VIRTUAL BIOLOGY COLLOQUIUM

Friday, 28 Jan 2022 | 4 pm | Online Zoom Session

Hosted by Dr Lau On Sun

Stochastic gene expression drives mesophyll protoplast regeneration



About the Speaker

Dr. Yuling Jiao earned his B.S. degree in Biochemistry and Molecular Biology at Peking University and his M.S. and Ph.D. in Molecular, Cellular and Developmental Biology at Yale University. As a postdoctoral fellow at the California Institute of Technology in the laboratory of Prof. Elliot Meyerowitz, he developed new techniques for cell type-specific transcriptome profiling. From 2010 to 2021, he was a Group Leader at the Institute of Genetics and Developmental Biology (IGDB). He switched his research interest to shoot morphogenesis. Since 2021, he has been a Boya Distinguished Professor at School of Life Sciences, Peking University. Dr. Jiao has been supported by the National Science Fund for Distinguished Young Scholars, and has received Science and Technology Award for Chinese Youth. He has served as the Country Representative and more recently Director Multinational Arabidopsis Committee, and as President of the Chinese Society for Plant Organogenesis. He is a on the Editorial Board of Plant Cell, and is an Associate Editor for Quantitative Plant Biology.

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By Yuling Jiao

School of Life Sciences, Peking University

Cell pluripotency is fundamental to biology. It has long been known that differentiated somatic plant cells may reacquire pluripotency, but the underlying mechanism remains elusive. In many plant species, a single isolated mesophyll protoplast may regenerate into an entire plant, which is widely used in gene transformation. Here, we identified two transcription factors whose ectopic activation promotes protoplast regeneration. Furthermore, we found that their expression was induced by protoplast isolation but at a very low frequency. Using live imaging and single-cell transcriptomics, we show that isolating protoplasts induces enhanced expression variation at the genome level. Isolating protoplasts also leads to genome-wide increases in chromatin accessibility, stochastic activation promotes gene enhances expression and protoplast regeneration. We propose that transcriptome chaos with increased expression variability among cells creates a cellular-level evolutionary driver selecting for regenerating cells.

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