

Colloquium

The Rapidly Expanding Histone Universe

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All eukaryotes organize their DNA into nucleosomes, consisting of an octamer of the four core histones H2A, H2B, H3, and H4, around which 147 base pairs of DNA are wrapped in two tight superhelical turns. Histones were an early acquisition in eukaryogenesis that allowed for massive genome expansion, a prerequisite for the complexity observed in modern-day eukaryotes. Histones are the targets of epigenetic modifications through the incorporation of histone variants and histone post-translational modifications, and require elaborate assembly and remodeling machinery for gene regulation. Who provided the chromatin starter kit to the early eukaryote? Many archaea organize their genomes with single, non-diversified histones that form slinky-like structures, without the requirement for additional machinery to assemble and disassemble nucleosomal structures. We hypothesize that these histones serve protective rather than regulatory functions and reflect adaptation to the often-extreme environment, and that different histone 'strategies' have evolved for different life styles. A subclass of giant viruses (ancient double-stranded DNA viruses that infect mostly amoebae) also encode their own histones, and these form meta-stable nucleosome-like structures with distinct features. Some additionally encode histone variants and linker histones, and histones can be fused in various combinations. Unexpectedly, we recently discovered that histories are sporadically present in the bacterial domain of life. In a stunning reversal of 'histone logic', these small histones can encase straight DNA rather than wrapping it around them. As such, histones are no longer a prerogative of eukaryotes but appear to be an ancient DNA packaging principle that has adapted to varying constraints in different domains of life.

Monday, February 3, 2025 11:30am - 12:30pm

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