

Editorial

Mining GOLD and new model organisms in biotechnology

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Are you aware that 41% of completely sequenced microbial genomes remain unpublished? Where can scientists find this information? The answer is provided by Siezen and Wilson's (2008) genomic update section article on unpublished, yet publicly available microbial genomes. The authors highlight that the GOLD (Genome OnLine Database, <http://www.genomesonline.org>) provides a complete and updated status of genome sequencing projects, and shows the dominance of the Joint Genome Institute and the J. Craig Venter Institute in the USA as the leading laboratories in the world in quantitative terms. Siezen and Wilson (2008) dig into GOLD and extract useful information on genome sequencing projects of relevance to the biotechnology field, such as the production of biofuels. Here they refer to the exciting world of cellulose and the potential of some *Clostridium* species for the synthesis of ethanol. They also show that the area of fine chemical production can benefit from sequencing projects such as that of *Actinobacillus succinogenes* that is the best known natural source for succinate, or the interest of a number of *Shewanella* strains to remove heavy metals. In all, Siezen and Wilson come to the conclusion that GOLD is one of the sources scientists need to consider to predict new pathways and products for biotechnology.

This new issue of *Microbial Biotechnology* presents an important research article on *Pseudomonas putida* KT2440 as a model system for white biotechnology. This strain was described about 25 years ago to be a plasmid-free derivative of the mt-2 strain (Nakazawa, 2002), and was soon shown to be a safe host for the cloning of soil bacterial genes (Timmis, 2002). Ever since, this microbe has been the subject of research on different many matters and scenarios and has been particularly used as a model for the development of the transcriptional loops in

the TOL pWW0 plasmid (Ramos *et al.*, 1997). The XylR protein, which is the ultimate regulator of the system, is the source of *in vitro* evolution that alters the effector specificity of this protein. XylR has turned out to be able to recognize 2,4-dinitro- and 2,4,6-trinitrotoluene through the accumulation of a number of point mutations. This has been elegantly developed and discussed by Garmendia and colleagues (2008) who further develop the use of modified regulators coupled to signal-emitting reporters, an area revised by Elad and colleagues (2008) in the previous issue of *Microbial Biotechnology*. In their study Garmendia and colleagues (2008) coupled XylR variants to a reporter system constituted by its natural Pu promoter. This original article reveals the potential of combining genetic engineering and signal output systems, and how it all works perfectly well in the model KT2440 host.

The heart of DNA biology and function is linked to the seminal observation by Avery and colleagues (1944) that DNA transformation of *Streptococcus pneumoniae* is the determinant that encodes the information of cell wall characteristics of these microorganisms. Ever since then, natural transformation has been described in a number of microbes including *Acinetobacter*, *Campylobacter*, *Chlamydia*, *Bacillus*, etc. Transformation is a key player in horizontal evolution, in which exogenous DNA is uptaken and incorporated into the host genetic background from which it replicates and is propagated. While there are no doubts on the role of transformations in DNA acquisition, the phenomenon has been constricted to a limited number of microbes. In this issue, Mirończuk and colleagues (2008) deal with the transformability of *Bacillus cereus*, a ubiquitous food-borne pathogen. Digging into the genome sequences these authors found that this microbe has an arsenal of genes necessary for DNA uptake and the authors hypothesize the lack of natural transformation could be linked to either the lack or low expression of *comR*, the gene encoding a key regulator. Mirończuk *et al.* proceeded to the cloning and expression of *comR* and show unequivocally that *cereus* can be subsequently transformed. This article brings the reader to a point in which the transformation of microbes in their niches needs to be explored in detail. The uptake of genes

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and the incorporation of heterologous DNA have been and are still the driving forces of microbial evolution.

The original article signed by Kim and colleagues (2008) shows the renewed interest of the scientific community on bacteriophages as potential antimicrobial therapeutic agents. After decades of oblivion in Western countries, the emergence of antibiotic-resistant strains and the lack of new antibiotics have witnessed the revival of research on the clinical use bacteriophages. In this field one of the key problems is the host's immune response that allows the virus to remain in the bloodstream for a very short time. The authors demonstrate in this study that conjugation of monomethoxy/polyethylene glycol (mPEG) molecules to structural proteins of purified bacteriophage particles, i.e. *Salmonella's* phage Felix-01 and *Listeria's* phage A511, in a process known as PEGylation, relieves the situation. PEGylated bacteriophages provoke a weaker immune response in both native and immune mice and their circulation time in the blood system increases in control mice.

Laccaria bicolor is a mycorrhizal fungus whose genome has been sequenced. The fungus establishes mutualistic symbiosis with a number of plants, which is relevant from a trophic point of view in forest ecosystems for mineral nutrition. Full exploitation of the genome will require assignment of functions, particularly to orphan genes, and mutagenesis is one of the ways to assign gene functions. In this issue, Kempainen and colleagues (2008) deal with the use of *Agrobacterium*-mediated gene transfer (AMT) to open new research avenues in fungal research. The authors describe a transformation vector that allows to generate random T-DNA tagged strains and to rescue DNA junctions. This molecular tool will be of great importance in ectomycorrhizal fungal genomics.

Microbial Biotechnology is getting us used to short and long reviews in areas of utmost interest for microbial biotechnology. Following the growing social interest on energy matters, Dr Larry Wackett offers an overview of the field of biofuels for motors, an issue of both economical and social concern due to the rising prices of petrol, and the chemical processes of petrol itself and petrol-derived products without forgetting the transition to renewable energies that society is increasingly demanding as petroleum-based technology will not be sustainable for much longer (Wackett 2008a). Wackett's review is a compendium of all the current possibilities involving biofuel microbial synthesis. Biofuels may not only constitute a means to partly overcome energy demands; as Rojo (2008) points out in his article highlighting Wackett's excellent review, biofuel research may also lead to new concepts in the development of new green biocatalytic

processes and products. Biofuels is a topic of great interest for society because of the expected economical outcome, an outburst of research is envisaged in this field.

The section on Web alerts by Wackett (2008b) deals on this occasion with a selection of web sites that focus on issues relating to systems biology of relevance to microbial metabolism and microbial biotechnology, areas in which relevant articles are expected to be published in *Microbial Biotechnology*.

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