OC6

A single transcription factor behind all bacterial dNTP synthesis revealed as a novel antimicrobial target

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Nowadays, the fear of infectious diseases is again increasing. Antibiotic-resistant bacterial strains are appearing worldwide, and so there is an urgent need to develop new antimicrobial drugs.

Ribonucleotide Reductases (RNRs) are essential enzymes that catalyse the reduction of ribonucleotides (NTPs) to their corresponding deoxyribonucleotides (dNTPs), thereby forming the building blocks for DNA synthesis and repair. A drug able to inhibit bacterial Ribonucleotide Reductase activity would completely inhibit bacterial growth.

Behind bacterial Ribonucleotide Reductase activity there is a complex regulon; although eukaryotic cells codify only for one RNR enzyme, bacteria can use three different RNR classes, granting them a huge adaptability. *Pseudomonas aeruginosa* is a major human opportunistic pathogen, causing severe lung chronic infections in cystic fibrosis and COPD patients. It codifies for all three RNR classes, in a complex regulon necessary for its adaptability and virulence.

The main focus of this work is a transcription factor, called NrdR, which is present in almost all bacterial species, and completely absent in eukaryotic organisms. This factor acts as a central regulator of all RNR enzymes in bacteria, hence being behind all dNTP synthesis. We have studied how NrdR regulates RNR activity in *P. aeruginosa*, being able to this point to propose a first model of the NrdR regulon, and being a step closer to new antimicrobial therapies.

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OC7

Improving enzyme cocktails for lignocellulose hydrolysis in biorefineries by rational protein design

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Plant biomass provides an abundant source of sustainable energy and chemical building blocks, mainly in the form of carbohydrates, which can be used in the newly established biorefineries through the release of fermentable sugars. Fermentation of these sugars can produce valuable commercial end products such as biofuels (i.e. bioethanol) and biochemicals. The improvement of enzymatic reactions to hydrolyze biomass to fermentable sugars is essential to improve the profitability of the process. An area of research directed at reducing costs and improving the yield of biofuel production processes is focused on improving the technical efficiency of the individual enzymes, or of the whole enzyme cocktails used to generate fermentable sugars from biomass. Using protein-engineering techniques, we have designed structural and functional mutants of different cellulolytic enzymes. Rational mutants have been designed through evolutionary trace studies, based on similar functions and relevant characteristics to acquire enhanced stability in specific culture conditions. This process is becoming a powerful tool for the rational design of engineered enzymes.

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OC8

Screening for bacterial laccases with potential bioremediation application

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Synthetic dyes are widely used in industrial processes such as textile dyeing or paper printing. However, these coloring agents present a hazard to the environmental because their toxicity [1]. Outstandingly, laccases are a promising biocatalyst able to detoxify these xenobiotic compounds. Eukaryotic laccases has been extensively studied [2]. Nevertheless, prokaryotic laccases still remain on explore [3]. Here, we report the production of bacterial laccases by *Streptomyces*, and *Bacillus* strains isolated from *Lasius niger*. Bacterial strains were grown in nutrient broth and enzymes were extracted by sonication. Laccases enzymatic assay was carried out [4] to investigate the potential of both genera in decolorizing chemical dyes. Congo red (azo dye) was used as substrate for the bacterial laccases and a commercial laccase was applied as positive control. Our results showed that strains belonging to both genera are able to decolorize azo dyes. Therefore, this is the first report of endozoic bacteria isolated from black ants (*L. niger* (L.)) as a novel source of microbial laccases with a potential biotechnological use.

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