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Divide and conquer: the road towards more stratified medicine for colorectal cancer

Dr Xin Wang

Assistant Professor and Assistant Head (Postgraduate Education),
Department of Biomedical Sciences, City University of Hong Kong

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Abstract

Colorectal cancer (CRC) is one of the leading causes of cancer-related deaths worldwide. Similar to many other malignancies, CRC is a heterogeneous disease, making it a clinical challenge for optimization of treatment modalities in reducing the morbidity and mortality associated with this disease. A more precise understanding of the biological properties that distinguish patients with colorectal tumors, especially in terms of their clinical features, is a key requirement towards a more robust, targeted-drug design, and implementation of individualized therapies. In the recent decades, extensive studies have reported distinct CRC subtypes, with a mutation-centered view of tumor heterogeneity. However, more recently, the paradigm has shifted towards transcriptome-based classifications, represented by six independent CRC taxonomies. In 2015, the colorectal cancer subtyping consortium reported the identification of four consensus molecular subtypes (CMSs), providing thus far the most robust classification system for CRC. In this talk, I will first briefly go through the historical timeline of CRC classification approaches; discuss their salient features and potential limitations that may require further refinement in near future. Subsequently, I will review recent efforts of the community, including our work, to push forward the clinical translation of CMSs. Despite the encouraging progress, several major challenges prevent translation of molecular knowledge gleaned from CMSs into the clinic. Finally, I will summarize some of these potential challenges and discuss exciting new opportunities currently emerging in related fields.

Biography

Xin Wang is an Assistant Professor and Assistant Head (Postgraduate Education) at the Department of Biomedical Sciences, City University of Hong Kong. He obtained his PhD at the University of Cambridge Department of Oncology and Cancer Research UK Cambridge Institute in 2013, where he identified molecularly distinct colon cancer subtypes using an unsupervised classification approach. From 2013 to 2015, He did his postdoc training at Harvard Medical School Department of Biomedical Informatics, where he applied advanced techniques in next-generation sequencing data analysis to study the role of BRD4-NUT fusion gene in NUT midline carcinoma and characterized LRF as an independent repressive transcription factor of fetal hemoglobin. In collaboration with cancer biologists and clinicians, he is currently working on dissecting molecular heterogeneity and subtype-specific regulatory mechanisms for biomarker development and identification of novel therapeutic targets in major malignancies such as breast, colon, pancreatic, ovarian and liver cancers.