

COMPARATIVE PROTEOMIC ANALYSIS OF COLLECTION AND CLINICAL-ISOLATE STRAINS OF PSEUDOMONAS AERUGINOSA

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Pseudomonas aeruginosa is an opportunistic pathogen that is a major cause of infection-related mortality among individuals with immuno-compromised systems. Fatality rates among patients infected with *P. aeruginosa* are higher than among those infected with any other opportunistic gram-negative bacterium, partly due to the incidence of multiresistant strains. Because of its relevance in hospital environments, there is a continuous effort to extend the knowledge on the biology of this human pathogen.

It is well known that *in vitro* serial passage of microorganisms causes changes in physiology and virulence-factor production. Thus, the collection strain PAO1 of *P. aeruginosa* is expected to display important differences at the proteome level with respect to new clinical isolates.

Here, we present a comparative proteome analysis of a new clinical multiresistant isolate present in several hospitals in the area of Barcelona and the collection strain PAO1. In order to perform this comparative analysis we have used the DIGE technology coupled with protein identification by mass spectrometry. The identification of differentially expressed proteins in these strains shall provide a basis for the interpretation of their phenotypic differences at a biomolecular level, with a special focus on infection and resistance mechanisms.

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