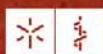


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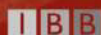


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Sphingomonadaceae* diversity and antibiotic resistance in water samples*Ivone Vaz-Moreira^{1,2}, Cátia Faria^{1,2}, Olga C. Nunes², Célia M. Manaia¹**¹CBQF/Escola Superior de Biotecnologia, Universidade Católica Portuguesa, Porto, Portugal;²LEPAE - Departamento de Engenharia Química, Faculdade de Engenharia, Universidade do Porto, Porto, Portugal

Sphingomonadaceae are ubiquitous bacteria in environment, including aquatic habitats. Nevertheless, their contribution for the acquisition and spread of antibiotic resistance in nature is poorly understood. We studied the diversity and the antibiotic resistance phenotypes of members of this family in isolates recovered from a drinking water treatment plant (n=6), tap water (n=55), cup filler of dental chairs (n=21) and a water demineralization filter (n=4). Bacterial isolates were identified based on the analysis of the 16S rRNA gene sequence and intra-species variation was assessed on basis of the *atpD* gene sequence analysis. Antibiotic resistance profiles were determined using the ATB PSE 5 strips (Biomérieux). The isolates were identified as members of the genera *Sphingomonas* (n=27), *Sphingobium* (n=28), *Novosphingobium* (n=12), *Sphingopyxis* (n=7) and *Blastomonas* (n=12). Susceptibility patterns were analysed and compared to the different sites of isolation and taxonomic groups. Colistin resistance was observed to be intrinsic (92%). The highest antibiotic resistance percentages were observed for the members of the genera *Sphingomonas* and *Sphingobium*, to the beta-lactams, ciprofloxacin and cotrimoxazol. Comparing the sites of isolation, the highest percentages of resistance were observed for tap and cup filler samples, where isolates of the genera *Sphingomonas* and *Sphingobium* predominated. These two genera presented different patterns of association of antibiotic resistance suggesting different paths of resistance acquisition. Antibiotic resistance patterns were often species- rather than site- or strain-related. This is the first study demonstrating that members of the *Sphingomonadaceae* family may play a role as potential reservoirs of antibiotic resistance in aquatic environments, namely in drinking water.