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What S.cerevisiae whispers about genome organization in human

The genome of higher Eukaryotes, and in particular of humans, is organized in 2 compartments in the space of the nucleus, the euchromatin which is favorable to gene expression, and the heterochromatin which is unfavorable, also called A and B compartments.

I often hear that the organization of the genome in nuclear space is very different in the yeast S.cerevisiae from nuclear organization of the genome in a human cell, and this is indeed the case for most differentiated human cell types. This is true, but there are also fundamental aspects that are conserved such as the existence of a "heterochromatin system", dependent on the HP1a protein in humans and the SIRc complex in yeast. Thus, the SIRc complex is found at the level of constitutive heterochromatin sequences, which are constituted in yeast by telomeres, and at the level of two loci, the HM "mating-type cassettes"- and we will consider that these sequences represent the B compartment in yeast. While B compartment, driven by the HP1a dependent heterochromatin system covers 50% of the human genome, i.e. 1.5Gb for a haploid genome, B compartment in yeast covers 0.25% of the genome, i.e. 30kb, which makes it a prime model system to study precisely "how heterochromatin works".

Indeed, yeast has been instrumental in understanding some basic rules of Eukaryotic genome organization (1, 2), as I will illustrate by presenting the concept of "heterochromatin ambiance".

1. Fourel G, Lebrun E, Gilson E. 2002. Protosilencers as building blocks for heterochromatin. Bioessays 24:828-35.
2. Fourel G, Magdinier F, Gilson E. 2004. Insulator dynamics and the setting of chromatin domains. Bioessays 26:523-32.

Auteur principal: FOUREL, genevieve (INSERM)

Orateur: FOUREL, genevieve (INSERM)