MedicalXpress

Clinical implications of cancer genomics—a special issue of PLOS Medicine

December 6 2016

This week's edition of *PLOS Medicine*, featuring four Research Articles and two Perspectives, begins a special issue devoted to research on cancer genomics. Research and discussion papers selected along with two leaders in the field, Guest Editors Elaine Mardis and Marc Ladanyi, will highlight progress in the study of important cancer types, and assess the clinical implications of progress in this fast-moving field.

In their Perspective article, James Topham and Marco Marra discuss the acquisition of genetic information from tumors, which in recent years has progressed from localized analyses of single genes, and subsequently panels of genes, that are important in specific cancer types, to whole-genome sequencing. Intensive effort is being applied to analyses of tumor genomes aimed at selection of appropriate therapies for individual patients, and the authors emphasize the need to study the dynamic nature of tumor genome sequences—which can change over time and adapt to cytotoxic and other treatments—to maximize the potential benefit for patients.

In a Research Article, Dr. Charles Perou of the University of North Carolina's Lineberger Comprehensive Cancer Center, Chapel Hill, NC, USA and colleagues study the evolution of tumors in two patients with triple-negative, basal-like breast cancer, a disease associated with lack of estrogen receptor, progesterone receptor, and HER2 which generally results in poor clinical outcome. For many cancer types, it is the metastases, or the spread of cancer cells from the original tumor to other parts of the body, that are life-threatening, and it is therefore of interest

to study the cancer after it has left the site of origin. The researchers studied whole-genome sequence and gene expression information from primary tumors and metastases obtained from the patients at autopsy, and report similar somatic mutation and copy number patterns across all tumors in an individual patient. This analysis identified multiple populations of cells, or clones, in the original tumor as well as in the metastatic sites. The findings suggest that metastatic potential is established early in the trajectory of this form of breast cancer, and that multiple clones from the primary tumor traveled together to distant organs.

Anindya Dutta and colleagues present a study of gene expression changes in large datasets derived from patients with brain tumors in a second Research Article—focusing on low-grade gliomas and glioblastoma multiforme, which is a particularly intractable form of the disease. The authors study expression of large numbers of long noncoding RNAs (lncRNAs), which are thought to be involved in governing the expression of other genes and thereby controlling important processes such as development and tumorigenesis. The authors found that a signature made up of selected lncRNAs was associated with length of survival in patients with low-grade gliomas. If validated in future work, these findings could lead to a way to estimate prognosis for patients with this type of tumor, which might be useful in planning treatment.

Further research and discussion articles addressing important topics in the area of cancer genomics will appear throughout the December, 2016 issue of PLOS Medicine.

More information: Topham JT, Marra MA (2016) Sequencing Strategies to Guide Decision Making in Cancer Treatment. *PLoS Med* 13(12): e1002189. DOI: 10.1371/journal.pmed.1002189