Data describing Tethered PaV1 infected juvenile lobsters introduced to occupied wild dens in the south-central Florida Bay (Lobster disease connectivity project)

Website: https://www.bco-dmo.org/dataset/556033
Version: 2015-04-13

Project
» Connectivity of disease in marine Ecosystems: multi-scale dynamics of a viral disease infecting caribbean spiny lobster (Lobster disease connectivity)

Contributors	Affiliation	Role
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Dataset Description

Field experiment in which uninfected or PaV1-infected tethered juvenile lobsters were introduced into dens with natural aggregations of lobsters whose abundance was again observed 24 hrs later.

Related References:

Methods and results appear in the following publication: Butler, M.J. IV, D.C. Behringer Jr., T.W. Dolan III, J. Moss, and J.D. Shields. (in press, 04/2015) Behavioral immunity suppresses an epizootic in Caribbean lobsters. PLOS ONE.

Methods & Sampling

We tested whether aggregations of healthy lobsters in natural dens differed in their response to the introduction into their den of an additional healthy lobster or a PaV1-infected lobster in a field experiment at three general locations in Florida Bay, Florida (USA)(approximate location coordinates: 24 56 29.72oN, 80 49 24.58oW; 24 50 30.55oN, 80 47 44.86oW; 24 50 17.04oN, 80 48 05.18oW) conducted on sites that had experienced a sponge die-off and thus where lobsters were highly aggregated. Lobsters (16 - 56 mm CL) were first collected by divers from natural habitats in the middle Florida Keys region, but not at the study site. The presence or absence of PaV1 in collected lobsters was assayed using PCR and all diseased lobsters used

in the experiment were visibly diseased (i.e., showed clinical signs of infection). Lobsters were tethered by tying a loop of monofilament (8 kg test) around their carapace (between the second and third periopods) with a snap swivel tied on the dorsal side of the carapace and the knot sealed with cyanoacrylate superglue. The snap swivel was clipped to a brick by a 50 cm long monofilament line. This arrangement permitted tethered lobsters to move freely and naturally within the limits of the tether, but they could not escape. Divers introduced either a single healthy or single visibly diseased juvenile lobster into separate, haphazardly selected natural aggregations of lobsters found under coral heads or within rocky holes. Dens were individually marked with numbered surface buoys so they could be relocated. We counted and estimated the sizes of all lobsters within each den prior to the introduction of the tethered lobster and then again 24 hrs later. Healthy tethered lobsters were released after the study, whereas diseased lobsters were returned to the laboratory and euthanized to prevent further spread of the PaV1 virus.

Data Processing Description

Data analyzed using a 2-way log-linear contingency table analysis to test for independence of the effect of PaV1 infection and tendancy for den aggregation to decrease or to increase/remain the same.

BCO-DMO Processing:

- added conventional header with dataset name, PI name, version date, reference information
- renamed parameters to BCO-DMO standard
- added lat, lon columns
- reformatted date from m/d/yyyy to yyyy-mm-dd
- replaced blank cells with nd

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Data Files

File
tether.csv (Comma Separated Values (.csv), 4.59 KB) MD5:45e0b8f6dfaf20649249ee74aa6b8062 Primary data file for dataset ID 556033

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Parameters

Parameter	Description	Units
site	site of tethering	unitless
date_start	date tethering began	yyyy-mm-dd
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
den_id	den identification number	unitless
den_type	type of den structure: spl = loggerhead sponge; sol = solution hole; c = coral head; spf = finger sponge; rock = rock	unitless
treatment	tethered lobster treatment: either PaV1 diseased or healthy lobster	unitless
length_carap_teth	carapace length of tethered lobster	millimeters
sex_teth	sex of tethered lobster	unitless
num_lobsters_start	number of naturally occurring lobsters observed in den at start of study	unit
length_carap_natl	estimated carapace length of lobsters observed in den at start	millimeters
num_lobsters_24hrs	number of naturally occurring lobsters observed in den after 24 hrs	unit
length_carap_natl_24hrs	estimated carapace length of lobsters observed in den after 24 hrs	millimeters
live_dead_teth	whether tethered lobster alive or dead after 24 hrs	unitless

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Deployments

Butler_FloridaBay

Website	https://www.bco-dmo.org/deployment/556102
Platform	Lobster habitat
Start Date	2004-07-15
End Date	2004-08-11
Description	Field expts with diseased lobsters

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Project Information

Connectivity of disease in marine Ecosystems: multi-scale dynamics of a viral disease infecting caribbean spiny lobster (Lobster disease connectivity)

Coverage: Florida Keys, USA and Carrbbean

Scientists are struck by how different terrestrial epidemiology is from that in marine ecosystems, a crucial difference being the more rapid spread of diseases in the ocean due to the presumed absence of barriers to waterborne dispersal. Yet, the movement of pathogens in the sea and its importance to disease dynamics in marine metapopulations is virtually unstudied. Marine pathogens do spread among distant host populations, as demonstrated by dramatic epizootics, but is this common or demographically relevant? Nearly all studies of marine diseases treat such events as transitory, focusing instead on local disease dynamics. This approach

suggests either that small-scale phenomena normally trump the influence of large-scale pathogen connectivity or, alternatively, that the dispersal of marine pathogens by highly motile adults or free-living waterborne pathogens is simply too intractable for empirical investigation. Yet, there is another perhaps unappreciated mechanism – dispersal by infected larvae. Most marine animals have life histories that include planktonic larvae, many of which are highly dispersive. If infected by pathogens, these “larval vectors” would provide an efficient mechanism for distributing pathogens at high concentrations directly into habitats where hosts dwell. More so than passive, waterborne pathogens that are subject to rapid dilution and have no means of targeting distant hosts.

We have evidence that long-distance pathogen dispersal in the sea via infected meroplanktonic larvae may be possible. The pathogen in question is an often lethal, pathogenic virus (PaV1; Panulirus argus virus 1) that infects the Caribbean spiny lobster, Panulirus argus – a species broadly distributed throughout the Caribbean where it supports the most valuable fishery in the region. We described the PaV1 virus in 1999 and since then have studied its pathology, epidemiology, transmission, and effects on juvenile lobster populations in the Florida Keys. Like others, our focus has been on local pathogen-host dynamics, but PaV1 infections in lobsters are now confirmed in distant areas of the Caribbean (Belize, Mexico, St. Croix) in regions that are demographically linked only by dispersing larvae that spend >6 mos. in the open ocean. We recently discovered that many lobster postlarvae recruiting to coastal nurseries in Florida are infected with PaV1, providing novel evidence for pathogen connectivity among distant host populations.

Focusing on the spiny lobster-PaV1 virus association as a case study, we propose an ambitious program of laboratory, field, and modeling research whose broader implications will better our understanding of the importance of dispersal by infectious agents on the spread and maintenance of disease in marine populations. The project builds upon data and techniques developed with prior NSF sponsorship, and brings together partners in developing Caribbean nations with a multidisciplinary group of scientists with long-standing research programs in larval biology, biophysical and ecological modeling, crustacean biology, molecular biology, and the study of marine diseases.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0928930
NSF Division of Ocean Sciences (NSF OCE)	OCE-0929086

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