THE CITY UNIVERSITY OF NEW YORK
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BIOLOGY DEPARTMENT SEMINAR SERIES

HOW DEVELOPMENTAL GENE REGULATION WORKS AND EVOLVES

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Date: **Tuesday, March 5th, 2024**
Time: **2:30 PM**
Location: **Room 6S-138**

Differential gene expression determines the diversity of cells and shapes in complex organisms, and it is primarily controlled by Transcriptional Regulatory Elements (TREs). Not surprisingly, genetic diseases and metazoan evolution predominantly involve TREs.

In our lab, we study developmental Gene Regulatory Networks (GRNs) among signaling and transcription factors in indirectly developing sea urchins and polychaetes. Developmental GRNs are transiently malleable during embryogenesis and in multipotent cells, where histone variant H2A.Z is strongly expressed. Experimental evidence supports an H2A.Z role enabling developmental GRN transitions, possibly by enhancing global TRE accessibility.

Our ATAC-seq genome-wide chromatin accessibility analysis during embryogenesis and differentiation revealed surprisingly early TRE accessibility that peaks during enhanced developmental potency and H2A.Zexpression. In addition, parallel Precision Run-On and sequencing (PRO-seq) experiments identified the precise location of transcriptionally engaged TREs genome wide.

The results reveal that may distal TREs associated with developmental gene regulation are transcriptionally paused, supporting a "ready-to-go" model during early development. Our PRO-seq characterizations in metazoans and unicellular sister groups suggest that the control of pause-release may represent an additional regulatory layer enabling metazoan evolution.

Furthermore, the comparative analysis of biochemical mechanisms in proximal, distal, constitutive, and inducible TREs suggests that developmental GRNs in metazoans emerged after the expression of constitutive transcription factors that regulate inducible genes during the life cycle of unicellular organisms became controlled by their own TRE targets.

This is a Clue event!