

## Podcast Interview: Lauren Schiebelhut

**PNAS:** Welcome to Science Sessions. I'm Paul Gabrielsen. Beginning in 2013, tide pools up and down the Pacific coast of America were struck with a devastating scourge. Sea star wasting disease afflicted several species of sea star, including the ochre sea star, *Pisaster ochraceus*. By 2015, 81% of the population had died. Today, the surviving sea stars are beginning to recover. But what was different about the survivors? Population geneticist Lauren Schiebelhut of the University of California, Merced and colleagues sampled the survivors to find out. They sampled both those that were adults at the time of the disease onset as well as those that were juveniles, offspring of the pre-disease population. The researchers noticed that the survivors displayed shifted genetic characteristics. While post-disease genetic monitoring is ongoing and the functions of those shifted genes are still under study, Schiebelhut says this event is an opportunity to observe natural selection processes in real time. She recalls how she felt near the beginning of the sea star wasting disease pandemic.

**Schiebelhut:** When we first heard about it it was more in localized populations, and so initially it was unclear, the scale of the problem. So when we eventually went out and saw it for ourselves, it was actually quite gruesome to see. The sea star will develop these white lesions, they lose their structural integrity, they'll drop arms, their arms will literally just crawl away from the rest of the body. And they simply, just as the name suggests, they just waste away in place and there's nothing left. *Pisaster ochraceus* was famously studied by Bob Paine in his "keystone species" concept. And so they're a really important predator in the rocky intertidal habitat and so the consequences of that were a little bit unclear initially, and then it started affecting more species than just *Pisaster*, so it became more alarming as time went on.

**PNAS:** She and her colleagues expected to see some signs of natural selection in the surviving population, but kept in mind the possibility that the disease may have just affected sea stars at random. In both adults and juveniles, they looked for the frequency of certain alleles in the sea star genome. Alleles are alternative forms of genes at specific locations in the genome. The *Pisaster* survivors displayed a shift in some allele frequencies, compared to the original population.

**Schiebelhut:** When we compare the population of *Pisaster* before the major mortality to the surviving population after the major mortality, we find significant shifts at particular locations in the genome. And then we also see the same types of shifts at the same locations between the original population of *Pisaster* and the new juveniles. And the third test we did was exploring whether that shift we see is actually consistent across geographic space. And overall, those three lines of evidence suggest that natural selection is at play here because all of the shifts happen in parallel. So that really points towards natural selection as being a main driver rather than just random mortality reshuffling what's already existent in the original population.

**PNAS:** At UC Merced, researchers in Michael Dawson's lab are working to annotate the *Pisaster* genome to investigate what functions the shifted alleles may have played in the sea stars' survival. So far, however, the functions of those genes are unclear. Also unclear is the genetic future of the ochre sea star.

**Schiebelhut:** So, one possibility is that the shifts will be maintained in the population, and we at least see that within this first generation after the major mortality and that this might incur some sort of resistance to the disease as it is right now. And another possibility is that as pressure from sea star wasting disease starts to dissipate over time, that we might start to see a shift in those allele frequencies back to that original baseline we collected, or just random shifts due to genetic drift going into the future. That is one thing we're interested in exploring, so we've been sampling annually since the event and so we have new cohorts of juveniles every year after that, and so we're looking at how that changes between each new generation, and then also how those shifts are being integrated into the mature, the reproductively mature, population of *Pisaster* as we go through time.

**PNAS:** Schiebelhut is also learning how a sea star's life cycle can affect their vulnerability to the disease.

**Schiebelhut:** The sea star wasting disease has not only affected *Pisaster ochraceus*, but it's affected about 20 other sea stars and each of those sea stars has their own life cycle or suite of life history traits that make them more or less vulnerable to this kind of mortality event. And so we're also exploring how that influences the recovery of the species. So even

though we have a lot of sea stars that were affected, this disease actually has quite different consequences for many of those species, and it's still out there on the coast today.

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