



“Gheorghe Asachi” Technical University of Iasi, Romania



---

P8

## AN EXTENSIVE ANALYSIS OF THE HYDROCARBON DEGRADING ABILITIES OF BACTERIA BELONGING TO THE SPECIES

### *Acinetobacter venetianus*

R. Fani<sup>1</sup>, M. Fondi<sup>1</sup>, I. Maida<sup>1</sup>, E. Perrin<sup>1</sup>, M.C. Papaleo<sup>1</sup>, G. Emiliani<sup>2</sup>, M. Galardini<sup>1</sup>, K. Mara<sup>1</sup>, F. Decorosi<sup>3</sup>, C. Viti<sup>3</sup>, L. Giovannetti<sup>3</sup>, F. Baldi<sup>4</sup>, A. Mengoni<sup>1</sup>, V. Orlandini<sup>1</sup>

<sup>1</sup>Department of Evolutionary Biology, University of Florence, Florence, Italy; <sup>2</sup>Tree and Timber Institute, National Research Council, Florence, Italy; <sup>3</sup>Department of Agricultural Biotechnology, University of Florence, Florence, Italy; <sup>4</sup>Department of Environmental Sciences, Cà Foscari University, Venezia, Italy

---

#### Abstract

In recent decades, accidental oil spills are one of the major sources of environmental pollution. Biodegradation is an efficient, economic and versatile method to detoxify a polluted environment. Indeed, the efforts of researchers are focused on oil bioremediation and, in particular, on the characterization of those microbial consortia able to grow in oil-contaminated soil and on their possible utilization in the treatment of such polluted environments. The aim of the present study was to characterize six *Acinetobacter venetianus* strains able to use diesel fuel oil as sole carbon source by integrating data coming from physiological experiments and whole genome sequencing. Data obtained showed that all the strains are hydrophobic both in LB and in MMV exception for the *A. venetianus* VE-C3 strain that resulted hydrophilic only in LB, suggesting the use of different strategies to adhere to pollutants by the representatives of this species. The production of emulsifying molecules was also tested, revealing that the two strains, out of the six strains tested in this work display an emulsifying activity. To gain deeper insights in the phenotypic traits of these strains, their utilization of different carbon and nitrogen sources was checked by phenotype microarray analysis, revealing (in some cases) deep differences and suggesting an unexpected metabolic heterogeneity. These physiological properties led us to choose these strains as candidates for the determination of their genome sequences in order to gain more insights into those genetic traits involved in the degradation of *n*-alkanes and the generic features representative for the species *A. venetianus*. Genome sequencing was performed with both Illumina and Roche 454 technologies and preliminary analysis of genome assemblies allowed us to identify important differences among all *A. venetianus* strains thus revealing the possible genetic basis of observed different phenotypic traits. Furthermore, the analysis of the emulsan gene cluster (embedding the genes responsible of the bioemulsifying activity) it was shown that the two strains RAG-1<sup>T</sup> and LUH7437 share a similar array of genes, thus explaining their similar emulsifying activity.

The whole body of data obtained showed that these strains afford an opportunity for analysis and manipulation of genes and gene products related to bioremediation, opening new possibilities for their large scale industrial application.

---