第80回　免疫学セミナーのお知らせ
Tsukuba Immunology Seminar

筑波大学医学セミナー

Single-cell and spatial multiomics of the developing human heart

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令和5年12月14日(木) 16：00ー17：30
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Abstract

The function of a cell is defined by its intrinsic characteristics and its niche. Here we integrate single-cell and spatial multiomics data to discover cellular niches within the human foetal hearts from the first and second trimesters. Foetal pacemaker cells exhibit distinct characteristics compared to adults, including gene expressions involved in innervation. In the ventricle, spatiotemporal transition along the transmural axis shows the morphological process of cardiomyocyte compaction. Using paired single-cell RNA and ATAC sequencing data, we highlight the maturation trajectory of cardiomyocytes and macrophages and infer vital gene regulatory networks and those co-regulations. Investigating somatic mutations enables us to perform lineage tracing analysis of cardiomyocytes and understand the branching point of pacemaker cells. Overall, the analyses provide a comprehensive map and insights into the human heart development.

References

Kanemaru K, et al., Spatially resolved multiomics of human cardiac niches. Nature 2023 Jul;619(7971):801-810.

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