MedicalXpress

Recycling histones through transcription

March 26 2015

Cells reuse a part of the histones which are used to pack DNA, according to a current study by Karolinska Institutet. The study, which is published in the journal *Genome Research*, was conducted on yeast cells, but it is likely that similar mechanisms are important for human beings as well.

Cells are also involved in energy saving and recycling. In this case it entails histones, the proteins which keep the cell's DNA packed by spinning it around itself like thread around reels of thread. The complex of DNA and histones is referred to as chromatin and it may be packed more hardly or loosely. The level of packing controls which genes are currently expressed by affecting how easy it is for transcription enzymes, referred to as RNA polymerase, to bind to DNA and read the DNA sequence. During transcription of active genes, the histones are temporarily removed from the chromatin so that the RNA polymerase can access the DNA.

In the current study, researchers studied how gene expression impacts the composition of the chromatin. Previous studies have shown that it is often newly-formed histones which are built into the chromatin during transcription.

"Instead we show that continuous transcription results in recycling of old histones," says Peter Svensson at the Department of Biosciences and Nutrition, one of the researchers behind the study.

Histones in the chromatin often have a number of modifications in the

form of chemical markers. The modifications differ between the active and quiet closed regions in DNA, and help the cell to remember which genes are not used.

"Patterns of these modifications take a long time to create and by recycling the histones the cell can keep the region active. We have also seen that the protein complex FACT is necessary to restore mature histones which are temporarily removed from the chromatin during transcription," says Peter Svensson.

The discovery indicates that transcription of genes has a histone-preservation function and that the cell can efficiently recycle the original histones. In this manner, it can save energy and at the same time preserve a cellular (epigenetic) memory in the chromatin. However, new histones which lack chemical markers or have other modifications than the mature histones are added in the chromatin when the genes move between the quiet and active stage.

In the new study yeast cells are used as the model system, while the involved proteins and their functions are largely evolutionarily preserved in human cells, and researchers believe that similar mechanisms probably have a general significance. The work was conducted with support of grants from the Swedish Research Council, the Swedish Cancer Society and Karolinska Institutet.

More information: "A nucleosome turnover map reveals that the stability of histone H4 Lys20 methylation depends on histone recycling in transcribed chromatin." *Genome Research*, first online 16 March 2015, DOI: 10.1101/gr.188870.114

Provided by Karolinska Institutet