Biocontrol: Crown-of-thorns no more
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Coral reefs face many threats, not least of which is the risk of recurrent outbreaks of *Acanthaster planci*, the crown-of-thorns starfish (COTS). A ferocious predator of reef-building corals, aggregations of COTS can denude kilometres of reef during outbreaks [1] (Fig. 1). Contending hypotheses for the cause of COTS outbreaks range from increases in nutrients and pollutants in the water column to warming sea surface temperatures [2]. On page 231, Hall *et al.* [3] report whole-genome sequences for *A. planci*, and perform analyses that provide much-needed momentum in the quest to curtail outbreaks of this starfish.

The authors sequenced two COTS individuals from distant regions of the Pacific Ocean — one from the Great Barrier Reef in Australia, and one from off the coast of Okinawa, Japan. Comparison of these genomes revealed high similarity in gene content and sequence identity (about 99%), in line with what is typically observed in marine animals that, like COTS, spawn by releasing eggs and sperm into the water, and have large population sizes and high dispersal capabilities. Coalescent analysis (in which computational models reconstruct the demographic history of populations using genomic information) suggested that the two COTS populations underwent similar changes in size over geological timescales, with an initial decline and subsequent recovery in the late Pleistocene, about 50,000 years ago.

Genetic analyses of COTS samples taken from many of the disparate marine regions in which the starfish are found have previously provided evidence [4] that *A. planci* is actually a species complex, consisting of four distinct clades that arose from an initial lineage in the Indian Ocean — Northern and Southern Indian Ocean clades, a Red Sea clade and a Pacific Ocean clade. Hall and colleagues' genomes afford a high-quality reference for future population-genomics analyses within and across the four clades. Such analyses could enable the identification not only of population-specific genetic variants, but also of local sequence adaptations to a particular environment [5].

The researchers compared their COTS genomes with those of other sequenced deuterostomes (the group of animals that includes vertebrates, echinoderms such as starfish and sea urchins, and hemichordates such as acorn worms), with the aim of identifying COTS-specific genes that could be targeted for biocontrol. This revealed some evolutionary conservation between the chromosomes of COTS, sea urchins and hemichordates. It also revealed that only a few gene families have more members in COTS than in related taxa, narrowing the authors' search for lineage-specific genomic innovations. Analysis of the complete collections of gene transcripts (the transcriptome) in various COTS tissues revealed that these expansions are in gene families that encode secreted proteins and receptor proteins expressed in external organs such as the spines, body wall and mouth region, indicating that they might be involved in communication between individuals.

Chemical communication is essential for species that live on the ocean floor to find mates and escape predation. COTS respond to chemical stimuli from other individuals by aggregating (known as positive chemotaxis) before mass spawning events. Hall *et al.* next investigated the molecules that might mediate these responses using a Y-maze choice experiment, in which the starfish moved down a channel then took either a left or right channel on reaching a junction.

The authors exposed starfish to a channel that contained proteins released from aggregating COTS and to a control clean water channel. They then performed a similar experiment using proteins from a predator, the giant triton snail *Charonia tritonis*. The aggregate exposure led to positive chemotaxis,
whereas predator exposure resulted in negative chemotaxis, with COTS moving away from the signal. The researchers analysed water samples to identify all of the proteins (the proteome) secreted by COTS in response to each stimulus. This uncovered approximately 400 proteins that were released into the water by the starfish during aggregation, predator evasion or both, including enzymes, components of COTS venom and signalling and structural proteins.

These analyses enabled Hall et al. to narrow down the list of COTS signalling proteins that might modulate behavioural responses to reproductive cues and predator avoidance in a lineage-specific manner. For instance, among the secreted proteins are a suite of ependymin-related proteins (EPDRs). The researchers showed that the gene family that encodes these proteins has undergone a rapid, lineage-specific expansion, giving rise to two copies of the set of genes, arrayed in tandem along the chromosome. These data lend support to the idea that EPDRs are recently evolved, COTS-specific communication molecules.

Another candidate family is the G-protein-coupled receptor (GPCR) proteins, which are known chemoreceptors [6]. Hall et al. find that GPCRs are highly enriched in external tissues, and some are expressed in a sex-specific manner, pointing again to a role in communication. Further analysis of the expression patterns of these proteins might help with the development of biocontrol technologies.

It remains unclear whether one or several factors trigger COTS population increases to densities that are lethal to corals [1, 2]. As a result, management and mitigation efforts have been hampered. Hall and colleagues' work clears the path to overcome such hurdles. In the future, analysis of the genomes of COTS populations from different regions of the world will better inform demographic models to tackle biocontrol by targeting region-specific genomic variants [7, 8]. These genomes will be crucial during years of acute outbreak throughout the Indo-Pacific basin, enabling researchers to identify mechanisms of local adaptation that differ between aggressive and non-lethal A. planci populations for more efficient outbreak management [8, 9].

The authors have produced a manageable list of proteins that should be tested for roles in chemical communication. These molecules can be biochemically evaluated for their cellular role in behavioural recognition of environmental cues, and bait compounds that mimic their activity can subsequently be developed. These COTS-specific baits could, in turn, enable faster and more-effective strategies for containing and ridding reef environments of overwhelming COTS outbreaks. As large groups of individuals are induced to aggregate, underwater robots specifically created for lethal injection of COTS could then be deployed across vast outbreak areas, replacing the human divers who currently perform this procedure [10].

Hall and colleagues' study emphasizes the power of whole-genome data in combination with other cell- and tissue-wide analyses and experimental approaches, not only to study natural history [5], but also for applied sciences such as pest control [9]. Containing COTS outbreaks suddenly seems a more attainable goal, at both regional and global scales.

Web Link(s):

Caption(s):

Figure 1: A crown-of-thorns starfish (Acanthaster planci) devours coral, leaving behind white bones.

Hall et al. [3] sequenced the genomes of two of these starfish, with the aim of providing information that might help to control starfish outbreaks.

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References


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