Abstract:

The variety of bacteria and their genomes sometimes causes conservation of homologue molecules to be displayed not in sequence but in secondary and tertiary structures. In the case of the regulatory 6S RNA, sequence homologues have been found in over 100 bacterial species so far. However, none were found in the genus *Streptomyces*. The unique genome of these soil-dwelling bacteria, known for their capacity to produce antibiotics, has a high G/C content and diverges substantially from distantly related bacteria. Yet in the non-coding 6S RNA it is the secondary structure that is crucial for its function. The 6S RNAs trap sigma factors by mimicking target promoter sequences in order to help with switching sets of expressed genes during developmental transitions. 6S-like RNA genes in *Streptomyces coelicolor* have been computationally predicted by comparison of *in silico* modelled secondary structures of known 6S RNAs. The aim of this thesis was the verification of these 6S-like RNA predictions. The experimental approach was based on RNA co-immunoprecipitation (RNA CoIP), as well as RT-PCR from RNA samples. The outcomes of this project are the detection of six novel ncRNA transcripts with possible 6S-like RNA functions, which also served as the wet-lab verification of the *in silico* prediction technique used to identify bacterial ncRNAs on the basis of structure conservation. More research needs to be conducted to resolve the role of the putative 6S-like RNA genes.

Keywords: 6S RNA, sigma factor, *Streptomyces*, antibiotics, physiological differentiation, gene expression