

# 巴斯德讲坛-资深系列 Pasteur Colloquium-Senior

## Dissecting the gene regulation network in human germline cells at single-cell and singlebase resolution



[Speaker] Prof. Fuchou Tang

[Time] 10:00-11:30AM, November 6, 2017

[Host] Prof. Lubin Jiang

[Venue] A0201, Life Science Research Building

#### [Speaker Introduction]

Dr. Fuchou Tang is Professor at BIOPIC, College of Life Sciences, Peking University. He is also Associate Director of Beijing Advanced Innovation Center for Genomics. He set up his own lab as a principal investigator at Peking University in 2010. Dr. Fuchou Tang's lab focuses on the epigenetic regulation of gene expression network during human early embryonic development and germline development. His lab pioneered the single cell sequencing field and has systematically developed a serial of single cell functional genomic sequencing technologies. His work has been cited for more than 5,000 times.

### [Abstract]

Human germline cells are crucial for maintenance of the species. However, the developmental trajectories and heterogeneity of human germline cells remain largely unknown. We performed singlecell RNA-seq and DNA methylome sequencing analysis of human germline cells in female and male human embryos spanning several critical developmental stages. We found that female fetal germ cells (FGCs) undergo four distinct sequential phases characterized by mitosis, retinoic acid signaling, meiotic prophase, and oogenesis. Male FGCs develop through stages of migration, mitosis, and cell-cycle arrest. Individual embryos of both sexes simultaneously contain several subpopulations, highlighting the asynchronous and heterogeneous nature of FGC development. Moreover, we observed reciprocal signaling interactions between FGCs and their gonadal niche cells, including activation of the bone morphogenic protein (BMP) and Notch signaling pathways. Our work provides key insights into the crucial features of human germline cells during their highly ordered mitotic, meiotic, and gametogenetic processes in vivo.



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