

# Abstract

*Corynebacterium glutamicum* is a Gram-positive non-sporulating soil bacterium which is used in biotechnology as a producer of amino acids, nucleotides, biofuels and alcohols. The aim of this thesis was to create a hybrid  $\sigma$  factor of RNA polymerase which would be able to recognize a matching hybrid promoter without effect on expression of the host genes. Based on the  $\sigma^D$  and  $\sigma^H$  amino acid sequence, two types of hybrid factors,  $\sigma^{DH}$  and  $\sigma^{HD}$ , were designed by the sequence combination of *sigD* and *sigH*. As an alternative approach, based on the *in silico* homology modeling, mutations of wild-type  $\sigma^H$  in the region recognizing the -35 promoter element of the  $\sigma^H$ -dependent promoter were introduced. Hybrid promoters were constructed by combining the -35 and -10 promoter regions that were derived from the  $\sigma^D$ - and  $\sigma^H$ -dependent promoters. Promoter activity was determined by using *gfpuv* reporter gene under the control of hybrid promoter. The expression of *gfpuv* in strains with hybrid sigma factors  $\sigma^{DH}$ / $\sigma^{HD}$  and hybrid promoters was rather low compared to strains that carried wild-type  $\sigma$  factor and the respective promoter. The aim of the thesis was achieved by using one of the mutant  $\sigma^H$  factor ( $\sigma^{\text{mutH}_{6A}}$ ) with alterations in the region recognizing the -35 element of the  $\sigma^H$ -dependent promoter. This mutant  $\sigma$  factor selectively drove transcription of the reporter gene from the hybrid *PsigDH* promoter.

**Keywords:** *Corynebacterium glutamicum*, sigma factor, promoter