

**Effect of high salinity and rhamnolipid production on biofilm-related gene expression  
by *Pseudomonas aeruginosa***

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*Pseudomonas aeruginosa* is an ubiquitous bacterium, commonly isolated from oil industry settings. Biofilms are complex structures, directly related to microbial-induced corrosion. In *P. aeruginosa*, biofilm formation involves many factors, such as the exopolysaccharides (EPS) Psl and Pel which are important matrix components. *P. aeruginosa* also produces rhamnolipids and type IV pili which play multiple roles in biofilm development. The present report focuses the impact of salinity on *P. aeruginosa* biofilm formation and the expression of some key target genes. The salt concentrations were 5 g/L, as standard, and 35 g/L, that mimics the *in situ* conditions of marine salinity. Two strains of *P. aeruginosa* were used: PAO1, the model strain, and its rhlA-minus derivative which does not produce rhamnolipids, and PA1, isolated from an oil industry field. Results obtained from both strains demonstrated a highly increased biofilm formation at high-salt concentration (35 g/L). Interestingly, the PA1 strain has shown a significantly higher biofilm formation when compared to strain PAO1. Results obtained for biofilm-related genes by qRT-PCR suggested that *P. aeruginosa* PAO1 adherent cells showed increased expression of the target genes (3 times) when grown in high salt concentration (35 g/L). PA1 strain adherent cells showed even higher increase in expression of those genes (4.5 times) when grown in high salt concentration. In the case of rhlA-minus *P. aeruginosa*, gene expression levels were lower (3 times) when compared to the wild-type strain, under lower salinity (5 g/L NaCl). However, in higher salinity no difference was observed, since the levels of biofilm formation and gene expression were similar in both wild-type and rhlA-minus strains. The results reported herein demonstrate the remarkable influence of higher salinity on biofilm formation and reveals some key genes involved in this phenotype variation.