

Supplemental Information:

Calculations for pathogen load proxies are shown in equations 1-4, where:

1NDN = first nearest diseased neighbor

2NDN = second nearest diseased neighbor

3NDN = third nearest diseased neighbor.

Equation 1: Distance to diseased neighbors:

$$\text{Distance to diseased neighbors} = \frac{(\text{distance to 1NDN})+(\text{distance to 2NDN})+(\text{distance to 3NDN})}{3}$$

Equation 2: Lesion severity:

$$\text{Lesion severity} = \frac{(\% \text{ visually actively affected tissue of 1NDN})+(\% \text{ visually actively affected tissue of 2NDN})+(\% \text{ visually actively affected tissue of 3NDN})}{3}$$

and binned by severity into low (≤ 25 % visually actively affected tissue), moderate (> 25 -75 % visually actively affected tissue), and high (>75 % visually actively affected tissue).

Equation 3: Size-weighted lesion severity:

$$\text{Size – weighted lesion severity} = \frac{((\text{size of 1NDN})*(\% \text{ visually activity affected tissue of 1NDN}))+(\text{size of 2NDN})*(\% \text{ visually activity affected tissue of 2NDN}))+(\text{size of 3NDN})*(\% \text{ visually activity affected tissue of 3NDN}))}{3}$$

Equation 4: Distance- and size-weighted lesion severity:

$$\text{Distance – and size – weighted lesion severity} = \frac{((\text{size of 1NDN})*(\% \text{ visually activity affected tissue of 1NDN}))/\text{distance to 1NDN}^2+(\text{size of 2NDN})*(\% \text{ visually activity affected tissue of 2NDN}))/\text{distance to 1NDN}^2+(\text{size of 3NDN})*(\% \text{ visually activity affected tissue of 3NDN}))/\text{distance to 1NDN}^2}{3}$$

Supplemental Table 1: Comparison of top four models explaining infection

likelihood. Coefficients for each variable are listed with the standard error of the mean in parentheses. Colony size was measured as the longest horizontal axis (cm). Reef position refers to reef flat (baseline condition where coefficient equals zero), reef crest (upper coefficient) or reef slope (lower coefficient). Baseline hazard is the baseline level of risk for any individual without accounting for host and pathogen heterogeneity in a location with no disease cases. Model fit was assessed using Akaike information criterion (AIC) with the best fit model described by the lowest AIC value.

Model	Colony size	Reef position	Initial lesion severity	Proximity to infected neighbors	Baseline hazard	AIC	Δ AIC
1	2.52^{-3} (1.4^{-3})	N/A	0.118 (0.005)	3.8^{-3} (0.001)	-12.26	941.44	0
			0.593 (0.005)				
3	2.46^{-3} (1.5^{-3})	0 (0.006)	0.109 (0.006)	3.87^{-3} (0.001)	-23.46	949.44	0.6
		0.002 (0.006)	0.519 (0.006)				
3	3.28^{-3} (1.5^{-3})	0 (0.006)	N/A	4.41^{-3} (0.002)	-10.22	953.79	7.35
		0.005 (0.005)					
4	N/A	0 (0.004)	0.13 (0.005)	0.004 (0.001)	-5.40	955.4	8.96
		0.002 (0.006)	0.796 (0.005)				

Supplemental Table 2: Range for optimal disease transmission. Coefficients for each variable are listed with the standard error of the mean in parentheses. Distance refers to the radius of concentric circles tested in the spatio-temporal point process regression model to determine the range in which disease transmission is highest. Zero indicates colonies were touching.

Model	Size	Lesion severity of nearest neighbors	Distance (m)	Distance coefficient	AIC
1	4.42^{-3} (1.58^{-3})	0.157 (0.05)	0	0 (0.025)	958.15
		0.879 (0.05)			
2	4.38^{-3} (1.57^{-3})	0.152 (0.05)	1	0.0114 (0.015)	957.54
		0.8 (0.05)			
3	2.54^{-3} (1.54^{-3})	0.126 (0.06)	5	8.89^{-3} (3.54^{-3})	946.54
		0.599 (0.06)			
4	3.11^{-3} (1.52^{-3})	0.118 (0.05)	10	4.45^{-3} (1.54^{-3})	943.71
		0.758 (0.06)			
5	2.58^{-3} (1.41^{-3})	0.112 (0.05)	15	3.85^{-3} (1.11^{-3})	941.44
		0.539 (0.05)			
6	2.70^{-3} (1.49^{-3})	0.0119 (0.06)	20	2.45^{-3} (8.25^{-4})	946.90
		0.003 (0.002)			
7	2.30^{-3} (1.48^{-3})	0.119 (0.05)	50	8.9^{-4} (2.9^{-4})	948.34
		0.0423 (0.006)			

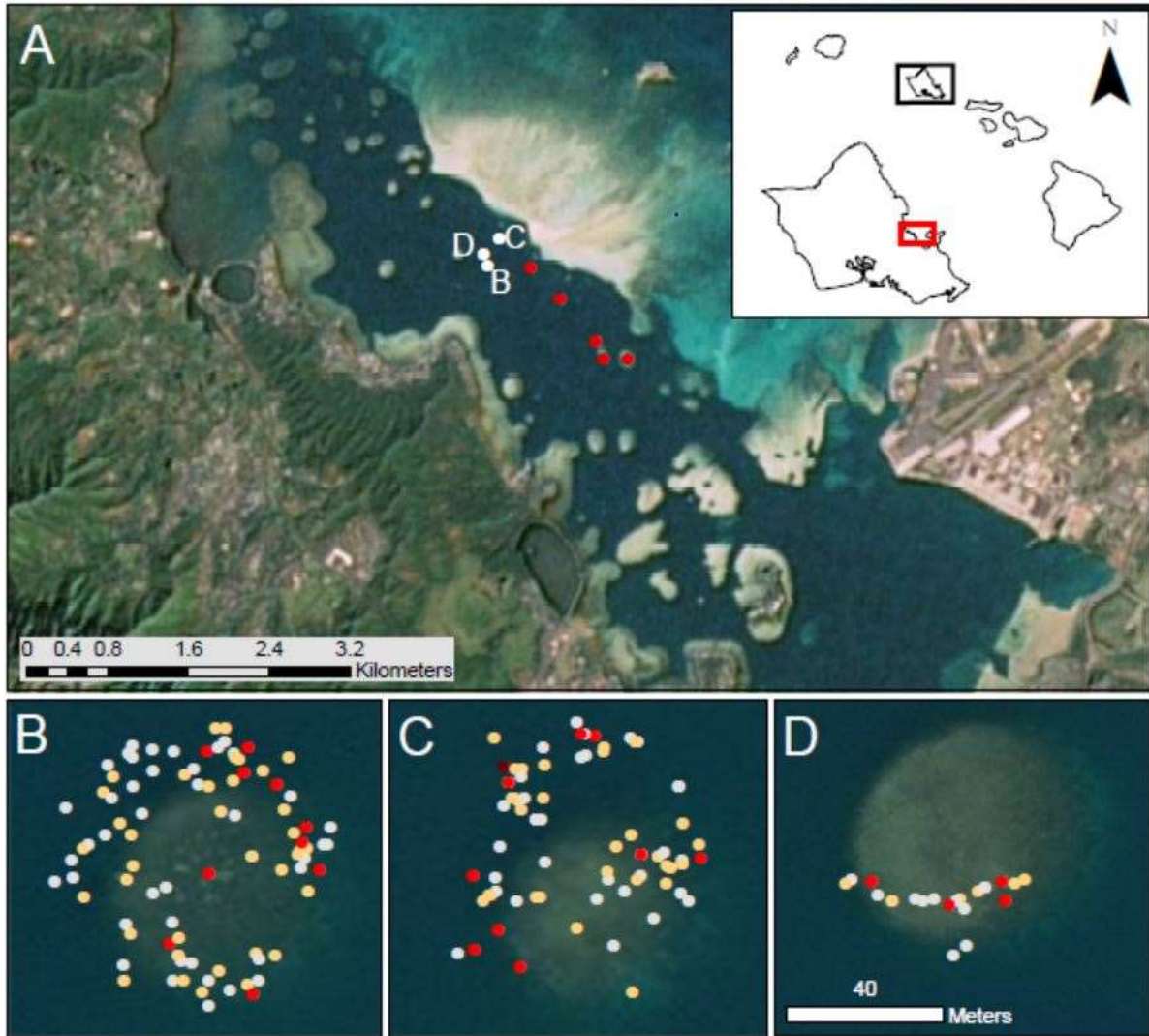


Figure S1: Map of survey sites. (A) Kāneʻohe Bay, Oʻahu, Hawaiʻi; inset shows Main Hawaiian Islands with Oʻahu enlarged. Red dots indicate patch reefs external to this study that were affected by the outbreak. White dots indicate survey sites at (B) Reef 21, (C) Reef 22, and (D) Reef 23. In maps B-D, the 200 focal colonies are represented by coloured dots indicating health state as healthy (grey), low severity (orange), moderate severity (red) and high severity (maroon) corresponding to 0, less than 25, 25–75 or greater than 75% tissue actively affected, respectively.

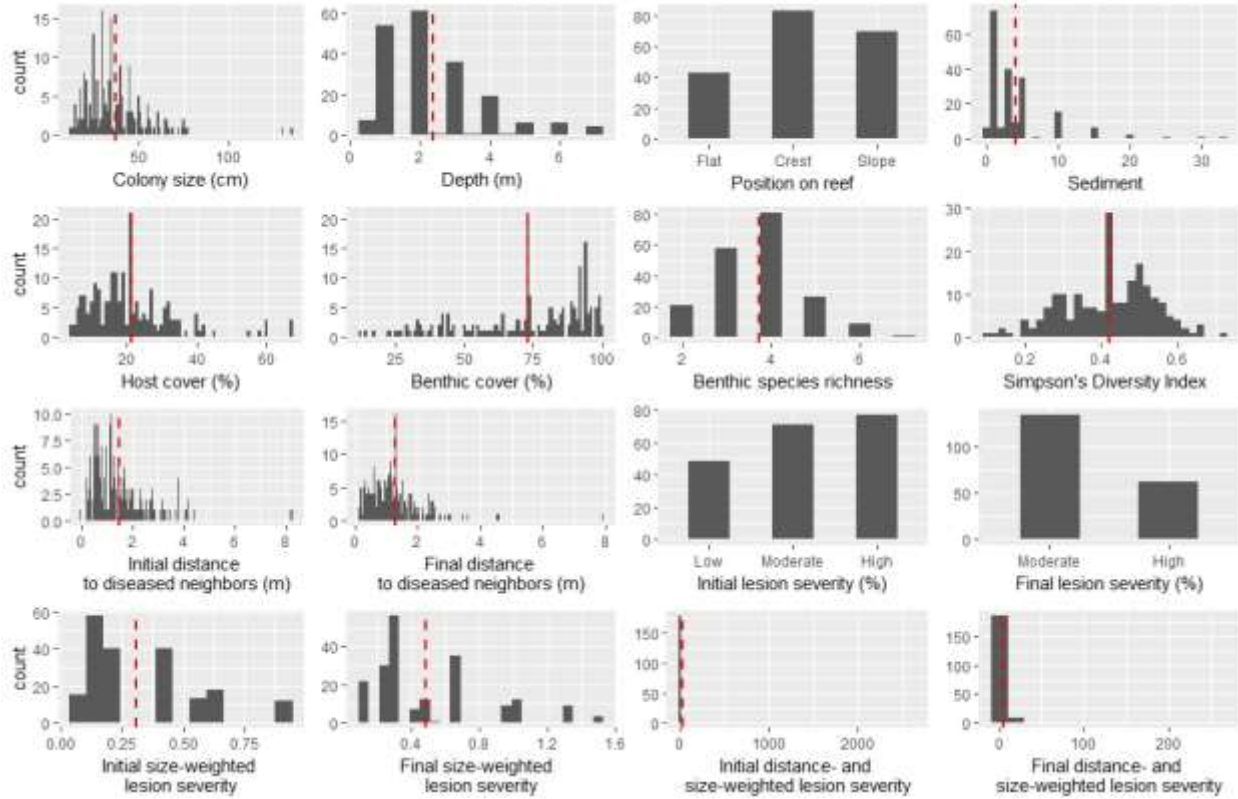


Figure S2: Distribution of host, pathogen, and environmental factors. Histograms show the range and distribution of each factor investigated in this study in the sampled population.

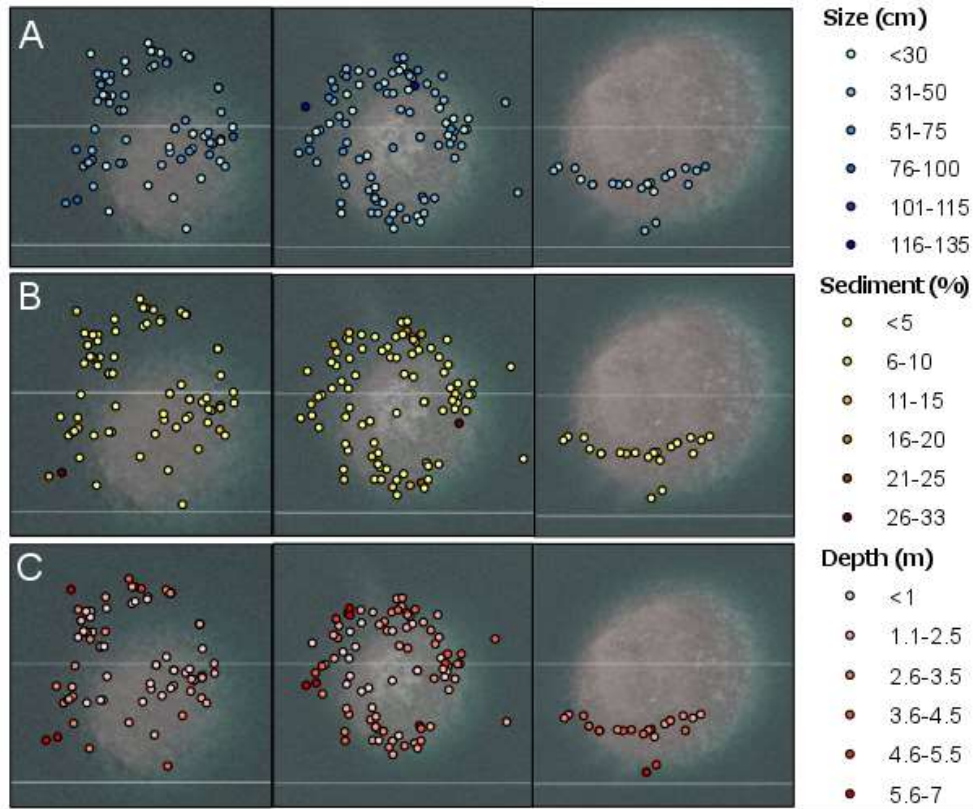


Figure S3: Spatial variation in host and environment factors. Variation in A) focal colony size; B) sediment on the focal colony's surface tissue; and C) depth of each focal colony. Dots represent the 200 focal colonies monitored during this study.

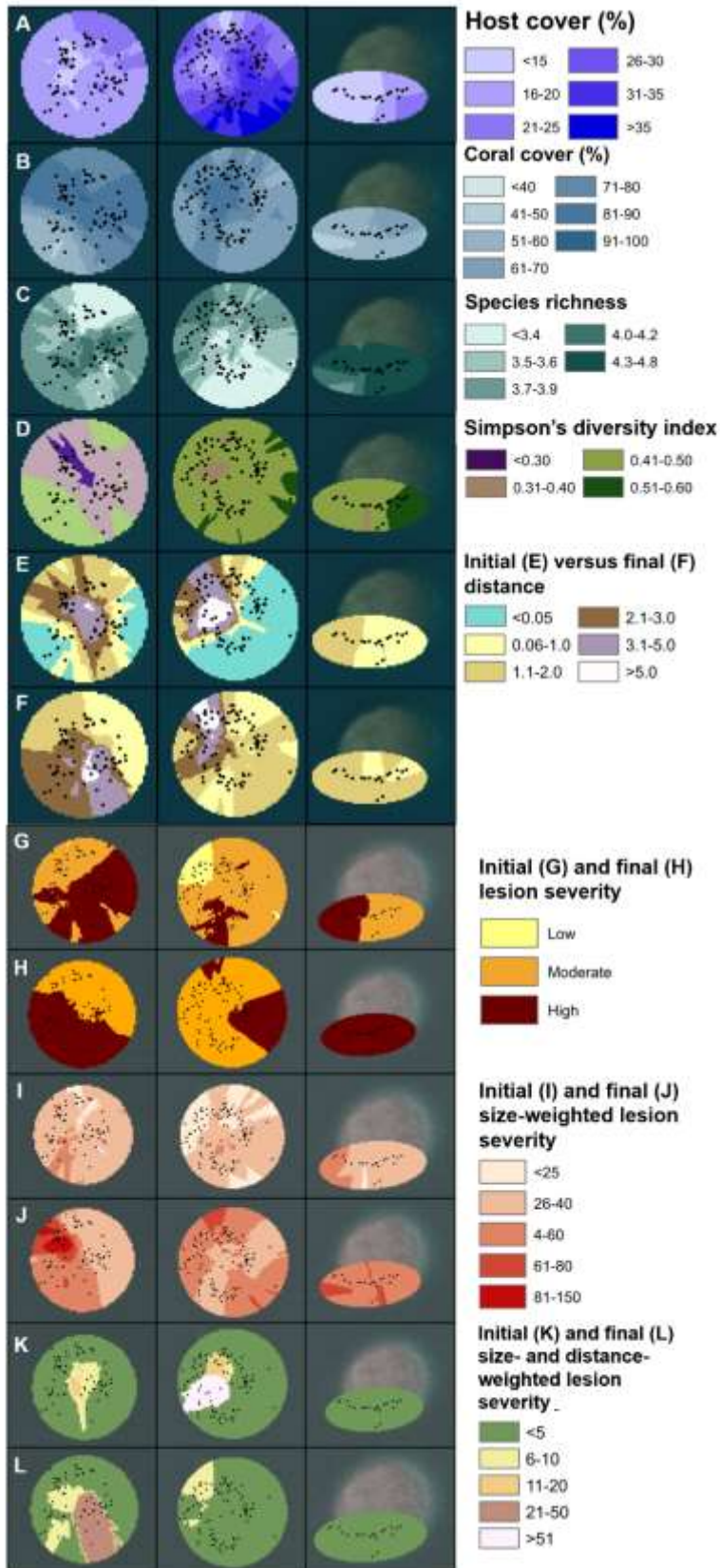


Figure S4: Spatial variation in pathogen and environment factors. Variation in A) host (*M. capitata*) cover, B) coral cover, C) species richness; D) Simpson's diversity Index; E) initial distance to diseased neighbors; F) final distance to diseased neighbors; G) initial lesion severity; H) final lesion severity; I) initial size-weighted lesion severity; J) final size-weighted lesion severity; K) initial size- and distance-weighted lesion severity; and L) final size- and distance-weighted lesion severity. The left panel is a map of patch reef 21, the central panel is a map of patch reef 22 and the right panel is a map of patch reef 23. Dots overlaying interpolated data represent the locations of the 200 focal colonies monitored during this study. Maps were interpolated from data collected surrounding each focal colony using the kriging function in ArcMap 10.4.