Conservation of regulation systems in firmicutes

Investigation of their promoter regions is an important step towards the understanding of global cell regulation networks. By coupling the current knowledge about experimentally proven transcriptional regulation with the currently available raw genetic data, a better understanding of the similarities and differences between various species could be obtained. Most of the bacterial transcriptional regulation data have however been obtained in two specific organisms, *Escherichia coli* and *Bacillus subtilis*, and comparative genomics is therefore necessary to evaluate to which extent the acquired knowledge is applicable to other bacterial species. Therefore, the annotated proteins of 66 complete firmicutes genomes, including that of *B. subtilis*, were compared to each other in order to build clusters of homologous proteins and their upstream intergenic regions. Potential binding sites for known *B. subtilis* transcription factors were then predicted in all the upstream intergenic regions using position specific weight matrices provided by DBTBS and the resulting binding site patterns were analyzed.

In order to provide a comprehensive representation of the known motif conservation pattern that remains easy to understand and interpret, new tools were developed that can generate a graphic for each cluster indicating on one side in which strains homologous proteins are found, and on the other side whether or not these proteins possess a certain transcription factor binding site in their upstream intergenic region. With this method, the existence of different regulation systems for the CtsR and HrcA heat shock response regulons within the firmicutes could for instance be shown. Our data suggest for example that the *Mycoplasma* stains, which are characterised by a very small genome size and lack CtsR, have placed the regulation of genes typically regulated by CtsR under the control of HrcA, or that in the *Staphylococcus* strains the HrcA regulons is not only regulated by HrcA itself, but also by CtsR.

By carrying out comparative analysis of a large number of related genomes, concentrating particularly on the conservation of the promoter regions of homologous genes, significant differences in the regulatory networks of not only a single strain, but of whole genus could be highlighted. This approach can therefore not only allow a refinement of the current understanding of bacterial regulation networks, but also provide new input for experimental research.