SFB 960-/BZR – Kolloquium

Donnerstag, 29.06.2017, 14:00 Uhr

H 53 (Neubau Biologie)

Prof. Dr. Chandra Kanduri

Institute of Biomedicine
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"Insights into long noncoding RNA-dependent disease-specific gene regulatory networks"

Long noncoding RNAs (lncRNAs) regulate gene expression by association with chromatin, but how they target chromatin remains poorly understood. We have used chromatin RNA immunoprecipitation-coupled high-throughput sequencing to identify 276 lncRNAs enriched in repressive chromatin from breast cancer cells. Using one of the chromatin-interacting lncRNAs, *MEG3*, we explore the mechanisms by which lncRNAs target chromatin. Here we show that *MEG3* and *EZH2* share common target genes, including the TGF-β pathway genes. Genome-wide mapping of *MEG3* binding sites reveals that *MEG3* modulates the activity of TGF-β genes by binding to distal regulatory elements. *MEG3* binding sites have GA-rich sequences, which guide *MEG3* to the chromatin through RNA–DNA triplex formation. We have found that RNA–DNA triplex structures are widespread and are present over the *MEG3* binding sites associated with the TGF-β pathway genes. Our findings suggest that RNA–DNA triplex formation could be a general characteristic of target gene recognition by the chromatin-interacting lncRNAs.

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