CDB SEMINAR

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Thursday, May 17

16:00~17:00 C1F CDB Auditorium

Transcriptional and posttranscriptional gene silencing at heterochromatic domains in fission yeast

Summary

Eukaryotic chromosomes are cytologically divided into two domains: heterochromatin and euchromatin. In heterochromatic domains, nucleosomes, the structural unit of chromatin, are packed into highly ordered and condensed structures, which play an essential role in various chromosome transactions including proper chromosome segregation, recombination suppression and gene silencing. However, it was not fully understood how exactly heterochromatin imposes gene silencing on underlying DNA.

We identified an RNAi effector complex named RITS (RNA-induced transcriptional gene silencing), which is essential for heterochromatin formation, and investigated the role of the RITS complex and RdRP (RNA-dependent RNA polymerase) in gene silencing. Through these analyses, we proposed that RNAi and other factors are components of a self-enforcing loop coupling heterochromatin assembly and siRNA production by RNAi, and that RNAi machinery tethering to chromatin causes posttranscriptional silencing in cis. In addition, we have recently reported that a novel complex SHREC (SNF2 and HDAC-containing repressor complex) mediates gene silencing at the level of transcription through two distinct activities, histone deacetylase and SNF2 ATPase, suggesting that chromatin remodeling as well as histone deacetylation is prerequisite for heterochromatic silencing. Furthermore, chromodomain proteins (e.g. Swi6 and Chp1) bound to histone H3 Lys9 methylation recruit both RNAi machinery and SHREC to heterochromatin, indicating that heterochromatin is a versatile platform for factors involved in both transcriptional and posttranscriptional silencing.

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