

Evolution & Behavior

When it comes to the giant bacterium *Achromatium*, everything is everywhere

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ABSTRACT

*Unlike typical bacteria, the giant *Achromatium* contains hundreds of unidentical chromosomes. *Achromatium* is present globally in different environments. This typically leads to speciation. Nevertheless, *Achromatium* shows minimal environment-specific phylogenetic differentiation. Instead, it harbors a globally identical functional inventory for which uses genes it needs for the specific habitat.*

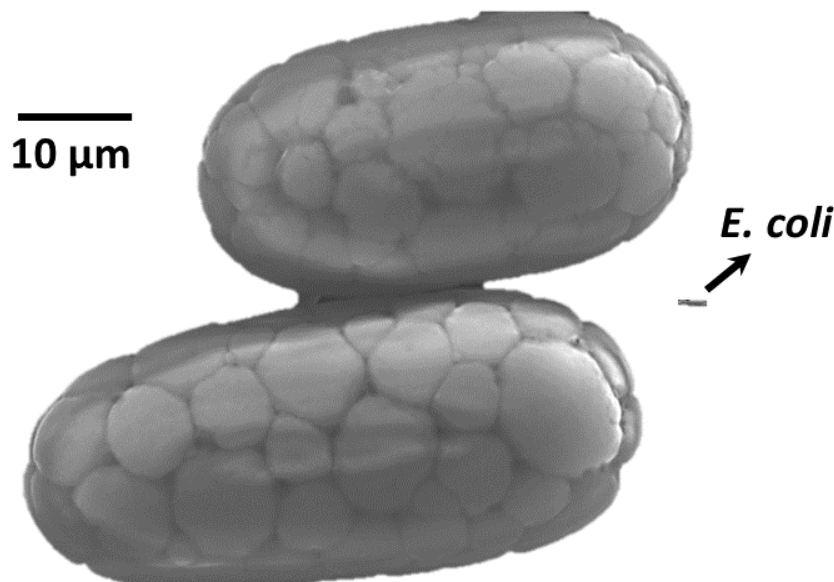


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Bacteria of the genus *Achromatium* are known since the 1890s. They occupy the uppermost layer of aquatic sediments at the boundary between the oxic water and the anoxic benthos where *Achromatium* uses sulfide for energy. *Achromatium* is recognizable by two distinctive features: (1) it is a giant bacterium with a volume 30,000 times larger than any typical bacteria, (2) it harbors “stones” (made of calcium carbonate) that fill most of its cell body.

Like other giant bacteria, *Achromatium* contains many chromosomes on which its genetic material is

encoded, typically around 300 chromosomes. However, unlike anything seen so far among bacteria, these chromosomes are not identical, making *Achromatium* the only known bacterium with multiple different chromosomes having numerous different versions of all functional genes including those known to occur only once in a bacterial genome.

We believe that this unprecedented genomic diversity is tightly linked to the stones in the cell. The cytoplasm is “squeezed” in between stones forming a thin network with occasional larger compartments. These

compartments are likely isolated one from another and so are the clusters of chromosomes trapped in them. Though these chromosome clusters had a common ancestor, they evolve independently from one another, giving rise to multiple alleles of the same gene in one single cell. When cells divide, chromosome clusters close to the division plane may mix, resulting in new genomic combinations. If the latter proves right, it is a single-cell bacterial representation of sexual-like reproduction, known thus far solely from *Achromatium*.

For more than a century, *Achromatium* was found exclusively in freshwater, known as the largest freshwater bacterium. Recently, however, it was also described from several saline environments. Therefore, we set to investigate the global distribution and diversity of the genus *Achromatium*.

To do so, we screened all publicly available DNA data obtained from sediments, for genes belonging to *Achromatium*. *Achromatium* was found to be universal, inhabiting a broad range of environments from the Arctic to the Antarctic. It occurs in shallow waters as well as in the ocean at depths of 4000 meters. It was found in hot springs but also in ice-cold water, in acidic and alkaline sediments, and also in hypersaline waters.

Typically, such a wide range of environmental conditions results in the establishment of new species, well-adapted to their specific environment. However, *Achromatium* defies this expectation. When comparing the sequences of phylogenetic markers or functional genes, no habitat-specific separation was observed. This is in contrast for example to the *Pelagibacter* clade, the most abundant group of aquatic bacteria, in which freshwater and marine species form separate phylogenetic groups.

Even more surprising was the lack of any functional difference between *Achromatium*-like sequences recovered from different environments. In a process called genome streamlining, bacteria typically adapt to their habitat, losing unnecessary genes. This seems not

to be the case for *Achromatium* and two results point to the possibility of an evolutionary strategy previously unknown. First, though the overall functional inventory was identical across environments, our data point to a difference in the copy number of genes among cells from different habitats. Second, when we investigated transcriptomic data, showing which genes of the total inventory are used, clear patterns were observed separating different habitats.

Thus, we propose that *Achromatium* accumulates functions with time. It adapts to different habitats not by losing unnecessary genes but rather by changing their copy numbers, enriching those it needs and “archiving” those it does not. Thereafter, *Achromatium* appears to regulate which genes it uses based on what it needs to survive in its current habitat. This previously undescribed strategy explains the ability of *Achromatium* to exist in environments with drastically different characteristics and suggests that it possesses the ability to overcome dispersal limitation by adapting each time to any environment it encounters.

Our understanding of *Achromatium* so far, consisting of its, likely, compartmentalized internal structure, and continuous shuffling of chromosomes, similar to sexual reproduction for the generation of genomic diversity and its evolutionary strategy of function accumulation and archiving, points to an organism with bacterial metabolism featuring many characteristics of advanced unicellular and multicellular organisms. However, whether *Achromatium* served a role in the evolution of sexual reproduction and the development of multicellular organisms or whether it is a unique bacterium with a special capability for adaptation remains to be further determined.

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