CHROMATIN ORGANIZATION MECHANISMS ACROSS THE YEAST GENOME

Eukaryotic genes are packaged into nucleosomal arrays that eminate from nucleosome-free promoter and termination regions. In Saccharomyces in particular arrays are highly organized, which includes tight positional linkage of array start sites and transcriptional start sites. Continuing downstream nucleosomes are uniformly spaced and contain a variety of histone marks and histone variants, which may be nonsymmetrically placed on one side of nucleosome versus the other, and have nucleosome position-specific enrichment. We have developed and used the ChIP-exo assay to assess subnucleosomal histone organization on a genomic scale. In addition, we have examined the distribution of chromatin remodelers at high resolution so as to gain an understanding of their involvement in creating nucleosomal arrays. Finally, we have now reconstituted nucleosomal arrays on a genomic scale with purified histones and remodelers, and are now working out the detailed contribution of individual remodelers to the physiological organization of arrays. One common denominator is the involvement of a physical barrier that sets where arrays start, and then a packing and spacing activity that sets the uniformity of arrays. Barriers can be established through underlying DNA sequences, adjacent nucleosomes, and through sequence-specific transcription factors.