

## **Coral-eating sea star invaders turn out to be locals**

## February 21 2012

Researchers at the Hawai'i Institute of Marine Biology (HIMB), the Joint Institute for Marine and Atmospheric Research (JIMAR), organized research units in the University of Hawai'i at Manoa's School of Ocean and Earth Science and Technology, and Rutgers University have disproven the secondary outbreak hypothesis in the Central Pacific.

One of the greatest biological threats to <u>tropical coral reefs</u> can be a population outbreak of crown-of-thorns (COT) <u>sea stars</u> (*Acanthaster planci*). Outbreaks can consume live corals over large areas, a change that can promote algal growth, alter <u>reef fish</u> populations, and reduce the aesthetic value of coral reefs, which in turn negatively affects tourism. Despite more than 30 years of research, the triggers and spread of COT outbreaks are not fully understood. Human impacts such as urbanization, runoff, and fishing have been correlated with outbreaks, but some outbreaks continue to occur in the absence of known anthropogenic triggers. Waves of a spreading outbreak that moves southerly along the Great Barrier Reef are termed secondary outbreaks because they are thought to be seeded from dispersing larvae of a primary outbreak upstream.

This secondary outbreak hypothesis has been widely accepted as the mechanism by which COT outbreaks spread across broad regions of the Pacific Ocean and impact remote locations such as Hawai'i, Guam, or French Polynesia - until now. A team of scientists from the Hawai'i Institute of Marine Biology and the Joint Institute for Marine and Atmospheric Research at the University of Hawai'i and Rutgers



University have recently used <u>genetic techniques</u> to evaluate the spatial scale at which COT outbreaks can occur via larval dispersal across the central Pacific Ocean. The results of this work have demonstrated that unlike on the <u>Great Barrier Reef</u>, COT larvae are not moving en masse among central Pacific archipelagos. In fact, contrary to expectations under the secondary outbreak hypothesis, all COT outbreaks in the study came from local populations. On a finer scale, genetic differences were detected among reefs around islands and even between lagoon and forereef habitats of the same island, indicating that the larvae of this species are not routinely reaching their full dispersal potential, and are certainly not fueling outbreaks at distant sites. This research has proved that outbreaks are not some rogue population that expands and ravages across central Pacific reefs. Instead, the authors hypothesize that nutrient inputs and favorable climatic and ecological conditions likely fuel outbreaks of local populations.

This work is particularly important because most current management strategies are focused on stopping secondary spread rather than preventing human activities that can start an outbreak. This study is the first genetic survey of COT populations in which both outbreak and non-outbreak populations are surveyed across a broad region of the Pacific and the results are pretty clear that outbreaks are not jumping across large expanses of open ocean. Dr. Rob Toonen, one of the researchers involved in this project, explains "the genetic differences found among COT populations clearly indicate that outbreaks are not spreading from the Hawaiian Archipelago to elsewhere. Furthermore, the similarity between outbreak and non-outbreaks are a local phenomenon. Our recommendation to managers is to seriously consider the role that environmental conditions and local nutrient inputs play in driving COT <u>outbreaks</u>."

More information: The full paper is free online at



dx.plos.org/10.1371/journal.pone.00311599

## Provided by University of Hawaii

Citation: Coral-eating sea star invaders turn out to be locals (2012, February 21) retrieved 28 April 2024 from <u>https://phys.org/news/2012-02-coral-eating-sea-star-invaders-locals.html</u>

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