

EDITO

The BaSysBio project aims at understanding the dynamic transcriptional regulation at a global scale in bacteria. A systems biology approach based on repeated cycles of mathematical model prediction and experimental validation is being developed to drive a quantitative understanding of the operation of complex living systems. In the past year, a large part of the BaSysBio efforts was focused on developing: 1) high throughput technologies enabling the quantitative measurement of cellular components; 2) mathematical models for large-scale transcriptional and metabolic control; 3) an information system to store, analyse and visualize the results; and 4) rigorous standardisation of experimental protocols.

In this first issue of the BaSysBio Newsletter, six of the project's major milestones are briefly introduced. More detailed and illustrated descriptions are also available on the BaSysBio web site.

Future issues of the BaSysBio Newsletter will report other scientific and technological achievements, and provide news about the various aspects of the project's life.

Philippe NOIROT, Project Coordinator – INRA, France

The glucose to malate shift: Intracellular metabolite concentrations

Uwe Sauer – ETH, Switzerland

A major problem in interdisciplinary collaborations between experimental biologists and computa-

tional groups are the different time-lines of the work flows. In our particular case, first data were necessary for model construction and for preliminary parameter estimations that provide guidance on the required measurement accuracy and resolution. Within the consortium it became quickly clear that metabolite concentration data would be required at a much earlier phase than anticipated...

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Bacillus subtilis Tiling arrays

Hanne Jarmer – DTU, Denmark

We have designed and used DNA tiling microarrays manufactured by NimbleGen, which cover the entire genome of *Bacillus subtilis*. The first set of data reveals the global transcription profile at the whole genome scale...

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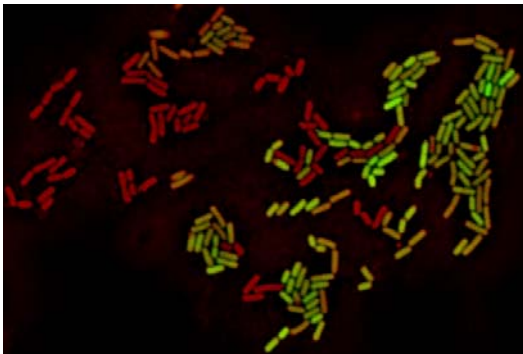
A cell array reporting on gene expression in living *Bacillus subtilis*

Anthony J Wilkinson – UOY, United Kingdom

The functions of living cells are determined by the repertoire of genes that are expressed. The chromosome of *B. subtilis* contains more than 4000 genes. Some of these genes have 'house-keeping' roles, which require that they are continuously expressed. Other genes have functions in the adaptation of the bacteria to changing environmental conditions such as an



alternative source of nutrients or a specific challenge such as oxidative stress. These genes are expressed only in response to specific signals or cues. Establishing the repertoire of genes being expressed under a given set of circumstances has traditionally involved laborious study of expression gene-by-gene or alternatively involved cell killing. In Workpackage 1.1 of BaSysBio, we are generating an array that can report simultaneously on the expression levels of several hundred genes in living cells...



Fluorescence microscopy image of *B. subtilis*

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A pressing need for standardisation in systems-level studies on living cells

Jan Maarten van Dijl – AZG, The Netherlands

All biological systems are extremely sensitive to their environment. As a consequence, small changes in the growth conditions of living cells – be it human or bacterial cells - may cause large variations in their quantitative cellular responses. Standardisation of procedures for cell handling and cultivation is therefore of the utmost importance

for any project addressing cellular functions and responses at systems level...

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Development of databases for large-scale experiments

Hans Peter Fischer – Genedata, Switzerland

Genedata has developed a central database to support the storage of experimental data produced within the BaSysBio consortium, as well as tools for analyzing the biological context of the data derived from molecular profiling studies...

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An essential signal transduction pathway controlling cell wall metabolism, virulence and biofilm formation in *Staphylococcus aureus*

Tarek Msadek – IP, France

In order to survive, bacteria have developed a variety of highly sophisticated and sensitive signal transduction pathways with which they adapt their genetic expression to meet the challenges of their ever-changing surroundings. These mechanisms enable bacterial cells to communicate with their environment, their hosts and each other, allowing them to adopt specific responses, or develop specialized structures such as biofilms or spores to ensure survival, colonization of their ecological niches and dissemination...

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