

CoryneRegNet – a Data Warehouse Containing Comprehensive Information on the Transcriptional Regulation of the Amino Acid Producer *Corynebacterium glutamicum*

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The industrially well-known amino acid producer *C. glutamicum* represents an excellent example for a “Genome-based Systems Biology” approach. The annotated *C. glutamicum* genome containing 3002 genes was successfully employed for metabolic reconstruction and production of oligo-based whole-genome microarrays. The presentation will concentrate on the analysis of complex regulatory networks of *C. glutamicum*. As an example, the transcriptional regulation of genes involved in sulfur metabolism of *C. glutamicum* will be presented. The regulatory network comprises one master regulator (the repressor McbR) and two activators (SsuR and CysR). For these three regulators, the target genes, the binding sites and the effector substances could be determined. In the meantime, there are further examples of master regulators known, namely SigH, LexA, RamA, DtxR, AmtR and the central regulatory hub GlxR. All transcriptional regulators analysed up to now were incorporated into a data warehouse designated CoryneRegNet (www.corynereenet.de), which discloses detailed information on the regulators, their target genes, operator sequences and regulatory interactions. It is a special feature of CoryneRegNet to enable the reconstruction and visualization of transcriptional regulatory networks at different level of regulatory hierarchy. At the moment, CoryneRegNet includes 72 of altogether 159 transcription factors of *C. glutamicum* exerting 806 regulatory interactions on 544 genes. About 92 % of these interactions are linked by regulatory motifs to build a single supercluster of the transcriptional regulatory network.