J Health Edu Res Dev 2018, Volume 6
DOI: 10.4172/2380-5439-C2-009

CloneSeq: Highly sensitive single-cell-based RNA-seq for comprehensive characterization of tumor cells

Oren Ram
The Hebrew University of Jerusalem, Israel

Tumors consist of cancer clones that are genetically and epigenetically different from one another. These clones compete for space and resources, such that some clones have a selective advantage over others. Different types of cancer treatment, both chemotherapy and targeted therapy, eliminate tumor cells while leaving behind clones that were resistant to treatment. These therapeutically resistant clones, which may consist of only a small number of cells, are a major cause of cancer deaths. The identification of mutations and/or characterization of cellular states that exist in a small fraction of cells is impossible using current bulk sequencing methods, which process a large number of cells. In order to characterize tumor subclones, as well as their specific phylogenetic relationships and their underlying phenotypes, measurement should be done in much smaller resolutions. Transcript expression levels and associated cellular states, such as RNA processing profiles and proliferation rates, as well as somatic mutations in expressed genes can be detected from RNA-Seq. Single cell RNA-seq should potentially enable reconstruction of the tumor's phylogenetic tree and render each cell in the tree with its functional state. However, single-cell RNA-seq poor sensitivity, limits our ability to detect the full spectrum of information requires for accurate profiling. In this talk, I will present a novel technology that enable high sensitive profiling of cancer single clones rather than single cells. This technology based on the capturing of single cells within 3D hydrogel spheres and expansion of cells into small clones. In the next step, the hydrogel spheres containing the clones are profiled using our in-house adaptation of the "InDrop" single cell RNAseq system. Data collected from PC9 cells (human adenocarcinoma cell line) shown clone-to-clone variation as well as superior resolution to detect cellular states comparing to single cell based assays. Further improvement of this technology is still needed and will be discussed in the talk with the exciting potential to next profile patient derived cells and to conduct drug screens for early detection of treatment resistant cells.

oren.ram@mail.huji.ac.il