NUS National University of Singapore

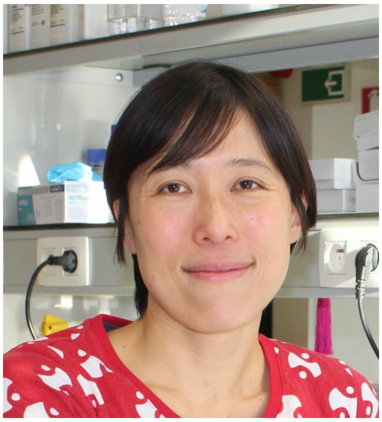
Department of Biological Sciences
Faculty of Science

SEMINAR

Tues, 9 Jul 2024 | 4:30 pm | DBS Conference Room 1

Hosted by Assoc Prof Low Boon Chuan

Cortical neurons exhibit cell-type specific maturation programme



By **Lynette Lim**

Vlaams Institute of Biotechnology (VIB), University of Leuven (KUL)

About the Speaker

Dr. Lynette Lim obtained her PhD from the National University of Singapore in 2012. She then received the EMBO fellowship and joined the lab of Oscar Marin at King's College London. There, she published seminal papers on cortical interneuron development in top-tier journals (Nature Neuroscience, Science, and Cerebral Cortex). Her discovery that unique developmental programs govern the formation of inhibitory circuits solidified her reputation in the field of cortical development. In 2020, she was appointed as Assistant Professor at the University of Leuven (KUL) and Group Leader at Vlaams Institute for Biotechnology (VIB) – Belgium. Dr. Lim has received numerous accolades. In 2019, she was awarded the Wellcome Trust Henry Dale Fellowship (respectfully declined). In 2021, Dr. Lim received the flagship Odysseus grant—a prestigious award aimed at attracting exceptional scientists to Flanders. Her laboratory aims to unravel the intricate molecular mechanisms governing interneuron diversification and maturation.

The mammalian neocortex is nature's most powerful intelligent machine. Our remarkable abilities to learn intricate tasks—from mastering languages to honing fine motor skills like drawing—underscore its significance. The postnatal period marks the peak of brain plasticity, witnessing substantial changes in circuit architecture in response to learning and external stimuli. While mounting evidence indicates this plasticity can be driven by changes in neuronal cell types, the precise molecular mechanisms and genes involved in guiding this post-mitotic cell fate acquisition are poorly defined. Here we combine single-cell RNA sequencing and spatial transcriptomics to characterize the emergence of neuronal diversity during the late embryonic and early postnatal phases in mice. Using the most diverse subclass of inhibitory neurons in the mouse cerebral cortex as a model, we found that the timing for cellular diversification is unique for different neurons, and particularly divergent between long-range neurons and interneurons. By elucidating the molecular logic that specifies neuronal identity, we aim to pave the way to build more flexible computational machines.