Biomedical Engineering Seminar Series

2 nd Semester, Academic Year 2019

Date: February 25, 2020
Time: 10.00 AM – 11.00 PM
Room 6373, 3rd level, Building 3,
Faculty of Engineering; Mahidol University

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"Molecular-based diagnostic platforms for infectious diseases and early detection of cancer"

(1)In diagnosing bacterial infection, rapid bacterial identification (ID) and antimicrobial susceptibility testing (AST) are critical to clinicians in order to provide an effective treatment in a timely manner. The gold standard, culture-based approach provides both ID and antimicrobial susceptibility but requires several days of turnaround time. A rapid bacterial diagnostic approach that is capable of bacterial ID/AST in heterogeneous samples within less than 4 hours by using digital PCR (dPCR) and digital high-resolution melt via microfluidic devices is developed. By utilizing dPCR, amount of nucleic acid can be quantified, which correlates to phenotypic responses of individual pathogens in a mixed sample and also shorten the required time of antibiotic exposure. In addition, a machine learning algorithm to automatically identify bacterial species based on melt profiles of 16S rRNA gene will be discussed.

(2)The vast majority of human cancers exhibit significant intratumor heterogeneity derived in largepart from heterogeneous DNA methylation patterns within the constituent subclonal populations. While heterogeneously-methylated, tumor-specific circulating cell-free DNA (cfDNA) derived from these subclones can be found in the plasma of most cancer patients, current methylation assessment techniques are fundamentally limited in their ability to detect, quantify and discriminate heterogeneously methylated DNA in fractions below 0.1%. Here, we present our recently developed quasi-digital approach called Discrimination of Rare EpiAlleles by Melt (DREAMing). This simple and inexpensive method relies upon high-resolution-melt (HRM) analysis to allow evaluation of tumor heterogeneity from liquid biopsies by quantifying the number and extent of methylation of individual partially and fully-methylated allele-copies at single-CpG-site resolution and single-copy sensitivity.

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