SEMINAR

生命科学セミナー

Interplay of transcription factors and epigenetic modifiers in gene expression stability

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Tue. 12th December 16:00 –17:00

KUIAS Main Building 2nd floor, Seminar Room

(Kyoto University Campus map #77)

The embryonic genome orchestrates gene expression during embryogenesis through the dynamic interplay of histone modifications and transcription factor accessibility. Histone tails, making up to 30% of histone mass, undergo critical post-translational modifications such as acetylation, influencing temporal and spatial gene activities around zygotic genome activation (ZGA). In Xenopus, a balance between histone acetyltransferases (e.g., Ep300) and deacetylases (e.g., Hdac1) is essential for cell fate decisions during gastrulation, with histone acetylation levels correlating with developmental plasticity. Our research reveals that Hdac1, maternally guided to the genome, plays a dual role. Hdac1 not only represses gene expression by sustaining a histone hypoacetylation state on inactive chromatin, but also maintains gene expression through participating in dynamic histone acetylation-deacetylation cycles on active chromatin. Our study illuminates Hdac1's integral role in the epigenetic modulation of the zygotic genome, providing a framework for understanding the molecular underpinnings of early vertebrate development.

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