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BIOLOGICAL SCIENCES: Evolution

Title: **Decimation by sea star wasting disease and rapid genetic change in a keystone species, *Pisaster ochraceus***

Mobile device title: Genetic aftermath of sea star wasting disease

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Abstract

Standing genetic variation enables or restricts a population's capacity to respond to changing conditions, including the extreme disturbances expected to increase in frequency and intensity with continuing anthropogenic climate change. However, we know little about how populations might respond to extreme events with rapid genetic shifts, or how population dynamics may influence and be influenced by population genomic change. We use a range-wide epizootic, sea star wasting disease (SSWD), that onset in mid-2013 and caused mass mortality in *Pisaster ochraceus* to explore how a keystone marine species responded to an extreme perturbation. We integrated field surveys with RADSeq data to (1) describe the population dynamics of mortality and recovery, and (2) compare allele frequencies in mature *P. ochraceus* before the disease outbreak to allele frequencies in adults and new juveniles after the outbreak, to identify whether selection may have occurred. We found *P. ochraceus* suffered 81% mortality in the study region between 2012 and 2015, and experienced a concurrent 74-fold increase in recruitment beginning late 2013. Comparison of pre- and post-outbreak adults revealed significant allele frequency changes at three loci, which showed consistent changes across the large majority of locations. Allele frequency shifts in juvenile *P. ochraceus* (spawned from pre-mortality adults) were consistent with those seen in adult survivors. Such parallel shifts suggest detectable signals of selection and highlight the potential for persistence of this change in subsequent generations, which may influence the resilience of this keystone species to future outbreaks.

Significance Statement

Opportunities to study microevolution in wild populations are rare and challenging. Annual monitoring allowed us to capture both the prelude to and aftermath of one of the largest marine mass mortality events on record in a keystone marine species. Median mortality of 81% across populations was recorded along with significant allele frequency shifts at multiple loci in the adult population. Shifts were consistent across locations and also occurred in new recruits, with few exceptions. These results indicate a long-term species-wide change in allele frequencies will persist through future generations. Population genomic monitoring, at a time when marine diseases and mass mortalities are on the rise, will be essential for documenting rapid genetic shifts in response to chronic and extreme events.

Introduction

As extreme disturbances potentially increase in both frequency and intensity (1, 2), a population's capacity to respond with standing genetic variation will become increasingly important for rapid adaptation (3–8). Impacts will be mediated via physiological tolerances and life-history traits that may reflect underlying genetic differences (9), and these genetic differences—among and within populations—may amplify or mute a species' sensitivity to change (4, 10). However, we know little about what determines which organisms are resilient or susceptible, whether or how impacted populations may recover, and if recovery increases resilience to future perturbations.

Standing genetic variation is shaped primarily by effective population size, selection, and the life history of species (11). Detecting changes in standing genetic variation due to selection in wild populations is challenging due to demographic processes in contemporary populations—such as range expansions, growth, and asymmetric migration resulting in complex spatial genetic patterns (12)—leading to potentially false conclusions about selective sweeps (13). A strategy to sidestep this problem involves identifying adaptive alleles in an ancestral population that have increased frequency in descendent populations; however, it is not always possible to know if a beneficial allele was secondarily introduced to the ancestral population (13). Additionally, selection can manifest in different ways in the genome, for example, a selected trait can be controlled by few genes of large effect or many genes of small effect; in the latter case the intensity of selection is diluted over many genes, resulting in only small changes in allele frequency (14). Marine taxa can pose particular challenges due to a suite of common traits—high fecundity, large population size, and high dispersal potential—acting to homogenize the gene pool and consequently restricting signals of selection to very small genomic regions (15), however, multiple studies have detected evidence of selection in such 'typical' species (16).

A recent epizootic provided opportunity to overcome many of these challenges. In 2013, a range-wide sea star wasting disease (SSWD) outbreak leading to mass mortality across the range of *Pisaster ochraceus* (17) created a rare opportunity to explore the genetic landscape in which selection acts, and to identify alleles that responded directly to the event through changes in frequency. A study of *Pisaster*

ochraceus immediately preceding the outbreak (18) was available to be coupled with samples following the disease outbreak, at multiple locations, along with quantitative surveys of mortality, to capture both the initial standing genetic variation and the aftermath of the largest documented non-commercial marine pandemic (19), which putatively was caused by a virus (17). Thus, individuals with different functional states (symptomatic–asymptomatic), and ‘parent’ and ‘daughter’ (sub)populations with differential responses (i.e. mortality rates), could be identified easily. Additionally, the epizootic offered the opportunity to explore how newly recruited *P. ochraceus*, which were spawned by pre-epizootic adults (Fig. S1), did or did not show similar genetic changes as the adult population. Thus, we were able to measure the actual change from the original standing genetic stock and identify candidate loci under selection during this disease outbreak.

The goals of this study are threefold: (a) to quantify the magnitude of mortality and recruitment in north central California, (b) ascertain whether selection may have shaped the surviving population of adult *P. ochraceus*, and (c) test whether juvenile *P. ochraceus* recruiting during the mortality event are most genetically similar to the pre-SSWD population (i.e. no detectable selection in recruits) or the surviving population (i.e. selection in parallel to adults). In doing so we aim to shed light on how this species, which in many ways is a typical marine species—large population size, broad range size, high gene flow, high fecundity, high dispersal potential (20)—responds to an extreme event and what signature this may leave on the subsequent generation.

Results

Mortality and recruitment in *P. ochraceus*

Following the outbreak of sea star wasting disease in 2013, median density of post-SSWD *P. ochraceus* adults ($0.005 \cdot \text{m}^{-2}$; quartiles Q1 = $0.003 \cdot \text{m}^{-2}$, Q3 = $0.018 \cdot \text{m}^{-2}$) was 81% lower than pre-SSWD densities ($0.028 \cdot \text{m}^{-2}$; Q1 = $0.013 \cdot \text{m}^{-2}$, Q3 = $0.045 \cdot \text{m}^{-2}$; Wilcoxon signed rank test, $V = 105$, d.f. = 1, $p = 6.104 \times 10^{-5}$; Fig. 1). For recruits (1.0–15.3 mm measured from center to arm tip; mean = 5.9 mm; median = 5.0 mm), there was a 74-fold increase in mean density ($0.006 \cdot \text{m}^{-2}$ pre-SSWD and $0.401 \cdot \text{m}^{-2}$ post-SSWD) driven by a subset of sites (Fig. 1) though the change was not statistically significant due to high heterogeneity and an abundance of zeros.

Sampling of genetic variation

After filtering 63 individuals with low coverage, 374 samples were available for genetic analyses: 142 pre-SSWD adults, 126 post-SSWD adults, and 106 recruits (Table S1). DDOCENT (21) identified a total of 3,546,608 variable sites. After filtering, we resolved 6,790 haplotypes (based on 7,303 SNPs) for 1,225 RAD loci, for which direct allele frequency shifts were measured. No significant population genetic structure was found in pre-SSWD adults ($F_{ST} = 0.0001$) or post-SSWD adults ($F_{ST} = -0.0037$) and no clonality was detected across all samples (i.e. zero duplicated multilocus genotypes). Genetic diversity was consistent among samples: pre-SSWD ($H_s = 0.434$), post-SSWD adults ($H_s = 0.432$), and recruits ($H_s = 0.433$) (Fig. S2).

Tests for selection in adult *P. ochraceus*

The DAPC revealed genetic differences between pre- and post-SSWD adult *P. ochraceus* (Fig. 2). The top 100 discriminatory haplotypes identified in the DAPC analysis had a mean change in frequency of ± 0.083 (SD = 0.040) discriminating pre- from post-epizootic *P. ochraceus* samples (Fig. 3); the mean frequency shift across all haplotypes was ± 0.018 (SD = 0.020). The BayeScan test for F_{ST} outliers yielded three outlier loci at an FDR of 0.10 (Fig. 3). These outlier loci were also detected within the top 100 discriminatory haplotypes from the DAPC analysis. Overall change in heterozygosity was negligible ($H_{o_PRE} = 0.421$; $H_{o_POST} = 0.423$), though heterozygosity for outlier loci did change in the surviving population, increasing at one locus and decreasing in the other two (Fig. S3).

Allele frequency changes in the three outlier loci (Fig. 4) were significant after a sequential Bonferroni adjustment for three tests (i.e. three loci) (Locus0379: $t = -2.93$, d.f. = 9, p -value = 0.01664; Locus1048: $t = 3.78$, d.f. = 9, p -value = 0.00434; Locus1166: $t = -4.49$, d.f. = 9, p -value = 0.00151) and largely consistent across geographic locations, with the most common haplotype in each outlier locus showing consistent directional changes in frequencies at 8/10 locations (Locus0379) and 9/10 locations (Locus1048 and Locus1166) (Fig. 4, Fig. S4). However, despite the geographic consistency, these results

were non-significant at $\alpha = 0.05$ for Locus1048 and Locus1166—which each changed similarly at 9/10 locations (Fisher’s Exact Test: $n = 10$, d.f. = 1, p -value = 0.0704, power = 0.72)—and for Locus0379, which changed similarly across 8/10 locations (Fisher’s Exact Test: $n = 10$, d.f. = 1, p -value = 0.1749, power = 0.48).

In a BLASTn query of the top 100 discriminating ddRAD loci, 85 loci mapped to echinoderm transcripts in EchinoDB (<http://echinodb.uncc.edu>; 22) (e-value < 1.0E-6) and 75 loci mapped to the *Pycnopodia helianthoides* transcriptome (23; Dataset S1).

Estimating genetic affinity of new recruits

DAPC results show 84.0% of the new recruits collected following the outbreak of SSWD assign to post-outbreak adult *P. ochraceus* (Fig. 2, Fig. S5) ($n = 106$, $\alpha = 0.01$, $\chi^2 = 48.906$, critical value = 6.635, d.f. = 1, power = 1.00). Comparisons of the frequencies of the top 100 discriminant haplotypes also reveal a greater magnitude of difference between pre- and post-SSWD adults than pre-SSWD adults and recruits (Fig. 3). However, though the magnitude differs, the direction of change is largely consistent; we find 82% of haplotypes ($n = 100$, $\alpha = 0.01$, $\chi^2 = 40.960$, critical value = 6.635, d.f. = 1, power = 1.00) share the same direction of change in frequencies in post-SSWD adults and recruits (relative to pre-SSWD adults) (Fig. 3B). Additionally, of those 82% with a similar direction of change, 80% of recruit allele frequencies represent an intermediate frequency between pre- and post-SSWD adults (Fig. 3).

Discussion

Pisaster ochraceus suffered elevated mortality, and experienced a coincident pulse of elevated recruitment, during the sea star wasting epizootic (Fig. 1). Direct comparisons of RADSeq data among pre- and post-SSWD adults and recruits revealed potential signals of selection as detected in parallel shifts in allele frequencies (Fig. 3 and Fig. 4). This was further corroborated by the BayeScan analysis at ~0.2% of loci (Fig. 3) and the largely consistent change in allele frequency across geographic locations (Fig. 4). While newly recruited *P. ochraceus* were the progeny of pre-SSWD adults (Fig. S1), shifts in allele frequencies in top candidate loci occurred in the same direction in the recruits as in the post-SSWD adult sample, relative to the pre-SSWD sample (Fig. 3); heterozygosity in recruits was intermediate between pre- and post-SSWD adults (Fig. S3). These parallel shifts in allele frequencies in independent samples of adults and recruits suggest a significant selection event concurrent with the sea star wasting disease epizootic.

Putative causes of allele frequency changes in *P. ochraceus*

Our empirical measurements of allele frequency changes in outlier and 100 top discriminating loci during the decimation of *P. ochraceus* by an epizootic disease are consistent with theory, which would predict that selection rather than genetic drift or gene flow would drive differentiation in highly abundant and fecund species (14). We also were able to empirically rule out gene flow as a cause of allele frequency changes because we sampled the surviving adults—likely ≥ 5 years-old given their size (24)—from the same pool of adults sampled before the SSWD outbreak; adult *P. ochraceus* do not disperse. Likewise, while larval dispersal may have contributed immigrant alleles, these were unlikely to influence conclusions based on region-wide comparison of pre-SSWD adults and recruits because *P. ochraceus* is well-mixed over large spatial scales (20) and the SSWD outbreak was range-wide. Moreover, while it can be difficult to distinguish between selection and drift using changes in allele frequencies between time series samples (25), empirically, it is improbable that drift leads to random allele frequency shifts in the same direction in post-SSWD adults and new recruits (Fig. 3). Consistency in the direction of allele frequency shifts in outlier loci across independently sampled geographic locations provides additional corroborating evidence consistent with selection (Fig. 4).

The weaker signal of selection in juveniles, relative to adults, can be explained by the life history of *P. ochraceus*. The answer lies in reconstructing the timeline of reproduction, disease onset, and recruitment (Fig. S1). *P. ochraceus* spawn from late March–May in Central California (26, 27)—slightly later to the north, e.g. late spring on San Juan Island (28) and May–early June in Oregon (29)—and have a pelagic duration of 6–8 weeks (30), though this species is apparently capable of much longer larval periods (up to 32 weeks) in the laboratory setting (31). This timeline would lead to intertidal settlement in approximately June–August. Even if we consider the earliest spawning (late March) (27) and shortest pelagic duration (6 weeks) (26) published for *P. ochraceus*, the earliest settlement of recruits would have

occurred in May 2014 (if spawned by post-SSWD adults). Although we did collect recruits during this month (Fig. S1, Table S2) we found they were the largest of all recruits sampled from December 2013 – May 2014 (Fig. S6), suggesting these recruits had been settled for some time. Recruits for this study therefore would have been spawned in the previous year, but likely not after major mortality from SSWD was seen in adults. Observations of sea star wasting disease were first documented in this region in late summer 2013 (<http://seastarwasting.org>). Given the lability of life history traits, one should also consider whether spawning could have occurred *after* adult mortality from SSWD, i.e. fall 2013; however, the size distribution of recruits observed from December 2013 to May 2014 (Fig. S6) indicates an earlier settlement, i.e. during summer 2013 (Fig. S1). The timeline indicates the recruits in this study settled during summer then were exposed to SSWD for approximately 4–12 months in the intertidal prior to collection. The post-outbreak adults were sampled approximately one year after recruits were sampled, meaning they would have experienced additional exposure relative to recruits before collection (Table S1). Thus, although juvenile *P. ochraceus* would have been spawned by pre-SSWD adults, they became genetically more similar to post-SSWD adults (Fig. 2 and Fig. S5) as shown by the top 100 discriminating haplotypes in the DAPC analysis because conditions were consistent with those seen in post-SSWD adults (Fig. 3). We consider sweepstakes reproductive success (32) and chaotic genetic patchiness (33) unlikely explanations of the observed patterns because both depend on chance mechanisms, which do not predict broad geographic consistency and the same subset of adults being reproductively successful and surviving a disease outbreak. A multiyear recruitment study of another large-population high-fecundity spawning echinoderm, *Strongylocentrotus purpuratus*, revealed no evidence for the sweepstakes reproductive success hypothesis (34). The more probable explanation for all statistical outlier loci behaving consistently across the large majority of sites, and juveniles shifting heterozygosity consistent with the shift seen in post-SSWD adults, is that juveniles underwent similar, but less strong, selective pressure as adults consistent with SSWD.

The limitations of reduced representation genomic techniques—e.g. the ability to detect signals of selection in polygenic traits (35) unless sweeps have been hard and recent, particularly when linkage disequilibrium is low (36–38)—and the challenges of studying the relative importance of selection in wild populations (39) were mitigated by the nature of our data set. These challenges can result in a lack of power to detect selection, not an increase in false positives. Paired temporal samples allowed direct measurement of allele frequency changes between the pre- and post-SSWD samples and helped to maximize power.

Of the 75 ddRAD loci that mapped to the *Pycnopodia helianthoides* transcriptome, 19 mapped to transcripts that were differentially expressed between asymptomatic and symptomatic *P. helianthoides* (Dataset S1; 23). While these results are consistent with a subset of putatively selected functional loci (Fig. 3), gene modeling and differential expression analyses are needed to describe the genomic context for the genetic shifts seen in *P. ochraceus*. Despite similar symptoms observed among asteroid species, there is potential for species-specific responses to SSWD. Responses to viral challenge experiments were not consistent among species, suggesting more complex and/or multiple etiologies are associated with SSWD (40).

The future of *P. ochraceus*

Pisaster ochraceus suffered major mortality between 2013–2014 associated with the SSWD epizootic (Fig. 1) (41), but also experienced record recruitment rates up to 300 times previous rates (41). Sea star wasting disease is still present in *P. ochraceus* populations in 2018 (42) and likely still exerting selection on susceptible individuals in otherwise seemingly somewhat resilient populations. Despite recently elevated recruitment rates, these new recruits will not contribute to reproduction for some time; *P. ochraceus* do not reach maturity until approximately 5 years of age (24), although maturation time could be shorter if *P. ochraceus* feed to satiation (43). This lag time makes predictions about recovery difficult, given continued persistence of the disease in *P. ochraceus*.

After a period of very low recruitment in *P. ochraceus*, ending 2012 (Fig. 1) (41), elevated pulses of recruitment have continued through at least 2017 in this region. All recruits after 2013 would have been spawned by the post-SSWD population, suggesting the shift in allele frequency should be maintained in future generations. For subsequent generations, given long-term consequences of genetic drift are diminished in populations that bottleneck for only a small number of generations and subsequently expand rapidly (44, 45), it seems unlikely genetic drift will be important given the large pulse of concurrent recruitment.

However, a number of factors could influence the trajectory of change in future populations. For example, elevated recruitment could introduce non-resistant alleles from other locations given heterogeneity in mortality and dilute the effects of selection for disease resistance (46). Additionally, sweepstakes reproduction is thought to be common in taxa with high fecundity and high larval mortality, whereby only a subset of adults contribute to successful cohorts of juveniles (32), potentially narrowing the gene pool on which selection can act in new recruits, however, we see no evidence of reduced genetic diversity in the recruits sampled, even within this single cohort (Fig. S2). Genotyping of individuals from subsequent pulses of recruitment is needed to determine genetic relationships between adults and juveniles, and to help us better understand the range of possible futures for *P. ochraceus* in the aftermath of this outbreak of sea star wasting disease.

A major concern for species affected by environmental change is that adaptation is outpaced by environmental change (47), but currently, our understanding of environmental stressors is incomplete. Although temperature has not been clearly linked to initial SSWD emergence it is perceived to play a role in exacerbating the disease (42), but whether the role is in elevated temperature (19, 48) or reduced temperature (41), or some combination is unresolved. Additional environmental factors known to influence *P. ochraceus* include CO₂ (49) and salinity (50), but how these might interact with SSWD is currently unknown. Clear genetic responses to SSWD have been documented in the sea star *Pycnopodia helianthoides*, with increased expression of genes associated with immune pathways (23). In *P. ochraceus*, asymptomatic individuals were more likely to be heterozygous at *EF1A* (51). It is conceivable, if observed shifts in allele frequencies in *P. ochraceus* are linked with increased survivorship leading to reproductive success, that *P. ochraceus* may fare better in future outbreaks of SSWD if caused by the same pathogen. Insight into this issue might be gleaned by comparing the recent outbreak of SSWD to prior geographically restricted outbreaks (52–54) and ongoing monitoring. Nonetheless, given its large population size, extensive gene flow, and the high standing stock of genetic variation on which selection can act (55), *P. ochraceus* seems to have a propensity to persist and respond to perturbation.

Materials and methods

Ecological surveys

Quantitative surveys of *P. ochraceus* were conducted at sixteen sites (Table S1; Fig. 1) the year preceding (Aug 2012 – May 2013) and following (Dec 2013 – May 2014, Jan 2014 and Dec 2014 – May 2015) the 2013 SSWD outbreak. At each site, we sampled two rocky intertidal areas (usually one on either side of a beach or headland and separated by approximately 100 meters), using quadrats to estimate juvenile abundance and transects to target larger adult *P. ochraceus*. (N.B. Sites A & K, Arena Cove & Bodega Reserve, [Table S1, Fig. 1] only had paired quadrat surveys.) All specimens were georeferenced using a Garmin C60X GPS (± 3 m precision). Data were reported as the number of individuals per square meter per site (Table S2).

Quadrats. We exhaustively searched 32–40 one-meter square quadrats per site (i.e. 16–20 per each of 2 areas), recording GPS waypoint, time, percent cover of major substrate and macrophytes, and abundances and sizes of *P. ochraceus*. Individuals were categorized as juvenile/recruit if their length from center to arm tip was ≤ 20 mm. Quadrat locations were selected by first finding one of the target habitat types—surf grass, low-zone red algae, coralline turf, cobble or boulder field, or urchin pools either empty or occupied—selecting a starting point haphazardly, and then using a random numbers table (range: 1–10 meters) to choose remaining quadrat locations.

Transects. To quantify changes in mature *P. ochraceus* density, we conducted GPS-tracked, 2m or 4m wide swath transects nested in each of two areas at each site. From a distance, an approximate starting point and orientation (with landmarks) for the starting transect was selected. Transects ran from the most shoreward to the most seaward possible suitable habitat at approximately 10 m intervals along shore, particularly targeting the low intertidal zone when the tide was maximally receded, with as many transects being done as permitted by the tide. The GPS auto-recorded a trackpoint every 6 seconds. To reduce error in estimates of the length and position of swathes (commonly ± 3 m), we smoothed tracks by averaging across windows of two consecutive trackpoints, and removed outlying trackpoints that led to a Euclidean distance ≥ 8 meters, since these were likely due to temporary drop-outs in satellite signal. We calculated total transect search area by multiplying the adjusted transect length by swath width. To estimate the change in density from pre- to post-SSWD *P. ochraceus* on transects we used individuals

with at least a 40 mm radius (which was chosen based on the minimum size of adult *P. ochraceus* observed at each site in 2012-13 surveys; Fig. S7) to ensure calculations were as inclusive of juveniles and adults as possible but influenced minimally by recruits of the previous 2 years (43).

Statistical analyses. Normality was tested in adult and recruit data sets using the Shapiro-Wilk Normality Test using *stats v3.3.2* in R (56). Given normality was rejected in adults and recruits (Shapiro-Wilk normality test, adults: $W = 0.502$, $p = 1.195 \times 10^{-8}$; recruits: $W = 0.324$, $p = 4.992 \times 10^{-11}$) the non-parametric Wilcoxon signed rank test was used to test for a change in density between pre- and post-SSWD outbreak samples using *stats v3.3.2* in R (56).

Sampling of genetic variation

We sampled tissue from mature *P. ochraceus* before the onset of sea star wasting disease at each of sixteen locations from Aug 2012 – May 2013 (Table S1; Fig. 1). Complementary samples of mature adults (Jan 2014 and Dec 2014 – May 2015) and new recruits (<1-year; Dec 2013 – May 2014) were collected, after the mid-2013 onset of SSWD. Tissue collection consisted of approximately a half dozen tube feet or 2–3 mm of arm tip, targeting ten adults and all recruits; samples were immediately preserved in 95% ethanol (Table S1). DNA was extracted using a silica based filter plate (PALL Corp., Cat#5053) (57). 50–100 ng of DNA in 25 μ l for each specimen was submitted to the Genomic Sequencing and Analysis Facility at the University of Texas at Austin (GSAF) for quantitation, normalization, double-digestion with the *EcoRI* and *MspI* restriction enzymes (58), size selection for 300 ± 50 bp using custom bead prep (GSAF), adaptor ligation, purification, and 2x150 paired-end sequencing on an Illumina HiSeq 4000.

Sequences were demultiplexed using *process_radtags* from *STACKS v.1.35* (59) allowing a maximum of 2 mismatches in the barcode. Raw sequences are deposited in the Sequence Read Archive of NCBI (SRP136569). *DDOCENT v.2.2.13* (21) was used to trim and map reads, and genotype SNPs using default parameters. Trimmed reads were directly mapped to the *P. ochraceus* draft genome (Ruiz-Ramos et al. unpubl. data; <http://genome.ucsc.edu/>) which was generated and assembled by Dovetail Genomics (Santa Cruz, CA) using Chicago, HiRise, and HiC technologies.

Genotyped SNPs underwent additional filtering, modified from Puritz et al. (60). Sequences were filtered using *VCFTOOLS v.0.1.15* (<https://vcftools.github.io/index.html>) (61) and custom scripts (<https://github.com/jpuritz/dDocent/tree/master/scripts>) (60). The final filtered vcf file had a 98% genotype call rate across all individuals (with maximum allowed missing loci per individual of 13%), minimum depth of 20, and a minor allele frequency of at least 0.01. Haplotypes were then called and filtered for potential paralogs or if missing in more than 10% of individuals using *RAD_HAPLOTYPED v.1.1.8* (62). The output genepop file of haplotypes was converted to Genetix and BayeScan format using *PGDSPIDER v.2.1.0.3* (63) for subsequent analyses. Haplotype frequencies were calculated using *popgenreport* in *PopGenReport v.3.0.0* in R (64). Heterozygosity, gene diversity (H_s), and F_{ST} were calculated using *basic.stats* in *hierfstat v.0.04-22* in R (65). Clonality was tested using *clonecorrect* after removing loci with missing data using *poppr v.2.5.0* in R (66).

Tests for selection in adult *P. ochraceus*

Four main approaches were used to identify changes between pre- and post-SSWD populations and test for signals of selection: (1) a discriminant analysis of principal components (DAPC) (67), (2) an F_{ST} -based outlier method implemented in BayeScan (68), (3) changes in heterozygosity, and (4) consistency in allele frequency change across separate geographic locations. Pre- and post-SSWD adult *P. ochraceus* populations were defined *a priori*.

The DAPC was performed on adult *P. ochraceus* (Table S1) using *dapc* in *adegenet v.2.0.2* in R (67) to identify loci distinguishing pre- and post-SSWD populations. The DAPC evaluates shifts at all haplotypes at a locus, making this analysis potentially more sensitive to detecting selection than F_{ST} -based outlier analyses which does not permit haplotype-specific comparisons. Pre- and post-SSWD groups were defined *a priori*. After running the a-score spline interpolation which identified the optimal number of principal components to retain to be 124, we retained 89 to follow the $<N/3$ rule to avoid overfitting (69). The proportion of conserved variance was 47.7% and one discriminant function (n groups – 1) was used. Haplotypes were sorted by loading from the DAPC and haplotypes with the highest loading per locus were retained. The top 100 haplotypes in this list were used to calculate changes in allele frequency in pre- and post-SSWD adults and recruits. As a preliminary exploration of the potential identity of these putatively selected loci, we used BLASTn (e-value $< 1.0E-6$) against EchinoDB (the

transcript database for echinoderms) (<http://echinodb.uncc.edu>; 22) and the *Pycnopodia helianthoides* transcriptome (23).

BAYESCAN v.2.1 (68, 70) was used to test for candidate loci under selection by using the difference in allele frequencies between pre- and post-SSWD adult samples. Default parameters were employed: thinning interval of 10 and 20 pilot runs for 5,000 iterations, with an additional burn in of 50,000; prior odds for neutral model was 10. The q -value was calculated for each locus and a false discovery rate (FDR) of 0.10, an analog of the p -value, was used to determine significance of outlier loci. To test whether geographic signals of selection might be present, we conducted two additional BayeScan analyses (default parameters) defining populations by geographic location (Table S1) *within* each time point (i.e. pre- and post-SSWD populations separately). No significant changes in any loci were found at FDR = 0.10, though sample sizes on a geographic location basis are small.

Heterozygosity was calculated across all loci and then separately for each outlier locus to identify whether heterozygosity was changing with SSWD.

Consistency in adult allele frequency change in the most common haplotype across geographic locations was assessed in any outlier loci identified by BayeScan using two approaches: a two-tailed paired t-test—comparing pre- and post-SSWD adults at each location—with a sequential Bonferroni adjustment for number of loci (71) and a Fisher's Exact Test (FET). Our criteria for including a geographic location in these tests was that it had ≥ 9 pre- and ≥ 9 post-SSWD adults (which yielded $n = 10$ locations; Table S1). For the FET, the change in allele frequency from pre- to post-SSWD for each location ($n = 10$) was classified as either “changing similarly” (i.e. meaning it shared a consistent direction of change with the overall change in frequency detected in the t-test), or “not changing similarly” (i.e. no change or a change in the opposite direction). We then compared these to the null expectation of random change, i.e. equal probability of similar or dissimilar allele frequency change—e.g. 5 locations with a similar shift and 5 with a dissimilar or no shift. We then used these values to conduct the FET. Recruits were excluded from this analysis because a portion of allele frequency changes from pre-adults could be immigrant.

Estimating genetic affinity of new recruits

To assess whether recruits were most genetically similar to pre- or post-SSWD adults, recruits were assigned by transformation using the centering and scaling of the adult data from the two-group DAPC using the same discriminant coefficients as the adults (69). Recruit assignment was evaluated using posterior membership probabilities with the `predict.dapc` function in *adegenet* v.2.0.2. We used separate χ^2 tests against a null hypothesis of (1) equal probability the recruits will assign to the pre- and post-SSWD adult samples and (2) equal probability recruit allele frequencies will be in the opposite or same direction of change as the post-SSWD adult sample, relative to the pre-SSWD adult population. Achieved power was calculated using G* Power 3 (72). Specific changes in allele frequencies for the top 100 discriminatory haplotypes (using only one haplotype per locus) identified in the DAPC analysis were calculated and compared in pre- and post-SSWD adults and recruits. For loci identified as outliers in adults by BayeScan, we also compared heterozygosity in recruits to pre- and post-SSWD adults.

Data accessibility: Raw sequence data are deposited in NCBI SRA (SRP136569). Commented bioinformatics code, raw SNP calls, filtered SNPs, and final haplotype calls are deposited at UC Merced Dash (refnumber).

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Figure Legends

Fig. 1 Spatial and temporal variation in abundance of *P. ochraceus* before and after the 2013 SSWD outbreak. (A) Map of study sites. (B) Densities of adults and recruits from before (white) and after (black) the outbreak shown by concentric bubbles; area of bubbles is proportional to density (adults: max density = $0.27 \cdot \text{m}^{-2}$; recruits: max density = $3.78 \cdot \text{m}^{-2}$). Adult densities had a median decrease of 81% (range: 9–100%). (C&D) Boxplots of mean density per square meter across surveyed sites for (C) adults and (D) <1-yr recruits. n.p. = no paired data. Map created with SimpleMappr, <http://www.simplemappr.net>.

Fig. 2 Discriminant analysis of principal components (DAPC) of 6,790 haplotypes from 1,225 ddRAD generated loci comparing pre- (n=142) and post-SSWD (n=126) populations of adult *P. ochraceus* and assignment of <1-year-old recruits (indicated by an ×) (n=106). The distribution of recruits is left-shifted relative to pre-SSWD adults. Cumulative variance explained by the number of retained principal components was 47.7%; one discriminant function was used (n groups – 1) in the DAPC (F-statistic = 276.4).

Fig. 3 Difference in allele frequency for (A) post-SSWD adults and recruits relative to the pre-SSWD adults for the top 100 discriminatory haplotypes (after filtering to retain a single haplotype per locus) identified in the DAPC analysis. The y=0 line represents no change from pre-SSWD allele frequencies. Absolute value of difference shown for post-SSWD adults. * indicates outlier loci from BayeScan (FDR = 0.10)—from left to right: Loc1048_Hap1, Loc0379_Hap3, and Loc1166_Hap2. (B) Total haplotypes showing the same v. opposite direction of frequency change in post-SSWD adults and recruits from pre-SSWD adult frequencies. Haplotype names are in Dataset S2.

Fig. 4 Consistent change in allele frequency from pre- to post-SSWD adults across geographic locations for the most common haplotypes in the putatively selected outlier loci identified in BayeScan (FDR = 0.10). * Direction of allele frequency change differs from other geographic locations for a particular locus. Only sites with *P. ochraceus* samples of $n \geq 9$ for both pre- and post-SSWD included (Table S1). Letters represent geographic sites; detailed locations are in Table S1.

Figure 1

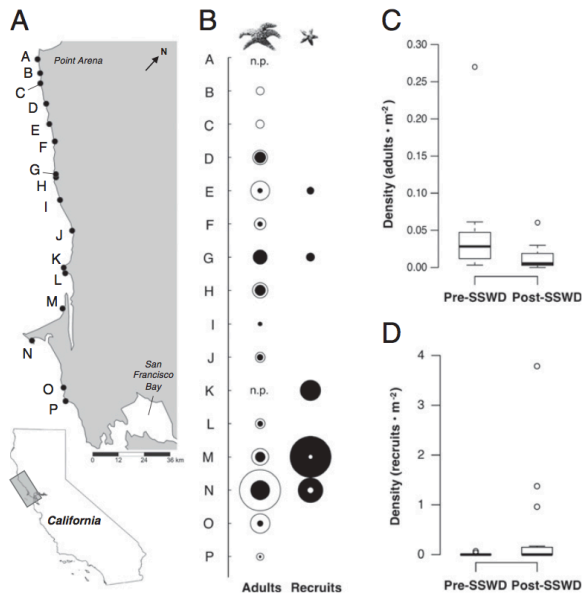


Figure 2

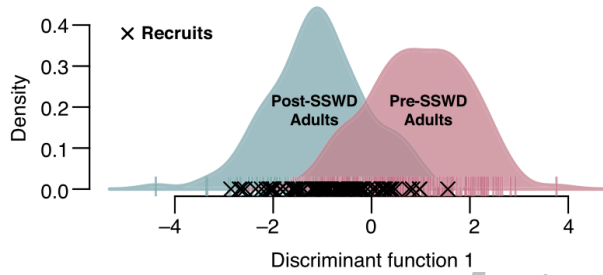


Figure 3

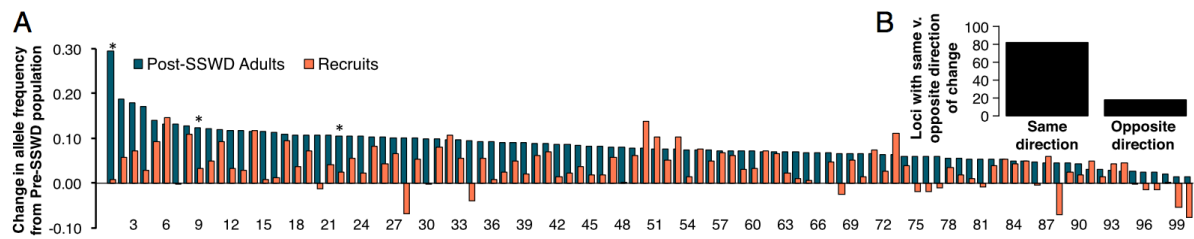


Figure 4

