PROJECT Stress in Mycobacteria – a bioinformatic approach

Bacteria of the genus *Mycobacterium* are acid fast, show a great hardiness and inhabit various environmental reservoirs, *e.g*. ground and tap water, soil, animals and humans. Mmycobacteria can form aggregates and biofilms, they can form spores and they are invasive, *i.e*. are invasive slow growing bacteria thatthey can grow and multiply within cells such as macrophages. They The genus *Mycobacterium* include non-pathogenic environmental bacteria, opportunistic pathogens and highly successful pathogens, *e.g*. *Mycobacterium tuberculosis* that cause tuberculosis (tbcTB; 10 million new cases per year).**Pathogenic**

We have initiated a systematic investigation of the response to stress in different mycobacterial strains with a focus on *Mycobacterium marinum*, a model system for *M. tuberculosis*, for a better understanding of the genetics and physiology of the pathogens' life cycle in molecular terms. Within this project we have completed the sequencing of the genomes of several *M. marinum* isolates that show phenotypic differences in reponse to stress. The master project will encompass a bioinformatic analysis of the available genomes with focus on the idenfication of genes that have a role in the stress reponse in mycobacteria.

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