

Evolutionary potential in a changing ocean

Ocean acidification is a marine repercussion of global carbon dioxide (CO₂) pollution. As atmospheric CO₂ dissolves into water, some of it reacts to form carbonic acid, bicarbonate and excess hydrogen ions. The resultant increase in acidity can damage the calcium carbonate shells of many marine invertebrates and impair the development of many marine fishes as well.

Ocean acidification is expected to increase with anthropogenic CO₂ production for the foreseeable future, and the ecological ramifications of this changing oceanic environment remain largely unknown. Recent research has begun to investigate whether and how marine species might adapt under the selective pressures of a rapidly acidifying ocean.

“The fundamental question is whether or not organisms can adapt to this threat,” said Hannes Baumann of the University of Connecticut (Groton), who studies marine fish and the effects of ocean acidification. Baumann and colleagues carried out an experiment with wild-caught Atlantic silversides, testing how well these fish can tolerate acidified water and whether that



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tolerance can be passed on to subsequent generations. They reared newly fertilized offspring in common-gardens—artificial habitats with nearly identical conditions that control environmental variables like food availability and water quality. Experimental habitats all contained water with a modified pH of 7.45, which represents the maximum acidity predicted for the open ocean in about 300 years (by comparison, control habitats contained unaltered water with a pH of 8.10). “Three hundred years is only five or six generations for whales or long-lived sharks,” noted Baumann, so species like these will have a short window of

opportunity in which to adapt or perish in a swiftly changing environment.

As they raised the silverside larvae, Baumann’s team kept track of how long each fish survived and collected DNA samples. Using genetic markers called microsatellites, the researchers determined the parentage of each fish and found that related larvae showed a similar ability to survive in acidified water (*Evol. Appl.* doi:10.1111/eva.12248; published online 13 February 2015).

This suggests that tolerance for higher acidity is a family trait among Atlantic silversides and that populations can potentially adapt to an ocean with higher acidity. This is good news for silversides, but for researchers it is also a proof-of-concept that quantitative genetics can help gauge the evolutionary potential of a species under selective pressure. “This is an experiment that can be performed in one generation,” said Baumann in a press release, and this is a valuable asset as diverse ecosystems face strong environmental changes in the coming years.

Gregory D. Larsen

A SIGNAL THAT SHIFTS GUT MICROBIAL COMPOSITION

Fluctuations in the composition and diversity of the gut microbial community can affect organismal health in various ways. Low microbial diversity in the gut can increase a person’s susceptibility to potential pathogens, such as *Salmonella* spp. And changes in the balance between the two bacterial taxa most prominent in the gut, Bacteroidetes and Firmicutes, are associated with conditions like obesity, diabetes, chronic inflammatory bowel disease, gastrointestinal cancer and stress. Medical researchers have therefore suggested that the ability to regulate microbial community composition might provide opportunities to treat these and other diseases.

One way of regulating community composition is by manipulating interactions between community members. Microbes use many mechanisms to detect and respond to the presence of other microbes. For example, bacteria produce small molecules called autoinducers in amounts proportional to the size of the population. By detecting these autoinducers, bacteria can regulate certain behaviors at the population level, including attachment, biofilm formation, motility and virulence. Such activities are relevant in the gut environment, leading researchers to believe that quorum sensing probably has a role in gut microbial community interactions.

Whereas many autoinducers are species-specific, autoinducer-2 (AI-2) functions across the bacterial kingdom; AI-2 produced by one species can influence others. This feature makes AI-2 an excellent candidate for mediating interactions in the mammalian gut microbial community, which includes hundreds of species. To investigate this potential role of AI-2, Karina Bivar Xavier (Instituto Gulbenkian de Ciência, Oeiras, Portugal) and colleagues manipulated AI-2 levels in the mouse gut using specially engineered *Escherichia coli* mutants and examined how these manipulations affected the composition of the gut microbiota.

The mice were first treated with streptomycin, which disturbed the normal microbiota, allowing *E. coli* to colonize the gut. Streptomycin reduced total bacterial load, decreased microbial diversity and substantially altered the relative proportions of Bacteroidetes and Firmicutes (from 48% and 43%, respectively, to 90% and 0.7%, respectively, after 28 d of treatment). Introduction of *E. coli* mutants that overproduce AI-2 reversed the effects of streptomycin by restoring the ratio of Bacteroidetes and Firmicutes bacteria (*Cell Rep.* doi:10.1016/j.celrep.2015.02.049; published online 19 March 2015). The results indicate that AI-2 can modulate the composition of the gut microbial community.

Xavier’s group concluded, “This work highlights the potential gain from understanding and manipulating the bacterial chemical repertoire operating within the bacterial community inhabiting the gut, towards the aim of tailoring the composition of the microbiota to our benefit.”

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