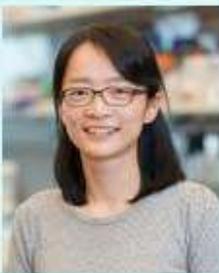


Taiwanese American Association of Pharmaceutical Sciences



2019 TAAP Symposium

Speaker Introduction



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**Emerging Field I:
Beyond DNA mutations:
The Roles of mRNA
Alternative
Cleavage and
Polyadenylation in Cancer**

Bio

Dr. Lee has long-term interests in the contribution of non-genetic aberration in cancer. She is currently a postdoctoral research associate at Memorial Sloan Kettering Cancer Center, where she has been studying the roles of mRNA processing events in tumorigenesis. At her work, she harnesses the power of a specific RNA-seq to identify errors hiding in RNA but not DNA. This work helps to elucidate how patients who harbor very few genetic mutations develop cancer and contribute to better understanding of cancer pathogenesis. It also has potential to provide more cancer treatment options. Prior to joining her current lab, Dr. Lee received her PhD from the University of Nottingham where she gained expertise in the fields of stem cell biology, pediatric brain tumor and epigenetics. She also gained expertise in the cancer epigenome while working at University College London.

Abstract

Genetic alterations are known cancer drivers, but not all patients harbor cancer-driving genetic aberrations. It has become increasingly clear that errors in mRNA processing also contribute to cancer progression. Alternative cleavage and polyadenylation (APA) generates mRNA isoforms differing either in their 3' untranslated regions or in the coding regions without changing DNA sequences. More than half of human genes express APA isoforms, but their biological significance and regulatory processes remain poorly understood. My current research has revealed widespread APA events in chronic lymphocytic leukemia where cancer cells utilize APAs to 1) mimic the outcomes of truncation mutations to affect tumor suppressor genes, and 2) alter protein complex assembly to gain oncogenic protein properties. These findings pave an unprecedented way to identify and investigate novel cancer-relevant genes that have been overlooked by conventional methodologies. The insights gained from my study will have broad biomedical impacts and offer additional prognostic and therapeutic opportunities.