Genetic characterization of *Klebsiella spp.* from surface waters in the North of Portugal

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The increase in *Klebsiella spp.* multidrug-resistant strains represent a serious threat to public health. Currently, growing resistance to antibiotics, particularly present in opportunistic enterobacteria, such as *Klebsiella spp.*, has been threatening human and animal health. However, comprehensive, and comparable data on its occurrence in surface waters are scarce, as well as phenotypic and genotypic data for several countries, including Portugal. Therefore, we aimed to investigate the prevalence of Klebsiella spp. in surface waters, as well as phenotypically and genotypically characterize the isolates. Sixty-five samples were collected from different surface waters in the North of Portugal, of which 31 (47,7%) were positive for *Klebsiella spp.* The antimicrobial susceptibility was performed by the Kirby-Bauer disc diffusion method against 11 antibiotics. High rates of antibiotic resistance were observed among these isolates for cefotaxime (41,9%), on the other hand, low rates of antibiotic resistance were observed among these isolates for meropenem (3,2%). The presence of different carbapenem genes (blaOXA, blaIMP, and blaKPC) was analyzed by PCR/sequencing in *Klebsiella spp.* isolates, as well as the presence of other resistance genes (e.g. blaCTX). The one with the highest prevalence was blaCTX (22,6%). However, in the carbapenem genes, amplification was not verified. This study provides relevant information about the prevalence of *Klebsiella spp.* in surface waters in Portugal. Therefore, there is a possibility of its spread into the environment, as well a potential risk of infection of humans and animals that are exposed to contaminated water sources.

Keywords: *Klebsiella spp.*; surface waters; antimicrobial resistance; resistance genes

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