Press Releases

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JAMSTEC
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Heterogeneous Symbiont Subpopulations Utilizing Different Energy Sources in a *Deep-sea Bathymodiolus Mussel* ~New Insights on Bacterial Symbiont Population's Adaptation to the Environment~

A research group led by Dr. Tetsuro Ikuta and Dr. Yoshihiro Takaki at the Japan Agency for Marine-Earth Science and Technology (JAMSTEC: Asahiko Taira, President) with Atmosphere and Ocean Research Institute at The University of Tokyo, Okinawa Industrial Technology Center, Okinawa Institute of Advanced Sciences, and Okinawa Science and Technology Promotion Center sequenced a whole-genome of the endosymbiont bacteria of a deep-sea mussel, *Bathymodiolus septemdierum* (Figure 1), a dominant species living at hydrothermal vents in the Izu-Ogasawara Arc.

They found that the symbiont population harboured in an individual *B. septemdierum* host is composed of several heterogeneous subpopulations that differ in gene sets for key metabolic enzymes. This heterogeneity may be beneficial for utilizing diverse energy substrates in the deep-sea vents, where the ambient conditions are variable. It provides new insights on how these mussels acclimate to their environment and survive in the deep ocean. These findings will help understand how symbiotic organisms alter their metabolic capabilities and expand their ecological range.

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Title: Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population.

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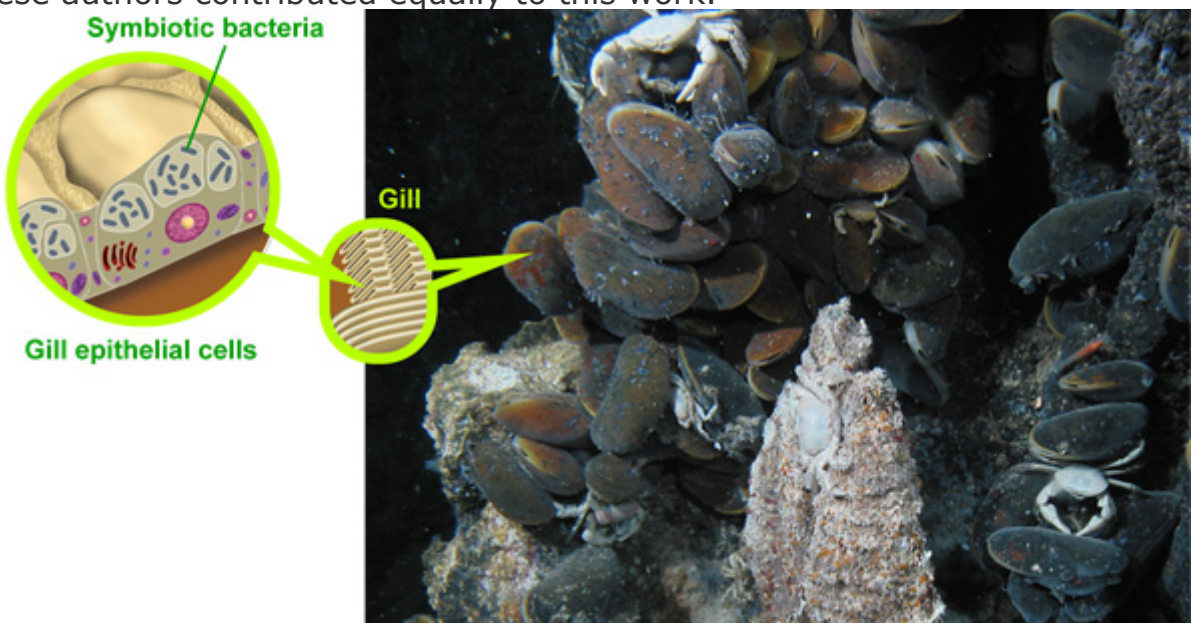

Illustrations by Nariyuki Yoshiwara

Figure 1: *Bathymodiolus mussels* have a symbiotic relationship with bacteria in their gills by obtaining them from the environment. The symbiont produces organic substances using energy obtained by oxidation of hydrogen sulphide or hydrogen, and then provides them to the host.

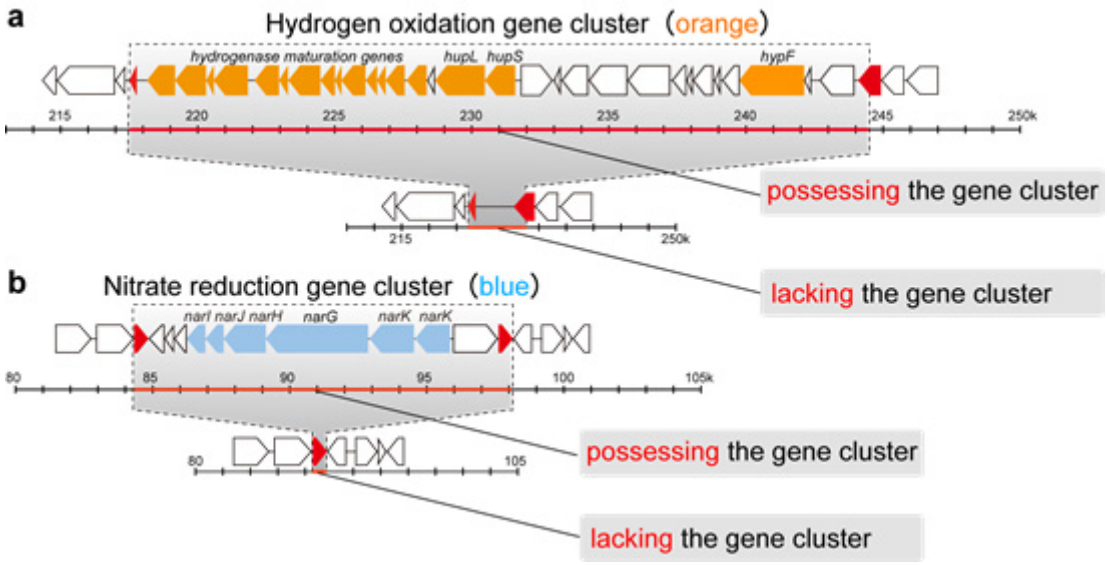

Figure 2: Genomic architectures revealed by whole genome sequencing of the symbiont of *B. septemdierum.* Genomic architectures with or without each gene cluster are shown here: (a) Hydrogen oxidation gene cluter; (b) Nitrate reduction gene cluster.

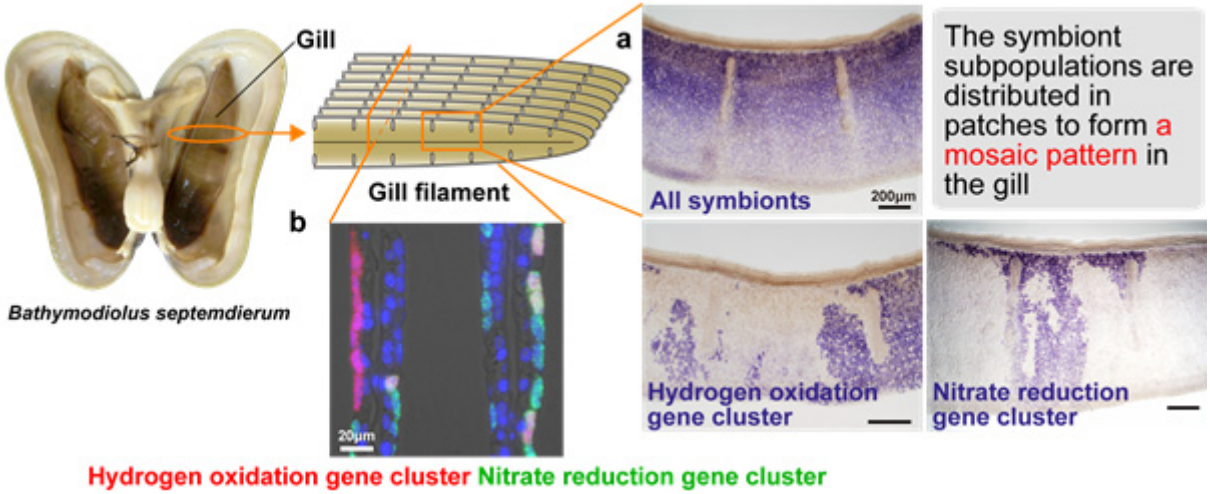

Figure 3: Patchy distribution of symbiont subpopulations: (a) The symbiont subpopulations in the gill were stained in blue-purple; (b) Red and green colours indicate subpopulation with hydrogen oxidation gene cluster and nitrate reduction gene cluster, respectively. Blue stain indicates DNA.

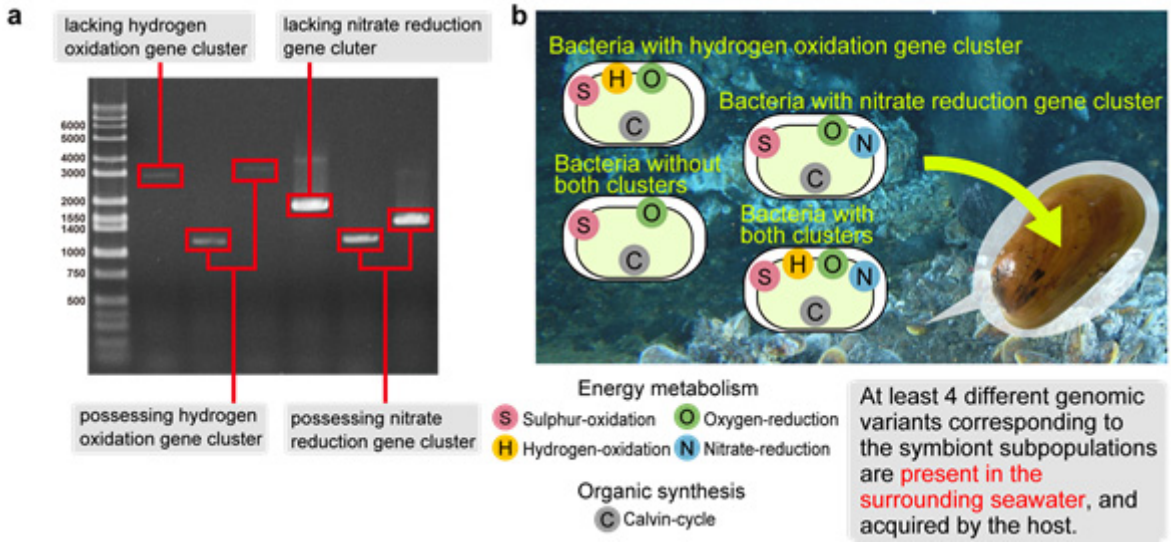

Figure 4: Model for production of heterogeneous symbiont subpopulations in a host individual: (a) PCR analysis using DNA extracted from seawater showing existence of different symbiont subpopulations in the surrounding seawater; (b) Model for production of heterogeneous symbiont subpopulations in a host individual.

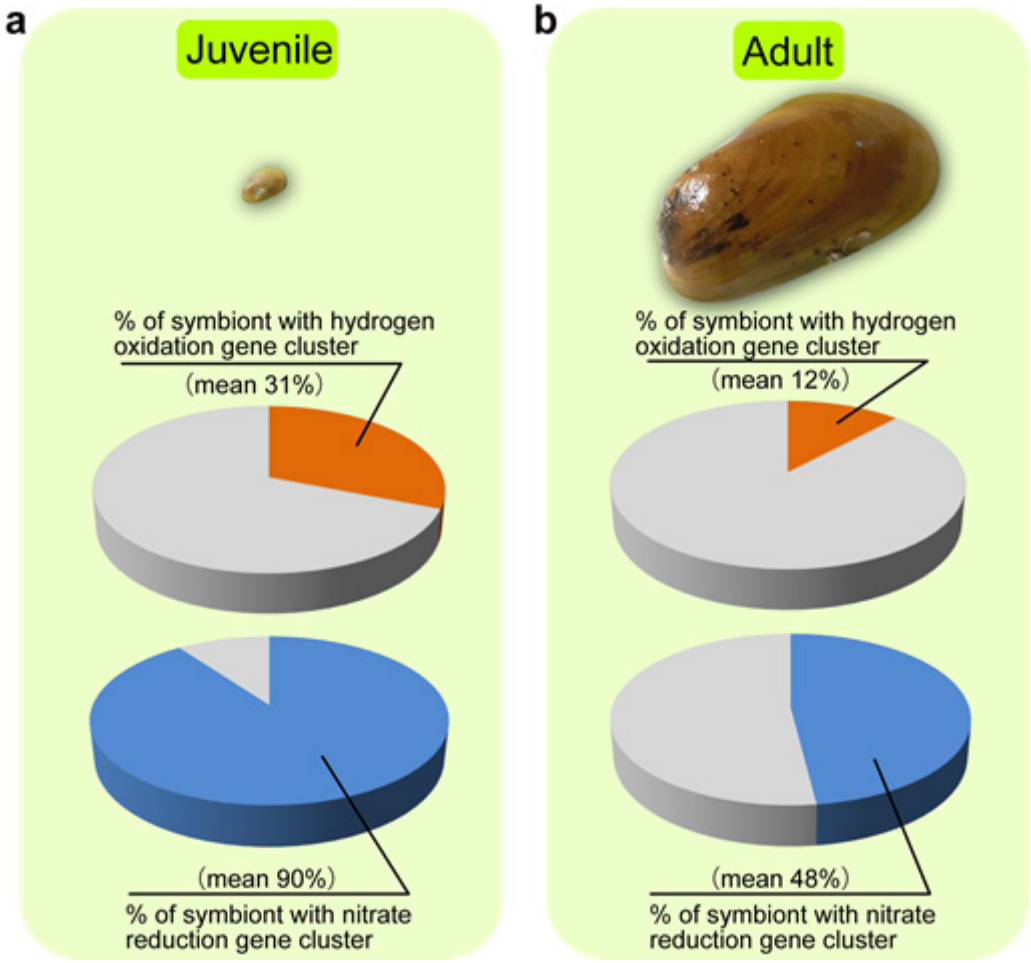

Figure 5: Proportion (%) of symbiont subpopulations with hydrogen oxidation gene cluster or nitrate reduction gene cluster in juvenile or adult hosts: (a) Mean proportions in six juveniles (cell length:2.8~5.0mm); (b) Mean proportion in six adults (cell length:110~120mm). The difference between (a) and (b) seems to be because certain subpopulations are selected during the host development or it may reflect different environmental conditions when the symbiont is acquired from the environment.

Deep-sea Bathymodiolus Mussels in the Izu-Ogasawara Arc
~Movie taken by *Hyper Dolphin*, a remotely operated vehicle~
(Video)

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