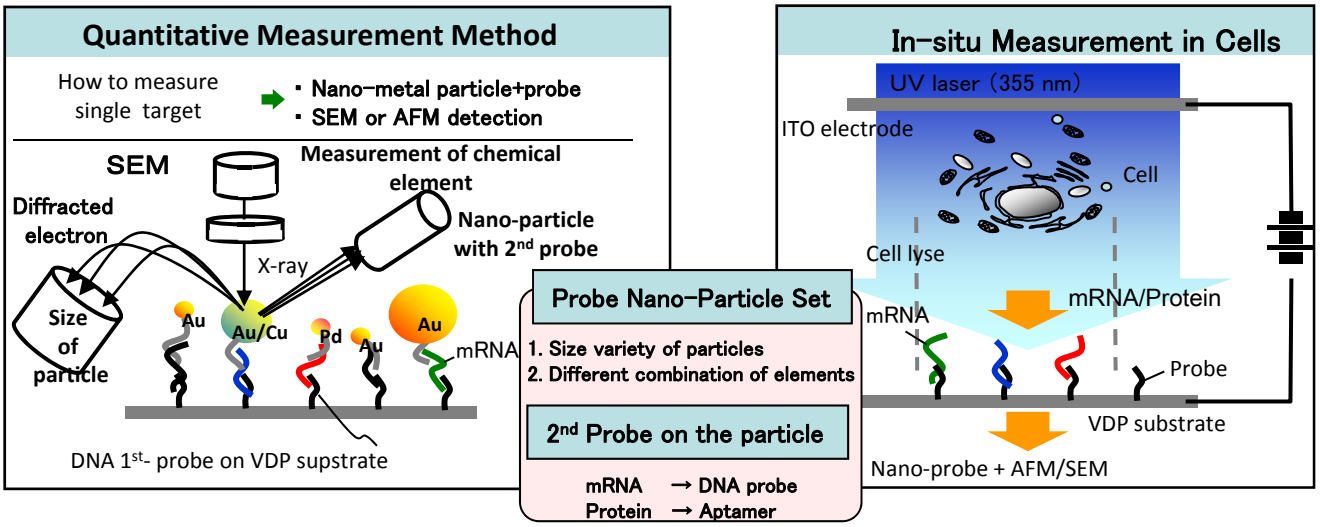
Four-year project

Single-cell-based quantitative genome/proteome analysis for epigenome era of life science

On-chip Molecular Cell Phenomics Project

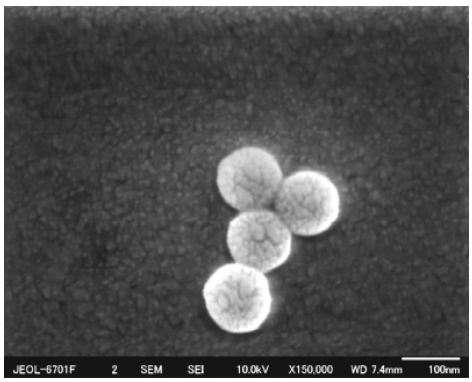
Project Leader
Kenji YASUDA



OBJECTIVE OF THIS PROJECT

In 20th century, knowledge of life science has been expanded dramatically started from the finding of genetic information carrier molecules, DNA. The genome analysis projects such as Human Genome Project showed us the importance of quantitative measurement of RNA expression and the existence of proteins to understand the characteristics of particular cells and phenomenon. And now, in 21th century, the importance of single-cell-based analysis of multicellular system becomes more and more for understanding the community effect of cell group, mechanism of differentiation within the organ and so on. However, we only have the cell-group-based measurement of mRNAs and proteins and those methods also lose the spatial information of the existence of those molecules in the cell.

In this project, we are going to establish new single-cell-based quantitative genome/proteome analysis method. The advantage of this method is that we can distinguish the 'characteristics' of individual cells within the cell groups in organ, and that we can measure the spatial distribution and the real quantitative numbers of particular biomarker molecules within a cell without using any of conventional methods like PCR, or DNA chips. These advantages will give us a chance to understand the new frontier of post genome researches like epigenetics, regenerative medicine, cellome and phenome. The future of this project will contribute for the evolution of the methods in the pharmaceutical industry, and creating new industries in Kanagawa Prefecture.



Gold-coated polystyrene beads（thickness 10nm、diameter 120nm）

Fig.1 Probe Particles

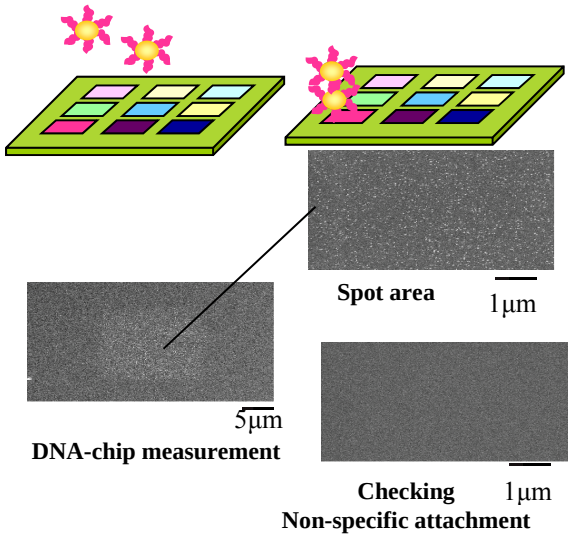


Fig.2 fM-order measurement DNA chip

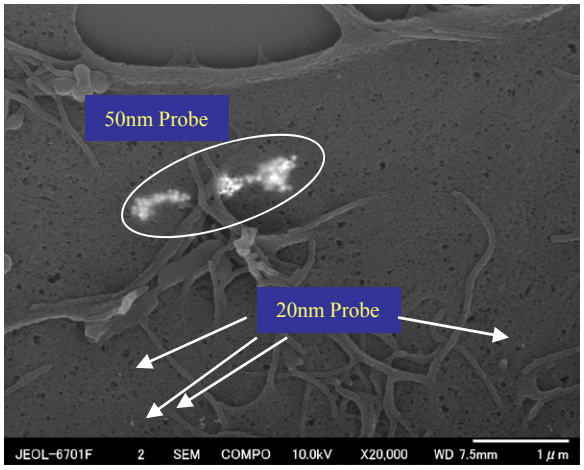


Fig.3 Nano-probes within a cell

Details

① Multi-tlabeled Nano Probe Set Development

We develop a set of different sizes of gold nano-particles having different elements as markers for distinguishing each particle. Using this probe set, we can use more than 200 different target probes simultaneously, which cannot be done using conventional fluorescent probles.

② fM-order Sensitive DNA Chip and Cell Preparation Method Development

Using Nano Prove Set, we develop the fM-order RNA quantitative measurement method, which can distinguish single and double strand RNAs within a cell. We also develop the method to fix cell components on the chip keeping their arrangements within a cell.

③ Single-cell-based On-chip Genome/Proteome Analysis

Using Nano Prove Set and the Chip on which cell components are fixed, we measure the arrangements of biomarkers within a cell quantitatively exploiting our newly developed scanning electron microscopy system.

Formation

Period: ２００８/４～２０１３/３
Member: Project Leader, Full-time Researcher, Par-time Researcher, Collaborator from Universities and Companies.
Place: KSP-East 3F