Assembly of specialised chromatin at Fission Yeast Centromeres

Alison L. Pidoux

Wellcome Trust Centre for Cell Biology and Institute of Cell Biology, School of Biological Sciences, the University of Edinburgh, Edinburgh, Scotland, United Kingdom.

Despite the conserved essential function of centromeres, centromeric DNA is not conserved between species. There is strong evidence indicating that centromeres are epigenetically regulated. Although centromeres normally assemble on preferred sequences, these sequences are neither necessary nor sufficient for centromere assembly. For instance, neocentromeres can form upon sequences that previously showed no centromere function. The presence of the histone H3 variant, CENP-A, is thought to be the epigenetic mark that specifies centromere identity.

We aim to understand how CENP-A assembly is influenced by sequence and by chromatin context. *Schizosaccharomyces pombe* centromeres are composed of a central domain which is assembled in CENP-A chromatin and forms the kinetochore, flanked by the heterochromatic (H3K9me2) outer repeat regions. We have previously shown that heterochromatin is required for establishment of CENP-A chromatin, but not for its maintenance. Our analyses suggest that histone acetyltransferases and deacetylases influence CENP-A establishment. In addition, analysis of requirements for CENP-A establishment lead us to propose that a key property of central domain sequences is their ability to direct an environment of low quality pervasive transcription that is permissive for CENP-A chromatin establishment.

Genome sequencing of three additional *Schizosaccharomyces* (*S. octosporus, S. japonicus* and *S. cryophilus)* species allowed partial assembly of putative centromere regions. In order to fully assemble the centromeres of these species we are employing PacBio sequencing of long reads in conjunction with analysis of CENP-A and H3K9me2 ChIP-seq to define chromatin domains. Intriguingly, although there is no homology between the centromere sequences of the four *Schizosaccharomyces*, the organization and architecture are similar. We are investigating the hypothesis that despite the lack of sequence conservation, the *Schizosaccharomyces* centromeres possess conserved properties that promote assembly of CENP-A chromatin and heterochromatin.