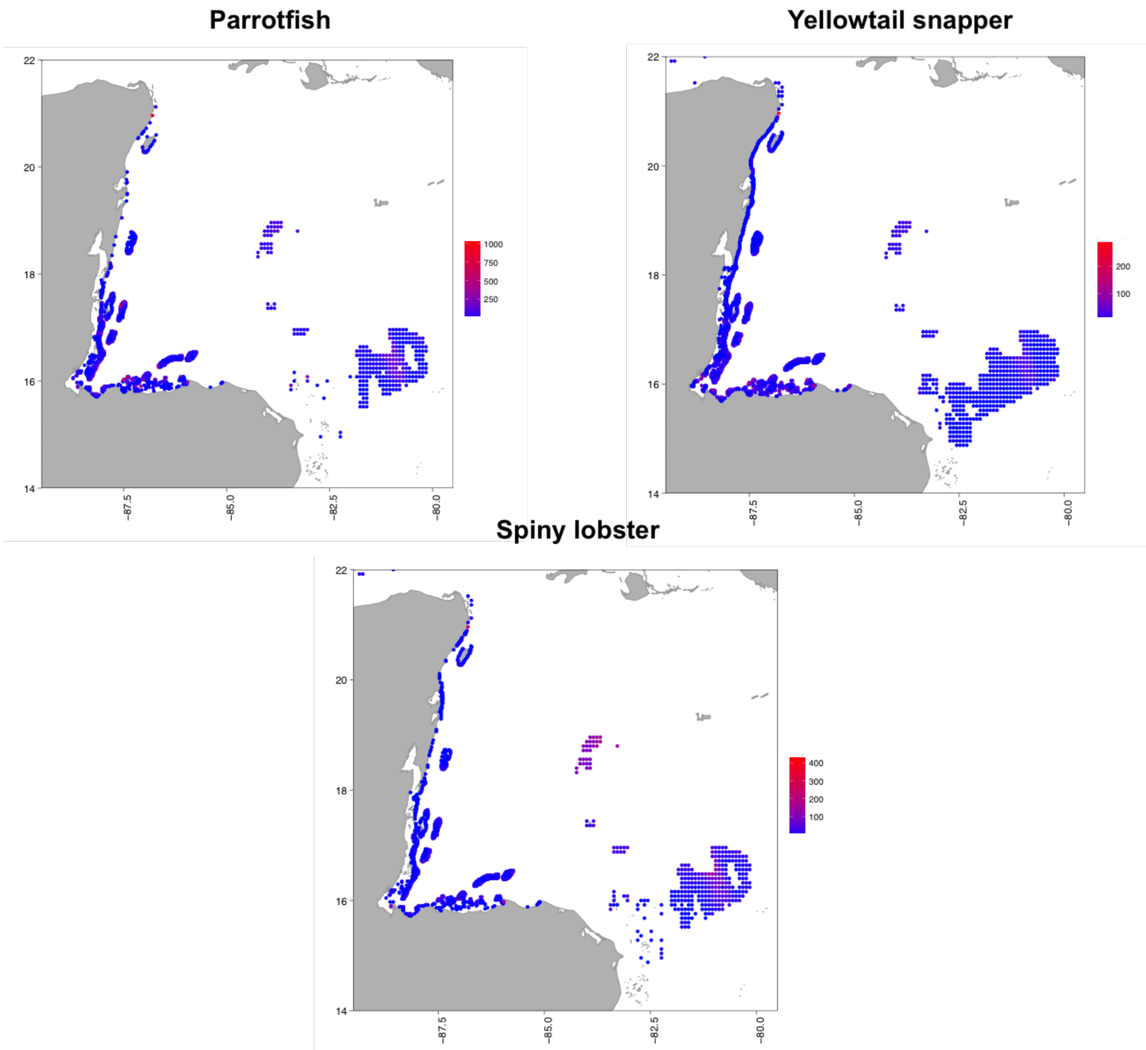


Figure 5: Proportion of settled larvae per settlement area, e.g. sinks. Areas with null transport success retention are not showed for ease of representation.

2. **Integrate ecological monitoring, genetic approaches, and fisheries data to measure the effects of MPA networks and develop targeted management strategies.**

With support from the Healthy Reefs for Healthy People Initiative (HRI, a Smithsonian Institution program), and three established non-governmental organizations, Centro de Estudios Marinos (Honduras), Comunidad y Biodiversidad (Mexico), and the Wildlife Conservation Society (Belize), we built a comprehensive MPA efficacy model using: 1) large-scale ecological datasets that document changes in the reef communities over the past 10 years, 2) site-specific environmental and habitat data, 3) spatial connectivity patterns for stoplight parrotfish and spiny lobster, and 4) fisheries catch data to measure the status of small scale fisheries linked to MPAs across Mexico, Belize, Guatemala, and Honduras.

Decadal analyses were conducted to detect trends in reef health, including commercial fish biomass, herbivorous fish biomass, percentage coral cover, and percentage fleshy macroalgae cover in each of the four countries and presented in the Healthy Reefs for Healthy People 2018 Report Card. In addition, data for 104 sites that were repeatedly surveyed in 2006 and 2016 based on a subsample of stratified randomized sites, the majority of which were outside MPAs, in addition to sites within No-take zones, Fished MPA zones, and sites in open fishing areas, finding: (a) an increase in coral cover in Mexico, Guatemala and Honduras, with no significant change observed in Belize; (b) significantly increased fleshy macroalgae cover for all four countries; (c) no significant changes in herbivorous fish biomass in any of the four countries; and (d) significant declines in commercial fish biomass in Belize and Guatemala, and no change in Mexico and Honduras. The number of sites included in No-Take zones also varied by country, for example in Belize partner NGOs manage most of the country's MPAs and provide HRI summary data (which was not included in this analysis but is included in the section below). Additional data will be collected and collated from the region during 2018, when available these data will be incorporated into these analyses to augment the time series data analyses to provide current estimates of the status of coral reefs and the fisheries they support.

We developed a model to evaluate the drivers behind observed trends in key MPA performance indicators that included explanatory environmental, biological, and habitat variables. These variables included sea surface temperature, surrounding mangrove, sea grass and coral reef habitat, net primary productivity, connectivity and a human impact index created by the Wildlife Conservation Society and Columbia University from nine global data layers covering human population pressure (population density), human land use and infrastructure (built-up areas, nighttime lights, land use/land cover), and human access (coastlines, roads, railroads, navigable rivers).

We obtained these data from global databases (National Oceanic and Atmospheric Administration's (NOAA) National Oceanographic Data Center Coral Reef Temperature Anomaly Database (CoRTAD), Institute for Marine Remote Sensing Moderate Resolution Imaging Spectroradiometer (MODIS), NASA Aquarius, Global Human Influence Index Dataset of the Last of the Wild Project, and United Nations Environment Program's World Conservation Monitoring Centre (UNEP-WCMC)), and the most recent habitat maps produced for the Mesoamerican Reef (MAR). We also incorporate level of enforcement, size, age, as compiled and evaluated in HRI's Eco-Audits, and isolation of each protected area into the datasets. The response and explanatory variables used in the model are listed in Table 2.

Table 2: Core variable used in ecological models

CATEGORY	VARIABLES	DATA SOURCE
Response or output variables (indicators of reef health)		
REEF FISH	Total fish biomass	Surveys
	Herbivore fish biomass	Surveys
	Piscivore fish biomass	Surveys
	Target/managed fish biomass and density	Surveys
	Herbivore species composition (e.g., PCA axes)	Surveys
BENTHIC	Coral cover (by species)	Surveys
	Coral species composition	Surveys
	Algae cover (by genus, functional groups)	Surveys
	Available substrate for coral recruitment (CCA, bare substrate)	Surveys
	Density of coral recruits	Surveys
Explanatory variables (some can be managed others cannot)		
HUMAN	Human Influence Index	GIS layer
	Access to fishing areas	GIS layer
	Gravity of human impacts	GIS layer
ECOLOGICAL	Reef connectivity (Connectivity indices for lobster, yellowtail, parrotfish, mutton snapper)	GIS layer
	Nursery and forage habitats (mangrove area/perimeters, seagrass areas)	GIS layer
	Coral species composition/functional traits	Surveys
ENVIROMENTAL	Reef complexity (rugosity)	Surveys
	Depth	Depth

	Sea surface temperature anomalies (DHW, TSA)	GIS layer
	Net Primary Productivity	GIS layer
	Wave exposure/storms	GIS later
MANAGEMENT	Years of protection	Management plans
	Management zones (GUZ, NTZ)	Management plans
	Size of no-takes	Management plans
	Level of enforcement	HRI EcoAudit

3. **Build local capacity to interpret and use scientific data in marine spatial planning and fisheries management**

A collaborative conference was held on Caye Caulker, Belize, from the 23rd to 25th October 2018, that included the 6th annual Healthy Reefs for Healthy People Initiative regional partner meeting and a two-day workshop to present NFWF project results. These events were combined to provide the greatest access to a wide audience of stakeholders from across the Mesoamerican reef region. A total of 55 participants from 42 institutions from across the four countries attended the three-day event, with representatives from government and non-government organizations (Figure 6).

Figure 6. Attendees of the Healthy Reefs for Healthy People Initiative 6th regional partner meeting.

Abel Valdivia presented the protected area evaluation and predictive tool that incorporated data from hundreds of Atlantic and Gulf Rapid Reef Assessments. The workshop provided valuable feedback from regional stakeholders on applications of the tool and ways to improve the tool for the end users. The tool will continue to be modified to better serve resource managers.

Preliminary connectivity data were presented during the third session of the conference, *Connectivity in the MAR*; which was divided into two components, (1) MAR – the importance of a connected ecosystem, and (2) How connected are we? Key species hold the clue. Courtney Cox ran the session, where genetic results were presented alongside larval modeling results of mutton snapper (*Lutjanus analis*), the yellowtail snapper (*O. chrysurus*), the queen conch (*Lobatus gigas*) and the spiny lobster (*P. argus*). The presentation focused on the uses of the data for evaluation and design of marine reserve networks at the regional level,. Due to the high levels of connectivity within the MAR, emphasis was given to a regional collaboration, and the need to expand the sphere of influence of individual marine reserves from the local community level to the regional level.

Outcomes

Outcomes from Activity 1: Three research studies on the connectivity of key species have been prepared and associated scientific papers are in development. Due to the delay in genetic processing, the scientific papers were not drafted in the timeframe we anticipated. We will complete the manuscripts over the next few months and submit for publication at a peer-reviewed scientific journal.

Outcomes from Activity 2: We presented the protected area evaluation tool to local managers and stakeholders at the joint conference with the Healthy Reefs for Healthy People Initiative. We are in the process of revising the tool based on feedback from participants in the workshop. The feedback included suggestions for additional species to include in the connectivity analysis. We are modeling larval dispersal of those species and will incorporate the results into the next iteration of the tool. We are also drafting the manuscript that describes the tool and practical applications such as developing targeted management strategies and monitoring the efficacy of MPAs to improve fisheries and support local livelihoods.

Outcomes from Activity 3: We collaborated with the Healthy Reefs for Healthy People Initiative, Centro de Estudios Marinos, and Comunidad y Biodiversidad, to communicate our findings to 55 participants from 42 institutions from across the four countries with representatives from government and non-government organizations. Participants were introduced to the tool, existing relationships were strengthened, and new collaborations were established during the workshops. We will use these relationships to continue trainings to ensure implantation of the tool.

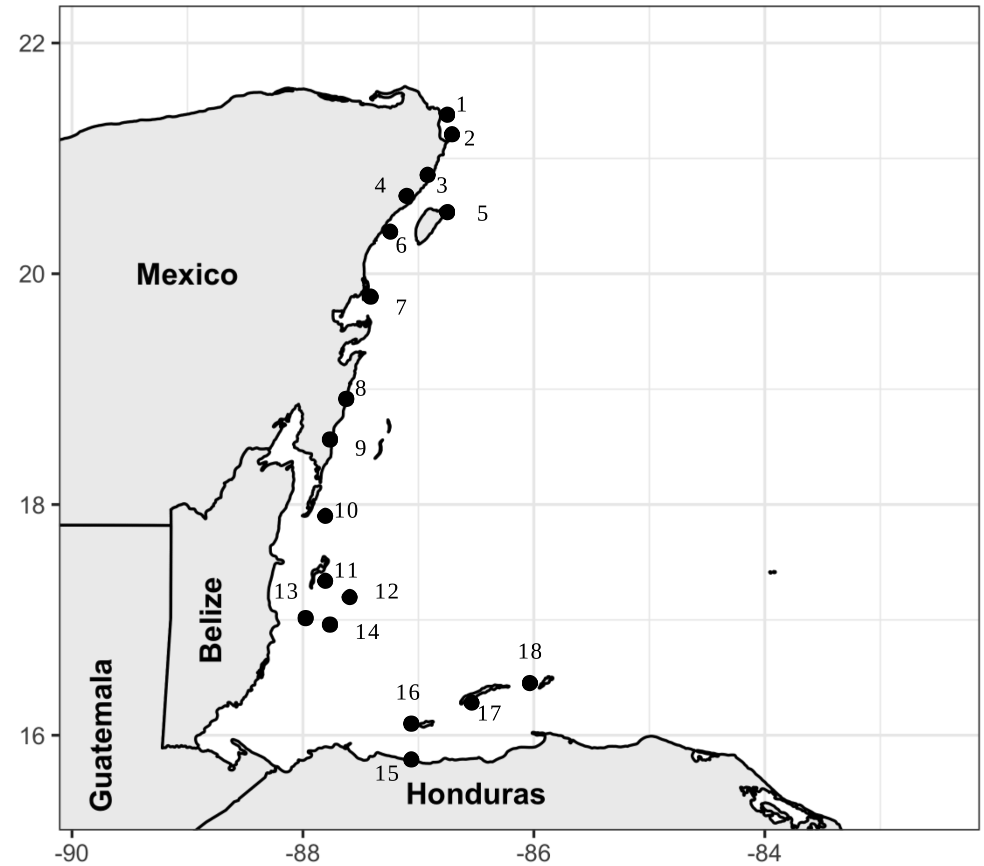
3. Looking Beyond the Grant (3 paragraphs)

We met our goals to assess genetic connectivity, develop a tool to evaluate and predict protected area effectiveness, and share our results with local stakeholders. Due to delays in the research permitting process we were not able to obtain genetic samples from Guatemala. In addition, we were not able to complete draft manuscripts for submission to scientific journals. The permitting process is often a cause for project delays in the Caribbean. However, in the future, we will collaborate with additional partners to expedite the process.

The feedback from the joint conference was extremely positive. Resource managers from governments and NGOs were excited about applying the protected area evaluation tool in their MPAs and other management areas. Conference participants provided valuable feedback allowing us to evolve the tool based on manager needs. The revised tool will be finalized and published in the public domain in the coming months.

The following are additional steps Rare is taking to achieve the specific conservation goals for this project:

1. Revise evaluation tool based on workshop participant feedback and publish tool in the public domain
2. Submit manuscripts to scientific journals communicating connectivity results and evaluation tool applications
3. Hold additional trainings on protected area evaluation tool



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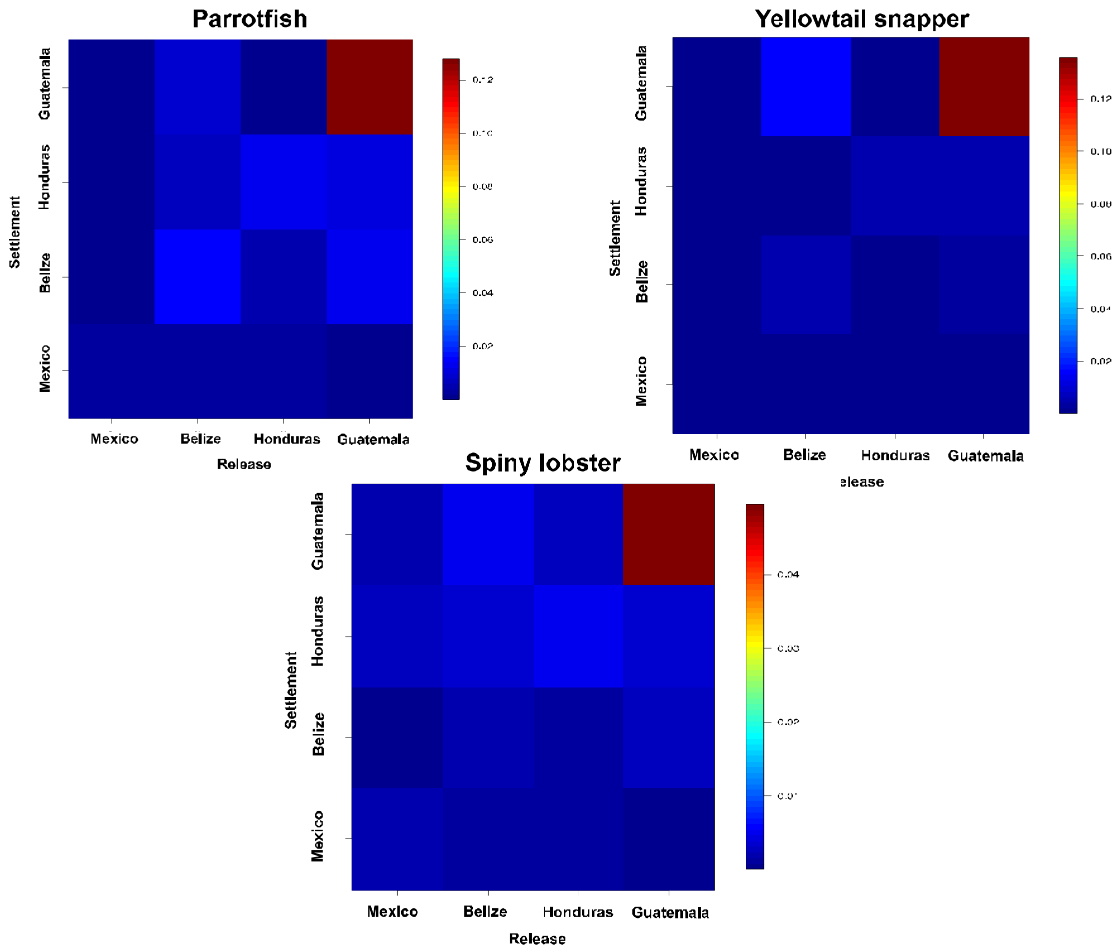

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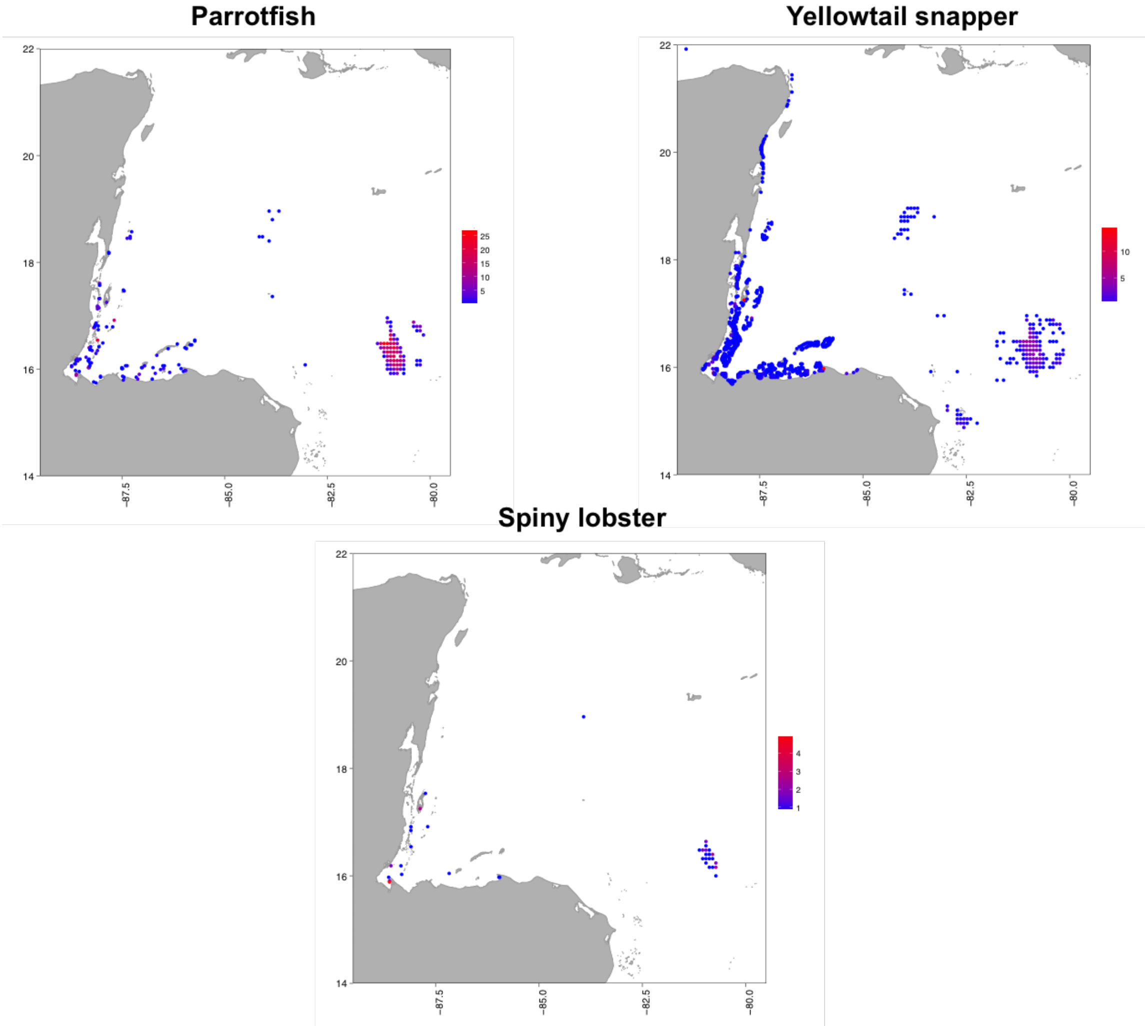

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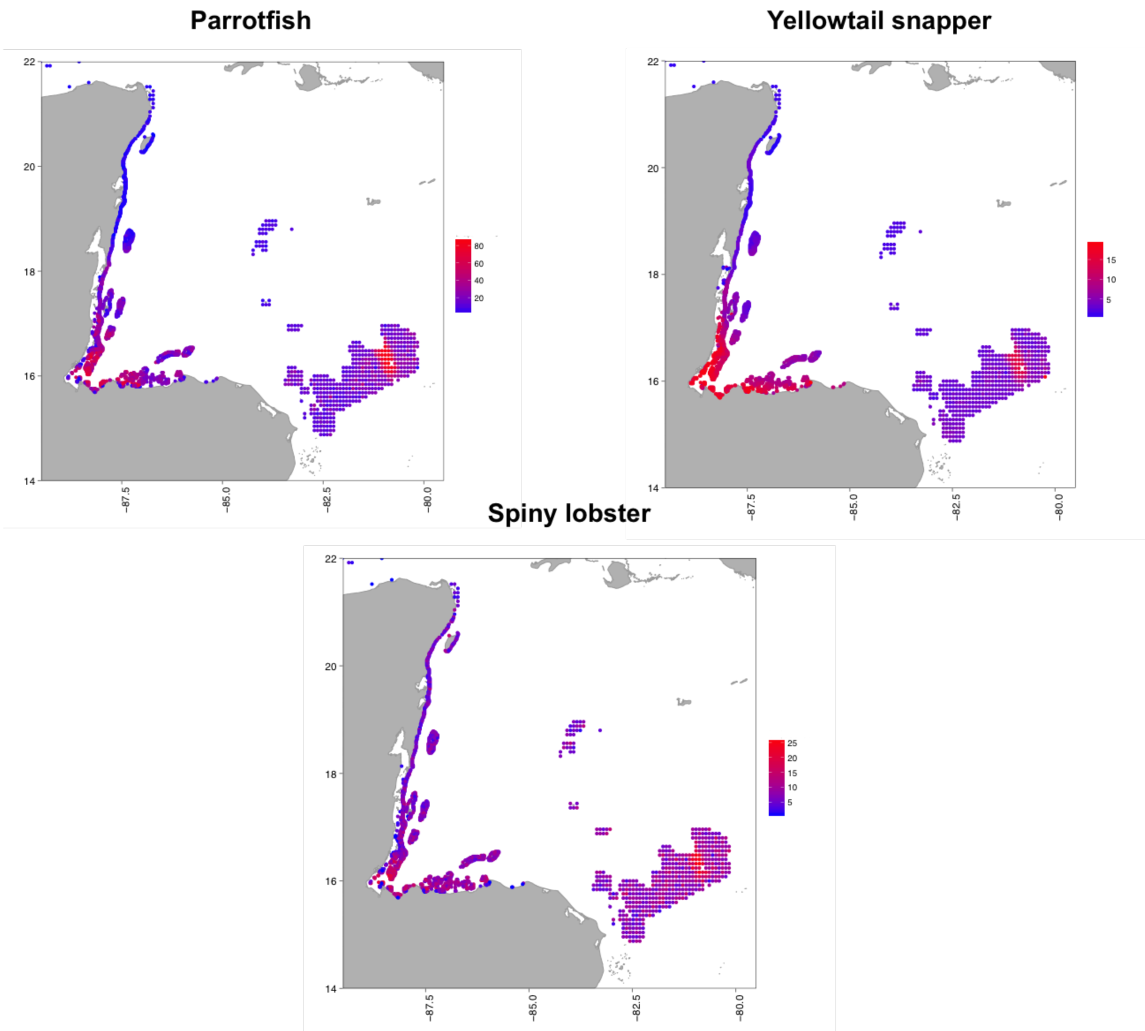
Larval sources and sinks



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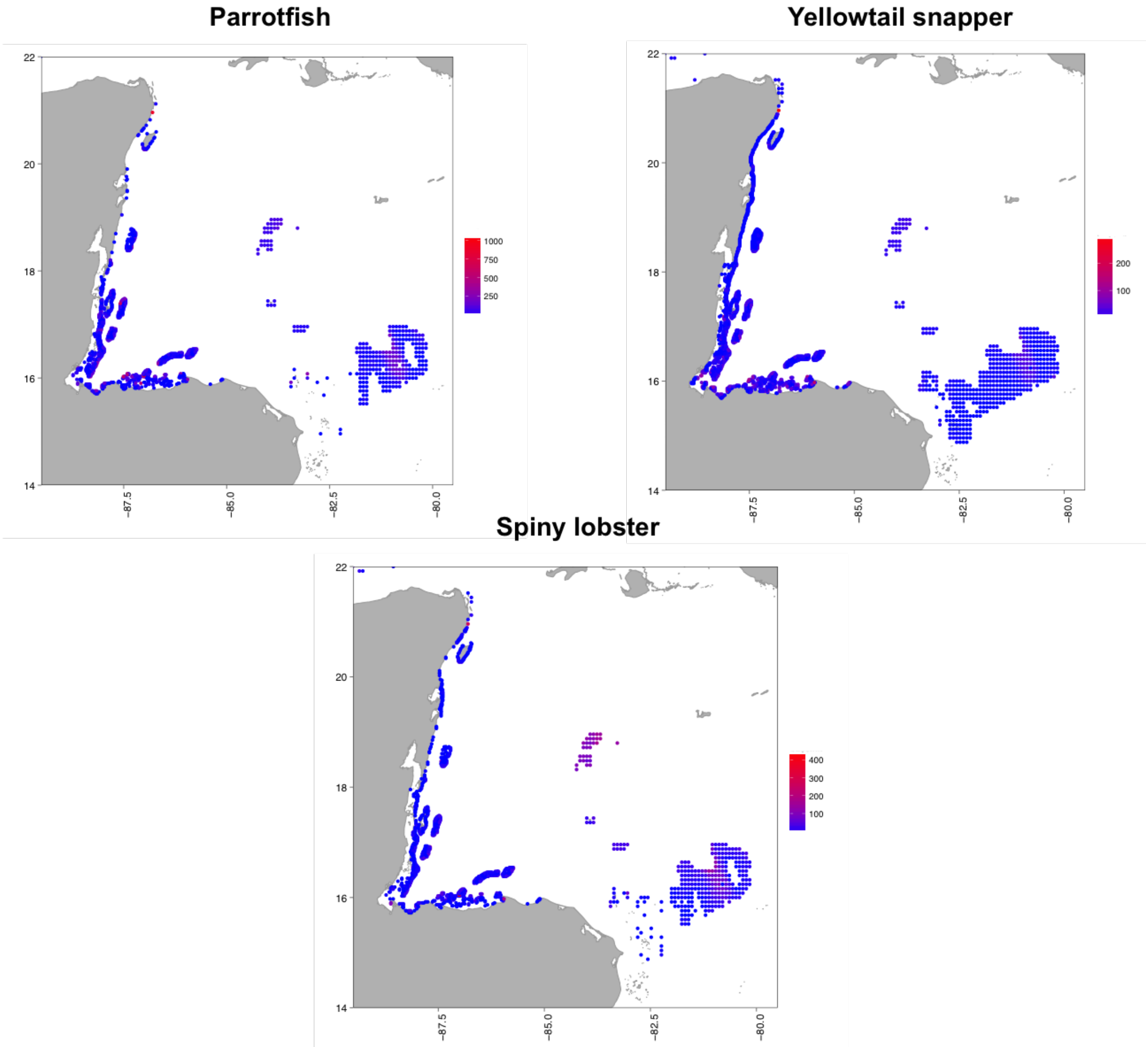

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