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SÉMINAIRE

Systematic protein-genome interaction maps reveal 5 chromatin types in Drosophila.

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The local protein composition of chromatin controls important processes such as transcription, replication and DNA repair, yet the diversity of chromatin and its distribution along chromosomes is still poorly characterized.Using DamID in Drosophila Kc cells, we generated high-resolution genome-wide binding maps of 53 chromatin proteins from a wide range of functional categories. For most of those proteins, no binding data was previously available.By constructing a non supervised classifier, we find that there are five principal chromatin types defined by unique yet overlapping combinations of proteins.Two types correspond to Polycomb and HP1-bound regions, respectively. The novel 'BLACK' chromatin type covers half of the genome and induces strong transcriptional repression on inserted transgenes. Remarkably, this chromatin type is devoid of the classic 'heterochromatin' proteins Polycomb and HP1. Thus, our data reveal the existence of a prominent repressive chromatin type that has largely been overlooked.Active genes are associated with one of the other two remaining combinations of proteins. H3K36 methylation is associated with only one of them, yet it was previously thought to mark every transcribed gene. In addition, active genes involved in growth and cell proliferation, and those involved in signal transduction are located in a distinct chromatin types.The five chromatin types modulate the interactions of transcription factors with DNA. We observe that most transcription factors bind their cognate motif only if it sits in the favored chromatin context. Our data rule out a simple exclusion mechanism but support a model whereby synergistic interactions target transcription factors to their binding site.Finally, genomic regions in the 5 chromatin types follow different evolutionary processes. The vast majority of synteny breaks with Drosophila pseudoobscura occurs in only one of the transcriptionally active types. Besides, the speed of evolution of genes located in that chromatin type is higher than for other types.In summary, our integrative approach identifies five major chromatin types, which are defined by unique combinations of proteins and have distinct functional properties.

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