G. Summary

To survive in the highly dynamic rhizosphere and successfully induce tumour formation, the phytopathogen *Agrobacterium tumefaciens* has to adapt its gene expression in response to constantly changing stimuli. Lately, it became more and more evident that sRNAs – often supported by the RNA binding protein Hfq – are strongly involved in the regulation of bacterial gene expression.

*In silico* predictions of sRNAs on the *A. tumefaciens* circular chromosome revealed several sRNA candidates, some of which were validated experimentally. One of these sRNAs represses expression of several ABC transporter proteins and was thus named AbcR1 (for ABC regulator). It is encoded in tandem with another, highly similar sRNA, AbcR2. Toeprint analysis and degradation experiments demonstrated that AbcR1 represses *atu2422* translation by binding to the ribosome binding site and induces its mRNA degradation. *atu2422* encodes a γ-amino butyric acid (GABA) binding protein. Uptake assays with wild-type cells and sRNA mutants showed that AbcR1 controls GABA import. Interestingly, GABA is part of the plant defence machinery and silences quorum sensing-related virulence functions in the bacterium.

High-throughput cDNA sequencing (RNA-seq) was used as a second strategy to discover sRNAs in *Agrobacterium* and to gain insight into the bacterial transcriptome. By this means, 388 transcriptional start sites upstream of annotated genes were mapped and 228 new sRNA candidates were identified on all four *A. tumefaciens* replicons. Differential expression of several sRNAs under diverse stress conditions was demonstrated. One putative sRNA transcript was drastically induced under virulence conditions. Some other sRNAs were found to be encoded in antisense orientation to virulence-related genes, suggesting involvement of these sRNAs in the infection process of *A. tumefaciens*.

A third project focused on the RNA chaperone Hfq. Interaction between the recombinantly produced protein and both AbcR sRNAs was demonstrated by gel retardation experiments. Several newly identified sRNAs were shown to be stabilized by Hfq *in vivo*. An *A. tumefaciens hfq* deletion mutant revealed increased abundance of several ABC transporter proteins and significant defects in growth, cell morphology, motility and tumour formation, reflecting its high physiological relevance.

In conclusion, this study provides valuable information about sRNA-mediated gene regulation and its impact on *A. tumefaciens* physiology.