ABSTRACT TEXT (2500 characters max.)

Comparative genomics of two *Pseudomonas aeruginosa* clinical isolates to elucidate the composition of their mobilomes

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Recently, we have set a collaboration with Hospital de Braga, located in the North of Portugal, that handles over 600 *P. aeruginosa* isolates per year, aiming to rouse a holistic research approach to provide relevant information and tools to the clinicians to circumvent the multi-resistance phenomena in *P. aeruginosa*. Since then, we have set procedures aiming a systematic phenotypic characterization of the clinical isolates and developed strategies for the identification of pathogenicity islands and SNPs among the clinical isolates via comparative genomics. In this context, we have determined the full genome sequence of two clinical isolates using the high-throughput system Illumina Genome Analyzer IIx. These two clinical isolates, named 138244 and 152504, are representatives of allelic sequence types ST175 (widely disseminated and associated with multidrug-resistance) and ST560 (rare allele), respectively. Importantly, under standardized experimental procedures, isolate 138244 did not produce pigments and evidenced an antibiotic pan-resistant phenotype whereas 152504 produced a high amount of pyocyanin pigment and was susceptible to all antibiotics tested. A comparative genomic analysis using the genome sequences of both isolates and of all *P. aeruginosa* strains deposited in Genbank so far, allowed the identification of the accessory genome content of both isolates. Apparently, isolate 152504 harbors in its genome 243 unique genes, often clustered together in the same locus. Based on the genome annotation information, the pool of unique genes mainly encode several virulence factors, chemical stress resistance systems as well as 106 hypothetical proteins, some of which predicted members of the secretome of *P. aeruginosa* 152504. The accessory genome of 138244 mainly includes genes associated with mobile elements (phages, transposases, integrons) and genes encoding for 190 hypothetical proteins. Currently, research approaches are focused on the functional elucidation of sets of genes encoding hypothetical proteins of both isolates and in the description and characterization of their secretomes.

This work was supported by the project PTDC/EBB-BIO/104980/2008 from the Foundation for Science and Technology (Portugal)