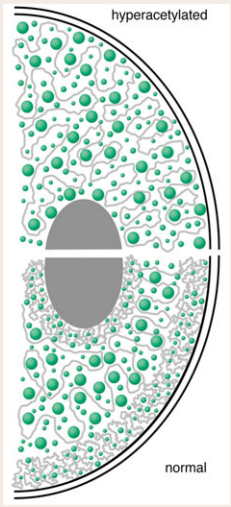
In this issue

by Jane Bradbury



Histone acetylation: an open pore policy

Histone acetylation is essential for the establishment of transcriptionally competent chromatin, but how it does this is unclear. Now, Karsten Rippe and colleagues demonstrate that histone acetylation dynamically regulates the accessibility of chromatin by 'opening it up' during interphase (see p. 5825). The authors have microinjected fluorescein-labelled dextran molecules of different sizes into HeLa cells and examined their nuclear distribution before and after histone acetylation. They describe three different chromatin condensation states that have different apparent pore sizes and show that increased histone acetylation uniformly changes the chromatin conformation to the most open of these states (which has a pore size of 60-100 nm). The authors suggest that, by opening up the chromatin structure, histone acetylation gives large nuclear assemblies, including 2-3 MDa protein complexes and the 40-80 nm RNA polymerase II transcription factories, access to previously inaccessible chromatin domains. By contrast, the nuclear distribution of smaller protein complexes is independent of histone acetylation.