

Supplementary Materials

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Methods

Determining Regions

R and the R packages 'rgdal', 'raster', and 'sp' were used to assign each data point to a single region. These regions included the Aleutian Islands, west Gulf of Alaska, east Gulf of Alaska, southeast Alaska, British Columbia (excluding the Salish Sea), the Salish Sea, the Washington outer coast (excluding the Salish Sea), Oregon, northern California, central California, southern California, and the Pacific coast of Baja California. From west to east then north to south, we used the following regional border cutoffs: the Aleutians began at Samalga Pass/Umnak Island at -169.5°W ; west Gulf of Alaska began at -157.7°W ; east Gulf of Alaska began at the eastern edge of Kodiak Island around -152.2°W ; southeast Alaska began at -138.1°W ; British Columbia began at the Alaska-Canada border at 54.7°N ; Salish Sea began at Campbell River around 50.0°N and included the Strait of Juan de Fuca and Puget Sound; Washington outer coast began near Neah Bay around 48.4°N , -124.8°W ; Oregon began at its northern border around 46.3°N ; northern California began at California's northern border at 42.0°N ; central California began at the San Francisco Bay at 37.8°N ; southern California began at Point Conception at 34.5°N ; Baja California began at the United States-Mexico border around 32.5°N ; and Baja California ended at 26.7°N at Bahia Asunción.

Epidemic Timeline - The Multi-Agency Rocky Intertidal Network (MARINE) database is the most comprehensive dataset of sea star wasting records, and is populated by a combination of observations submitted by the public through seastarwasting.org, MARINE long-term monitoring data, Partnership for Interdisciplinary Studies of Coastal Oceans (PISCO) network diver surveys, and various community science programs. Thus, it was uniquely well suited for this analysis. While this dataset is powerful, there are some limitations to our analysis of epidemic phases. When estimating the 'date SSWD first observed', the true date is likely somewhat earlier since the first day of infection likely occurred before the first recorded observation. However, we do not think the true date is later than reported since the MARINE database included a requirement for photo verification of disease symptoms by an expert during the early phase of the epidemic.

For calculating the date first observed and outbreak date, we elected to pool data from both intertidal *Pisaster ochraceus* and *P. helianthoides* since *P. ochraceus* has more observations than *Pycnopodia*, enabling more accurate estimates of outbreak timing among regions ($N = 450$ and $N = 247$ sites, respectively). To determine if the timing was similar between species, we performed a two-sample Kolmogorov-Smirnov test (k.s test in dgof package v1.2 in R) on the count of sites over time when the first observation of SSWD occurred, and compared the two species. We found that *P. ochraceus* had slightly earlier dates of first SSWD observation than *P. helianthoides* (Fig. S3). Since the disease apparently spread quickly in the water, it probably was nearly simultaneously present in subtidal and intertidal habitats at a given site. Thus, it is likely that the slight lag in date first observed for *P. helianthoides* was due to the easier access to intertidal *P. ochraceus* than subtidal *P. helianthoides*. However, it is also possible that this lag was truly a difference in disease dynamics between the warmer

intertidal and cooler subtidal, but we were not able to address this question because there were not enough within-site comparisons to explore in our dataset.

When estimating ‘outbreak date’, we first fit a normal distribution to the date SSWD was first observed at each site, then calculated the date of the 10th percentile to approximate the date at which 10% of the sites with a region had reported SSWD observations. No symptomatic sea star observations were recorded in the Aleutians or Baja California and thus our ability to estimate crash date is limited. Only three observations were recorded in the western Gulf of Alaska and these estimated an outbreak date of Aug 25, 2016. Konar et al. (2019) never recorded a symptomatic sea star in the Katmai Peninsula (western Gulf of Alaska), but the initial decline occurred between June 2016 and June 2017, so an outbreak date of Aug 25, 2016 is reasonable (1). We also used Aug 25, 2016 as the outbreak date for the adjacent Aleutians region only for purposes of splitting the data into phases, though it is unclear whether the disease affected this region (pers. comm. B. Konar). For Baja California, we used the southern California outbreak date of Nov 6, 2013, and it is likely that this date estimate is accurate since populations declined shortly thereafter.

Unlike ‘date SSWD first observed’ and ‘outbreak date’ we defined ‘crash date’ using the *Pycnopodia* population changes to determine disease progress. Ideally the timeline of the epidemic would rely on metrics of signs of disease in the field such as prevalence or disease occurrence. However, SSWD kills individual *Pycnopodia* within days to weeks, and can move through a population within weeks to months (2–4). Consequently, it is likely that seasonal or annual surveys at a given site or region missed peak disease prevalence or any occurrence of disease entirely. We calculated the ‘crash date’ by fitting a logistic regression model to the occurrence of *Pycnopodia* over time for each region. We fit a logistic regression model to the occurrence of *Pycnopodia* from 1/1/2012 to 12/31/2019 to model the shape of the population decline for each region (Fig. 1a). From these models, we 1) estimated regional *Pycnopodia* occurrence rates on 1/1/2012 and 12/31/2019, 2) calculated the predicted occurrence value corresponding to a 75% decline in starting versus ending occurrence in each region, and 3) solved the inverse logistic equations for the date at which this occurrence value was predicted. We note that the disease itself is still present in many or all of the regions after the crash date, and that it is possible the disease may still be in the epidemic phase in some regions (e.g., Alaskan regions).

While this worked well for most regions, we had to modify this procedure for several regions. For instance, in southern California the abundance of data was resulting in an estimated crash date before the outbreak date. To remedy this, we restricted southern California models to fit data from 1/1/2013 to 12/31/2019, instead of 1/1/2012 to 12/31/2019. We lumped data from the Aleutians and the western Gulf of Alaska to increase the sample size in the model and because these regions likely had similar disease timing and population trends (pers. comm. B. Konar, 1).

Density and Occurrence Models

For the shallow models, we tested how density and occurrence varied with population phase (historic/current), region, and their interaction. For all shallow models, we dropped Baja California and southern California because the ‘current’ surveys consisted entirely of zeros, so this prevented the models from fitting the data. We also lumped the Aleutian Islands and west Gulf of Alaska into ‘western Alaska’ and the Washington outer coast and Oregon into the Pacific Northwest (excluding the Salish Sea). We also compared graphs and models with and without fjord habitats in British Columbia (CCIRA dataset), and elected to drop these data because the current anomalously high densities of sea stars in these habitats have no historical comparison, and these data were masking the declines in density that were evident in

other datasets in the region. We instead investigate these populations in the remnant population analyses elsewhere. For density models at deep depths, data were limited to only a few regions, so we did not compare regions and we tested only how density varied with population phase (historic/current). For occurrence models at deep depths, we merged the data into three ‘super-regions’ (Alaska, British Columbia including Salish Sea, and the outer coast of the contiguous US).

SDM modeling

Time Periods - We modeled *Pycnopodia* distribution for pre-outbreak populations using species and environmental data from 2009-2012 and for current populations using data from 2017-2020. We chose to limit the pre-outbreak model to 2009-2012 because a) of the very patchy nature of long-term *Pycnopodia* observations that would greatly increase spatial heterogeneity in sampling effort and b) we wanted to represent the state of the population directly prior to the outbreak. To the first point, only a single dataset goes back to 1967, and only 6 of the 30+ datasets goes back before 1990. We specifically limited the species distribution models to 2009-2012 and 2017-2020 because we wanted to minimize the impacts of differential sampling effort between the two periods. Maxent models are sensitive to uneven sampling effort, and we tried to minimize this whenever possible. We felt that including data from 1967 - 2012 for the pre-outbreak model would a) pit 35 years of sampling pre-SSWD against just 3 years of sampling post-outbreak and b) could bias models towards older data that was not representative of populations near the beginning of SSWD.

Variable selection – We used prior studies on *Pycnopodia* to identify useful abiotic variables to include in our Maxent SDMs. For instance, Hemery et al. (2016) found depth, mean annual temperature, and mean annual salinity to be the three most important factors in predicting *Pycnopodia* distributions in Oregon (5). Additionally, Bonaviri et al. (2016) found *Pycnopodia* abundances in the Channel Islands to be structured along a temperature gradient (6). Based on these studies, we identified depth, temperature, and salinity as important variables to include in our models.

Other variables we considered for inclusion were mean chlorophyll, substrate type, latitude, dissolved oxygen, mixed layer depth, water movement, and temperature at depth. However, we were unable to find datasets for dissolved oxygen, mixed layer depth, measurements of water movement, and temperature at depth that had both the sufficient spatial extent and resolution to use in our models, and thus were unable to include these variables. Another consideration for model selection was collinearity amongst variables. The remaining variables under consideration, temperature, salinity, chlorophyll, substrate type, latitude, and depth, are interdependent and thus will have some levels of collinearity. We were most concerned about potential collinearity of temperature with other variables, particularly latitude. We used linear models to assess correlation between these variables at points where *Pycnopodia* were observed. While all variables were significantly correlated with temperature, only latitude showed an adjusted R^2 value > 0.015 with an R^2 value = 0.14 (p -value < 0.001) (Fig S5).

As noted in [12], it is considered best practice to avoid including collinear variables within Maxent models, and thus we preferred to use either a temperature metric or latitude. We tested Maxent model fit when one variable was substituted for the other. When latitude was added to the models and the temperature metric dropped, both the pre-outbreak and current models had a decreased fit (AUC by 0.28 and 0.31, RTG by 0.07 and 0.2 for pre-outbreak and current respectively). Thus, model fit declined when including latitude instead of temperature, which indicated that we should use the temperature metric. We felt further justified in this decision considering that previous work has found a relationship between temperature and SSWD progression whereas we are unaware of any hypothesized relationship between latitude and SSWD [8,9,10]. Outside of temperature, the collinearity of the remaining variables was

investigated (e.g. salinity and depth), and again, while the relationship was often highly significant between variables, the adjusted R^2 value rarely rose above 0.1.

After eliminating latitude, we were left with temperature, salinity, chlorophyll, depth, and substrate type. We decided to include mean chlorophyll measurements for two reasons: 1) as a proxy for general productivity and food availability in the system at large spatial scales and 2) because a recent investigation into the cause of SSWD indicated that the addition of organic material to a system could spur the disease (11). We included substrate type as this is a key component of the physical environment for benthic invertebrates. While the resolution of our dataset (~11 km grid cells) conceals much fine-scale variability that is likely important for *Pycnopodia*, we were unable to find abiotic data at higher resolutions that also encompassed our entire study area. However, given that we were ultimately studying the species from a biogeographic scale spanning an entire ocean basin, we felt that 11 km² was high enough resolution to provide insight into the associations of *Pycnopodia* with their environment across their range. We used substrate data from the University of Colorado at Boulder's dbSEABED inventory for substrate (<https://instaar.colorado.edu/~jenkinsc/dbseabed>).

At 11 km resolution and covering the entire range of *Pycnopodia*, the best measurements of salinity we were able to find were 30-year climatological means produced by NOAA (https://www.nodc.noaa.gov/OC5/regional_climate/). With temperature, however, we had more options. We considered using mean temperature (measured using NASA's Moderate Resolution Imaging Spectroradiometer (hereafter MODIS) satellite data), the standard deviation in temperature (using MODIS satellite data), marine heatwave frequency (7), degree days over 14°C (6), and the 90th percentile of MODIS temperature measurements. All models performed similarly when substituted into the Maxent model and had similar predictive abilities (based on their AUCtest value). Thus we chose the 90th percentile of MODIS temperature measurements because we felt it had the most biological relevance to *Pycnopodia* based on previous investigations into the relationship between wasting and temperature (8–10).

Environmental Data - After collecting environmental data from the sources listed above we calculated mean chlorophyll and 90th percentile of temperature for the 2009-2012 period for the pre-outbreak model and for the 2017-2020 period for the current model. This was possible due to the availability of high-resolution, gridded, 8-day raster datasets of these variables derived from NASA's MODIS Aqua sensor on Google Earth Engine. We have now added this information to the manuscript. It is unlikely that depth changed substantially at large spatial scales between the two periods so depth data were not recalculated for the two different periods.

Ideally, we would have calculated mean salinity and substrate type for both the 2009-2012 and the 2017-2020 period. At this time, neither variable is easily mapped from remote sensing, but must rather be mapped in situ using depth profiles run from vessels. Thus, the data available for these variables is neither regular enough nor fine-scale enough to map these variables across the entire continent for each time period. For both datasets, the best maps available with the needed resolution (11 km grids) were only available as static maps created using long-term data. Despite the shortcomings of these static long-term representations of salinity and substrate variability, we believe that they do represent continental-scale patterns in substrate and salinity. For instance, in this region, salinity is most strongly influenced by the addition of freshwater from large rivers in the northern part of the range. While changes to these rivers from climate change are likely impacting ocean salinity at the river/ocean interface, it is unlikely that the patterns associated with these major rivers have disappeared between the early 2000s and the late 2010s. Furthermore, we tested how using a long-term climatology of temperature vs. 2009-2012/2017-2020 temperature data impacted the models, and found that neither the pre-outbreak or current model was sensitive to this change.

Substrate data were initially provided as four separate categories defining the percent of the substrate made of 1) mud, 2) sand 3) gravel and 4) rock at each location, which we transformed to 5 substrate categories by conducting K Means clustering: 1) sand dominated, 2) mud dominated, 3) sandy with rocky outcrops, 4) mixed sandy and muddy substrate, and 5) gravel dominated.

Background Data - We used our compiled *Pycnopodia* dataset, which includes presence and absence/non-detection information, to create a kernel density estimate of sampling effort across the study area from 2009-2012 and 2017-2020. These kernel density estimates were then used to create a set of 5000 background points that had a similar spatial sampling bias as the presence data to mitigate the effects of uneven sampling effort across the region (referred to as a ‘biased background’ approach in (11)).

Model Selection - We used ENMeval to choose the feature classes and regularization parameter combinations for our *Pycnopodia* Maxent models (12). ENMeval provides a suite of modeling statistics for Maxent models including training AUC, test AUC, AICc, and several threshold-based statistics. Unfortunately, the literature is somewhat unclear on which metrics are the most important in choosing a Maxent model (11,13–15). Based on the literature, we chose to use 1) the difference between training AUC and test AUC in order to prioritize models that had improved predictive capacity and 2) AICc to avoid overly complex models. Test and training data were cross-validated using the ‘checkerboard 1’ option to minimize the impacts of spatial autocorrelation on test and training models.

While the models with the lowest AICc often included hinge feature classes, these models produced response curves that looked highly overfit and had relatively high AUCdiff (around 0.15). Thus we narrowed our focus to models that include Linear, Quadratic, and Product functions, which were more biologically interpretable and less prone to overfitting (11). Additionally, increasing the regularization parameter to be greater than the pre-set value = 1 did not consistently improve AICc or AUC metrics and thus we used the pre-set value = 1 in our models.

Estimating Tau - We utilized the logistic output of Maxent which requires a mathematical transformation of the raw Maxent output. This transformation involves scaling the raw output by the probability of presence at an ‘average’ site in the model, also known as τ . The pre-set value of $\tau = 0.5$ in Maxent. The average probability of presence of *Pycnopodia* changed drastically between the pre-outbreak and current models due to SSWD. Thus, we needed to account for this by adjusting τ between the pre-outbreak and current models (11). There are few well-established methods for estimating τ , so we estimated it as the total occurrence rate for *Pycnopodia* out of all available surveys in each time period (i.e. 2009-2012 and 2017-2020). While this metric undoubtedly misses some of the nuance behind the parameter τ , these estimates will at least help account for the gross differences in *Pycnopodia* presence rates across their range between the two periods.

Table S1. List of datasets used in the study. *Washington outer coast and British Columbia excludes the Salish Sea.

Dataset	Institution	Contact	Region(s)	Survey Type	Years	References / Websites
ADFG	Alaska Dept of Fish and Game	Tom Dean	east Gulf of Alaska	SCUBA Dive	1990-1999	Jewett et al. 1995
AFSC	Alaska Fisheries Science Center	Nancy Roberson	Aleutians, west and east Gulf of Alaska, southeast Alaska	Trawl	1983-2018	www.fisheries.noaa.gov/region/alaska
CACS	Center for Alaskan Coastal Studies	Katie Gavenus	east Gulf of Alaska	Intertidal Survey	2014-2020	www.akcoastalstudies.org
CCIRA	Central Coast Indigenous Resource Alliance	Tristan Blaine, Alejandro Frid	British Columbia*	SCUBA Dive	2018-2020	https://www.ccira.ca/
CDFW-BML	California Dept of Fish and Wildlife & Bodega Marine Laboratory	Laura Rogers-Bennett	northern California	SCUBA Dive	1999-2018	marinescience.ucdavis.edu
CDFW-MARE	California Dept of Fish and Wildlife & Marine Applied Research & Exploration	Mike Prall, Dirk Rosen, Andy Lauer mann	northern, central, southern California	ROV Dive	2005-2016	www.maregroup.org
COBI	Comunidad y Biodiversidad	Eduardo Diaz, Jorge Torre, Fiorenza Micheli	Baja California	SCUBA Dive	2009-2019	https://cobi.org.mx/en/
FHL	Friday Harbor Labs	David Duggins	southeast Alaska	SCUBA Dive	1976-1988	Duggins 1983
Glacier Bay NP	Glacier Bay National Park and Preserve	George Esslinger, Ben Weitzman	southeast Alaska	SCUBA Dive	2018-2018	Donnellan et al. 2002
Gulf Watch Alaska	Gulf Watch Alaska	Brenda Konar, Ben Weitzman	west and east Gulf of Alaska	Intertidal Survey	2005-2017	Konar et al. 2019
Gwaii Haanas	(1) Gwaii Haanas Parks Canada (2) Haida Fisheries Program (3) Florida State University	(1) Lynn Lee (2) Dan McNeill (3) Dan Okamoto	British Columbia*	SCUBA Dive	2017-2020	https://www.pc.gc.ca/en/pn-np/bc/gwaiihaanas
Hakai	Hakai Institute	Alyssa Gehman	British Columbia*	SCUBA Dive	2014-2018	www.hakai.org
iNaturalist	iNaturalist	California Academy of Sciences	all except Baja California	Community Science Observation	1978-2020	www.inaturalist.org
MARINe-Dive	Multi-Agency Rocky Intertidal Network	Melissa Miner	east Gulf of Alaska, British Columbia*, Salish Sea, Oregon	Community Science SCUBA Dive	2013-2019	https://marine.ucsc.edu/data-products/collaborative-monitoring/index.html
MARINe-Observation	Multi-Agency Rocky Intertidal Network	Melissa Miner	all except Aleutians	Community Science Observation	2012-2019	http://data.piscoweb.org/marine1/seastardisease.html
MBNMS	Monterey Bay National Marine Sanctuary	Steve Lonhart	central California	SCUBA Dive	2003-2012	https://sanctuariesimon.org/dbtools/project-database/index.php?ID=100312
MexCal-UABC	Universidad Autónoma de Baja California	Rodrigo Baes	Baja California	SCUBA Dive	2017-2020	Beas-Luna et al. in prep

NOAA	NOAA- National Marine Fisheries Science	Aimee Keller	Washington*, Oregon, northern, central, southern California	Trawl	2004-2008	Harvell et al. 2019; https://www.nwfsc.noaa.gov/data/map
OceanWise	Oceanwise - Vancouver Aquarium	Donna Gibbs	all except Aleutians, west Gulf of Alaska, northern California, Baja California	Community Science SCUBA Dive	1967-2019	https://ocean.org/
OCNMS	Olympic Coast National Marine Sanctuary	Ole Shelton, Greg Williams	Washington*	SCUBA Dive	2015-2019	https://olympiccoast.noaa.gov/
ODFW- Marine Habitat	Oregon Dept of Fish and Wildlife	Scott Marion	Oregon	ROV Dive	2001-2018	https://www.dfw.state.or.us/MRP/habitat/
ODFW- Marine Reserves	Oregon Dept of Fish and Wildlife	Lindsay Aylesworth,	Oregon	SCUBA Dive	2010-2019	https://oregonmarinereserves.com/
PISCO	U of California Santa Cruz & Santa Barbara	Dan Malone	Oregon, northern, central, southern California	SCUBA Dive	1999-2019	http://www.piscoweb.org/ke lp-forest-study
REEF	Reef Environmental Education Foundation	Christy Pattengill-Semmens	all except Aleutians, west and east Gulf of Alaska	SCUBA Dive	1994-2020	Harvell et al. 2019; https://www.reef.org/reefs-invertebrate-and-algae-monitoring-program
Reef Check	Reef Check	Jan Friewald	northern, central, southern California	SCUBA Dive	2006-2017	https://www.reefcheck.org/california-program/
Simon Fraser-Lee	Simon Fraser U	Lynn Lee	British Columbia*	SCUBA Dive	2010-11	Lee et al. 2016
Simon Fraser-Salomon	(1) Simon Fraser University, (2) Fisheries and Oceans Canada, (3) Gwaii Haanas Parks Canada, and Council of the Haida Nation	(1) Anne Salomon, (2) Hannah Stewart and (3) Lynn Lee	British Columbia*	SCUBA Dive	(1) 2009-2013 (2) 2013-2016	(1) Trebilco et al. 2014 (2) Burt et al. 2018
Simon Fraser-Schultz	Simon Fraser U & Vancouver Aquarium	Jessica Schultz	British Columbia*, Salish Sea	SCUBA Dive	2009-2014	Schultz et al. 2016
UAF-Dive	U of Alaska Fairbanks	Brenda Konar	Aleutians	SCUBA Dive	2016-2017	www.uaf.edu/cfos/people/faculty/detail/brenda-konar.php
UCSC	U of California Santa Cruz	Kristy Kroeker	southeast Alaska	SCUBA Dive	2016-2020	kristy-kroeker.squarespace.com
UW	U of Washington*		Washington*	SCUBA Dive	1987	Kvitek et al. 1989
VIU-Watson	Vancouver Island U	Jane Watson	British Columbia*	SCUBA Dive	1987-2019	https://scitech.viu.ca/biology/faculty/jane-watson-phd
WDFW-Dive	Washington Dept of Fish and Wildlife	Taylor Frierson and Henry Carson	Salish Sea, Washington*	SCUBA Dive	1984-2019	https://wdfw.wa.gov/
WDFW-Trawl	Washington Dept of Fish and Wildlife	Taylor Frierson and Henry Carson	Salish Sea	Trawl	1991-2019	https://wdfw.wa.gov/

Table S2. Dates and associated information describing the epidemic timeline among regions. Gray text indicates low confidence due to limited data. ^These dates were inferred based on the dates in neighboring regions. *British Columbia and Washington outer coast exclude the Salish Sea.

	Determined using 1 st symptomatic sea stars at each site				Determined using declines in occurrence of <i>Pycnopodia helianthoides</i>		
Region	N sites surveyed	Date SSWD First Observed	Outbreak Date	Emergence Duration (mo.)	N surveys	Crash Date	Epidemic Duration (mo.)
Aleutians	0	no data	^2016/08/25	no data	15	2018/02/07	^17.5
west Gulf of Alaska	3	2016/08/25	2016/08/25	no data	36	2018/02/07	^17.5
east Gulf of Alaska	14	2013/11/04	2015/06/04	19.0	222	2018/02/02	32.0
southeast Alaska	63	2013/08/21	2014/06/25	10.1	156	2018/09/17	50.8
British Columbia*	37	2013/11/07	2014/01/04	1.9	1515	2017/08/13	43.3
Salish Sea	369	2013/03/30	2013/11/03	7.2	9759	2017/12/15	49.4
Washington outer coast*	22	2013/06/07	2013/06/25	0.6	157	2017/08/25	50.0
Oregon	65	2013/04/24	2014/04/11	11.6	438	2016/12/16	32.2
northern California	47	2013/08/07	2013/09/07	1.0	195	2016/01/03	27.9
central California	79	2013/07/15	2013/09/20	2.2	1035	2015/06/11	20.7
southern California	64	2013/10/18	2013/11/06	0.6	2694	2014/05/18	6.3
Baja California	1	2013/10/18	^2013/11/06	0.6	269	2014/01/08	2.1

Table S3. Logistic regression model results of declines in occurrence from 2012-2019 for shallow depths (except in southern California, where 2013-2019 data were used). These models were used to estimate *Pycnopia helianthoides* population crash dates among regions, and delineate epidemic and post-epidemic phases. *British Columbia and Washington outer coast excluding the Salish Sea.

Term	N	df	Chi Sq.	P	R ²
western Alaska	51	1	3.66	0.0556	0.054
east Gulf of Alaska	222	1	21.92	<.0001	0.073
southeast Alaska	156	1	9.14	0.0025	0.054
British Columbia*	1515	1	233.12	<.0001	0.112
Salish Sea	9759	1	1464.68	<.0001	0.110
Washington outer coast*	157	1	40.88	<.0001	0.191
Oregon	438	1	47.63	<.0001	0.080
northern California	195	1	89.17	<.0001	0.378
central California	1035	1	591.65	<.0001	0.438
southern California	2694	1	95.33	<.0001	0.186
Baja California	269	1	591.65	<.0001	0.302

Table S4. Data descriptors and density and occurrence metrics for *Pycnopodia helianthoides* populations in historic (before outbreak date in each region) and current (2017-2019) population phases, reflecting impacts of the Sea Star Wasting Disease outbreak from 2013-2017: a) populations in shallow depths (< 25 m) split by region; b) populations in deep depths (>25 m) globally; and c) Populations at all depths globally. Gray text indicates low confidence due to low sample size or inconsistent sampling efforts. *British Columbia and Washington outer coast excluding the Salish Sea.

Region	Population Phase	Density (<i>Pycnopodia</i> km-2)					Occurrence (% surveys present)				
		N Surveys	Mean	SD	SE	% Decline Density	N Surveys	Mean	SD	SE	% Decline Occurrence
a) Regionally at shallow depths (< 25m)											
Aleutians	Historic	9	83,333	132,288	44,096	40.0	23	35%	49%	10%	-115.6
	Current	2	50,000	70,711	50,000		4	75%	50%	25%	
west Gulf of Alaska	Historic	45	27,444	34,093	5,082	100.0	73	53%	50%	6%	100.0
	Current	5	0	0	0		6	0%	0%	0%	
east Gulf of Alaska	Historic	152	120,193	304,314	24,683	93.8	168	78%	42%	3%	58.9
	Current	54	7,438	22,288	3,033		78	32%	47%	5%	
southeast Alaska	Historic	47	118,715	98,711	14,399	96.0	106	81%	39%	4%	20.8
	Current	31	4,758	12,499	2,245		84	64%	48%	5%	
British Columbia*	Historic	1,091	23,095	46,650	1,412	87.9	2,239	63%	48%	1%	68.9
	Current	220	2,794	9,000	607		568	20%	40%	2%	
Salish Sea	Historic	244	101,049	873,132	55,897	92.4	12,235	81%	39%	0%	52.9
	Current	87	7,641	15,511	1,663		3,457	38%	49%	1%	
Washington outer coast*	Historic	9	85,724	100,015	33,338	99.6	140	95%	22%	2%	70.6
	Current	15	304	895	231		43	28%	45%	7%	
Oregon	Historic	72	44,137	41,983	4,948	100.0	742	60%	49%	2%	92.2
	Current	19	0	0	0		85	5%	21%	2%	
northern California	Historic	192	33,526	32,542	2,348	99.2	220	89%	31%	2%	94.9
	Current	85	267	1,397	152		88	5%	21%	2%	
central California	Historic	1,041	38,755	47,778	1,481	99.5	1,580	83%	37%	1%	96.0
	Current	169	181	1,140	88		361	3%	18%	1%	
southern	Historic	1,062	35,790	82,750	2,539	100.0	2,768	22%	42%	1%	99.3

California	Current	268	0	0	0		1,240	0%	4%	0%	
Baja California	Historic	81	2,586	6,049	672	100.0	87	25%	44%	5%	100.0
	Current	128	0	0	0		128	0%	0%	0%	
b) Globally at deep depths (> 25m)											
All	Historic	1,976	636	2,852	64	96.2	13,710	18%	38%	0%	55.3
	Current	177	24	94	7		697	8%	27%	1%	
c) Globally at all depths											
All	Historic	6,021	27,552	189,911	2,447	94.3	34,091	49%	50%	0%	52.3
	Current	1,260	1,580	8,322	234		6,891	23%	42%	1%	

Table S5. Generalized linear model results analyzing the trends in *Pycnopodia helianthoides* for a) densities and b) occurrence at shallow depths (≤ 25 m), and c) densities and d) occurrence at deep depths (> 25 m) among regions and population phases. Population phases compared historic (before the outbreak date in a given region) and current (2017-2020) populations. In a) and b), we lumped the Aleutian Islands and west Gulf of Alaska into ‘western Alaska’, the Washington outer coast and Oregon into the ‘Pacific Northwest’ (excluding the Salish Sea) and dropped southern California and Baja California because current populations had zero *Pycnopodia*. In d) Three super regions were classified as Alaska, British Columbia including Salish Sea, and the outer coast of the contiguous US).

Term	df	Chi Sq.	P
a) Shallow Density Model			
Population Phase	1	0.5	0.473
Region	7	8600.1	<.0001
Population Phase * Region	7	684.2	<.0001
b) Shallow Occurrence Model			
Area	1	2.0	0.156
Population Phase	1	744.7	<.0001
Region	7	50.3	<.0001
Population Phase * Region	7	269.1	<.0001
c) Deep Density Model			
Population Phase	1	137	<.0001
d) Deep Occurrence Model			
Area	1	1.8	0.1851
Population Phase	1	870.8	<.0001
Super region	2	74.5	<.0001
Population Phase * Super region	1	203.8	<.0001

Table S6: Maxent permutation importance, a measurement of variable predictive capacity, for the five environmental variables used to predict *Pycnopodia helianthoides* distributions in pre-outbreak (2009-2012) and current (2017-2020) Maxent species distribution models.

Variable	Pre-Outbreak (2009-2012)	Current (2017-2020)
90th Percentile of Temperature (°C)	9.0%	39.6%
Depth (m)	74.5%	41.8%
Mean Chlorophyll (mg/m-3)	2.6%	10.7%
Mean Salinity (PSU)	13.6%	6.3%
Substrate Type	0.3%	1.7%

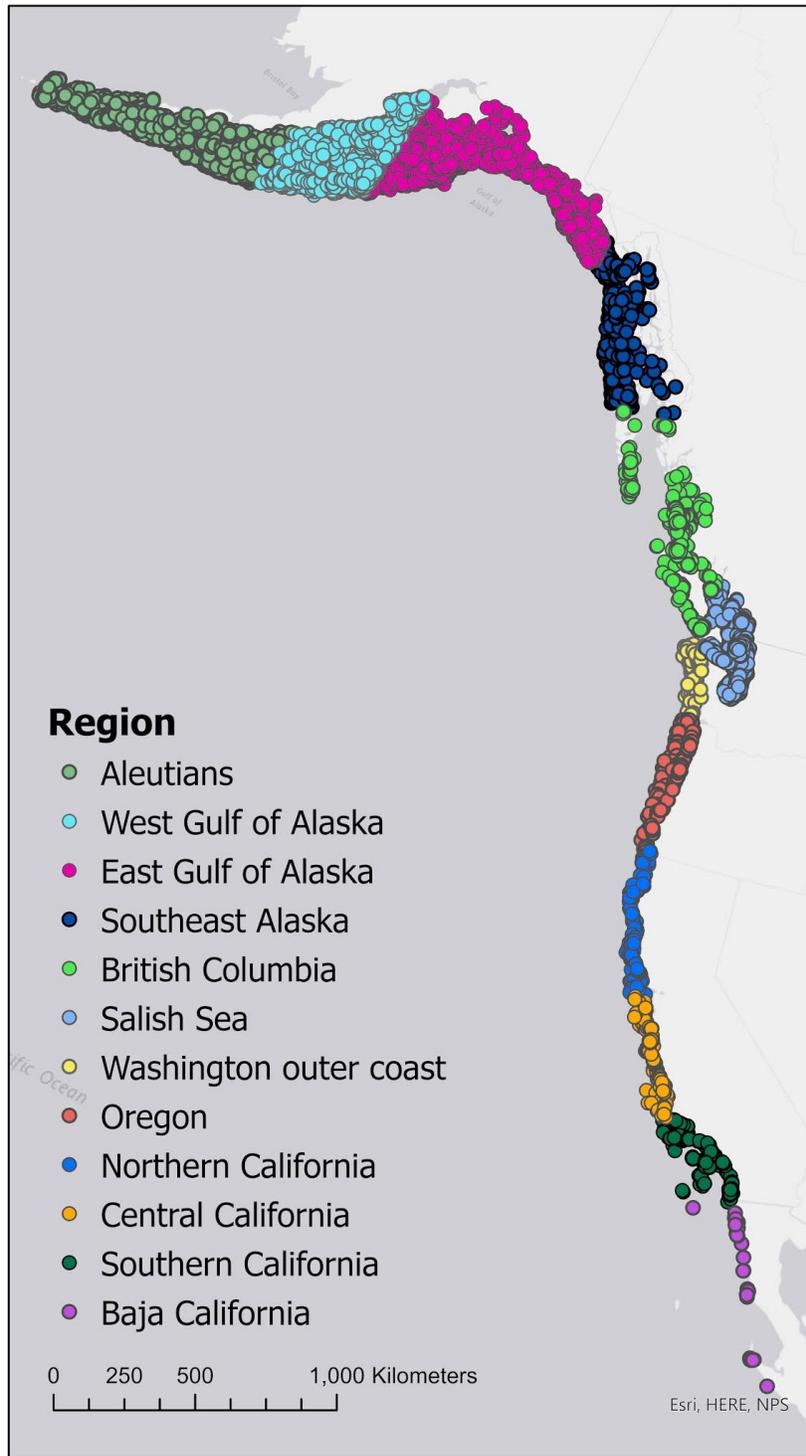


Figure S1. Map of the 48,810 *Pycnopodia helianthoides* surveys gathered for this study spanning 1967-2020. Colors indicate the 12 regional designations assigned to the data.

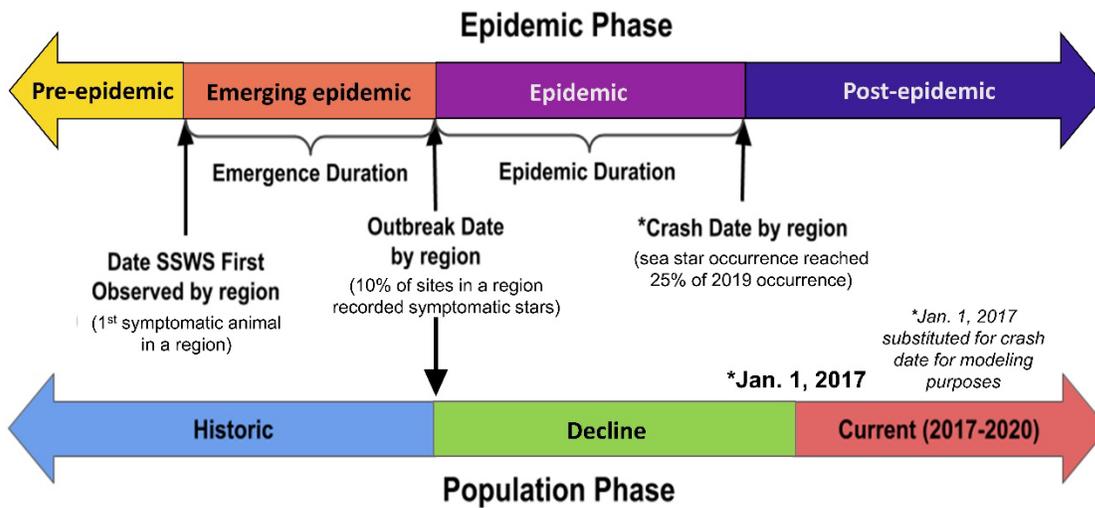


Figure S2. Notable events and phase definitions for both the sea star wasting disease epidemic and sunflower sea star populations.

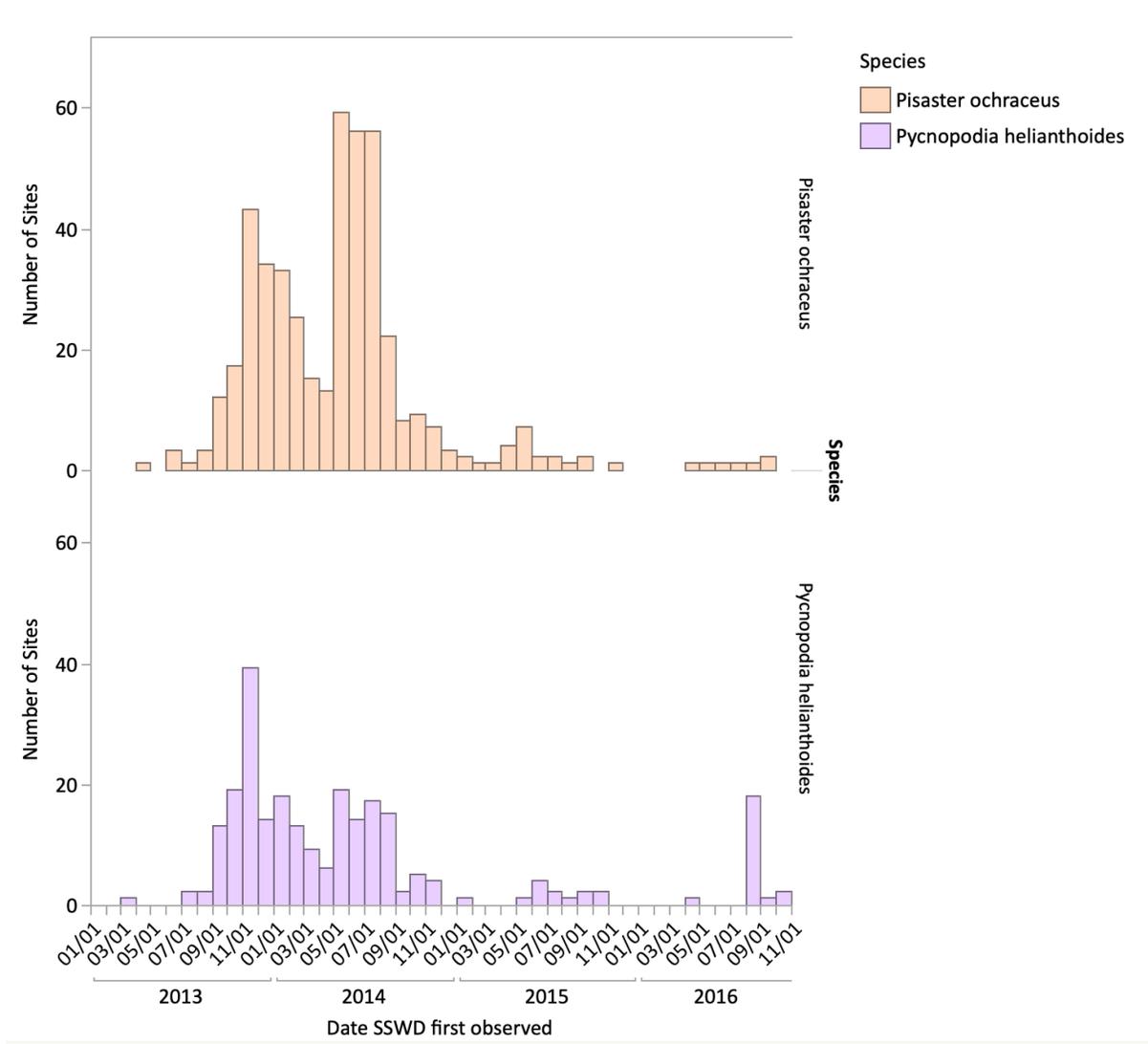


Figure S3. Comparison of the date SSWD was first observed in *Pisaster ochraceus* and *Pycnopodia helianthoides* for each site in the MARINE database (Multi-Agency Rocky Intertidal Network).

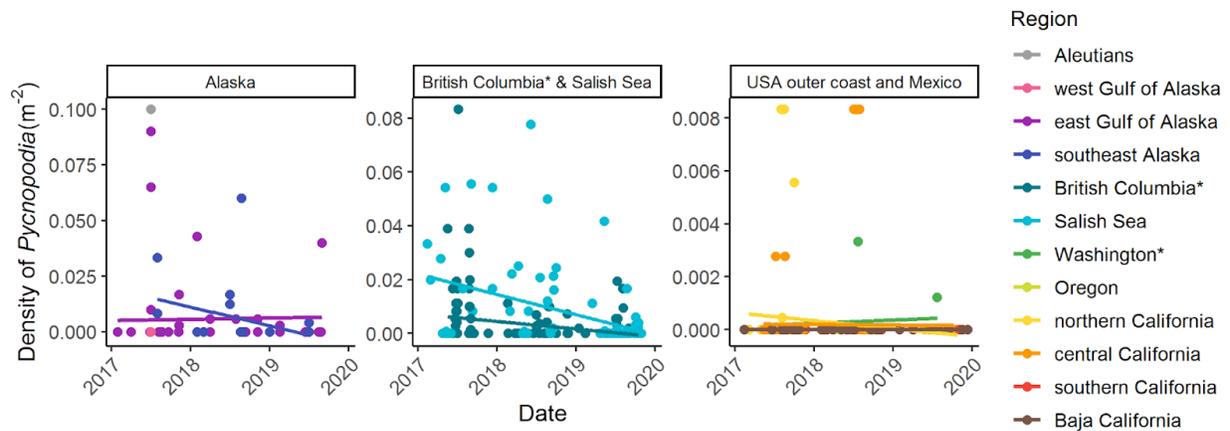


Figure S4. Regional densities of *Pycnopodia helianthoides* populations from 2017-2019 with lines representing modeled linear trends in density over time in each region. *British Columbia and Washington exclude the Salish Sea.

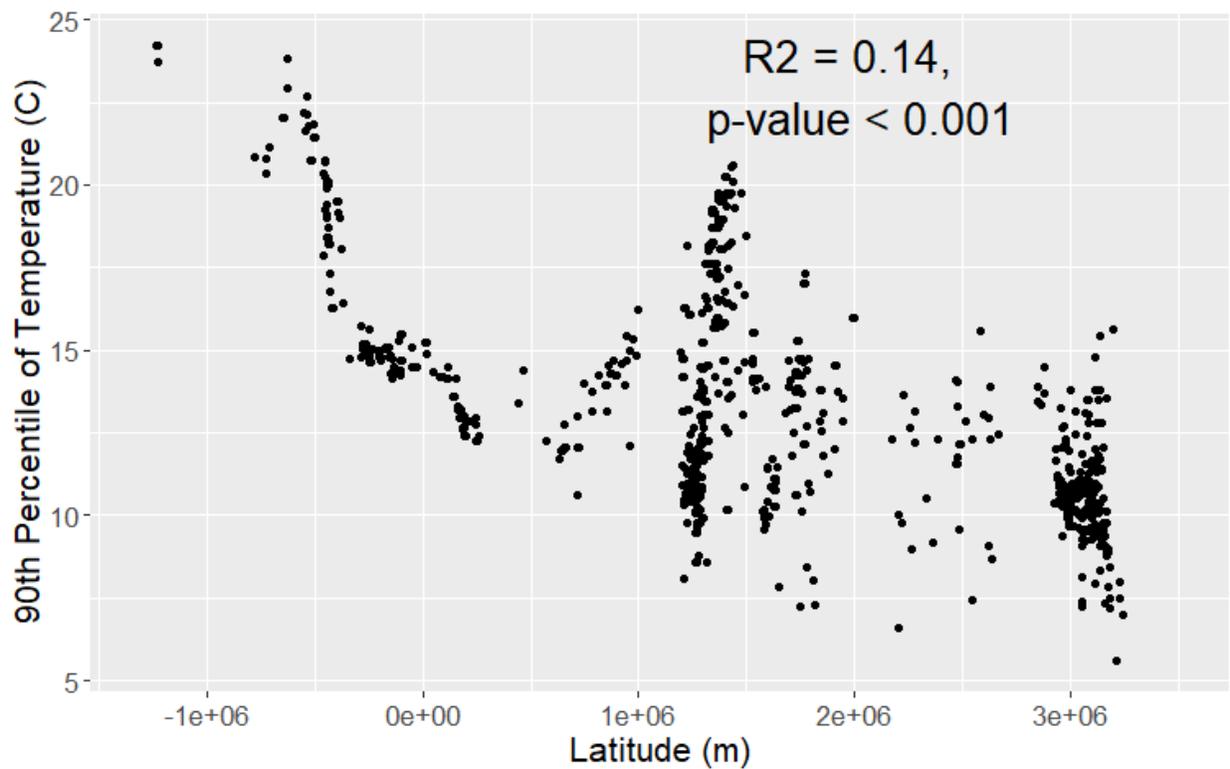


Figure S5. Relationship between Latitude (m) and 90th Percentile of Temperature ($^{\circ}\text{C}$) of observed *Pycnopodia helianthoides* used in the Maxent species distribution models (both pre- and post-outbreak models). The R^2 and p-value of a linear model between the two variables are reported. Latitude is reported in North American Albers Conic Equal Area.

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