P015 Transcriptome changes and cAMP oscillation in an archaeal cell cycle

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The cell cycle of all organisms includes mass increase, replication of the genetic material, segregation of the genome, and cell division. It is tightly regulated and typically includes cell cycle-specific oscillation of the levels of transcripts, proteins, signalling molecules and posttranslational protein modifications.
For the analysis of the cell cycle of *Halobacterium salinarum* a synchronization procedure was optimized, so that nearly 100% of all cells divide in a time interval that is 1/4th of the generation time. Cell cycle-dependent transcription changes were analysed using a genome-wide DNA microarray. The transcript levels of 87 genes were found to be cell cycle-regulated (3% of all genes). They could be clustered into seven groups with different transcription level profiles. Cluster specific sequence motifs were detected around the translational start side. Notably, many genes that have oscillating transcripts levels in eukaryotes are not regulated on the transcriptional level in *Halobacterium salinarum*. Analysis of cell cycle-specific proteome changes is currently under way.
Synchronized cultures were also used to identify putative small signalling molecules. It was found that *Halobacterium salinarum* contains a basal cAMP concentration of 200µM, considerably higher than that of yeast. cAMP oscillation could be observed in synchronized cell cultures. The cAMP concentration is shortly induced directly prior to and after cell division, indicating that cAMP might be an important signal for cell cycle progression.