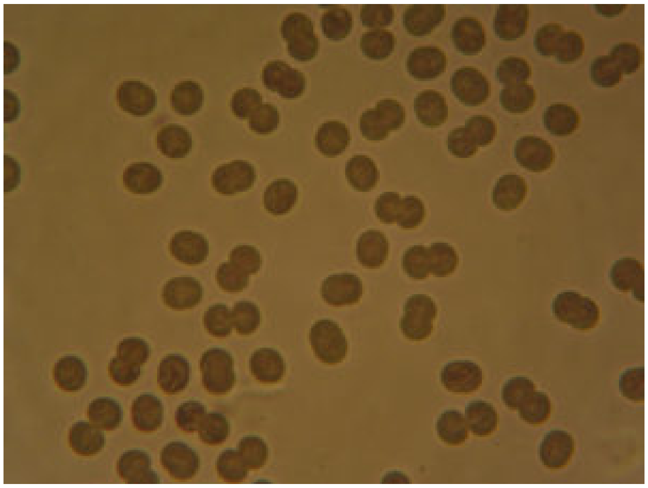
Why identify microscopic photosynthetic bacteria called Cyanobacteria?

Cyanobacteria, the small, harmless bacteria, are invisible to the naked eye. Cyanobacteria photosynthesize like all plants do and thus produce the oxygen we breath. In nature they can be found almost everywhere from the open ocean, to deserts and thermal springs.

Identification and classification of cyanobacteria is a difficult task due to the way these organisms reproduce. There are no male and female cyanobacteria that can produce fertile offspring; instead each organism divides into two and produces two identical clones. This fact poses limitations to our ability to explore their ancestry. Moreover, different species do not have enough morphological differences to accurately identify them, like we can differentiate between e.g. a human and a chimpanzee.

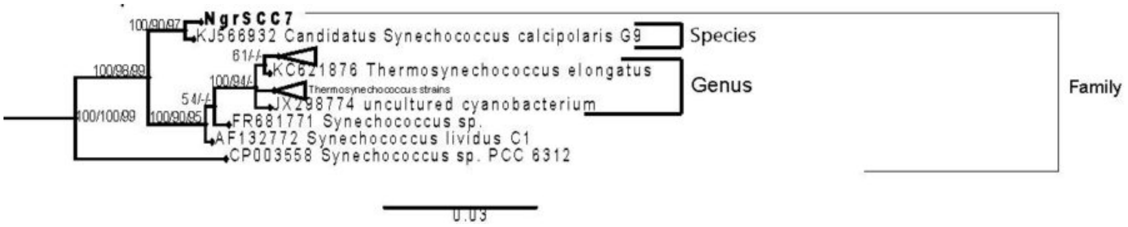


Unicellular cyanobacterium.

It is important to be able to identify these organisms because different species have different technological applications like *Spirulina* which is a well-known food supplement or *Nostoc* which is the prominent fertilizer in rice cultivation.

The best practice to classify cyanobacteria is to use a polyphasic taxonomic approach i.e. to use as much taxonomic information as possible and not just one trait like morphological discrepancies. One of the most used tool in cyanobacterial classification is the exploration of their DNA, especially some conserved regions of their DNA, which are known to have changed only slightly during their evolution and are universally found in all species. With the use of some sophisticated algorithms which take into account complex evolutionary models, we are able to get an estimate of their evolutionary relationships. Usually we visualize these relationships in tree-like structures which are called phylogenetic trees. In these trees, lines connect the different species and evident clusters can be inferred to represent certain taxonomic classes like species, genera or families.

In Greece, which is located in the southeast part of Europe, many thermal springs can be found scattered all over the country. These thermal springs host many cyanobacterial conglomerates, which are called mats. In our study we sampled 9 thermal springs of Greece and isolated in the lab 17 different species. We were the first to implement a polyphasic approach to cyanobacteria of the Greek thermal-springs.



Phylogenetic tree of cyanboacteria.

Our results highlighted the abundant diversity of thermal spring environments with many new species and at least 6 new genera and provide new evidence in the taxonomy of Cyanobacteria. It pointed out the urgent need to continuously update the taxonomic relationships, instead of thinking of taxonomy as something stable and finalized.

The journey to better understand the complex evolutionary relations between cyanobacteria has a big and harsh way ahead of it, but it is an interesting one that can question our current understanding of how these great organisms have evolved over the billion years of their existence.

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Publication

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