

Abstract

The aim of this thesis was to characterize the function of sigma factors of the bacterium *Corynebacterium glutamicum* and to analyze the promoter sequences which are recognized by individual sigma factors. Sigma (σ) factors are the subunits of RNA polymerase, which allow recognizing the sequences of specific promoter regions of the gene and initiating its transcription. The *C. glutamicum* genome carries genes encoding the primary sigma factor σ^A and six alternative sigma factors, σ^B , σ^C , σ^D , σ^E , σ^H and σ^M , whose expression is changed depending on the growth conditions and in response to the stimuli from the surrounding environment. Regulation of gene expression at the level of transcription is one of the mechanisms of the adaptation of cells to changes of living conditions. At the conclusion of this work, a model of the regulatory network of sigma factors, which is a core of the complex regulatory network controlling all processes in the cell, is proposed.

Key words: sigma factor (SF), RNA polymerase, *Corynebacterium glutamicum*, transcription, promoter