

**Abstract:**

*Streptomyces* are medically important soil-living bacteria that undergo morphological changes from spores to aerial hyphae and are important producers of bioactive compounds including antibiotics. Their gene expression is tightly regulated at the early level of transcription and translation. In the transcriptional control, sigma factors play a central role; the model organism *Streptomyces coelicolor* possesses astonishing 65 sigma factors. The expression of sigma factors themselves is controlled on the post-transcriptional level through the action of sRNAs that modify their mRNA level. However, only several sigma factors in *Streptomyces* have known regulons and also their sRNAs-mediated regulation has not been studied so far.

According to previously measured gene expression data, we selected several highly expressed sigma factors. Using mutant strains with HA-tagged sigma factors, regulons of two important sigma factors, SigQ and HrdB, were analyzed by ChIP-seq procedure. Other sigma factors were further studied to see if they possess asRNAs, using 5' and 3' RACE method and northern blotting.

Our data confirm the essentiality of HrdB sigma factor during the vegetative phase of growth. The other sigma factor, SigQ, has been revealed to be an important regulator of nitrogen metabolism and osmotic stress response coinciding germination.

We also uncovered three novel *cis*-asRNAs corresponding to sigma factors SigR, SigB, and SigH; moreover, the last two are thought to mediate a complex formation with RNase III. Based on these data asRNA-sigma factor-regulon transcriptional control pathway can be suggested.

Key words: *Streptomyces*, sigma factor, *cis*-asRNAs, mRNA, RACE, northern blot, RNase III