

A novel genus of bacteria associated with *Sphagnum*

Kulichevskaya, I.S., Suzina, N.E., Liesack, W. & Dedysh, S.N. (2010). *Bryobacter aggregatus* gen. nov., sp. nov., a peat-inhabiting, aerobic chemo-organotroph from subdivision 3 of the *Acidobacteria*. *International Journal of Systematic and Evolutionary Microbiology* **60**, 301–306.

Most readers will be familiar with the bryological interest to be found in a peat bog, ranging from the obvious collection of *Sphagnum* species to the more hidden assemblage of delicate hepatics. Many will also be familiar, or at least aware, of the associated invertebrate life that is often observed down the microscope. However, there is one group of organisms that will rarely if ever be encountered by the average bryologist, but which are of fundamental importance to the ecology of not only peat bogs, but all habitats – bacteria.

A group of microbiologists from the Russian Academy of Sciences, Moscow, have studied the microbial communities of *Sphagnum*-dominated acidic wetlands in Siberia for a number of years, and have found that a characteristic component of such communities are members of a group of acid-loving bacteria called the *Acidobacteria*. Although members of this group are globally distributed, they are difficult to grow in culture and are consequently poorly understood. Taxonomists have divided the *Acidobacteria* into eight subdivisions, but only two of these include fully characterized representatives.

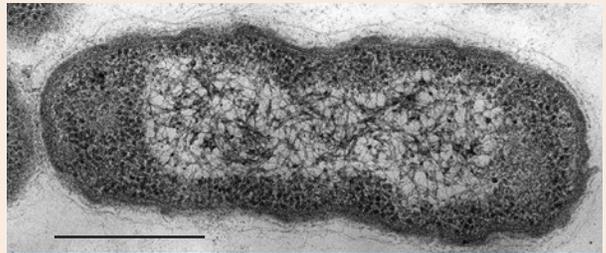
However, using specially developed low-nutrient growth media in conjunction with enrichment techniques, the team has successfully isolated and identified several peat-inhabiting members of the *Acidobacteria*.

Bacterial species are generally identified by using a series of biochemical, physiological and genetic tests, in addition to morphological characteristics. After performing the various tests on a number of cultures of bacteria extracted from peat soil samples taken from various *Sphagnum*-dominated bogs, such as Bakchar (west Siberia) and Obukhovskoe (European west Russia), the researchers realized

that three of the isolates were very similar to each other, and might even represent members of one of the subdivisions of *Acidobacteria* for which no described species are known.

The determination of novel isolates of bacteria to genus and species level is based on DNA sequence similarity of the 16S rRNA gene. This gene has been chosen as a 'standard' by which all bacterial species are measured as it is known to have a constant and slow rate of mutation so that relationships between species can be reasonably accurately measured by the level of DNA sequence similarity in that gene – the more similar the DNA sequence, the closer the relationship.

The three strains possessed nearly identical 16S rRNA gene sequences, and based on the results of a phylogenetic tree derived from the 16S rRNA gene sequences of other known members of the *Acidobacteria*, it was clear that



△ Electron micrograph of an ultrathin section of a cell of *B. aggregatus*. Bar, 0.5 µm.

the three strains did indeed belong to a subdivision of the *Acidobacteria* from which no isolates had been previously fully described. In addition, their molecular similarity to other fully characterized members of the *Acidobacteria* was low enough to warrant their placement in a completely new genus.

The new genus name was derived from the Greek word for moss (*bryon*) and the Latin word for a short rod (*bacter*), thus *Bryobacter*, a rod-shaped, moss-associated bacterium. The specific epithet refers to the isolates' propensity to form cell aggregates.

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