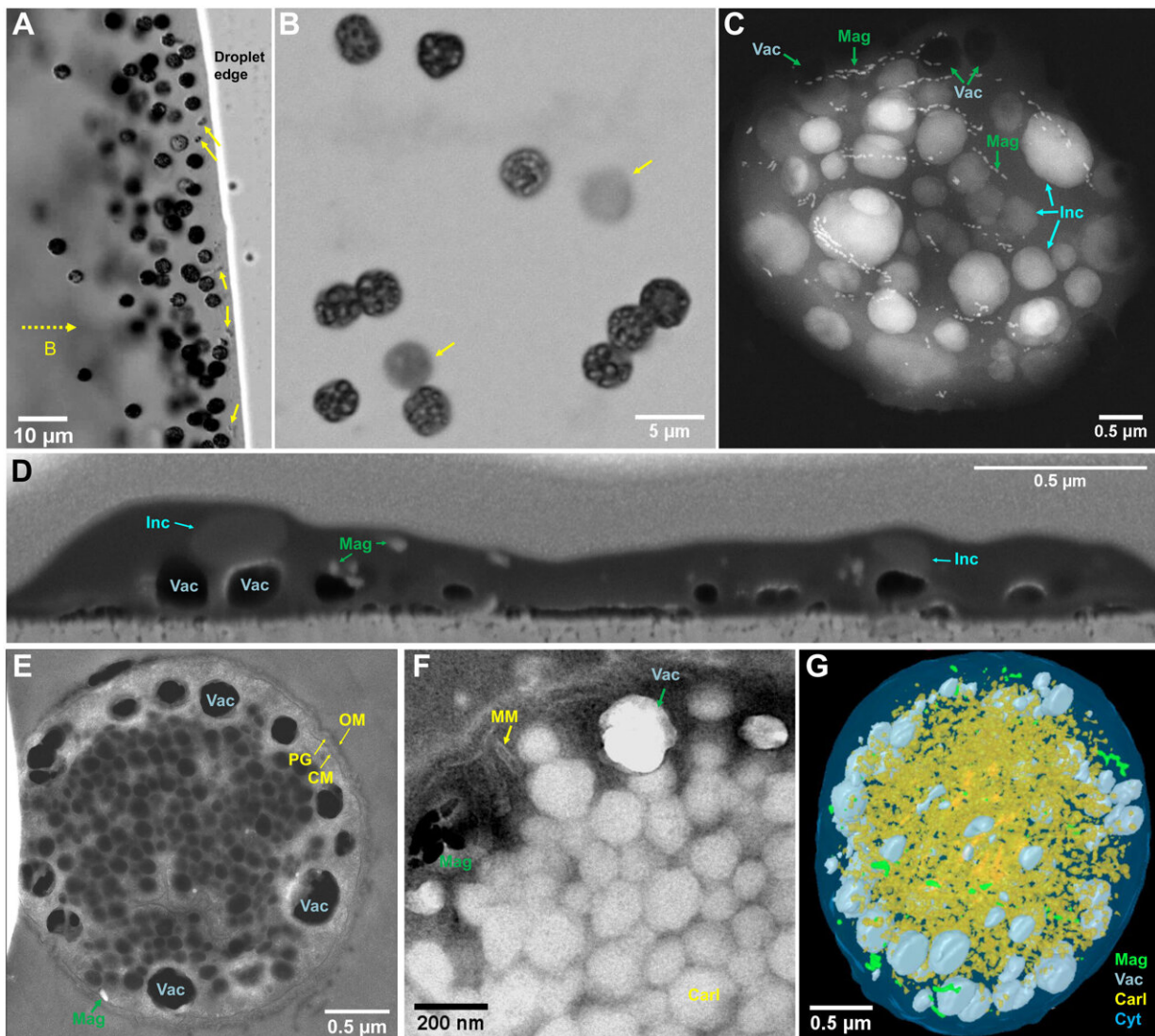


Researchers discover intracellular biosilicification in prokaryotes

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Morphology and ultrastructure of the magnetotactic strain WYHC-5. (A) Optical micrograph showing living coccoidal MTB (WYHC-5). They swim out from the

sediment located to the left of the image (sediment not shown) along the external applied magnetic field lines (dashed line with arrow) and gather on the water droplet edge. A few other types of small MTB are indicated by yellow arrows. (B) Optical micrograph of WYHC-5 cells magnetically collected from sediments in laboratory microcosms. The bacteria were stained by crystal violet before optical microscopy observations. Two out-of-focus cells are indicated by yellow arrows. (C) STEM image of one typical WYHC-5 cell acquired in the STEM-HAADF showing multiple chains of magnetosome magnetite (Mag), numerous electron-dense inclusions (Inc), and electron-transparent vacuoles (Vac). (D) SEM image of air-dried WYHC-5 cell selected from a series of FIB sections showing that the vacuoles, magnetosome magnetite, and electron-dense inclusions are relatively independent from each other within the cell. The empty vacuoles remain approximately spherical in shape, suggesting that they have a rigid enclosed structure. (E) STEM-HAADF image of an ultrathin section of a freeze-substituted WYHC-5 cell showing (i) the typical Gram-negative cell wall (CM, cytoplasmic membrane; OM, outer membrane; PG, peptidoglycan) and (ii) vacuoles adjacent but separated from the CM. (F) Bright-field TEM image of an ultrathin section of a freeze-substituted WYHC-5 cell showing empty magnetosome membrane (MM; the inside magnetite crystal might have been lost during sample preparation), and the aggregate of polyhedral carboxysome-like bodies (Carl). (G) 3D FIB-SEM reconstruction and visualization of one freeze-substituted WYHC-5 cells [green, magnetosome magnetite; gray, vacuole; yellow, carboxysome-like body; light blue, cytoplasm (Cyt)]. The FIB-SEM sections and 3D reconstructions for air-dried and freeze-substituted WYHC-5 cells are provided as movies S2 and S3, respectively. Credit: *Science Advances* (2022). DOI: 10.1126/sciadv.abn6045

Biosilicification—the formation of biological structures composed of silica—has wide distribution among eukaryotes. It plays a major role in global biogeochemical cycles and has driven the decline of dissolved silicon in the oceans throughout geological time.

A research team led by Profs. Li Jinhua and Pan Yongxin from the

Institute of Geology and Geophysics of the Chinese Academy of Sciences (IGGCAS) has discovered a novel magnetotactic bacterium that forms intracellular, amorphous silica globules.

This finding reveals intracellularly controlled silicification within prokaryotes and suggests a previously unobserved influence on the biogeochemical Si cycle that was operational during early Earth history.

The study was published in *Science Advances* on May 13.

Silicon is the second most [abundant element](#) in Earth's crust after oxygen. It is an essential element for life, both on land and in the ocean. The formation of biological structures composed of silica, known as biosilicification, is widely distributed in eukaryotes.

It has previously been proposed that the radiation of biosilicifying eukaryotes during the Phanerozoic drove secular decreases in dissolved silicon (DSi) in the global ocean, ultimately resulting in the low DSi concentrations seen today. However, strong evidence of such a process has remained elusive during the Precambrian.

Prof. Li Jinhua discovered one particular group of magnetotactic cocci in sediments collected from Lake Weiyanghu (WYH), located in Xi'an City, Shaanxi Province, China. This bacterium, tentatively named strain WYHC-5 and phylogenetically affiliated with the Nitrospirae phylum, belongs to a deep-branching group of magnetotactic bacteria (MTB).

"Electron microscopy analyses showed that strain WYHC-5 can accumulate a large amount of silicon within its cells in the form of amorphous silica globules, aside from forming magnetite-type magnetosomes and sulfur inclusions," said Prof. Li.

The results of metagenomic analysis of the WYHC-5 genome have

revealed the presence of a key gene possibly involved in silica deposition. Further assessment has revealed that the intracellular silica globules are also present in some other strains affiliated with the Proteobacteria phylum.

This study thus provides previously unrecognized structural and molecular evidence for intracellularly controlled biosilicification in prokaryotes. The results suggest a possible influence on the biogeochemical silicon cycle during early Earth history.

These findings also expand the record of silicifying prokaryotes from the genus *Bacillus* belonging to the Firmicutes phylum and the cyanobacterium *Synechococcus* to several MTB species affiliated with the Nitrospirae and the Proteobacteria phyla. However, the biosilicification pattern (i.e., the form and location of silicified products) is obviously different among bacterial groups.

The MTB strain WYHC-5 accumulates silicon intracellularly in the form of amorphous silica globules due to an estimated DSi concentration approximately 3,500-fold higher than that in surrounding water used for experiments. Therefore, it represents both a novel and a highly effective mode of prokaryotic biosilicification.

Phanerozoic cherts are primarily composed of silicified skeletons and thus are biological in origin. However, the origin of Precambrian cherts has long been an enigma, due to a lack of evidence that silica-secreting organisms were present in the Precambrian in sufficient abundance to have had a significant influence on the Si cycle. All MTB alive today are microaerobic and anaerobic, and versatile in their C, N, S, P and Fe metabolisms. They are also environmentally ubiquitous, living in various freshwater, brackish, marine, and hypersaline habitats, and even in hot springs.

"Taken together, these facts support the possibility that MTB lived in hypoxic environments in the Archaean Ocean at a point in early Earth history. Therefore, prokaryotes may play a role in driving the biogeochemical Si cycle in both modern environments and early Earth history, provided that prokaryotic biosilicification has an ancient origin rather than a recent horizontal gene transfer," said Prof. Pan.

More information: Jinhua Li et al, Intracellular silicification by early-branching magnetotactic bacteria, *Science Advances* (2022). [DOI: 10.1126/sciadv.abn6045](https://doi.org/10.1126/sciadv.abn6045)

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