

Single cell analysis chip for spatial transcriptome of cell network and tissues

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In order to analyze biomolecules in tissues or cultured cell networks, we are developing a chip which can analysis mRNA in each single cell on 2D plane with the positional information of the cells. This chip consists of the array of cell-analysis-units which have a function to extract the cytoplasm from single cell and to hand out them to a next generation sequencer. This task will be achieved with microfabricated piezoelectric Lead-Zirconium-Titanate (PZT) actuators controlled by an active matrix thin film transistor (TFT) array. These are fabricated by newly developed low-temperature solution-based processes using functional Ink, which is advantageous for low-cost and large-area production of active elements.

PZT has excellent piezoelectric characteristics and can be fabricated by solution processes. To obtain a device-quality PZT film, however, its conventional processes required high annealing temperature ($> 600\text{ }^{\circ}\text{C}$), which damages the transistor array integrated to control actuators. By UV/O₃ treatment, we successfully decreased the process temperature below 450°C which is critically important for integration with TFTs [1-3]. By using this process, we fabricated the PZT actuator array with TFT active matrix and confirm piezoelectric operation.

Besides the development the chip, we tried to optimize the quality of mRNA analysis from single cell on chip. A HEK293 cell with green fluorescent protein expression was used as a test cell. The cell was positioned on the micro hole of chip. By increasing the suction pressure, the cytoplasm was extracted to the reverse side of the chip through the micro hole. The mRNA in the extract was analyzed by next generation sequencer and we found that mRNA of more than 14000 genes are recovered from the single cell using our chip through the hole.

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References

- 1) T. T. Phan, et al., *Applied Physics A*, 122 (2016) 623.
- 2) T. T. Phan, et al., *J. Micromech. Microeng.* 27 (2017) 014004.
- 3) R. Shimura, et al., *Sensors & Actuators: A.*, 267 (2017) 287-292.