

Single-cell transcriptome analysis for realization of effective regenerative medicine



- Lecturer: Dr. Itoshi NIKAIDO
(Unit Leader, Bioinformatics Research Unit
RIKEN Advanced Center for Computing and Communication Japan)
二階堂 愛 先生
(理化学研究所 情報基盤センター
バイオインフォマティクス研究開発ユニット／ユニットリーダー)
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- Place: Lecture room 4, Medical Education & Library Building 4F
医学教育図書棟4階 第4講義室

ABSTRACT

We must avoid involuntary transplanting heterogeneous cell into our body for safely realization of regenerative medicine. Development of a highly reproducible and sensitive single-cell RNA sequencing (RNA-seq) method would facilitate the evaluation of cellular non-genetic heterogeneity in transplanted cells.

In this lecture, I will introduce various single-cell omics technologies regardless of experimental or bioinformatics techniques. Especially, I report a novel single-cell RNA-seq method called Quartz-Seq that has a simpler protocol and higher reproducibility and sensitivity than existing methods [1]. I show that single-cell Quartz-Seq can quantitatively detect various kinds of non-genetic cellular heterogeneity, and can detect different cell types and different cell-cycle phases of a single cell type. Moreover, this method can comprehensively reveal gene-expression heterogeneity between single cells of transplanted cells. I also introduce that cutting edge bioinformatics technique for analysis single-cell RNA-seq uncover spacial and temporal information from snapshot of single-cell transcriptome data.

Furthermore, we developed a novel reverse transcription to extremely reduce dropping-out low-abundant mRNAs in experimental replications. Finally, we develop and introduce a high-throughput single-cell RNA-seq to realize several thousands single-cell RNA-seq to find rare cellular sub-populations from tissues and organs.

References

1. Sasagawa Y*, **Nikaido I***, Hayashi T, Danno H, Uno KD, Imai T and Ueda HR. Quartz-Seq: a highly reproducible and sensitive single-cell RNA sequencing method, reveals non-genetic gene-expression heterogeneity. Genome Biology. 14. 2013 (*Equally contributions)
2. Yoshimoto N, Kida A, Xu J, Kurokawa M, Iijima M, Niimi T, Maturana AD, **Nikaido I**, Ueda HR, Tatematsu K, Tanizawa K, Kondo A, Fujii I & Kuroda S. An automated system for high-throughput single cell-based breeding. Scientific Reports 3, Article number: 1191. 2013.

- Inviter: Ass. Prof. H. Takizawa (Dept. of IRCMS- I) / 滝澤 仁 准教授(国際先端医学 I)
- Essay/レポート宛先(To Ass. Prof. Takizawa): htakizawa@kumamoto-u.ac.jp
- Essay/レポート宛先(CC: Student Affairs Sec. / 医学教務): iyg-igaku@jim.kumamoto-u.ac.jp