

Comparative genomic analysis of gene clusters of *Pseudomonas aeruginosa* that define specific biofilm formation in deciphering target regions for novel treatment options.

Abstract

Pseudomonas aeruginosa is an opportunistic pathogen associated with numerous nosocomial infections that are difficult to treat as a result of natural resistance to various antibiotics, particularly because of biofilm formation. The purpose of this study was to determine the evolutionary relationship of *P. aeruginosa* biofilm formation genes and their distribution within different strains. In total, 13 genes responsible for biofilm formation by *P. aeruginosa* were identified and used in the study. The BLAST Ring Image Generator (BRIG) analysis was used to visualize the distribution of biofilm formation genes between different strains of *P. aeruginosa*. Phylogenetic analyses of the biofilm formation genes indicated a strong co-evolution of a majority of these genes, n=10. Exceptions were the genes *fliC*, *algD*, and *algU* which may have been exchanged by horizontal gene transfer or evolved faster than the other genes of this functional group as they are more important in terms of a proper response of the biofilm formation to specific environmental stimuli in different habitats. The BRIG analysis revealed that the *pslE*, *pslG* and *pslJ* genes were all located around the same locus (2450kbps) in a variable region of the genome of strains of *P. aeruginosa* giving credence to the coevolution between these set of genes. Findings of this study could inform identification of potential target genes for therapeutic agents.