

## **Abstract**

An important feature of bacteria is an ability to adapt to changing environment by regulating gene expression. Level of gene expression and its right timing depends mainly on activation or repression of the gene by transcriptional regulators and recognition of the respective promoter by the sigma factor which is a subunit of RNA polymerase. Transcription regulators with sigma factors and other control elements, form a complex regulatory network.

The regulatory network in *Corynebacterium glutamicum* is one of the best studied networks among gram-positive bacteria owing to genome sequencing and application of a number of techniques at the genome level. There has been a lot of success in understanding the roles of individual regulators and interactions between regulators in response to changes in environment.

This work summarizes currently known knowledge of mutual relationships between sigma factors, the influence of sigma factors on transcriptional regulators and their cooperative effect on the initiation of transcription. In the thesis, a regulatory network of sigma factors in *C. glutamicum* and a regulatory cascade in response to the stress situation is schematically created.

**Key words:** sigma factor (FS), *Corynebacterium glutamicum*, transcription regulator (TR), transcription, regulation