MS03-P111 - LATE | DNA RELAXASE TRAA OF THE G+ PLASMID PIP501 AS KEY PLAYER IN BACTERIAL CONJUGATION

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The accelerated emergence of antibiotic resistant bacteria is one of the biggest threats to human health in the world. Dissemination of antibiotic resistance and virulence determinants in clinical settings is caused by horizontal gene transfer even among only distantly related bacteria, and is mediated by a multi-protein complex termed type IV secretion system (T4SS), encoded by conjugative plasmids. The T4SS of the broad host-range, self-transmissible plasmid pIP501 consists of 15 proteins, which assemble into the Gram-positive cell wall-spanning mating core complex, the cytosolic relaxosome and the coupling factor connecting the components.

This project aims to bring about a crystal structure of the relaxase TraA, the central element of the relaxosome, and further elucidate function and intermolecular interactions thereof within its T4SS. With the pipeline for new antibiotics to treat drug-resistant infections running dry, there is an immediate need for novel therapeutics, and in the light of the DNA-mobilizing enzyme TraA acting as initiator, regulator and terminator of bacterial conjugation, we view comprehending its structure and detailed function as potential key to impede the rapid dissemination of antibiotic resistance genes.