CDB SEMINAR

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15:00~16:00 A7F Seminar Room

NUCLEAR DYNAMICS IN FISSION YEAST *SCHIZOSACCHAROMYCES POMBE*

Summary

We have developed *Schizosaccharomyces pombe* as a model system to study nuclear organisation and its impact on gene regulation. Firstly we have used the heterochromatic mating-type region to investigate the impact of repressive chromatin on nuclear architecture. We have found that both cis and trans-acting factor are important for correct sub-nuclear organisation of the mating-type region (Alfredsson-Timmins et al JCS 2007). Further studies indicate that a balanced dosage of the trans-acting factors is also important. Moreover we have investigated the short-term response to nitrogen starvation in the fission yeast. Nitrogen depletion leads to a fast induction of a large number of genes in *S. pombe* and is thus suitable for genome-wide studies of chromatin dynamics during gene regulation. Intriguingly, some of the upregulated genes are found in clusters. Previous studies from our group revealed that two of these clusters, named Chr1 and Tel1, are found at the nuclear periphery under uninduced conditions but change localisation to a more interior position 20 minutes after the onset of nitrogen starvation (Alfredsson-Timmins et al Chromosoma 2009). Preliminary data indicate that the relocalisation of the Chr1 cluster is necessary for full induction of the genes. By performing microarray analysis we detect that after 20 minutes of nitrogen starvation, 118 transcripts are upregulated. Surprisingly, this upregulation is associated with nucleosome eviction of equal magnitudes in the promoters and in the coding regions. Moreover, a strong increase in the histone modification H3AcK9, and a minor increase in H4AcK5, is also found in the upregulated genes. Two highly induced genes in the Chr1 cluster, *urg1*$^{+}$ and *urg2*$^{+}$, display a substantial nucleosome loss in their coding regions, with only 20 % of the nucleosomes being left after induction. We conclude that nucleosome depletion during transcriptional activation is not necessarily limited to promoter regions.

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