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Diversity and antibiotic resistance of Acinetobacter spp. in water from the source to the tap

C.A. Narciso Da Rocha[1], I. Vaz-Moreira[1], L. Svensson-Stadler[2], E.R.B. Moore[2], C.M. Manaia[1]
[1]Escola Superior de Biotecnologia - Universidade Católica Portuguesa, Porto, Portugal
[2]Culture Collection University of Gothenburg and Department of Infectious Disease, Gothenburg, Sweden

Acinetobacter spp. are ubiquitous bacteria in the environment and hypothetic reservoirs of antibiotic resistance in drinking water. *Acinetobacter* spp. isolated from a drinking water treatment plant and from tap water, served by that plant, were identified and typed based on the analysis of the *rpo*B, *gyr*B and *rec*A partial gene sequences. Antibiotic resistance was characterized, using the disc diffusion method, and each isolate was classified as wild or non-wild type, according to the observed phenotype.

The strains of *Acinetobacter* spp. could be affiliated to 11 different species, four of which represent presumably new species. Most of the isolates were related to the species *A. johnsonii* and *A. lwoffii*. These two groups, as well as others related to the species *A. parvus* and *A. tjernbergiae*, were detected both in the water treatment plant and the tap water. Other strains, related to the species *A. pittii* and *A. beijerinckii*, were isolated only from tap water. Most of the isolates (80 %) were susceptible to all of the 12 antibiotics tested. In contrast, non-wild phenotypes for tetracycline, meropenem, ceftazidime, streptomycin, among others, were observed in water-treatment plant samples and/or in the tap water samples. Although, in general, this study reports a low antibiotic resistance risk of the Acinetobacter spp. in water, the potential of these bacteria to acquire and disseminate resistance via drinking water is demonstrated.