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## BOOK OF ABSTRACTS

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Sociedade Portuguesa de Microbiologia

  
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### P57. Do *Klebsiella pneumoniae* environmental strains maintain clinically relevant genomic and phenotypic traits?

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Extended-spectrum  $\beta$ -lactamase (ESBL)-producing *Klebsiella pneumoniae* are well-known pathogens, increasingly reported in the environment. This fact represents a human health concern since third-generation cephalosporins are frontline antibiotics used to treat infections caused by this species. A major question is whether environmental ESBL-producing *K. pneumoniae* can infect humans. To address this question, this study compared clinical and environmental *K. pneumoniae* strains regarding genetic and phenotypic traits and assessed their potential infectious capacity. Therefore, 59 isolates (25 environmental and 34 clinical) of cefotaxime-resistant *K. pneumoniae* were characterized based on antibiotic resistance phenotype, plasmids content, and horizontal gene transfer capacity. A subset of these isolates was tested for infection capacity in *Galleria mellonella* (23 environmental and 24 clinical) and for whole genome sequencing (7 environmental and 11 clinical). Most environmental (80%, 20/25) and clinical isolates (94%, 32/34) were multidrug resistant. Environmental isolates presented mostly 2 plasmids (48%, 12/25) while clinical isolates presented 1 or 2 plasmids (41%, 14/34 each), however bacterial conjugation was more frequent among clinical (76%, 26/34) than environmental isolates (40%, 10/25). *G. mellonella* health index was lower after infection with clinical (most of the infected isolates scored 1) than with environmental isolates (most of the infected isolates scored 6). A screening of the whole genome sequences, made in parallel with data available in public databases (in total 73 environmental and 78 clinical), targeting 6 groups of genes related to antibiotic and metal resistance, virulence, efflux systems, oxidative stress and quorum sensing, evidenced the existence of 1383 gene variants. A total of 438 genes out of the 1383 were common to all isolates, while 460 and 485 genes were found exclusively in environmental and in clinical isolates, respectively. A screening of the whole genome-deduced amino acid sequences demonstrated a common putative proteome, related with all functional categories, in environmental and clinical isolates (n=2715), although the number of exclusive amino acid sequences was higher for clinical isolates (n=577 in clinical vs. n=205 in environmental). These results suggest the adaptation of *K. pneumoniae* to environmental or clinical niches, although highlight that putative clinically relevant traits may persist in bacteria thriving in the environment.