OPEN ACCESS Freely available online

Journal of Clinical Research & Bioethics

Editorial

Role of Genomics in Treatment of Cancer

Rosy Stephen*

Department of Oncology, University of Texas, Texas, USA

DESCRIPTION

The study of cancer genomes has revealed abnormalities in genes that drive the development and growth of numerous types of cancer. This knowledge has enhanced our understanding of the biology of cancer and led to new styles of diagnosing and treating the disease. For illustration, the discovery of cancer-causing inheritable and epigenetic changes in tumors has enabled the development of curatives that target these changes as well as diagnostic tests that identify patients who may profit from these therapies. Food and Drug Administration (FDA) in 2011 have approved one similar targeted medicine called vemurafenib (Zelboraf), for the treatment of some cases with carcinoma who have a specific mutation in the BRAF gene as detected by an FDA-approved test.

Although a large number of inheritable differences that drive the development and progression of numerous types of cancer have been linked through large-scale research studies, some tumor types haven't been deeply characterized. In order to define the full set of driver mutations and other differences to DNA and RNA in numerous cancers, new technologies and the knowledge gained from former genomic studies could be used. Studies that compare genomic information from excrescences and normal tissue from the same case allow researchers to discover genomic changes that may drive cancer.

Another occasion is to expand the current use of genomic styles to probe the molecular base of clinical phenotypes. This approach could help experimenters identify inheritable changes that may distinguish aggressive cancers from idle bones, for illustration. Analogous approaches could be used to study the molecular base of response to a given remedy, as well as mechanisms of resistance to treatment.

The wealth of data arising from cancer genome studies decreasingly will be integrated with cases, medical histories and clinical data. These integrated results could be used to develop more customized approaches to cancer opinion and treatment, as well as to improve methods of prognosticating cancer threat, prognostic, and response to treatment. Genomic tools will also be essential for analyzing results from precision drug clinical trials, similar as those being conducted by NCI's Public Clinical Trials Network.

Comprehensive analysis of cancer genomes has revealed a great deal of diversity in the inheritable abnormalities plant within cancers of a single type. Also, intermittent inheritable differences within these cancers are frequently involved in only a small chance of cases. Relating which inheritable changes initiate cancer development and discovering rare inheritable differences that drive cancers are thus challenges for the field. Another challenge is acquiring high- quality natural samples demanded for genomic studies, particularly for excrescence types that are uncommon or rare, or those not treated primarily by surgery.

Developing cell lines and beast models that capture the diversity of mortal cancer is also an unmet need. Models of rare cancer subtypes may be absent or underrepresented, and there are no models for numerous intermittent inheritable lesions in mortal cancer. Managing and assaying the vast quantities of data involved in genomic studies are fresh challenges for the field. This area of exploration requires an effective bioinformatics structure and decreasingly involves benefactions of data and expertise from cross-disciplinary teams.

Correspondence to: Rosy Stephen, Department of Oncology, University of Texas, Texas, USA, E-mail: stephenrosy@gmail.com

Received: November 03, 2021; **Accepted**: November 17, 2021; **Published**: November 24, 2021

Citation: Stephen R (2021) Role of Genomics in Treatment of Cancer. J Clin Res Bioeth. 12:e389.