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HU: A KEY PLAYER FOR NUCLEOID ORGANIZATION AND COMPACTION IN DEINOCOCCUS RADIODURANS

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In all organisms, genomic DNA is compacted several orders of magnitude and yet must remain accessible for essential DNA-related processes including DNA replication, repair and transcription. Most of our knowledge of the organization and dynamics of nucleoids originates from studies of rodor crescent-shaped bacteria. We have used *Deinococcus radiodurans*, a relatively large, spherical bacterium, well-known for its exceptional radioresistance, to study the structure and dynamics of the nucleoid. Using conventional and super-resolution microscopy approaches, we have revealed that its nucleoid is highly compact at all times, but also surprisingly dynamic, adopting six distinct configurations, including the previously described toroid, as it progresses through its cell cycle [1]. A major player in the organization of bacterial nucleoids is the highly abundant histone-like HU protein that largely coats the genomic DNA. Using a combination of biochemistry, biophysics, microscopy and molecular dynamics simulations, we have investigated HU's mode of DNA binding and its ability to condense the genomic DNA. Taken together, these findings demonstrate that bacterial nucleoids are highly organized and dynamic structures, which are tightly regulated by cell shape and cell cycle progression, and suggest that the HU protein plays a key role in this process.



Fig. 1: (A) Schematic representation of a bacterial nucleoid (green). Nucleoid associated proteins (NAPs) and in particular the abundant HU protein, are largely responsible for the high degree of compaction of the nucleoid.
(B) Schematic representation of the various shapes and structures adopted by the nucleoid of *D. radiodurans* as it progresses through its division cycle (Phase 1 to 6). Scale bar: 1µm. The QR code provides a link to a simulated movie of this dynamic process.

[1] K. Floc'h, co-authors. (2019). Cell morphology and nucleoid dynamics in dividing *D. radiodurans*. **bioRXiv**. DOI: <u>10.1101/582304</u>.