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Poster

IDENTIFICATION PIPELINE OF *ANAPLASMATACEAE* TYPE IV EFFECTOMES.

Silou S.,[1,2,3]* and Meyer D. F.[1,2]

1 CIRAD, UMR ASTRE, F-97170 Petit-Bourg, Guadeloupe, France
2 ASTRE, Univ Montpellier, CIRAD, INRA, Montpellier, France
3 Université des Antilles, 97159 Pointe-à-Pitre, Guadeloupe, France
* To whom correspondence should be addressed. Email: stephanie.silou@cirad.fr

Abstract: *Anaplasmataceae* family includes obligate intracellular pathogenic *Ehrlichia* and endosymbiotic *Wolbachia* bacteria. A key factor of bacterial pathogenesis and symbiosis with eukaryotic cells is the ability to evade the innate immune system and hijack the host cellular pathways. A*naplasmataceae* use effector proteins (T4Es) to manipulate cellular processes in order to survive and proliferate.

It is still difficult to predict and study the repertoires of T4Es in *Anaplasmataceae.* Identifying such type IV effectomes is crucial to comprehend how the bacterium establishes symbiosis or pathogenesis. Deciphering bacterial interactions with mammalian or vector cells will foster development of alternative strategies to fight against the pathogen or prevent pathogen transmission by the vector. We propose a pipeline to identify T4 effectomes in *Anaplasmataceae*. We first use S4TE 2.0 software as a prediction tool for T4Es. The predicted effectors are confirmed using secretion assays in *Legionella pneumophila* and with cellular biology approaches. Then, we screen the effectome library for intracellular localization, for particular cellular phenotypes, and for protein partners or chromatin interactions. We then investigate for potential post-translational modifications of effectors after secretion (phosphorylation, truncation). Finally, we do phenotypic screening after ectopic expression in yeast. For each remarkable phenotype, the corresponding effector genes is silenced using PNA technology.

This computational based- medium-throughput screening of *Anaplasmataceae* type IV effectors will accelerate the dissection of bacteria-host mutualistic or pathogenic interactions and will highlight the evolutionary history shared by these bacteria. These results will promote the development of novel strategies to prevent vector-borne transmission of pathogens and alternative therapeutics