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Poster: Salmonella chromatin reorganization upon SPI-1 expression

Salmonella enterica serovar Typhimurium (*S.* Typhimurium) is a facultative intracellular bacterium that is a major cause of foodborne gastroenteritis in humans. It has the ability to infect numerous cell types, thanks to a broad arsenal of virulence genes. The majority of the genes encoding the most important virulence factors of *S.* Typhimurium are located within the highly conserved *Salmonella* pathogenicity islands (SPIs). There are 17 SPIs; among them SPI-1 encodes for a Type 3 Secretion System and several effector proteins needed to trigger the invasion of epithelial cells. SPIs expression is tightly regulated by a complex regulatory network in which nucleoid-associated proteins (NAPs) are among the key regulators. Besides acting as transcriptional regulators, NAPs also play an important role in bacterial chromosome architecture. Thus, we propose that the expression of SPIs in response to environmental stresses (e.g., infection) might promote changes in *S.* Typhimurium chromosome conformation that could be driven by the differential binding of NAPs. By using HiC, we studied for the first time the 3D organization of *S.* Typhimurium chromosome in conditions mimicking infection and promoting the bistable expression of SPI-1. Our results show that, irrespective of SPI-1 expression, the chromosome of *Salmonella* is partitioned into two structurally distinct entities: the *terminus* (*ter*) and the non-*ter* regions. In the non-*ter* region, long-range DNA contacts can extend up to ~1Mb and in the *ter* region, contacts are constrained up to ~600Kb by the MatP protein. Furthermore, expression of SPI-1 revealed a local reorganization of the chromatin at the SPI-1 locus. Remarkably, by applying HiC to sorted SPI-1 ON subpopulations, we unveiled transcriptionally induced virulence domains (VIDs) within SPI-1 locus. The contribution of NAPs to the chromatin remodeling observed is been currently investigated. Altogether, our results revealed for the first time the global 3D organization of the *Salmonella* genome in conditions mimicking epithelial cells invasion and the specific folding of SPI-1 chromatin upon virulence expression.

Auteurs principaux: Dr KORTEBI, Mounia (Institute for Integrative Biology of the Cell (I2BC), Genome Biology Department, Gif-sur-Yvette, France); Dr BOURGE, Mickaël (Imagerie-Gif CYTO, Department of Platform, I2BC); Dr DORMAN, Charles (Department of Microbiology, Moyne Institute of Preventive Medicine, Trinity College Dublin, Dublin, Ireland); Prof. BURY-MONÉ, Stéphanie (Institute for Integrative Biology of the Cell (I2BC), Genome Biology Department, Gif-sur-Yvette, France); Dr BOCCARD, Frédéric (Institute for Integrative Biology of the Cell (I2BC), Genome Biology Department, Gif-sur-Yvette, France); Dr LIOY, Virginia (Institute for Integrative Biology of the Cell (I2BC), Genome Biology Department, Gif-sur-Yvette, France)

Orateur: Dr KORTEBI, Mounia (Institute for Integrative Biology of the Cell (I2BC), Genome Biology Department, Gif-sur-Yvette, France)