

All are Welcome!

Decoding the Genetic Landscape of Human Evolution

17 DEC 25 MONDAY 3PM

AUDITORIUM LEVEL 1

The 3-fold expansion of the cerebral cortex is the defining feature of human evolution. This extraordinary transformation occurred over a remarkably short evolutionary time span of ~7 million years. However, the causal mechanisms and pathways that govern size control of the developing brain have not yet been systematically investigated. The focus of my research program will be to use comparative studies of humans and great apes to pinpoint the cellular and molecular principles that led to the emergence of our unique human features. Our approach draws inspiration from classical developmental genetics paradigms such as the Heidelberg screens, which identified many of the key signaling pathways that govern morphogenesis. However, while the core elements of these pathways are highly conserved from fruit flies to humans, unique aspects of human development arise from altered timing, regulation, and complexity. Performing parallel screens in closely related species allows us to identify key species differences in development. We plan to observe the balance of self-renewal and differentiation in neural progenitor cells, the key cell type that gives rise to virtually all neurons. By making perturbations to neuronal progenitor cells at genome-wide scale, we will systematically identify the key pathways that regulate human brain expansion.

Recent Publications:

1. R. She, T. Fair, R. A. Saunders, B. J. Pavlovic, J. S. Weissman, A. A. Pollen, Comparative landscape of genetic dependencies in human and chimpanzee stem cells, Cell 2023 Jul 6;186(14):2977-2994
2. R. She, J. Luo, J. S. Weissman, Translational fidelity screens reveal eIF3 as a key regulator of start codon selectivity, Nucleic Acids Research 2023 Jul 7;51(12):6355-6369
3. R. She, D. F. Jarosz, Mapping Causal Variants with Single-Nucleotide Resolution Reveals Biochemical Drivers of Phenotypic Change, Cell 2018 Jan 25;172(3):478-490.e15

Our Speaker



Richard She is a Nanyang Assistant Professor in the School of Biological Sciences at NTU. He did his Ph.D. work in yeast genetics with Dan Jarosz, using large inbred crosses to fine-map the DNA variants that give rise to complex traits. He then joined Jonathan Weissman's lab for his postdoc, where he built CRISPR tools to identify unique species-specific vulnerabilities in human and chimpanzee stem cells.

Richard She
Nanyang Assistant Professor
Nanyang Technological University

Hosted by Dr Yu Fengwei

TEMASEK LIFESCIENCES LABORATORY

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