MS09-1-3 TraM – a DNA binding protein of pIP501 – a broad-host-range plasmid
#MS09-1-3

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Abstract
The spread of resistances to antibiotics in bacteria is a serious global health problem. Conjugative plasmid transfer mediated by Type IV Secretion Systems (T4SS) is the most important means to transfer antibiotic resistance genes among bacteria. It is present in Gram- positive (G+) and in Gram- negative (G-) bacteria as well as in archaea. Conjugative plasmids of incompatibility group Inc18, primarily found in enterococci and streptococci, have a remarkably broad host range of conjugative transfer and hence play an important role in the propagation of multi drug resistant germs [1]. Several human pathogens are among them. Their abundance in wild life and farm animals increases the potential of its circulation. To date there is no existing structure of a T4SS of G+ bacteria, but several of G- bacteria [2]. pIP501 is one of the best studied Inc18 plasmids. Its transfer region is organized in a single operon encoding 15 putative transfer proteins.One of them is the DNA binding transmembrane protein TraM. TraM has three domains, an extracellular and an intracellular domain connected by a transmembrane domain. The investigation of TraM includes biophysical, biochemical and structural characterization. We are on the way to determine the residues of TraM, which are involved in DNA binding. We designed two different N-terminal constructs varying in length, TraM94 and TraM167. The structure of TraM94 was recently solved in our group. In contrast to the monomeric TraM94 TraM167 is a trimer in solution like the C-terminal domain of TraM, whose structure was solved in our group already some years ago [3].

References
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