



Bioinformatics Playing a Lead Role in Cancer Therapeutics

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Editorial

Due to new and powerful technologies, the volume of biological data collected during the course of biomedical research has exploded. In last two to three decades, this world has witnessed a rapid progress of biomarkers and bioinformatics technologies. Cancer bioinformatics is one of such important omics branches for experimental/clinical studies and applications. The availability of these data, and the insights they may provide into the biology of disease, can be used in a big way for precision medicine. At the same time mining the volume of "Big Data" to answer the complex biological questions that could bring precision medicine into the mainstream of clinical care is an evident challenge in oncology.

It is well understood that a dysregulated expression of miRNAs plays a significant role in development of human cancer [1-2]. The importance of miRNAs in cancer is accentuated by the fact that they can function as oncogenes by down regulating tumor suppressor genes [3] or as tumor suppressor genes by down regulating oncogenes [4]. According to an estimate by National Cancer Institute (NCI), USA, just the research performed using next-generation sequencing of patient genomes will produce one Exabyte data by end of 2017 from studies of patients with cancer. The data generated is so complex that it would become unrealistic to think of finding a solution. Hence basic as well as applied miRNA research is being enhanced by cutting edge computational tools and databases freely accessible through online sources.

It is well known that microRNA targeting pathways of human disease provide a new and potential powerful candidate for therapeutic intervention against various pathological conditions [5]. In oral cancer, miRNAs have been shown to affect cell proliferation [6], apoptosis [7], and diagnosis and even in chemotherapy. Keeping in view the immense use of bioinformatics, a study was conducted by authors to identify the genes involved in inflammation of oral cancer and find out the key miRNA by constructing a micronome using Cytoscape software [8]. Dysregulated genes obtained from oral cancer gene databases were analyzed and only experimentally proven miRNAs of inflammatory genes were included in the study. In addition protein-protein interaction network was constructed using Search Tools for Retrieval of Interacting Genes (STRING) database. The constructed micronome revealed miR-19a/b as a key regulator for SOCS3 during cancer related inflammation of oral squamous cell carcinoma [8]. Such type of micronomes can be constructed for a number of cancers in different tissues of interest and bioinformatics can be explored for development of more specific target oriented drug delivery systems at a very fast pace.

Bioinformatics can be further integrated with available data and insights from 5000 years old texts in Ayurveda for personalized medicine, tailoring prevention, diagnosis, and treatment based on the molecular characteristics of a patient's disease. Huge flow of data has necessitated the need of computational support for collection, storage, retrieval, analysis and correlation of data sets of complex information. Use of bioinformatics enables researchers to observe economy and devise noble targeted drug delivery systems. With the adoption of advanced bioinformatics, it has become easier for researchers to overcome various challenges of time consuming and expensive procedures of evaluation of safety and efficacy of drugs at a much faster and economic way. Bioinformatics may be a major game player and trend setter for personalized medicine in cancer therapeutics and other diseases in near future.

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