Exploring the genome catalogs of *Pseudomonas* using next generation sequencing technologies

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Bacteria belonging to the *Pseudomonas* genus possess an intricate ability to tolerate and thrive in very challenging environments such as the Human lungs, the deep sea or highly polluted soils. Such competence resides in their wide nutritional and metabolic versatility and in a intricate network of adaptation mechanisms. In other words, the necessary code to efficiently cope with a wide variety of different substrates, biotic and/or abiotic stress conditions is included in their genomic catalog. Therefore, they hold great potential, as a source of novel biomolecules and cell factories, for different biotechnological applications, namely in the fields of biocatalysis, biosensors, bioremediation, and biomedicine. The main goal of our group is to develop the necessary knowledge base and analytical resources to establish selected *Pseudomonas* spp. and/or their biomolecules as biotechnological tools, using an integrative biology approach by the application of high-throughput technologies.

In this context, we have used Next Generation Sequencing technologies to decode the genome catalog of three selected *Pseudomonas* isolates. The environmental *Pseudomonas sp*. M1 strain was selected due to its remarkable ability to metabolize a wide variety of xenobiotics/recalcitrants [1-3] whereas two *Pseudomonas aeruginosa* clinical isolates were used to shed some light into the *P. aeruginosa* accessory genome (mobilome) and how genomic diversity translates into phenotypic diversity [4].

Details on the strategies used to reconstruct and decipher the genome of the selected *Pseudomonas* isolates, and on the current status of each project will be presented. Future research approaches will also be addressed mainly focused on an extensive exploitation of the genomic potential of the three *Pseudomonas* strains, envisaging the understanding of the genomic complexity of these bacteria and its full biotechnological/biomedical potential.

[1] **Santos P.M., Sá-Correia I.** (2007) J. Biotechnol **131:**371-378.
[2] **Santos P.M., et al** (2007) OMICS **11:**233-251.
[3] **Santos P.M., Sá-Correia I.** (2009) Proteomics **9:**5101-11.
[4] **Soares-Castro et al** (2011) J. Bacteriol. **19:**5573

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