



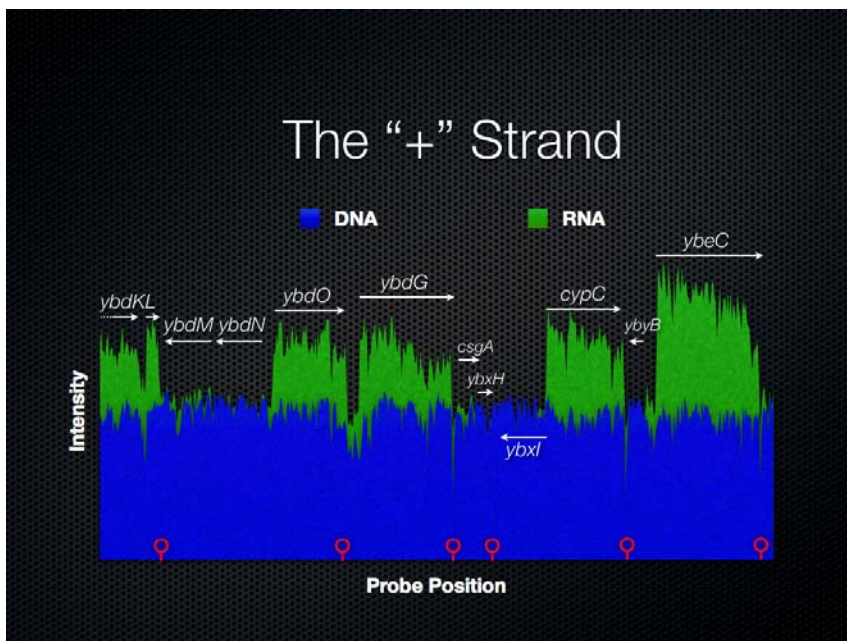
BaSysBio is a collaborative research programme (Integrated Project) funded by the European Commission under the 6th Framework Programme in the Life Sciences, Genomics and Biotechnology for Health

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.

DNA tiling microarrays are composed of ~385,000 oligonucleotide probes “tiling” the genome of *Bacillus subtilis* on both strands, with a distance of 22 nucleotides (nt) between the beginnings of each probe. The probes are allowed to vary in length in order to minimize the difference in the melting temperature (isothermal). The DNA tiling array will allow the global mapping of transcribed regions under various environmental conditions, and will considerably enrich the current knowledge about transcriptional units. The quality of the microarrays (or chips) was tested to validate their use by the whole BaSysBio consortium. Genomic DNA and total RNA were extracted from *B. subtilis* cells growing exponentially in rich medium (Luria Broth). Four biological replicates were prepared, and for each, total RNA, its corresponding cDNA, and genomic DNA were labeled and hybridized to NimbleGen tiling chips. The hybridization signals measured from RNA samples were stronger than those originating from cDNA, facilitating the monitoring of transcripts on each DNA strand. Also, we found that the genomic DNA did not hybridize uniformly, indicating that parts of the sequence used for the design contain either mismatches or regions affecting the hybridization. Using the Circular Binary Segmentation (CBS) method originally developed by Olshen, et al. (2004), both strands of the chromosome were divided into segments (>2,000 segments/strand) based on both the signal intensity level and consistency. Each of the resulting segments was hereafter assigned as either “transcribed” or “not transcribed” depending on the signal intensity. The results from this study are very promising as 50% to 75 % of all known transcripts, depending on the cut-off setting, have been identified. Altogether, they validate the DNA tiling microarrays for use by the BaSysBio consortium, which represents an important milestone for the project.



The signal intensity on the forward strand is represented as a function of the position on the genome (from 222 kb to 223 kb). The signals arise from the hybridization of genomic DNA (blue) and total RNA (green). The positions of rho-independent terminators are shown in red, and the genes located in this region are shown as white arrows.

From Work-Package 1.2 – DNA tiling arrays

Contributors: S. Rasmussen & H. Jarmer (DTU)

January 2008

contact: hanne@cbs.dtu.dk and simon@cbs.dtu.dk

