Understanding the workings of the Schizosaccharomyces pombe genome in three dimensions

J.M. O'Sullivan

(Liggins institute, University of Auckland, Grafton, Auckland 1032, New Zealand.

Gravida: National Centre for Growth and Development, University of Auckland, Auckland, New Zealand.)

contact: justin.osullivan@auckland.ac.nz

Genomes have evolved as three-dimensional structures to fulfill a variety of functions, such as chromosomal replication and epigenetic silencing. New methods of analysis allow us to integrate the three-dimensional organization of genomes, patterns of epigenetic modifications and nuclear functions into an over-arching theory of the nucleus. Here we present the three-dimensional spatial organization of the *Schizosaccharomyces pombe* epigenome through the cell cycle. Euchromatin and heterochromatin are clearly separated within the nuclear space, except in proximity to the spindle pole body, while origins of replication are spatially separated according to firing time and frequency. Known features of genome organization (*e.g.* the clustering of telomeres and retrotransposon long terminal repeats (LTRs)) are observed throughout the cell cycle. There are clear correlations between transcript levels and chromosomal interactions, consistent with a role for interactions in transcriptional regulation at specific stages of the cell cycle. Surprisingly, deletion of the histone methyltransferase Clr4 has little effect on the global organization of heterochomatin and euchromatin, although it does affect the localization of early and late firing replication origins. Our work paves the way for the utilization of global genome structure models to understand the spatial positioning of genomic loci within the *S. pombe* nucleus.