Poster Presentation

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Insights on small-molecules inhibitors and protein-protein interactions of the T4SS

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ABSTRACT: Bacterial T4SS are complexes, constituted of 8 to 12 conserved proteins, used by many gram-negative bacteria for the translocation of proteins and DNA-protein complexes as well as for the transportation of DNA-protein complexes across their cell envelope. T4SS are excellent model targets for the development of antivirulence drugs as it is an essential virulence factor for many bacterial pathogens, such as Brucella. Antivirulence drugs that deprive the pathogen of its essential virulence factor, the T4SS, would constitute alternatives to or enhancements of current antibiotic treatment. VirB8, a conserved assembly factor in T4SS forms dimers that are very important for T4SS function in these pathogens. Due to its multiple interactions, VirB8 is an excellent model for the analysis of assembly factors but also a possible target for drugs that could target its protein–protein interactions, which would disarm bacteria by depriving them of their essential virulence functions.

[1] *Smith, M. A., Coincon, M., Paschos, A., et al. (2012). Identification of the binding site of Brucella VirB8 interaction inhibitors.,* ***[2]*** *Paschos, A., den Hartigh, A., Smith, M. A., et al. (2011). An in vivo high-throughput screening approach targeting the type IV secretion system component VirB8 identified inhibitors of Brucella abortus 2308 proliferation.*

Keywords: Type IV secretion system, Bacterial virulence, small-molecule inhibitor