

GENETIC CHARACTERIZATION OF *KLEBSIELLA SPP.* FROM SURFACE WATERS IN THE NORTH OF PORTUGAL

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Introduction

The increase in *Klebsiella spp.* multidrug-resistant strains represent a serious threat to public health. Thus, currently human, and veterinary medicine is threatened worldwide by a growing resistance to antibiotics, particularly present in opportunistic Enterobacterial pathogens (e.g., *Klebsiella spp.*). The focus of the One Health perspective is the role of interconnected ecosystems in the emergence and spread of antimicrobial resistance.

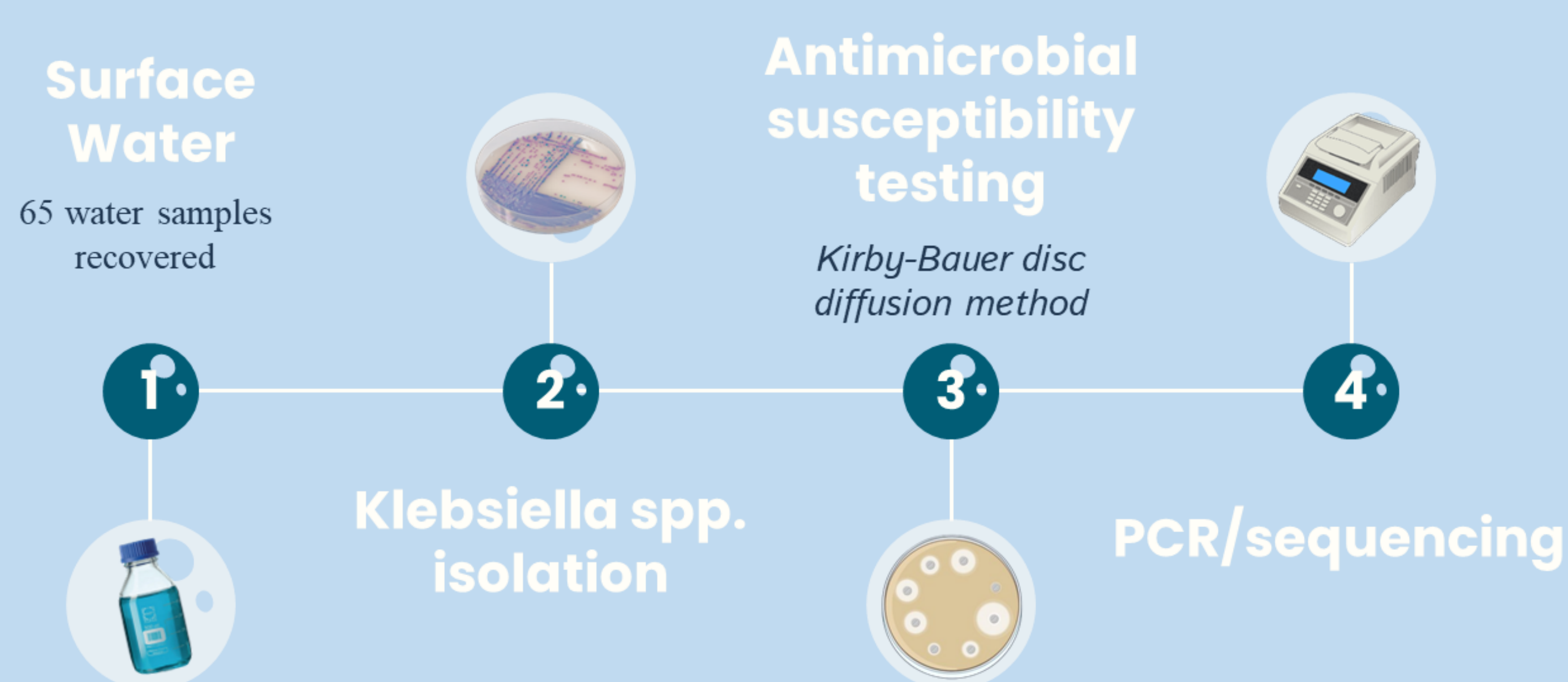
The approach mobilizes multiple sectors, disciplines and communities at varying levels of society to work together. This way, new and better ideas are developed that address root causes and create long-term, sustainable solutions.

Objective

The aim of this work was investigating the prevalence of *Klebsiella spp.* in surface waters, as well as characterize the isolates phenotypically and genotypically.

Methodology

Surface water samples were collected weekly over a period of 6 months in the northern of Portugal.



Conclusion

Our study provides information on the prevalence of *Klebsiella spp.*, which is of clinical importance in surface water in Portugal. These findings indicate their possible dissemination in the environment and the potential risk of colonization and/or infection of humans and livestock associated with exposure to contaminated water sources.

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Results

From the 65 samples, 31 *Klebsiella spp.* were isolated. Furthermore, 12 (38,7%) of the 31 *Klebsiella spp.* isolated were categorized as MDR (multidrug resistant), since they showed resistance to 3 or more classes of antibiotics. High rates of antibiotic resistance were observed among these isolates for cefotaxime (n=13; 41,9%). As a result, was obtained a high prevalence of gene amplification for blaCTX (n=8; 25,8%).

