

Disease dynamics in marine metapopulations: modelling infectious diseases on coral reefs

Susanne H. Sokolow^{1*}, Patrick Foley³, Janet E. Foley¹, Alan Hastings² and Laurie L. Richardson⁴

¹Department of Veterinary Medicine and Epidemiology, ²Department of Environmental Science and Policy, University of California, Davis, CA 95616, USA; ³Department of Biological Sciences, California State University, Sacramento, CA 95819, USA; and ⁴Department of Biological Sciences, Florida International University, Miami, FL 33199, USA

Summary

1. Coral reefs are experiencing devastating mortality due, in part, to emerging disease. Despite this growing problem, the long-term consequences of infectious disease in marine ecosystems remain poorly understood, and the application of epidemiological models to marine disease systems represents a research priority for managing resources in the world's oceans.

2. Metapopulation models may provide a framework for modelling coral population dynamics at the regional scale, and we use this approach to investigate the effects of infectious disease. The model presented here incorporates a susceptible-infected or 'S-I' disease into a system of patchily distributed, dynamic coral hosts, and highlights some basic differences that set many marine disease systems apart from their terrestrial counterparts.

3. The model predicts several possible long-term outcomes of disease introduction, and suggests that the consequences of disease may vary considerably among different pathogens and regions. Due to the long time-scales for coral dynamics, epizootics are expected to be prolonged with recovery slow at the regional scale.

4. Our model results show how infectious disease can substantially alter host metapopulation dynamics, with some non-linear relationships which are likely to affect the response of these systems to management and environmental change. For example, higher rates of coral colonization can have variable consequences for host population occupancy (i.e. coral cover) when infectious disease is considered, and chronic diseases with long-lived pathogens pose the highest risks for regional coral extinction.

5. *Synthesis and applications.* We present a tractable epidemiological model within a metapopulation framework and compare the model output with empirical data for a white plague type II (WP2) outbreak among coral of the upper Florida Keys. We conclude that this model fits well with the spatial and temporal patterns of WP2 over a decade. Despite terrestrial–marine differences, many patterns derived from our model are consistent with epidemiological principles. Thus, the careful application of these principles within the context of marine management may be a promising research frontier. Although we focus on coral disease, the methods and results may apply to other marine metapopulations.

Key words: coral conservation, coral health, disease management, emerging infectious disease, epidemiology, marine ecology, model, simulation

Introduction

Coral reefs are in global decline, with diseases increasing in both prevalence and spatial extent (Hughes 1994; Harvell *et al.* 1999b; Porter *et al.* 2001; Ward & Lafferty 2004; Weil

et al. 2006). Some coral diseases have caused severe, documented population declines in certain coral species (Aronson & Precht 2001; Richardson & Voss 2005). Anthropogenic factors and global climate change may also contribute to coral decline, and these stressors are hypothesized to worsen the effects of infection in coral (Harvell *et al.* 1999b; Hughes *et al.* 2003; Pandolfi *et al.* 2003; Sutherland *et al.* 2004).

*Correspondence author. E-mail: shsokolow@ucdavis.edu

Regional outbreaks (epizootics) of disease have been documented among many coral populations (Richardson *et al.* 1998a; Santavy *et al.* 1999; Green & Bruckner 2000; Harvell *et al.* 2004; Williams & Miller 2005). Some diseases, such as sea fan aspergillosis and white plague type II, clearly exhibit multi-year epizootics (Kim & Harvell 2004; Richardson & Voss 2005), but many coral diseases are only beginning to be monitored on a long-term basis at broad geographic scales. Despite some intense monitoring efforts for white plague type II (this study), yellow band syndrome (Bruckner & Bruckner 2006), sea fan aspergillosis (Kim *et al.* 2006), and white syndrome (Bruno *et al.* 2007), much is unknown about transmission dynamics and the long-term consequences of most coral diseases.

With marine diseases continuing to emerge, several questions arise, including: (i) what are the long-term consequences of infectious diseases on coral resilience and persistence; (ii) what factors affect overall regional disease dynamics and long-term outcomes; and (iii) what management options increase the probability of coral persistence when considering infectious disease?

To explore these questions, a novel analytical model of coral–pathogen metapopulation dynamics is presented here. The model is adapted as a simulation to allow the addition of demographic stochasticity and to enable a comparison to qualitative patterns for the coral disease white plague type II in the Florida Keys, USA. This model incorporates features common in the marine environment into a basic ecological framework, to begin to explore the effects of changing environmental conditions, management, and infectious disease pressures on marine ecosystems.

METAPOPOPULATION STRUCTURE OF CORAL REEFS

A metapopulation, here, is defined as a group of organisms in a network of patches connected by intermediate levels of migration and local extinction. Coral reef environments are inherently patchy. At the ‘regional scale’, encompassing about 10^1 – 10^3 km along a coastline or around a submerged island, one useful method for exploring coral dynamics may be the metapopulation modelling approach (Mumby 1999; Mumby & Dytham 2006), particularly at spatial scales appropriate to the dispersal distances of coral planulae (larvae). It has been assumed that marine populations are well connected via long-distance dispersal of planktonic larvae; however, mounting evidence demonstrates that connectivity in the marine environment may be more limited, and self-recruitment within reef regions is common (Cowen *et al.* 2006; Vollmer & Palumbi 2007).

LIMITATIONS OF TERRESTRIAL EPIDEMIOLOGICAL MODELS FOR MARINE ECOSYSTEMS

Some aspects of marine systems make inherent assumptions of terrestrial disease models inappropriate. For example, adult hosts (especially invertebrates) in the marine environment are often sessile (McCallum *et al.* 2004; Cowen *et al.*

2006), and disease agents may move more widely and rapidly within the water column than on land (McCallum *et al.* 2003). Additionally, pathogens adapted to the marine environment may survive for longer periods outside the host (Harvell *et al.* 2004), and can be sensitive to environmental conditions such as water temperature, salinity, or pH (Tamplin 2001; Remily & Richardson 2006).

Terrestrial-marine differences make direct application of most epidemiological models difficult to interpret for marine systems. For example, transmission rates in epidemic models typically depend on contact rates among susceptible and infectious hosts (McCallum *et al.* 2001), and this concept is not interpretable when hosts, such as coral, are sessile for most of their lives. Rather, movement and survival of pathogens outside hosts must be incorporated.

Another concept of most epidemic models is that of the susceptible ‘individual’ (i.e. one individual defined as one person, animal, plant, etc.). In contrast, some marine invertebrates, like coral, are actually comprised of a multi-cellular animal in a mutualistic relationship with an intracellular dinoflagellate (zooxanthellae). These complexities have led to the recent use of the term ‘holobiont’, which includes the animal hosts, their normal microbiological flora, and their intracellular zooxanthellae, as the individual unit of study for coral, and some other marine invertebrates (Reshef *et al.* 2006). Finally, coral are usually arranged in groups of asexually produced colonies which may be capable of interacting with predators and pathogens as ‘super-organisms’, where lesions in one region effect responses from other regions of the colony (Kim *et al.* 2000). We argue that a metapopulation approach (i.e. focusing at the scale of patches of hosts), with explicit inclusion of a free-living pathogen stage, may be the best method for modelling disease in these systems, especially where hosts, like coral, are made up of complex mutualistic groups of interacting sessile, long-lived, colonial organisms and pathogens are likely to be widespread and may be long-lived and highly mobile.

Together with the long time-scales of coral population dynamics, a lack of baseline data in marine ecosystems makes uncertainty a dominant factor in marine research. Simple and generalizable models are needed to allow exploration of disease effects in a wide parameter space and over long time-periods, so that management decisions can be guided by science.

A CASE STUDY: WHITE PLAGUE TYPE II

White plague type II (WPII) is an infectious disease of hard corals which occurs throughout the Caribbean and was first described during an outbreak in 1995 in the Florida Keys (Richardson *et al.* 1998b). The etiology, pathogenesis, and transmission of WPII are fairly well described (Richardson 1998; Richardson *et al.* 1998b; Richardson & Voss 2005). The disease is caused by a marine bacterium, *Aurantimonas corallicida* (Richardson *et al.* 1998b; Denner *et al.* 2003). Signs of infection include rapid tissue death which spreads across the colony surface (Fig. 1). WPII infects a range of scleractinian coral species, predominantly the elliptical star



Fig. 1. White plague type II on a *Montastraea* spp. colony in the Florida Keys (photo by S. Sokolow). WPII causes a sharp line between apparently healthy tissue (darker) and freshly exposed coral skeleton (white), and tissue loss typically progresses upward from the base of the colony at a rate of up to 2 cm day⁻¹.

coral, *Dichocoenia stokesi*, which experienced severe population declines during the recent Keys-wide WPII outbreak (Richardson & Voss 2005).

Spatial data from the Florida Keys and the Virgin Islands demonstrate that colonies infected with WPII can be found in local clusters (Richardson *et al.* 1998b; Kaczmarek *et al.* 2005) and that transmission can occur rapidly: the disease spread throughout the upper Florida Keys within 4 months of its first identification (Richardson *et al.* 1998b). As is the case for many other coral diseases, the WPII pathogen

appears to fluctuate seasonally, with the highest prevalence in the summer months of June to October (Richardson *et al.* 1998b; Remily & Richardson 2006). It is unknown whether the WPII pathogen moves freely within the water column or in association with a reservoir or fomite (such as algae, fish, or marine sediments); however, it appears that the WPII pathogen is highly mobile or ubiquitous, with rapid spread throughout the entire Florida Keys and the wider Caribbean during the last decade (Croquer *et al.* 2003, 2005; Borger & Steiner 2005; Voss & Richardson 2006).

Materials and methods

CORAL–PATHOGEN METAPOPULATION MODEL

To investigate the long-term effects of infectious diseases on reefs, we propose and explore a coral–pathogen metapopulation model (see Fig. 2). We expand upon existing epidemiological models by adapting the metapopulation approach (Levins 1969; Hess 1996) to a dynamic system of sessile hosts and also by explicitly tracking an environmental pathogen population as in Anderson and May (1981, model G) and Codeco (2001).

For simplicity, our model assumes no vertical transmission or individual recovery. These assumptions are reasonable since no evidence exists for vertical transmission for any coral disease to date, and recovery of killed tissue is rare for most coral diseases studied (Borger & Steiner 2005; Kim *et al.* 2006). Thus, the coral–pathogen metapopulation can be modelled as a susceptible–infected or ‘S–I’ disease system via the following three differential equations, where S is the proportion of susceptible patches, I is the proportion of infected patches out of a constant total number of patches in the metapopulation network: susceptible + infected + empty patches, and W is the free-living pathogen population; (for parameter definitions see Table 1):

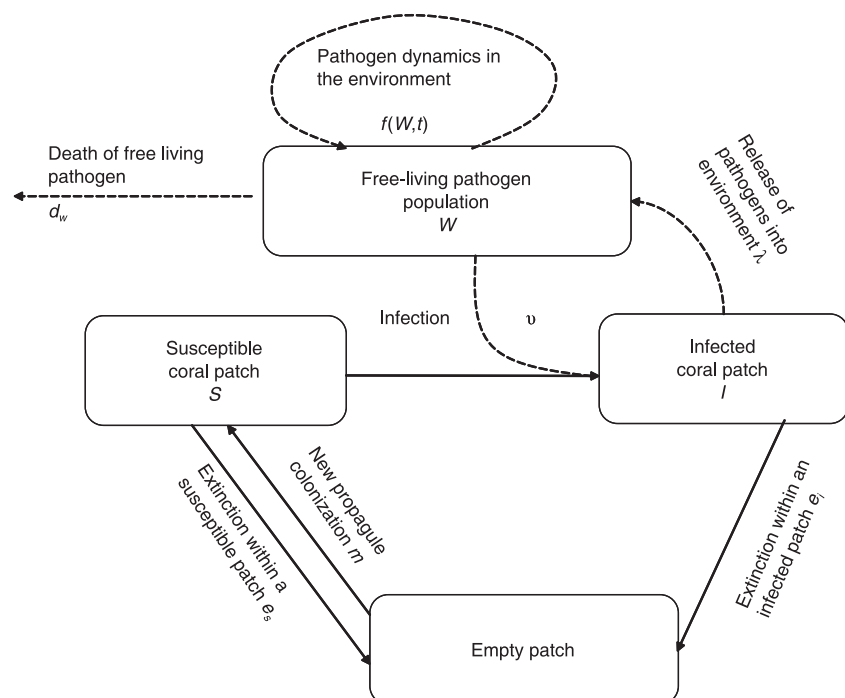


Fig. 2. Schematic representation of the coral–pathogen metapopulation model.

Table 1. Parameter definitions

Parameter	Explanation
m	A colonization (or connectivity) term encompassing coral fecundity within a patch (propagule generation) as well as propagule dispersal, settlement, and post-settlement survival
e_s	The local extinction rates of susceptible (healthy) coral patches
e_i	The local extinction rates of infected coral patches (note: it is assumed, by definition, that $e_s < e_i$, that is infection has a negative impact through disease-induced mortality and thus infers a higher probability of extinction)
v	A 'transmission efficiency' term that represents the probability that a free-living pathogen will invade when it comes into contact with a susceptible patch of coral hosts, causing a local disease outbreak within a patch
λ	The rate at which infected hosts shed pathogens into the environment or free-living pool
$f(W)$	A function governing the population dynamics of the free living pathogens (in the simplest case explored here, free-living particles undergo exponential decay where $f(W) = -d_w W$ with $1/d_w$ equal to average time that an infectious particle exists in the environment). This simple case (where $f(W) = -d_w W$) was also described analytically by a mathematical stability analysis (see Supporting Information, Appendix S2)

$$\frac{dS}{dt} = m(S + I)(1 - S - I) - e_s S - vWS \quad \text{eqn 1}$$

$$\frac{dI}{dt} = vWS - e_i I \quad \text{eqn 2}$$

$$\frac{dW}{dt} = \lambda I + f(W) \quad \text{eqn 3}$$

For exploration using simulations, the model was translated into a set of three difference equations in R version 2.7.0 (The R Development Core Team, <http://www.r-project.org/>, accessed 13 August 2008). Demographic stochasticity was incorporated by enforcing stochasticity in the value of a variable at time $t + 1$ (selected from a Poisson distribution) if the population at time t was very small: < 3 patches or individual pathogen particles (see Supporting Information, Appendix S1 for simulation details and original code for the R functions). Disease introduction was simulated by adding a single dose of one hundred infectious particles to the system as an initial condition. For the simulations: the time step used was 1 day, and the total number of patches in the metapopulation was set at 5000. Results were plotted and compared qualitatively. A wide range of plausible parameter values was compared to generate predictions about the effects of changes (such as increases or decreases in colonization, pathogen survival, or extinction rates) on disease dynamics and coral metapopulation persistence.

WHITE PLAGUE TYPE II DATA COLLECTION

Data for white plague type II (WPII) used in this analysis were collected by one of the authors (L.L.R.) and colleagues for over a decade. Methods consisted of direct observation of reef sites by a team of divers noting all corals exhibiting signs typical of WPII infection within each of the surveyed areas. Survey effort (total number of sites surveyed) varied from year to year. Years during which either no data were collected or only one site was surveyed were omitted from this time series. Where there were more than one survey season per year, only the survey which occurred closest to late summer was included to ensure the most consistency across years. The majority of sites were surveyed more than five times. Sites were generally located at or around permanent mooring buoys throughout the Florida Keys National Marine Sanctuary and the surrounding reefs; however these buoys were sometimes lost in storms or

renumbered (Richardson & Voss 2005). Therefore, care was taken to identify the approximate location by GPS coordinates and reef name to ensure comparability in spatial location from year to year to the best extent possible. The area surveyed was roughly equal among sites and averaged about 200 m². If one or more diseased colonies were detected within the surveyed reef area, the site was considered positive for disease; if no diseased colonies were detected, the site was considered negative for disease. Disease prevalence for this data set was defined as the total number of diseased sites divided by the total number of surveyed sites within each survey period. Confidence intervals were calculated for each survey using the function 'prop.test' from the R base package.

Results

THE THEORETICAL CORAL-PATHOGEN METAPOPULATION

In the absence of disease, the coral metapopulation system has a stable equilibrium for patch occupancy dependent on the rate of coral colonization and local extinction (with a non-zero, stable equilibrium as long as colonization exceeds extinction); thus, our model collapses into a simple Levins (1969) metapopulation model framework when disease is absent. With the addition of an initial dose of pathogenic particles into the free-living population, three possible outcomes occur: (i) disease extinction and patch occupancy recovery (epizootic dynamics), (ii) disease persistence and patch occupancy reset to a new lower equilibrium level (disease persistence or enzootic dynamics), or (iii) coral and pathogen extinction or quasi-extinction (the term 'quasi-extinction' is used to indicate that stochastic variability can be necessary to drive populations completely extinct when they reach very small size.).

After pathogen introduction, the size and length of an outbreak and the probability of disease persistence in the coral metapopulation are dependent on a dynamic balance between the loss and generation of infected and susceptible patches. Analytical solutions and stability analyses (Supporting Information, Appendix S2), in addition to insights from numerical simulations (Figs 3, 4), demonstrate thresholds

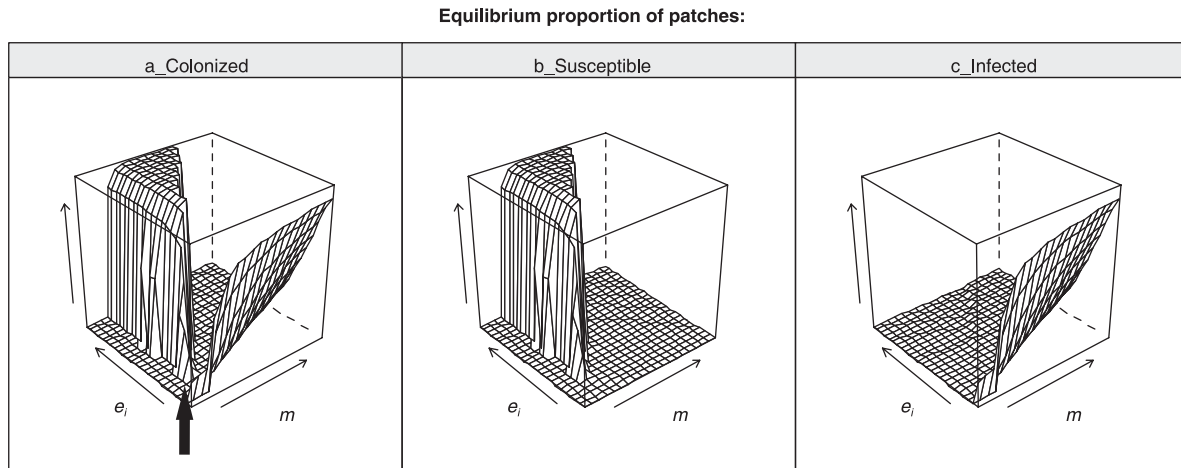


Fig. 3. Equilibrium disease dynamics in the parameter space defined by the colonization rate of susceptible patches (m) and the extinction rate of infected patches (e_i). Graphs represent the proportion of patches at equilibrium: (a) colonized (by both infected and healthy coral), (b) susceptible (colonized by healthy coral) and (c) infected (colonized by infected coral). The parameter m varied from 0.00008 to 0.002 at equal increments and e_i varied from 0.0001 to 0.005 at equal increments (represented by the grid on each surface). The z axis in a–c ranges from 0 to 1. The other parameters, when not varied as described above, were kept constant as follows: initial % colonized patches = 90%, initial per cent infected = 0%, initial number of infectious particles = 100, $I_0 = 0$, $W_0 = 100$, $e_s = 0.00001$, $d_w = 0.01$, $v = 0.00001$, $\lambda = 100$. In all cases, simulations ran for a total of 182 500 days, or approximately 50 years. The bold arrow in panel (a) marks the parameter combination used for Fig. 6.

above which the disease persists, and below which the disease fades out of a region after introduction.

Figures 3 and 4 show some non-linear and complex effects of changes in parameters on both equilibrium and transient dynamics for a wide range of plausible parameter values. For example, increasing colonization or extinction rates can have either positive, negative, or negligible effects on the equilibrium dynamics, depending on initial conditions and the magnitude of the change (Fig. 3). Positive effects of increasing connectivity are more likely when it is initially low, but negative effects of increasing connectivity can occur when it is sufficiently high (Fig. 3).

As demonstrated in Fig. 3, patches are colonized exclusively by healthy coral at equilibrium for parameter combinations where epizootics fade out of the system, such as when connectivity is low and disease virulence is high (low m , high e_i). Conversely, patches are colonized almost exclusively by infected coral (enzootic disease) at equilibrium when connectivity is high and disease virulence is low (high m , low e_i). Because all new coral are born susceptible in our model (i.e. no vertical transmission), there is always a non-zero proportion of susceptible patches any time there are any coral present in the system. At parameter combinations where disease persists indefinitely, new susceptible patches are relatively rapidly converted to infected patches, and thus, the proportion of susceptible patches remains low or negligible at equilibrium. Despite this, there can be prolonged transient periods (years to decades) where coral metapopulations have variable proportions of diseased and healthy patches.

Some transient infection dynamics are shown in Fig. 4, such as the maximum proportion of patches infected at the initial phases of an outbreak (outbreak intensity) and the total duration of an outbreak (outbreak length). Diseases

with both low virulence and long-lived pathogens (low e_i , low d_w) are likely to have the highest impacts on host populations due to high intensity outbreaks of relatively long duration. Conversely, diseases with high virulence and short-lived pathogens (high e_i , high d_w) tend to have comparatively low intensity, short outbreaks. Furthermore, diseases with discordant combinations of e_i and d_w – high virulence but long-lived pathogens (high e_i , low d_w) or low virulence and short-lived pathogens (low e_i , high d_w) – tend to have, on average, moderate intensity outbreaks of moderate duration, except nearing the threshold for endemic disease (lowest e_i) where outbreaks can be also of high intensity and duration even when free-living pathogens are short-lived.

PATTERNS IN THE OBSERVED CORAL DISEASE DATA – WHITE PLAGUE TYPE II

Based on map information obtained from the Florida Geographic Data Library (<http://www.fgd.org/>, accessed January 2007), the Florida Keys region contains approximately 6000 reef patches ranging in size from about 12 m² to over 1 × 10⁶ m², and the average patch size is approximately 7000 m². Within the extent of the sampled region (Fig. 5), there are approximately 1100 patches of reef ranging in size from about 12 m² to 1 × 10⁶ m², with an average patch size of approximately 8000 m².

Regional-scale time-series data tracking the disease status of coral sites infected with WP2 revealed an overall epizootic curve beginning early in 1995, peaking within a year after the first reports of the disease, followed by a prolonged period of moderate prevalence and finally regional decline to very low to undetectable levels within a decade (Fig. 6). Unfortunately, after 2005, the long-term monitoring efforts declined due to

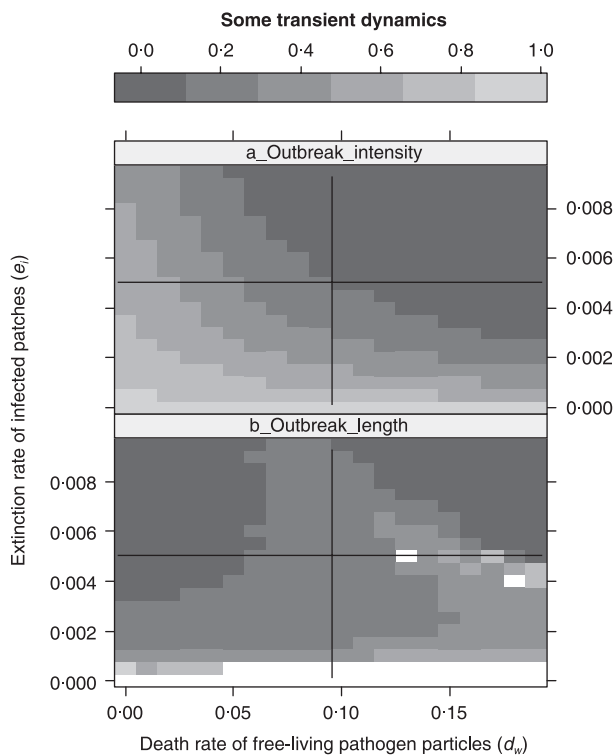


Fig. 4. Transient dynamics in the parameter space defined by e_i and d_w . Shading corresponds to the magnitude of each transient measurement: (a) outbreak intensity, defined as the maximum proportion of patches infected at any point during an outbreak, ranging from 0 (no patches infected) to 1 (all patches infected); and (b) outbreak length, scaled to the observation period, ranging from 0 (no outbreak) to 1 (outbreak lasted 50 years), with blank/white indicating that the outbreak exceeded 50 years (enzootic disease). The parameter e_i ranged from 0.00001 to 0.01 at equal intervals and d_w ranged from 0.001 to 0.1 at equal intervals. The remaining parameters were as in Figs 3 and 6. Each panel is broken into four quadrants which are, clockwise from the upper left corner: high disease virulence and long-lived pathogens; high disease virulence and short-lived pathogens; low disease virulence and short-lived pathogens. Note that the quadrant characterized by low disease virulence and long-lived pathogens leads most consistently to long, high-intensity outbreaks.

closure of a local research centre. However, anecdotal observations have revealed sporadic, but comparatively rare, sightings of the disease in the region since the outbreak subsided in 2005 (L. Kaczmarek, personal communication).

Given a plausible set of parameter values (see Supporting Information, Appendix S1), Fig. 6 shows that model predictions for disease levels within the upper Florida Keys region agree with (occur inside of the confidence intervals for) all years of observed data, except one: 1997. The observed deviations from expected disease levels were negative (disease was lower than predicted) in 1997, 2001, and 2005, and positive (slightly higher than predicted) in the other years surveyed.

The spatial tracking of infected sites reveals a lack of any dominant directional trajectory nor any other clear spatial pattern since the first reports in 1995, but rather the data

demonstrate a sporadic pattern of colonization and local fade out of disease in patches of coral hosts throughout the Keys over time (Fig. 5), suggestive that metapopulation dynamics may fit well with the observed spatial configuration of infection at the regional scale.

Discussion

We present a general, mean-field model incorporating susceptible-infected, or 'SI', disease dynamics within a marine metapopulation framework. Our mechanistic model predicts some patterns in coral disease dynamics that fit well with spatial and temporal data from a decade-long WPPI outbreak in the Florida Keys. The current model not only lays a foundation for explicitly including disease in management and ecological research in marine settings, but also highlights the potential for expansion in the future to include more complexities such as external forcing through climate, seasonal, and abiotic factors, or alternative modes of transmission. Results from the model offer preliminary insights into the dynamics of infection at the metapopulation level, and help guide our understanding of the potential effects that management and environmental change may have on the long term population ecology of disease in marine systems.

WHAT FACTORS AFFECT OVERALL REGIONAL CORAL DISEASE DYNAMICS?

The observed dynamics of WPPI fit well with predictions from our epidemiological model (Fig. 6). This suggests that the trajectory and fate of marine metapopulations after pathogen introduction may be predictable from epidemiological models if the parameters can be estimated. However, there were some fluctuations around the model predictions in the observed WPPI data (Fig. 6). There was a particularly strong deviation in 1997 which may have simply been due to the low sample size that year (only six sites were sampled). However it may be that the deviation in 1997, as well as in other years, was driven by external forcing from factors not yet considered in the model, such as climate variables, water circulation patterns, and movement of potential vectors or reservoirs of disease. The 1997–1998 season was one of the most anomalous on record with respect to sea surface temperature and El Niño global weather conditions, and environmental extremes may have affected disease risk (Harvell *et al.* 1999b; West & Salm 2003). The influence of these environmental factors on coral disease dynamics is an important area of current and future research.

In our model, long-term disease establishment is more likely for relatively lower virulence diseases. This finding is consistent with the finding of Hess (1996). Our model expands Hess' result to include not only diseases with low mortality rates (low e_i , Figs 3, 4), but also diseases for which pathogens survive for relatively longer periods outside their hosts (low d_w , Fig. 4). These patterns are emphasized because it may be difficult to generate alarm or management action for diseases which appear to have low virulence in the short term;

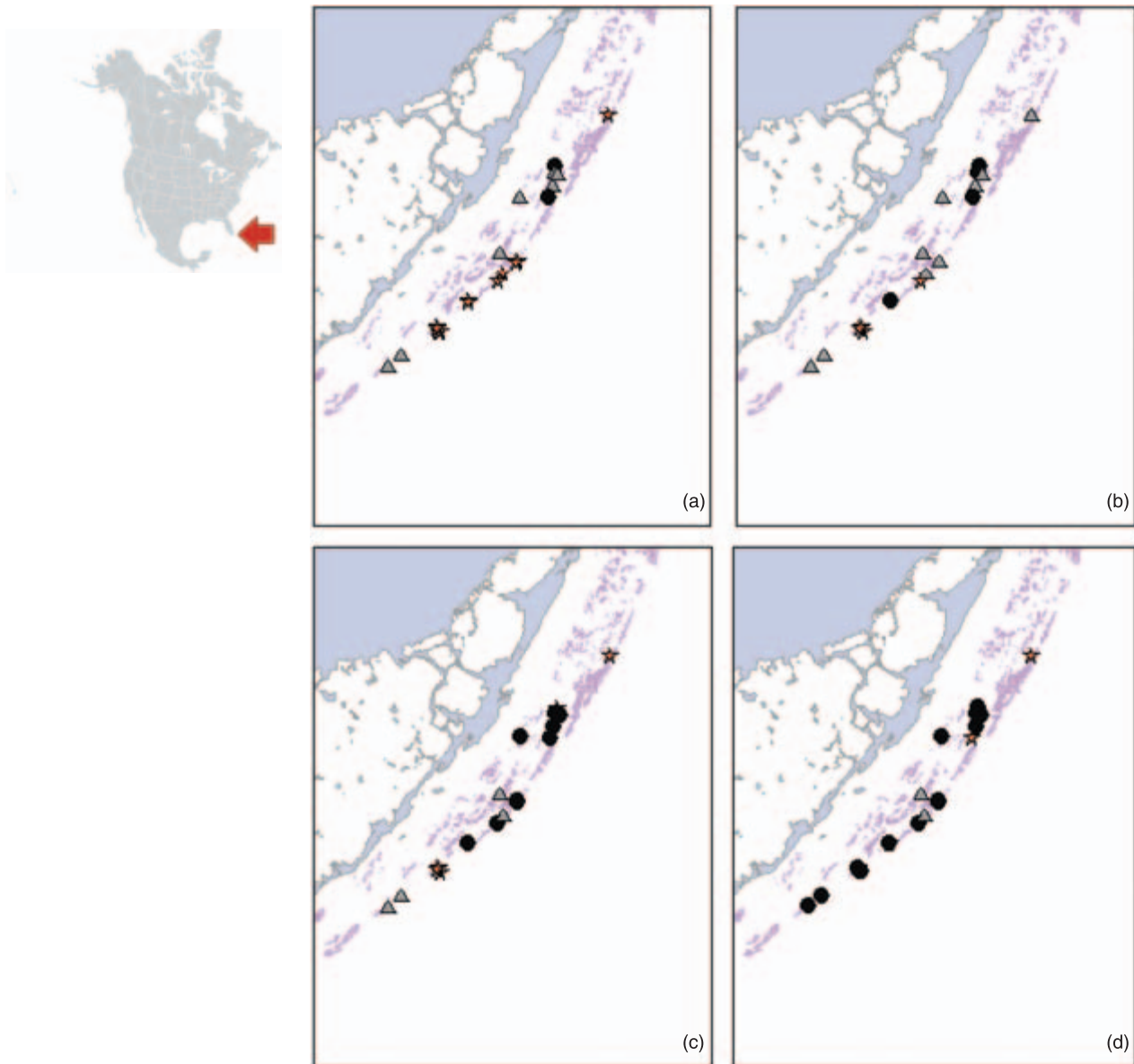


Fig. 5. The spatial distribution of white plague type II (WPII) infections on reefs in and around the Florida Keys National Marine Sanctuary (shown at the arrow on the map in the upper left corner) during the sampling periods in (a) 1995, (b) 1998, (c) 2002, and (d) 2004. Triangles, reef patches not examined in that sampling season (but which were examined during other time points in the study); stars, positive sites: one or more cases of WPII were observed; circles, negative sites: no cases of WPII were observed. The basemap for a–d was obtained from: Florida Geographic Data Library <http://www.fgdl.org/>; shaded areas represent land and submerged reef patches and white areas represent non-reef ocean floor, usually sand or seagrass.

however, these chronic diseases may be very influential for determining the long-term health of regional host metapopulations. The phenomenon that chronic diseases can lead to higher sustained disease prevalence within host populations is widely recognized in epidemiology and may contribute, for example, to why HIV (a chronic infection) has become persistent at high prevalence in some human populations while Ebola (an acutely lethal disease with a high case fatality rate) mainly occurs in rare and sporadic, small-scale epidemics (Borchert *et al.* 2000; Levin *et al.* 2001). Our results support

the prediction that if future climate scenarios allow marine pathogens to survive better in the ocean, through sea-surface warming or less severe winters, longer and more severe outbreaks may be expected.

According to our model results, higher connectivity among marine populations may have either beneficial or detrimental effects on overall host persistence when infectious disease is considered. A negative effect of higher connectivity occurs when disease is allowed to persist where it would otherwise fade out in a more isolated system (Fig. 3), and this is more

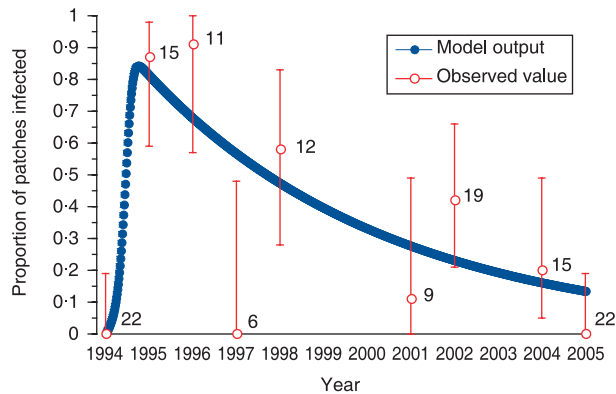


Fig. 6. Observed and theoretical patterns for the proportion of infected coral patches over time. Solid circles: example model output based on simulated disease introduction into the region in early 1994, and parameter values: $S_0 = 0.9$, $I_0 = 0$, $W_0 = 100$, $e_s = 0.00001$, $d_w = 0.01$, $v = 0.00001$, $\lambda = 100$, $m = 0.0002$, $e_i = 0.0005$. Open circles: the temporal pattern of observed white plague type II infections among patches of coral in the Florida Keys National Marine Sanctuary and surrounding reefs from 1994 to 2005 (with 95% confidence intervals signified by error bars). Numbers represent the number of sites surveyed in that year. Note the apparent anomaly in 1997. Parameter values used for this figure are further discussed in the online supplemental material (Supporting Information, Appendix S1) and are within the range displayed in Fig. 3 (marked by an arrow).

likely to occur when connectivity (or recruitment) is already fairly high. On the other hand, higher connectivity and resultant higher gene flow are thought to promote coral resilience to large-scale disturbances such as warming events and bleaching (Hughes *et al.* 2003). In applying this result to marine disease management, it is noteworthy that many coral systems, especially in the Caribbean, are already highly degraded and likely have severely depressed recruitment (Hughes & Tanner 2000). Where recruitment rates are very low, increases in connectivity are generally considered beneficial for host metapopulation survival and resilience.

IMPORTANCE OF MANAGING INFECTIOUS DISEASE FOR CONSERVATION OF CORAL REEFS

In our deterministic analytical model (see Supporting Information, Appendix S2), coral metapopulation extinction by infection is not possible. Indeed, single-host infections are not expected to cause extinction (Anderson & May 1986). However, in conjunction with other stressors, or in more complex situations where pathogens can spill over from alternative hosts, extinction by infection can and does occur (Daszak & Cunningham 1999; Woodroffe 1999; Daszak *et al.* 2001; Lips *et al.* 2006; Smith *et al.* 2006). The inclusion of even a small amount of stochastic variability in our simulation model presents a scenario in which infectious disease can cause extinction of the host metapopulation if disease drives patch occupancy below a 'quasi-extinction threshold' (Lande 1993; Smith *et al.* 2006) beyond which the effects of other

stressors or demographic and environmental stochasticity lead to imminent regional extinction.

Because many coral species are currently threatened by multiple stressors, including climate change, fishing pressure, and pollution (Carpenter *et al.* 2008; Jackson 2008), and because most coral diseases affect multiple host species (Sutherland *et al.* 2004), extinction by infection is a concern that warrants further study. As an example, white band disease has been implicated in the widespread devastation of *Acropora* spp. coral in the Caribbean region, and consequently these once dominant reef-builders were recently listed under the US Endangered Species Act (Precht *et al.* 2004; Anon 2006).

WHAT MANAGEMENT OPTIONS INCREASE THE PROBABILITY OF CORAL PERSISTENCE WHEN CONSIDERING INFECTIOUS DISEASE?

Infectious disease within marine ecosystems presents a difficult problem for management since most marine management strategies, such as fishing regulations and marine protected areas, do not directly address disease risk (McCallum *et al.* 2005). Unfortunately, traditional disease management strategies that rely on interventions such as culling, vaccination, and treatment are probably unrealistic at the regional scale for most marine systems, and currently, there are not many available management options for coral disease.

Our results show that many management strategies have the potential to affect infectious disease dynamics, either directly or indirectly, when they alter such key parameters as host colonization, pathogen survival in the environment, disease transmission, and mortality (e.g. Figs 3 and 4). Because of complex thresholds which can be influenced by many parameters simultaneously, management may affect disease in sometimes predictable and sometimes counter-intuitive ways. For example, increases in coral recruitment have been a demonstrable outcome from marine protected area establishment (Mumby *et al.* 2007). An important prediction to clarify with empirical studies is: does marine protected area establishment affect regional disease levels, and if so, how?

It remains ambiguous, based on our current model results, whether the net effects of marine protected area establishment will be positive or negative with respect to infectious disease. Our model predicts that in some cases, increases in coral recruitment rates could lead to higher prevalence and longer persistence of infectious disease inside compared with outside protected areas. Despite this potential, by reducing the effects of other compounding stressors, the benefits of reserves probably outweigh the risks. However, reserve establishment alone may not directly reduce disease risk, and other management strategies may be needed to complement reserve establishment when infectious disease is a concern. For example, the potential for regulating anthropogenic factors associated with connectivity, such as shipping traffic or the movement of humans and equipment, has been relatively unexplored. Also, evidence is increasing that mitigating the effects of climate change may be an important factor for

disease management in the oceans (Colwell 1996; Harvell *et al.* 1999a, 2002; Rosenberg & Ben-Haim 2002; Bally & Garrabou 2007; Carpenter *et al.* 2008). More research in these areas is clearly warranted.

While to date, uncertainty about disease parameters precludes specific management recommendations, our study presents a framework that can guide future empirical work. For example, our case study of white plague type II demonstrates the utility of coordinated efforts to monitor a subset of permanent sites (or 'patches') within each region for the presence or absence of infectious disease, and this could represent a substantial improvement over the more common practice of haphazard local disease monitoring (Downs *et al.* 2005). We hope that epidemiological models, building on the one presented here, will facilitate the explicit incorporation of infectious disease dynamics into management strategies in the future. In the final sections, we outline some future directions which could further strengthen predictions, guide management, and place epidemiological modelling into the wider framework of coral disease research and conservation.

FUTURE DIRECTIONS

Integrating disease dynamics with external forcing and coral–algal competition models

The mean-field model presented here assumes that transmission is dependent on the average density of susceptible hosts, the average number of infectious particles in the environment and a constant transmission probability when infectious particles contact susceptible patches of hosts. This is a plausible transmission model for some infectious coral diseases at the regional scale, especially for those that appear to be locally clustered, such as white plague (Kaczmarek *et al.* 2005) and black band disease (Borger 2003; Page & Willis 2006). However, it is possible that some marine diseases follow more complex modes of transmission, such as strong reliance on local environmental conditions or spatial distributions of vectors. For example, a recent study found that outbreaks of the coral disease, white syndrome, occurred most commonly on reefs that had high coral cover but also typically followed warm years (Bruno *et al.* 2007). Expansion of our current model to examine the effects of seasonality and environmental forcing represents an important future direction.

Also, our disease model assumes, for simplicity, that the potential substrate for coral colonization remains constant over time, and ignores competition between coral and algae for space. When adult coral are killed by disease or other disturbances, the liberated substrate may not always be available for colonization by new coral but rather may be overtaken by macroalgae, rendering the substrate no longer available for future colonization once the algae become established (Mumby & Dytham 2006; Mumby & Hastings 2008). Thus, a more realistic scenario would integrate coral–algal competition with the dynamics of infectious disease, and this warrants further study.

Estimation of parameters

We show that for coral disease, and possibly other marine systems, parameters may be most useful for management if these are estimated at the level of populations or patches of hosts. Few of the epidemiological parameters employed within our metapopulation model (Table 1) can be estimated reliably for any coral disease to date, representing a critical area for future research. Coordination among scientists to compile multiple long-term, large-scale, and spatially explicit data sets on host and disease parameters at the regional and metapopulation scales will be necessary before general patterns can be reliably concluded.

The ecological and spatial dynamics of emerging marine diseases are complex. Yet management decisions are imminently necessary and thus must be guided by theory as well as available empirical data. Application of epidemiological and ecological models, with modifications appropriate to marine systems, can be successful tools for generating testable predictions for large-scale and long-term processes governing infectious disease dynamics in the marine environment. Our model results, as well as emerging patterns for several marine diseases, suggest that infectious disease can have substantial effects on marine metapopulation persistence, and understanding the role of infectious disease in these systems should be considered a conservation priority.

Acknowledgements

The authors thank I. Hanski for encouragement with the early concept, J. J. Stachowicz, E. C. Chamberlin, and three anonymous reviewers for useful comments on manuscript drafts, J. D. Voss, E. R. Remily, J. D. Lorber, and L. Kaczmarek for help in acquisition and compilation of field data, R. K. Plowright and N. Gottdenker for helpful suggestions on programming in R, and E. H. Girvetz for GIS technical assistance. S.H.S. was supported by a sub-award of the NOAA NURC/UNCW no. NA030AR4300088 and block grant awards from the Ecology Graduate Group UC Davis.

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Received 14 December 2008; accepted 2 March 2009
 Handling Editor: Marc Cadotte

Supporting Information

Additional supporting information may be found in the online version of this article:

Appendix S1. Simulation details and original code for the basic R function utilized

Appendix S2. Analytical solutions and stability analyses

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