Unravelling a novel packaging of chromatin in dinoflagellates.

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Over the last few decades, chromosome architecture together with epigenetic modifications have been shown to play a major role in the control of nuclear processes such as gene expression, and are central in the regulation of cellular processes in disease and inheritance. Dinoflagellates possess an enlarged genome with multiple gene copies and an unusual chromosome organization that is compacted throughout the cell cycle. In addition, they lack a recognizable nucleosome structures with only a very low expression of histones. We have seen that they have also acquired a novel nucleoprotein called **D**inoflagellate **V**irus **N**ucleo**P**rotein (DVNP) that is only present in some marine viruses. This protein presents many similarities to histones and is thought to play a central role in this new genome architecture. These peculiarities raise several interesting questions as to how dinoflagellates have evolved mechanisms to organize and regulate chromatin compaction and gene expression in the absence of nucleosomes. To gain a clearer view of the nuclear organization of dinoflagellate chromosomes and the gene coding sequences within them, we are using chromosome conformation capture technologies (HiC) to define the global three-dimensional genome architecture and describe general chromosomal domains and compartments. In addition, to better understand the role of DVNP in this architecture, we are analyzing the post-translational profile of this protein as well as its binding pattern along the genome. Together, these local as well as genome-wide approaches will define the link between DVNP expression and the architectural features determined by HiC. Our aim is to generate a general picture of the architecture of the nuclear genome of dinoflagellates. This will identify alternative chromatin compaction mechanisms that are divergent from the classical nucleosome/histone code, so far observed in eukaryotic cells.