B·DEBATE International Center for Scientific Debate BARCELONA

CRG Centre for Genomic Regulation

LEONIE RINGROSE

CV

PARTICIPANT AT:

CODING AND NON-CODING FUNCTIONS OF THE GENOME
BARCELONA CONFERENCE ON EPIGENETICS AND CANCER

October, 29th-30th, 2015, Barcelona

Leonie Ringrose, Professor at Humboldt University, Berlin, Germany

Leonie Ringrose graduated in Molecular Biology at the University of East Anglia (Norwich, U.K) in 1989. She then moved to Germany where she spent three years as a patent examiner at the European Patent Office in Munich. After this she returned to research, and obtained her PhD at the European Molecular Biology Laboratory (EMBL) in Heidelberg in 1997. During this period her research interests focused on the kinetic analysis and mathematical modelling of recombination pathways using the site-specific recombinases FLP and Cre, and mathematical and experimental analysis of DNA looping. In 1998 she mo¬ved to the laboratory of Dr. Jean-Maurice Dura in the Institut de Génétique Humaine in Montpellier, France. In this first post doc she started work on the epigenetic regulation by Polycomb and Trithorax group proteins. After another postoc in the laboratory of Dr. Renato Paro in the University of Heidelberg she started as a group leader at the Institute of Molecular Biotechnology (IMBA) in Vienna, Austria in 2006. Leonie Ringrose has recently accepted a professorship at the Integrated Research Institute for the Life Sciences at the Humboldt University in Berlin, where she continues to work on the quantitative analysis of epigenetic regula¬tion. The goal of her group is to understand how a system whose components are in constant flux can ensure both stability and flexibility of gene expression states. For that propose, they use a combination of quantitative live imaging, mathematical mo¬delling, computational approaches and molecular and developmental biology to understand the interaction of the Polycomb and Trithorax group proteins with their chromatin targets and non-coding RNAs.

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ABSTRACT

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Non-Coding Rnas in Polycomb/Trithorax Regulation

In Drosophila and vertebrates, many Polycomb (PcG) target sites are transcribed into non-coding RNA. This observation, in combination with the fact that several Polycomb and Trithorax Group (TrxG) proteins can bind to RNA in vitro has given rise to the proposal that interactions of PcG and TrxG proteins with specific non-coding RNAs are responsible for targeting to specific sites in vivo. However, there are also results that argue against a simple targeting function for ncRNAs. The idea that PcG complexes themselves recognise specific RNA sequence or structural motifs is inconsistent with several observations. For example, we and others have recently shown that the PcG complex PRC2 interacts promiscuously with RNA in vitro, and that this interaction leads to an inhibition of histone-methyltransferase activity of both fly and vertebrate PRC2. A key future challenge will be to reconcile the lack of inherent specificity of PcG and TrxG proteins for specific RNAs in vitro, with the exquisite specificity of some ncRNAs in affecting PcG and TrxG function in vivo. I will discuss current progress towards this goal.

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