Unraveling the impact of chromatin dissociation dynamics of lncRNAs in gene expression regulation

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ABSTRACT

Long non-coding RNAs (lncRNAs) constitute a large and diverse class of molecules that can play key roles in the nucleus or the cytosol of the cell. Grouping lncRNAs based on shared molecular features and understanding principles of their subcellular and subnuclear localization can help to mechanistically elucidate their functional regulatory potential in gene expression regulation. We recently developed a method using nascent RNA transcriptomics to profile chromatin dissociation dynamics of newly transcribed RNAs across the genome, and classified mRNAs and lncRNAs based on distinct chromatin dissociation rates [1]. Notably, enhancer-transcribed lncRNAs show enhanced release from chromatin and higher propensities for interactions with specific RNA-binding proteins (RBPs), including some bona fide mRNA processing factors. We will discuss our progress toward functional validation through acute protein depletion of key RBP candidates and present results from experiments aimed at modulating the chromatin association of specific lncRNAs.

REFERENCES

[1] Ntini et al. 2024. *Cell Syst,* **14(10)**: 906–922.e6.