Tracing the temporal-spatial transcriptome landscapes of the human fetal digestive tract using single-cell RNA-sequencing

With the support by the National Natural Science Foundation of China, the research team directed by Prof. Tang FuChou (汤富酬)at the Biomedical Pioneering Innovation Center (BIOPIC), College of Life Sciences, Peking University, and Prof. Qiao Jie (乔杰) at Peking University Third Hospital recently dissected the gene expression profiles of the four main organs of human fetal digestive tract and the adult large intestine *in vivo* at single-cell resolution, which was published in *Nature Cell Biology* (2018, 20(6): 721—734). The first author of the paper is associate professor Gao Shuai (高帅) at the College of Animal Science and Technology, China Agricultural University.

The development of the digestive tract is critical for proper food digestion and nutrient absorption. The study analyzed the main organs of the digestive tract, including the esophagus, stomach, and small and large intestines from human embryos between 6 and 25 weeks of gestation and the large intestine from adults using single-cell RNA-seq analyses. In total, 5,227 individual cells were analyzed and 40 cell types clearly identified. The corresponding detailed information, including the cell identity, developmental stage, cell number, cell cycle index, and cell-type-specific markers, were revealed. Moreover, the research team presented the first analysis uncovering the transcriptomic features and developmental dynamics from fetal to adult stages at single-cell resolution.

In addition, the regulation patterns of signaling pathways, such as the IHH signaling pathway, TGF-β and BMP signaling pathways, during human fetal development were investigated. The physiological functions involved in the digestion and absorption of proteins, were initially established and then specifically enhanced in the small intestine. The team also identified the immune cells, including T cells, B cells and macrophages in the embryonic digestion tract and found that most of them arise in the late stages of small and large intestine development.

The findings offer a comprehensive transcriptome resource for human fetal digestive tract development as well as the large intestine in adults at single-cell resolution. This analysis of the gene expression patterns of each organ in both temporal and spatial dimensions provides guidelines to estimate the status of cells differentiated from pluripotent stem cells *in vitro*. It may facilitate the diagnosis and treatment of digestive-tract-related diseases, such as gastrointestinal tract cancer.

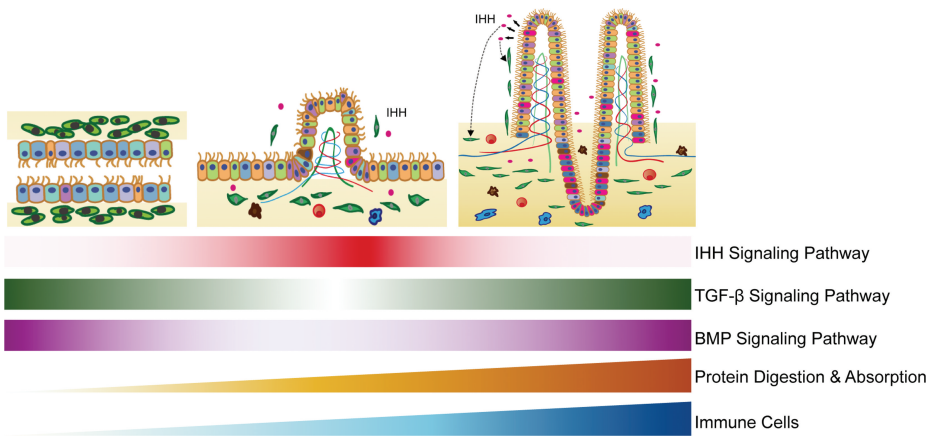

Figure Schematic diagram showing the morphology changes, signaling pathway regulation and cell-cell interactions during small intestine developmental process.