



CHROMATIN

Evolutionary insights into nucleosomes

Nucleosomes are the fundamental unit of chromatin in eukaryotes, and work in recent years has revealed close ties between nucleosome occupancy, composition and modification, and gene expression. Nucleosomes comprised of homologues of histones H3 and H4 were discovered in some archaea in the 1990s, but little has been known about their distribution or function. Ammar *et al.* now present the first genome-wide map of archaeal nucleosomes, and this work uncovers conserved features suggesting ancient roles for nucleosomes in gene regulation.

The authors studied the halophilic archaea *Haloferax volcanii*, which has a total genome size of 4 Mb. To map nucleosomes in this species, they crosslinked the histones to DNA and then used micrococcal nuclease to digest the DNA exposed between the nucleosomes (an approach known as

micrococcal nuclease sequencing (MNase-seq)). Fragments protected by histones were then sequenced and mapped to the *H. volcanii* genome to provide a map of nucleosome occupancy. The density of nucleosomes on the archaeal genome was greater than the density observed for eukaryotic genomes, which is consistent with previous suggestions that archaeal nucleosomes are smaller than eukaryotic nucleosomes (that is, they contain a histone tetramer instead of an octamer). Other global features — such as the periodic pattern of occupancy ('peaks' at nucleosomes and 'troughs' between them) and enrichment for G/C nucleotides at nucleosome midpoints — are similar to eukaryotes.

Ammar *et al.* then used RNA sequencing (RNA-seq) to characterize the transcriptome of *H. volcanii* and used this data set to explore the links

between nucleosome occupancy and gene expression. The patterns they found were strikingly similar to those seen in eukaryotes. For example, they found nucleosome-depleted regions (NDRs) flanked by well-positioned nucleosomes at transcription start sites and NDRs at transcription termination sites. They also found that the degree of nucleosome occupancy is correlated with gene expression.

So what might these findings tell us about the evolution of chromatin? As archaeal genomes are small and do not need to be packaged into a nucleus, the authors propose that the ancestral role for chromatin was not higher-order genome organization and compaction. Instead, they suggest that the original function of nucleosomes was in regulating gene expression and that the packaging roles could have emerged with the evolution of eukaryotes.

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ORIGINAL RESEARCH PAPER Ammar, R. *et al.* Chromatin is an ancient innovation conserved between Archaea and Eukarya. *eLife* **1**, e00078 (2012)

FURTHER READING Bell, O. *et al.* Determinants and dynamics of genome accessibility. *Nature Rev. Genet.* **12**, 554–564 (2011)