2.5.32

Are plants a solution for textile wastewater treatment?

L.C. Davies* , **R. Ferreira**, **G. Cabrita**, **J. Novais**, **S. Martins-Dias**

IBB-Institute for Biotechnology and Bioengineering, Centre for Biological and Chemical Engineering, Instituto Superior Técnico, Lisboa, Portugal

Azo dyes are extensively used in the textile industries for dyeing fabrics, therefore they are expected to be adherent, long lasting, resistant to sunshine, not fading through oxidation during the washing process; however these characteristics constitute a major problem while treating dye-wastewaters. Most of the synthetic dyes are xenobiotic compounds that are poorly removed by the use of conventional biological wastewater treatments and even when the azo dyes are degraded colorless aromatic amines known to be mutagenic and carcinogenic are released. This situation poses an environmental disposal problem to industry and concomitantly a health problem to society by the contamination of drinking water and soils, especially in developing countries such as India and China.

In the Environmental Biotechnology area, constructed wetlands (CWs) have been successful in the treatment of a model molecule such as an azo dye, Acid Orange 7 at pilot scale. The role of plants, so-called phytoremediation, while integrated in the dye-wastewater treatment system have been addressed in our group, highlighting the fact that the plants most used in CWs (*Phragmites*) have an enzymatic array that is activated in the presence of this azo dye, which has been confirmed by *in vitro* trials. We have observed, for instances that peroxidases from *Phragmites* were able to breakdown the azo bond of AO7 and degraded the aromatic amines by-products. Nevertheless the role of *Phragmites* in industrial wastewater treatment systems related with the molecular biochemical processes of the detoxification pathways are still to be clarified. We are currently trying to identify genes and enzymes involved within this process by measuring mRNA accumulation for target enzymes before and after *Phragmites* are exposed to pollutants. Up to now, gene sequences of enzymes such as catalase, glutathione peroxidase and superoxide dismutase were gathered. At the same time we aim to analyze *Phragmites* proteome with and without oxidative stress conditions. So far, the methodologies that lead to plant proteome extraction are being established enabling differential display analysis. The information gathered from genomics and proteomics may contribute to the understanding of the phytoremediation process and how it can be enhanced. This will be in the future a step forward on wastewater treatment and soils decontamination.

doi:10.1016/j.nbt.2009.06.734

2.5.33

Recovery of γ-decalactone produced by *Rhodotorula aurantiaca* from the culture broth using Macronet resins

M. Alchihab* , **J.M. Aldric**, **M. Aguedo**, **J. Destain**, **J.P. Wathelet**, **P. Thonart**

Gembloux Agricultural University, Gembloux, Belgium

During the biotransformation of castor oil into γ-decalactone, *R. aurantiaca* produced both the lactone form and its precursor (4-hydroxy-decanoic acid). After six days of culture, a maximum yield of γ-decalactone of 6.5 g/L was obtained after acidification at pH 2.0 and heating at 95°C for 30 min. The parameters of γ-decalactone adsorption on three Macronet resins (MN-202, MN-102 and MN-100) were investigated in water. Adsorption isotherms of γ-decalactone for the three Macronet resins were linear. Then, the trapping of γ-decalactone produced by *R. aurantiaca* on these resins was carried out. γ-Decalactone was effectively retained by all the studied Macronet resins. The resin MN-202 trapped γ-decalactone more efficiently than MN-102 and MN-100. The percentage of adsorbed γ-decalactone on the resins MN-202, MN-102 and MN-100 were respectively 85, 75 and 81% whereas around 50% of γ-decalactone was then desorbed. We propose an industrial process using Macronet resins to extract γ-decalactone from culture broth of *R. aurantiaca*.

doi:10.1016/j.nbt.2009.06.735

2.5.34

Hydrophobic tags for protein purification by HIC: quantitative criteria for selection

O. Salazar* , **M. Robinson**, **C. Quilodran**, **C. Montecinos**, **M.E. Lienqueo**

University of Chile, Santiago, Chile

At large scale, protein purification is mainly carried out through chromatographic techniques, amongst which are affinity chromatography, ion exchange chromatography, hydrophobic interaction chromatography and gel filtration chromatography. Each of these techniques exploits a specific feature of the target protein relative to the rest of the contaminant proteins. Unfortunately, in some cases there is no specific characteristic that facilitates such purification. For this reason, in some cases genetic engineering has been used to modify the target protein by fusing polypeptide tags that give particular features to target proteins. The most widely used polypeptide tags are histidine tags, which allow fused proteins to be purified by ion metal affinity chromatography (IMAC). Unfortunately, this chromatographic technique is, in some cases, very expensive and incompatible to be used at large scale procedures. For this reason, the use of polypeptide tags exploiting other properties such as hydrophobicity has been considered. Although adding hydrophobic tags has advantages, they also show disadvantages such as loss of protein stability, a decrease in protein expression levels and protein aggregation, resulting in loss of recovery levels of the fusion protein. Although data exist