Institute for Basic Science

Center for Molecular Spectroscopy and Dynamics

COLLOQUIUM

■ **SPEAKER**

Dr. Kyuwan Lee (Intel Corporation)

■ **TITLE**

Quantitative Hyperspectral Imaging of Single Molecule Variants in Live Cells

■ **ABSTRACT**

A single molecule is a fundamental component of the chemical and biological processes, and structural variants of molecules, such as mRNA isoforms causing cancer, are playing critical roles in a variety of diseases even though their expression levels are extremely low. However, there is currently a lack of quantitative technologies for monitoring single-molecule isoforms in inside the live cells. In this seminar, I show that a combination of plasmonic dimer probes and hyperspectral imaging can be used to detect and quantify single molecule variants in different conditions. The probes are made from plasmonic nanoantennae functionalized with molecular probes targeting specific structure of a single molecule, forming nanoantenna dimers or multimers that exhibit distinct spectral peaks and shifts due to plasmonic coupling. With this approach, I present a spectral imaging technique that the spatial and temporal distribution of multiple BRCA1 mRNA variants in the malicious tumor cells can be monitored to reveal the correlation between cancer and the low-expressed mRNA variant by measuring the hybridization dynamics of the nanoplasmonic dimers. This study provides insights into single molecules and their transport in living cells, which could improve our understanding of more advanced molecular complexes in pharmacogenomics, genomic diagnosis, and molecular therapies through newly developed biophysics and biotechnology methods.

Despite the significant advantages of current hyperspectral imaging in providing a high and stable signal to noise ratio for single-molecule detection, the long scanning time may not be applicable for the observation of molecule's translational dynamics. Future work may involve the development of a fast spectral imaging metrology for the tracking of the single molecule dynamics in living cells, such as tumor-related miRNA's response to the chemotherapy, followed by the statistical quality controls by three-sigma limits rule. With this molecular foundry approach, it is possible to unveil the

temporospatial correlations between expression levels of transcripts and proteins for the cancer diagnosis, and eventually, to build a molecular circuit for the manipulation of disease processes.

■ DATE AND VENUE

Apr. 26, 2016 (5:00-6:00 p.m.)
Seminar room 116, R&D Center