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► **To cite this version:**

Michael Koczerka, Olivier Grépinet, Isabelle Lantier, Marie Morillon, Justine Deperne, et al.. In vivo expression kinetics of the PagN Salmonella entry factor. EMBO | EMBL Symposium: New Approaches and Concepts in Microbiology, Jul 2021, Heidelberg, Germany. . hal-03444015

HAL Id: hal-03444015

<https://hal.inrae.fr/hal-03444015>

Submitted on 23 Nov 2021

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In vivo expression kinetics of the PagN Salmonella entry factor

Salmonella are among the top-ranked foodborne pathogens, inducing a wide variety of diseases ranging from gastroenteritis to typhoid fever, depending on the infecting serovar, the host and its genetic background. As a facultative intracellular pathogen, it can induce its own internalization in non-phagocytic cells through at least 3 different bacterial factors: the SPI-1-encoded T3SS-1, and two outer membrane proteins, Rck and PagN. The pagN gene is part of the PhoP-PhoQ regulon, and was identified, through the use of in vivo expression technology, as a gene required for Salmonella Typhimurium survival in BALB/c mice. It encodes for a widely conserved, 27 kDa protein displaying both structure and function homology with the proteins Hek and Tia of E. coli. This invasin allows Salmonella to invade cells through a Zipper-like mechanism, following interaction with heparan sulfate proteoglycans. However, its precise role in vivo remains to be determined including the cells targeted by this invasin. In this study, we aimed to precisely determine the kinetics of expression of this entry factor in mice. Bioluminescent S. Typhimurium reporter strains carrying transcriptional fusions were used to track the transcription of pagN in three murine models reproducing the different pathologies induced by Salmonella : typhoid fever, gastroenteritis and asymptomatic carriage. We observed a transcription of pagN in the intestine independently of the genetic background of the host and the inflammatory state of the animals. Moreover, pagN transcription was detected at later time points in lymphoid organs following the systemic spread of the pathogen in the typhoid fever reproducing model. Further analyses are in progress, focusing on the identification of the cells targeted by PagN.

Michael Koczerka is the recipient of an EMBO|EMBL Symposia fellowship, jointly funded by EMBO and the EMBL Advanced Training Centre Corporate Partnership Programme.

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