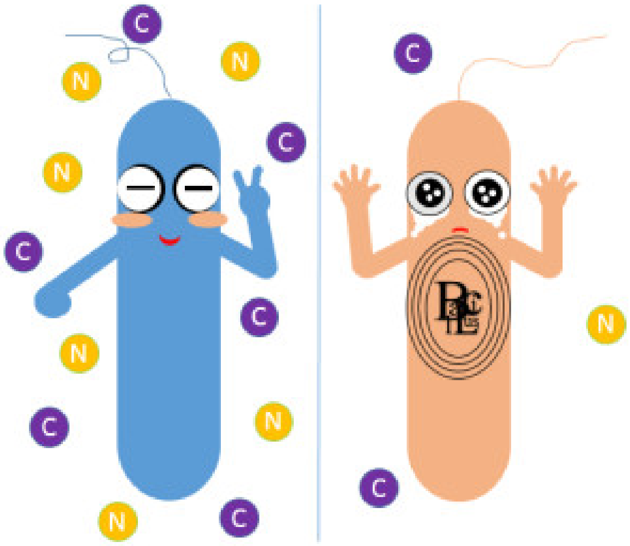
Endospore formation: a mechanism for microbial response to unfavorable environment

The strain included in the report is *Bacillus* sp. CHD6a, a member of the phylum *Firmicutes* isolated from the shallow-sea hydrothermal vent systems off northeast Taiwan's coast. *Bacillus* is a genus of Gram-positive, rod-shaped and ubiquitous in the environment.



A diagram showing the bacteria without and with endospore

Each *Bacillus* strain usually produces a single internal endospore. Endospore formation is mostly triggered by the nutrient-depleted or harsh environments. The shape of the endospore in *Bacillus* is oval, and its position within cell is subterminal or central. During the sporulating cell division, an asymmetric two compartments are formed. The larger one is mother cell and the smaller one is forespore. The endospore maintains a tough, dormant and non-reproductive form under the whole stressful conditions, and contains bacterial chromosome, ribosomes and a great number of dipicolinic acids. The spore protection layer consists of four parts: exosporium, spore coat, spore cortex and core wall. Endospores or spores are resistant to ultraviolet radiation, extreme heat or freezing, desiccation and other stress, wherein its chromosome is kept in a safe environment. It can bring itself back to the vegetative state under favorable environmental conditions, even after a few centuries dormant state.

A great number of genes involved in (endo-) spore formation are detected in the genome of *Bacillus* sp. CHD6a, which represents ~3% of genomic size. The formation of endospore is usually triggered by the expression of histidine sensor kinases (including KinA, KinB and KinC), and then they go through six stages (Spo0 and from SpoII to SpoVI) to be mature spores.

The characteristic of forming endospore in genus *Bacillus* makes them cope uncomfortable environmental conditions and to be widely distributed in diverse habitats. With the development of technology and more microbes studied, more and more microbial evolutionary and adaption mechanisms would be found.

Wenxin Lin, Qiang Zheng, Nianzhi Jiao
State Key Laboratory of Marine Environmental Science, Institute of Marine Microbes and Ecospheres,
Xiamen University, Xiamen 361102, People's Republic of China.

Publication

Genome sequence of Bacillus sp. CHD6a, isolated from the shallow-sea hydrothermal vent.
Lin W, Chen H, Chen Q, Liu Y, Jiao N, Zheng Q
Mar Genomics. 2016 Feb