Degradation of cholesterol by *Rhodococcus* sp. strain CECT 3014

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The ability to bioconvert steroid compounds is well documented and has been utilized by the pharmaceutical industry to synthesize novel steroid products. In order to find new and potent aerobic steroid degraders or transformers, we carried out screening experiments with cholesterol, testosterone, or other steroid compounds as the only carbon and energy source for bacterial growth.

Among Gram-positive bacteria, several *Rhodococcus* species are able to degrade different steroid compounds. We focused our study on *Rhodococcus* sp. CECT 3014, a Gram-positive bacterium that is able to grow using either cholesterol or testosterone as carbon and energy source. These features make this strain a good candidate system to study the enzymatic pathways that concern the steroid catabolism. In this work, we present new results about the physiology of this bacterium. We also describe the isolation and characterization of several *Rhodococcus* sp. CECT 3014 genes involved in the catabolism of cholesterol and/or testosterone.

**Keywords:** Cholesterol, steroid compounds, bioconversion, biotransformation, *Rhodococcus*

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**Desulfovibrio vulgaris Hildenborough transcriptomic analysis by Restriction fragment functional display (RFFD)**

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Sulphate-reducing bacteria reduce sulphate with electrons from carbon substrate thereby producing hydrogen sulphide. This reduction is anaerobic, however the metabolic activity of SRB in anaerobic zones is frequently higher than in neighbour aerobic zones. The large tolerance to oxygen of SRB is surprising, some are able to respire oxygen in a process coupled to chemoheterotrophic conservation of energy and ATP production. In the case of *Desulfovibrio vulgaris* Hildenborough, sequencing of its genome has confirmed the presence of oxidative sulphate-degrading genes. In order to understand why aerobic respiration occurs in *D. vulgaris*, we propose a comparative study of gene expression under aerobic and anaerobic conditions, in wild-type and oxygen-respiration deficient mutants, focusing on the identification of genes related to the aerobic metabolism. Genes encoding regulators of oxygen response are of special interest. RFFD technique, here described, constitutes a powerful tool to do such study.

**Keywords:** *Desulfovibrio vulgaris*, gene expression, RFD, oxygen response