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BOOK OF ABSTRACTS

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P-146 - WHOLE-GENOME SEQUENCING OF LABRYS PORTUCALENSIS F11 AND RHODOCOCCUS SP. FP1 PROVIDES GENETIC INSIGHTS INTO THEIR XENOBIOTIC METABOLIC FEATURES

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Background

Bacteria with diverse xenobiotic-degrading capacities, harboring multiple catabolic pathways, are extremely promising for degradation of environmental pollutants. *Labrys portucalensis* F11 and *Rhodococcus* sp. FP1 were isolated from sediments collected at the industrial chemical complex of Estarreja, northern Portugal. Both strains have demonstrated ability to degrade several aromatic compounds under aerobic conditions, including pharmaceuticals (fluoroquinolones[1], fluoxetine[2], diclofenac and estradiols) and industrial and agro-chemicals (fluorobenzene[3], fluorophenol[4], fluoroanilines[5] and bisphenols). Understanding the metabolic potential of *Labrys portucalensis* F11 *and Rhodoccus* sp. FP1 could provide the basis for their application in bioremediation processes.

Method

Genomes were sequenced using Illumina HiSeq 2500 platform and FASTQ reads assembled using an algorithm based on de Bruijn graphs. Gene prediction and genome annotation was performed using Rapid Annotation Subsystems Technology (RAST) v2.0.

Results & Conclusions

The genome of *Labrys portucalensis* F11 comprises 7,952,755 bp with a GC content of 63.5% whilst the genome of *Rhodococcus* sp FP1 is composed of 9,630,728 bp with 67.2% of GC content. For F11, a total of 7406 coding DNA sequences (CDS) were predicted, of which 3224 (44% of CDS) were assigned to subsystems. For FP1, out of the total 9094 CDS, only 3258 (ca. 36% of the total CDS) were allocated in subsystems. On both cases, the most abundant subsystems were those involved in the metabolism of amino acid derivatives and carbohydrates. In addition, both genomes harbor genes involved in the catabolism of aromatic compounds, representing about 3.2 and 4.5% of the total protein-encoding genes of F11 and FP1, respectively. Metabolism of aromatics begins with ring hydroxylation and genes encoding enzymes for this step such as dioxygenases and monooxygenases were present on both genomes. In addition, genes predicted to encode different ring-cleaving dioxygenases that catalyze the dearomatization steps, namely, gentisate 1,2-dioxygenase, catechol 2,3-dioxygenase, protocatechuate 3,4-dioxygenase and catechol 1,2-dioxygenase were also present on both genomes. This work provides new insights into the genetic determinants that may help devising strategies for bioremediation of environments polluted with xenobiotics.

References & Acknowledgments

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