Delving into the molecular mechanism behind deep-sea bacteria's pressure tolerance

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The Mariana Trench is the deepest feature of the Earth's surface. The water column there exerts a pressure of more than one thousand times normal atmospheric pressure at sea level, enough pressure to crush an SUV. Yet many organisms thrive in this seemingly inhospitable environment. A Japanese research team has been investigating how deep-sea bacteria adapt to such high-pressure conditions. They have identified a structural change that confers pressure-resistant properties on a particular protein found in bacteria.

The findings, which the team will present at the meeting of the American Crystallographic Association (ACA), held July 28-Aug. 1, in Boston, Mass., may one day help guide the design of enzymes for use in high-pressure chemical industrial processes.

In general, pressure, like that caused by a water column thousands of feet deep, deforms proteins. As the proteins change shape, water can penetrate the protein's interior. Some proteins are better able to resist this incursion of water, but the molecular mechanisms of the pressure resistance aren't yet well understood.

"Our group is focusing on high-pressure protein crystallography, using 3-isopropylmalate dehydrogenase (IPMDH) as a model protein. The goal is to delve into the principles of the molecular mechanism of the pressure tolerance of proteins by comparing the structures of IPMDHs from organisms that thrive in high-pressure environments and those that are sensitive to high-pressure pressure environments," explains Nobuhisa

Watanabe, a professor at the Synchrotron Radiation Research Center, Nagoya University.

To create the high pressures necessary for their studies, the team uses a diamond anvil cell (DAC), which consists of two opposing diamonds with a gasket compressed between the culets (the small, flat facet at the bottom of the diamonds).

The team's big discovery so far is that the initial water penetration at the molecular surface of the side opposite to the active site of IPMDH is unique.

"At the site of the penetration, there is a difference of amino acid between IPMDHs from bacteria that thrive in high-pressure environments and those that are sensitive to it. Based on this data, we substituted one amino acid at the site of the IPMDH from pressure-sensitive bacteria and checked its activity under pressure," says Watanabe. "And as we expected, only this one residue-substituted IPMDH, which has 364 amino acids in total, achieved pressure resistance comparable to the bacteria that thrive in high-pressure environments."

This means that it may soon be possible to synthesize designer pressure-resistant proteins. The team plans to continue their high-pressure studies of several other proteins to try to discover the physical principles behind pressure resistance mechanisms that enable bacteria to thrive in high-pressure conditions.

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