QUANTITATIVE & SYSTEMS BIOLOGY COLLOQUIUM:

Maternal Transcription Factors and Epigenetic Modifiers in Regulating Cell Fate Determination During Zygotic Genome Activation

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Abstract:

We study the mechanisms by which pluripotent embryonic cells in Xenopus tropicalis initiate distinct cell fate specifications, focusing on the essential roles of maternal transcription factors (TFs) and histone modifications during the zygotic genome activation. We elucidate a coordinated sequence of events starting from maternal TF binding to germ layer specific cis-regulatory modules (CRMs), followed by the recruitment of RNA polymerase activity, enhancer RNA expression, and the transcription of germ layer specific target genes. Additionally, we examine epigenetic changes around the CRMs, finding that Histone Deacetylase 1 (Hdac1) and Polycomb Repressive Complex 2 (PRC2) specifically associate with germ layer-specific CRMs. Contrary to expectations, Hdac1's role is not limited to repressing gene expression by maintaining a histone hypoacetylation state on inactive chromatin. Hdac1 also supports gene expression by participating in dynamic histone acetylation-deacetylation cycles on active chromatin. This dual functionality of Hdac1 highlights its crucial role in the epigenetic regulation of the zygotic genome, offering insights into the molecular underpinnings of early vertebrate development.

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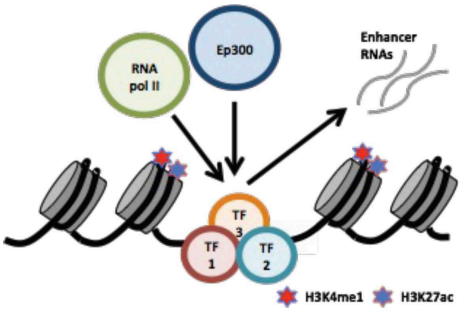

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