Genome Mining, Prioritization and Expression of Biosynthetic Gene Clusters in the Actinomycete genus *Amycolatopsis*

Simone Edenhart[1], Martina Adamek[1], Mohammad Alanjary[1], and Nadine Ziemert[1]*

[1]University of Tuebingen, Interfaculty Institute of Microbiology and Infection Medicine, German Centre for Infection Research (DZIF), Tuebingen, Germany
*nadine.ziemert@uni-tuebingen.de

In the last years, next generation sequencing has become cheaper and faster than ever. Usage of genome mining tool, enable us to search the genomes of Actinomycetes for biosynthetic gene clusters (BGCs) of secondary metabolites in this massive, constantly growing amount of sequencing data. These tools revealed many so far unknown BBCs in bacteria and thus a great potential for new, interesting natural products. Therefore, the challenge is now to triage the most promising pathways to guide laborious wet-lab experiments, assist with the dereplication of already known compounds and predict interesting bioactivities based on genomic data. For this, the Antibiotic Resistant Target Seeker (ARTS) was developled. ARTS is a user-friendly web tool that automizes “target directed genome mining efforts” and screens actinobacterial genomes for putative antibiotic housekeeping genes. ARTS thus allows the user a fast and efficient genome-based prioritization of bacterial strains with the potential to produce antibiotics with interesting and potentially novel modes of action.

We applied ARTS on the Actinomycete-genus *Amycolatopsis,* which is known for the production of glycopeptide antibiotics like rifamycin, balhimycin and ristomycin. Additionally, we combined it with genetic and molecular networking algorithms to detect unique BGCs with potentially new targets. After identification the most promising BGCs for drug discovery, we now aim to express them heterologously by TAR-cloning.