

What drives the diversity of electricity-producing cable bacteria?

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Salinity gradients are a characteristic feature of coastal ecosystems and thus are considered one of the main drivers of microbial diversity. Indeed, the recently discovered electricity-producing cable bacteria are currently classified into two main genera: *Candidatus* Electronema for freshwater systems and *Candidatus* Electrothrix for marine systems. However, this classification is based on a relatively small number of 16S rRNA gene sequences and 5 fragmented genomes. Although efforts to complete the genomes are ongoing, the overall diversity of cable bacteria remains uncertain and is likely still underestimated.

Our objective was thus to expand and unify the current database of 16S rRNA gene sequences assigned to cable bacteria. Firstly, lab incubations of sediments from a broad range of salinities were set up. A total of 9 sites were studied, including low (salinity <3) and medium salinity (salinity 10-29) sediments from the Magazzolo river mouth in Sicily and the Ebro delta in Spain, and marine sediments (salinity ≥ 30) from the Rattekaai salt marsh in the Netherlands, two sites in the Belgian coastal zone and one in the Ebro delta.

Collected bulk sediment was incubated in cores in order to enrich for electrogenic cable bacteria. High-resolution microsensor profiling (O_2 , H_2S , pH and electric potential) of sediments was conducted to scan for the unique geochemical fingerprint of electrogenic sulfide oxidation by cable bacteria. Upon the development of this geochemical profile, single cable bacteria filaments were extracted from the enrichment incubations to sequence the full-length 16S rRNA gene. Secondly, public 16S rRNA gene databases were mined in search of additional cable bacteria sequences to include a wider variety of environments. In total, more than 130 sequences from around the globe were compiled and used to construct an updated phylogenetic tree of cable bacteria.

Our results indicate that the current diversity of cable bacteria is largely underestimated as 4 potential new genus-level and 32 new species-level clades were identified. 16S rRNA gene sequences from our brackish samples from Spain and Sicily alone could not be assigned to any of the described cable bacteria species and thus possibly represent new species.

While cable bacteria often inhabit sulfidic, organic-rich environments, the sediments from Sicily and the Belgian coastal zone are low in free sulfide. Therefore we hypothesize that, next to salinity, the availability of reduced sulfur species may play an important role as a driver of cable bacteria diversity. In addition, our data challenges the previous classification into a strictly marine and a strictly freshwater genus as several phylogenetic clades appear to tolerate large salinity ranges. With the expanded diversity, future studies will reveal if there is a link between the morphology and the phylogeny of cable bacteria.

Keywords

Electrogenic Cable Bacteria; Microbial Diversity; Coastal Sediments; 16S Rrna Gene Sequencing; Salinity Gradients