

## Summary

Since many millennia, mycobacteria cause infectious diseases in humans. The most life-threatening of these diseases is tuberculosis (TB), which is caused by *Mycobacterium tuberculosis*. As the current BCG vaccine does not fully protect against TB and antibiotic resistant strains appear due to the inappropriate use of medicines, it is essential to study the virulence mechanisms of *M. tuberculosis* in order to prevent TB from becoming an untreatable disease. These mechanisms were studied in this thesis, by using the genetically closely to *M. tuberculosis* related species *Mycobacterium marinum* as a model for pathogenic mycobacteria. The specialized protein transport system ESX-5, which is unique for pathogenic species, was studied in detail and found to play an important role in the infection process and the uptake of fatty acids, which is linked to the initiation of latency. For the homologous and highly important ESX-1 protein transport system, a new substrate and regulator protein could be identified. Finally, a genome-wide DNA sequencing study has led to the identification of mycobacterial factors that are required for a successful infection of phagocytes derived from several types of hosts. Together, these studies can contribute to the development of new vaccines, for example by targeting candidate virulence factors found in the sequencing study, or aid in the development of new therapeutic strategies aimed to increase effectiveness of TB treatment.