分子生物学教室セミナー

Epigenetic and transcriptional regulation of neuronal activity-response genes during development

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Venue: ZOOM
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Appropriate transcriptional responses to environmental stimuli are fundamental for sensory circuit formation. How epigenetic chromatin states regulate neuronal activity-regulated transcription during development is poorly understood. To address this issue, we carried out epigenetic and transcriptional profiling of neuronal activity-response genes during mouse somatosensory neuron development. We found that in developing sensory neurons, prior to sensory activity-dependent induction, immediate early genes (IEGs, e.g. *Fos*) are embedded into a unique ‘bipartite' Polycomb chromatin signature. Namely, IEGs carry active H3K27ac mark on promoters and enhancers, but repressive Polycomb-H3K27me3 mark on gene bodies. The bipartite chromatin signature originates from conventional Polycomb ‘bivalent’ chromatin. Polycomb H3K27me3 marking of IEG gene bodies inhibits productive mRNA elongation, dampening basal productive transcription, while still allowing for fast stimulus-dependent mark removal and mRNA induction. We revealed a novel epigenetic chromatin mechanism regulating the rapidity and amplitude of the transcriptional response to relevant stimuli, while preventing inappropriate activation of IEGs at pre-sensory stages.
In addition, I want to introduce my new laboratory, opening in the DANDRITE-Nordic-EMBL in Denmark very soon. I will investigate epigenetic and transcriptional basis of memory engram plasticity, be taking advantage of the beyond state-of-the-art genomics technologies.

References:
1. Kitazawa, T., et al., *Nature Genetics*. 2021 Mar;53(3):379-391.
A unique bipartite Polycomb signature regulates stimulus-response transcription during development.
2. Kitazawa, T., et al., *Curr Opin Neurobiol*. 2018 Oct 17;53:210-219.
Barrelette map formation in the prenatal mouse brainstem.

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