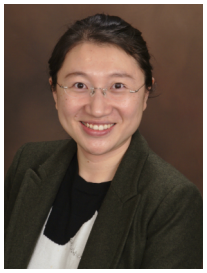
Title: Advanced Molecular Technologies for Cancer Diagnostics and Treatment



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Proposal

Cancer has been listed as the second most common cause of death worldwide. More than 1 million new cancer cases were diagnosed each year. Successful medical treatments are extremely limited by heterogeneous factors, such as tumor microenvironment, social, physical variations and tumor stages. The development of multidrug resistance also seriously hurdles the effectiveness of anticancer drugs. Instead of “one treatment fits all”, more personal diagnostics and clinical trial are required for future biomedical practice to combat cancer.

Advanced molecular technologies, including genomics, transcriptomics and proteomics, have profoundly impacted the modern cancer diagnostics and chemotherapy. The most extensive application of advanced molecular technologies is the Next Generation Sequencing (NGS), which provides sensitive and high-throughput digital data of either whole genome sequence or targeted gene sequences of cancer cells. Raw sequencing data could be either mapped to reference genome or subjected to *de novo* genome assembly. Coupled with advanced computational analysis, single nucleotide polymorphisms (SNPs) or InDel (Insertions and Deletions) could be detected for genotyping. Some other striking applications include massive parallel sequencing of hundreds of breast cancer samples to identify novel gene mutations related to cancer; or transcriptome sequencing to quantify the gene expression levels at different cancer stages.

Whole genome sequencing benefits us with precise disease detection but is limited to the empirical value in clinical application. Non-coding RNA sequence or long repetitive sequences may interrupt with correct genomic assembly and annotation; moreover, genomic variations are not always correlated to the structural or functional differences of proteins. Therefore, proteomics, triplicating the complexity of genomics, has brought our prediction to practice. Cell surface and membrane proteins are attractive targets for identifying novel biomarkers, antigens or drug transporters. By using trypsin shaving, biotin labeling or glycoprotein capturing, these proteins will be isolated from cytoplasmic contaminants and identified by liquid chromatography tandem mass spectrometry (LC-MS/MS).

We invite authors to submit original research as well as review articles to this special issue in **Journal of Cancer Research Updates** that will help improve advanced molecular detection in cancer diseases. Potential topics include, but are not limited to:

1. Discover novel genes, proteins or signal pathways related to cancer disease
2. Laboratory and clinical evaluation of new biomarkers, antigens or drug binding target
3. Clinical trials for cancer diagnostics and treatment based on genomics or proteomics data
4. Statistical analysis of selected cancers based on surveillance, epidemiology or advanced molecular detections
5. Novel advances in cancer prevention, diagnostics and treatment