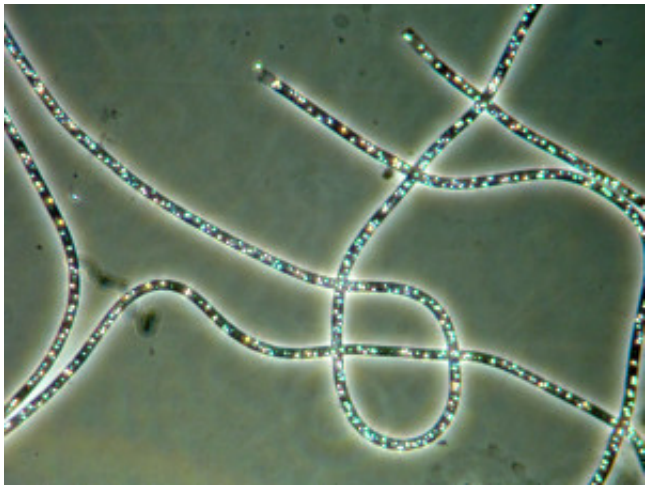
Life on sulfur. Why we need complete genomes

The ability of bacteria to grow on inorganic compounds like sulfur was discovered by Russian microbiologist Sergey Winogradskij in 1888. First, he studied a sulfur bacterium of the *Beggiatoaceae* family to demonstrate that it can produce energy from inorganic compounds and use this energy to utilize carbon from carbon dioxide (CO_2) to sustain life. Other bacteria are able to use different inorganic compounds like nitrogen, hydrogen, iron and arsenic to produce energy as well. This process is known as chemolithotrophy and facilitates their ability to sustain life without oxygen.



The photo demonstrates the bacterial filaments of Beggiatoa leptomitifomis neotype D-402? with granules of elemental sulfur. The size of this bacterium can be as long as 100 micron and even longer

In our published work, we studied *Beggiatoa leptomitifomis neotype* D-402[?], which is a unique representative of freshwater sulfur bacteria. The figure demonstrates the bacterial filaments with granules of elemental sulfur. The size of this bacterium can be as long as 100 micron and even longer. These bacteria are known for being able to survive in very harsh environments due to their ability to live on sulfur and atmospheric nitrogen without any oxygen. In the future, this knowledge could potentially be harnessed for planetary terraforming and also answer the question of what life may have looked like on early Earth.

Genome sequencing and its corresponding annotations may lead to the discovery of potential abilities of microorganisms, finding unusual enzymes and consequently new metabolic pathways, and finally performing biological engineering to improve microorganism properties for practical applications in biotechnology. Additionally, complete genomes help elucidate evolutionary relations of these organisms in the tree of life. However, there are only a few non-complete genomes for the

family of *Beggiatoaceae* currently available due to the difficulties involved in culturing these organisms in the lab.

Unfortunately because current sequencing technology does not allow the reading of many millions of letters from the complete genome directly, scientists have relied on DNA fragmentation to circumvent this challenge. Most platforms can only read substantially short pieces of DNA fragments, which comprise on average 50-400 letters. The overlapping reads can be assembled into one piece and create a complete bacterial chromosome. However, bacterial genomes have so called repeat sequences, which can prevent performing a complete assembly if your largest read is shorter than the repeat itself. The newly developed SMRT sequencing technology overcomes this problem by being able to read much longer pieces of DNA fragments up to 30,000-40,000 letters long. The instrument for SMRT sequencing is based on the incorporation of fluorescent nucleotides by a special DNA polymerase and has the power of 150,000 fluorescent microscopes put together. Moreover the SMRT sequencing can detect additional modifications on DNA molecules and predict what type of restriction-modification barrier we dealing with. Thus these data may be used to develop efficient transformation systems.

Alexey Fomenkov[1] *and* ***Margarita Y. Grabovich***[2]
[1]*New England Biolabs, Ipswich, MA. USA*
[2]*Department of Biology, Voronezh State University, Voronezh, Russia*

Publication

Complete Genome Sequence of the Freshwater Colorless Sulfur Bacterium Beggiatoa leptomitiformis Neotype Strain D-402T.
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