Scalable multi-omics approach to identify biomimetics that control marine pests: the crown-of-thorns starfish case

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Résumé

Pest species dominate natural and built marine habitats worldwide, largely because of their ability to colonise habitats beyond their own, outcompete resident species, and prolifically reproduce. Although most pests are invasive, some take over because of changes to their native ecosystem. One notorious case of the latter is the crown-of-thorns starfish (COTS), a coral reef resident that consumes corals and destroys reefs. The high seasonal fecundity of COTS is an important natural contributor to localised outbreaks, although changes in larval food availability and abundance of predators have been attributed to these outbreaks. COTS synchronously spawn in the summer, with a single female releasing up to 50 million eggs. In this presentation I will describe our efforts to identify communication factors that underlie COTS reproduction by combining transcriptomic and proteomic analyses with behavioural assays. This includes (i) a scalable, environmentally-benign approach to identify putative communication proteins released under experimental and natural conditions, and (ii) targeted and replicated transcriptomes from wild COTS (translocation of COTS to aquaria has a marked impact on normal gene expression). These analyses are consistent with COTS releasing a proteaceous macromolecular complex in the summer that is differentially perceived by males and females, and controls prespawning and spawning behaviours. Like COTS, the life histories of most marine pests rely on chemical communication to colonise, reproduce and overrun a habitat. The multi-omic approach used for COTS provides an example of how to identify life history factors that can be used in marine pest biocontrol programs.

Mots-Clés: coral reefs, echinoderms, pest species, proteomics, transcriptomics

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