Isolation of lytic phages for clinical antibiotic resistant *Pseudomonas aeruginosa*

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ABSTRACT

Pseudomonas aeruginosa as a relevant opportunist pathogen involved in nosocomial infections. *P. aeruginosa* uses an arsenal of virulence factors to cause serious infections and one of the most worrying characteristics of this bacterium is its low antibiotic susceptibility. The low susceptibility to antibiotics can be attributed to a concerted action of multidrug efflux pumps with chromosomally-encoded antibiotic resistance genes and the low permeability of the bacterial cellular envelopes. Furthermore, *P. aeruginosa* can develop acquired resistance either by mutation in chromosomally-encoded genes or by the horizontal gene transfer of antibiotic resistance determinants. Today, prevention and control of bacterial resistance requires new antimicrobial agents, the prudent use of existing ones, new vaccines and enhanced public health efforts to reduce transmission of bacterial resistance. Bacteriophages and their lytic enzymes can be an alternative to antibiotherapy towards the reduction of *P. aeruginosa*, without causing elimination of beneficial microorganisms.
In this work, 4 *P. aeruginosa* strains, namely ATCC, CECT 111, PAO1 were used to screen for phages present in hospital effluents. Overall, 17 different bacteriophages were isolated. These newly isolated phages were tested against 35 antibiotic multi-resistant clinical strains provided by the São Marcos hospital (Braga) and their lytic spectra studied. Most phages were well capable of infecting different isolates, however some phages had quite a narrow spectrum of activity. The best four phages were selected and characterized according to their structural proteins and one-step growth.