

The global diversity of electricity-producing cable bacteria

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Around 10 years ago, it was discovered that electrical currents are naturally running through the seafloor. Soon thereafter, it was found that long, multicellular filamentous bacteria are generating these currents. These so-called “cable bacteria” belong to the family *Desulfobulbaceae* and consist of centimeter-long chains encompassing 1000's of cells. Cable bacteria display a unique “electrogenic” metabolism via which electrons are transported from one end of their filamentous body to the other, thus creating large currents that span centimeter distances. A better understanding of these enigmatic cable bacteria would benefit microbial ecology, but could also spur new applications in bio-electricity. One important question is whether the capability of long-distance electron transport has evolved only once, and is limited to a narrow group of bacteria, or whether it is present in multiple groups of bacteria. Cable bacteria can be found worldwide but the knowledge regarding their diversity and abundance is still fragmented. Thus far, two genera of cable bacteria have been described: *Candidatus* Electronema, which inhabits freshwater sediments, and *Candidatus* Electrothrix which lives in marine sediments. Recent observations show that different cable bacteria morphotypes exist (varying in diameter size) and co-occur within the same marine sediment. Likely, the diversity of cable bacteria is underestimated by the currently available data.

The objective of this study was to improve the understanding of the diversity of cable bacteria. To this end, we screened a variety of different marine sediment environments, and sequenced the 16S rRNA gene of resident cable bacteria. The existing phylogenetic tree was amended with these new sequences as well as with sequences acquired from 16S rRNA sequence archives.

Sediment sampling was conducted in the Belgian zone (St. 130, St. 700) aboard the RV Simon Stevin and at a brackish site in Sicily, Italy. In order to enrich the cable bacteria, sediment cores were incubated in the laboratory. As it is possible to extract single cable bacteria from the enrichment incubations, 16S rRNA gene sequences can be obtained for individual filaments. Additional sequences were obtained from multiple sites in The Netherlands, Australia and the USA. A multiple sequence alignment was conducted to compare the sequences and to enable subsequent phylogenetic analysis.

The new phylogenetic tree presents a substantially expanded diversity of cable bacteria and shows branches that link to several hitherto undescribed genera and species. In particular, Station 130 in front of the Belgian coast, emerged as a treasure chest for undiscovered cable bacteria diversity. Cable bacteria filaments extracted revealed several 16S rRNA gene sequences that cannot be assigned to the two previously described cable bacteria genera (94.5 % sequence identity cutoff).

In conclusion, our results show that the diversity of cable bacteria is still greatly underestimated. Even though cable bacteria are distributed worldwide, their local diversity seems to be higher than expected, with several different species and genera occurring at the same geographic sites. Future studies will show if and how cable bacteria genera can be distinguished from each other in terms of morphology and physiology.

Keywords: Cable bacteria; Microbial biodiversity; Electrical sediments; Phylogeny; Sequencing