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CANCER – will Molecular Methods and Bioinformatics Help Us to Reduce Cancer Mortality or Researches have Way ahead

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Editorial Article

On earth there is no human being who is not subjected to the risk of cancer. The only definite way to avoid cancer is not to be born. Study of cancer patterns in human population have contributed to knowledge about its origin. In 2015, there were 8.8 million deaths globally because of cancer [1].

70% of deaths occurred in developing countries. One third of mortality is due to increased body mass index, lack of exercise, tobacco and drinking alcohol. Infections such as hepatitis and human papilloma virus which cause carcinomas are responsible for 25% of deaths [2]. Although both genetic and environmental factors are responsible for the development of cancer, but environmental influences appear to be dominant risk factors for most cancer. Presentation of malignancies in the last stage and unreachable diagnosis and treatment are common. Pathologists play a major role in the early diagnosis of cancer. In 2017, only 26% of developing countries reported having pathology services available in public sector. However, more than 90% of developed countries reported, to have treatment services available. The total annual economic cost of treating cancer patients in 2010 was calculated at approximately 1.16 trillion US dollar [3].

Only 1 in 5 underdeveloped and developing countries have the necessary data to drive cancer policy. Cancers commonly found in males are prostate, lung and colon, in female's breast, lung, colon and rectum and in children leukemia, brain tumors and lymphoma. Cancer is mainly due to successive mutations in genes and because of these mutations there is change in cell function. Different mutations leading to conversion of proto-oncogene to oncogene include chromosomal translocation, point mutations, deletion, and amplification and insertion activation.

Along with genetic, epigenetic modifications such as DNA methylation, histone modification and nucleosome position are leading to the development of cancer cells. Studies are undergoing to explore epigenetic modifications leading to cancer development. Different molecular methods have helped to determine change in protein structure as well as detecting novel cancer biomarkers. Recently, a comprehensive gene panel was performed in Non-Small cell lung cancer cases.

The National Comprehensive Cancer Network [NCCN] guidelines include testing for ROS1, RET, BRAF, ERBB2, and MET in such patients [4]. This testing sets the stage for genotype-driven decision-making and has the potential to significantly impact cancer mortality. The ideal panel of genes targeted is constantly expanding. The next generation sequencing in breast cancer research is mainly used in the following three aspects: genome DNA sequence analysis (including the whole genome sequencing, exon sequencing, targeting gene sequencing), RNA transcription group sequencing (including the whole transcriptome analysis, small RNA sequencing, and noncoding RNA analysis), epigenetic sequencing (including chromatin immunoprecipitation sequencing, methylation analysis sequencing) [5]. Immunohistochemistry and next generation sequencing of genes has introduced new lines of treatment that is targeted therapies. These drugs block or interfere with molecules involved as checks in cell cycle and this lead to uninhibited proliferation of cancer cells. These include hormone therapies, signal transduction inhibitors, gene expression modulators, apoptosis inducers, angiogenesis inhibitors, immunotherapy and toxin delivering molecules. Recently studies are being carried out on immunotherapy treatment and nanotechnology for inhibiting cancer cell growth.

Studies have discovered that in male patients with advanced and untreatable prostate cancer with specific DNA repair mutations can be treated with immunotherapy. Pathologists and cytopathologists are putting efforts to maximize the amount of tumour DNA for Next Generation Sequencing but this is yet to be standardized.

Pathology has made day by day progress during the last few decades. Today, there is a need of implementation of molecular techniques to pathological samples especially cytopathology samples, as it can increase access to testing, reduce turnaround times to results and reduce the need for repeated procedures.

This journal is focused to build a bridge among researchers, academicians and clinicians from different fields to discuss their knowledge and interdisciplinary forum. It will keep all the participants abreast with the latest updates in the field of cancer. It will also provide a platform where participants will learn and share the current trends in the specified areas and also express their thoughts on various aspects of professional importance.

The journal would consider both investigative and experimental studies in vitro and in vivo related to human and animal tissues with clear relevance to carcinogenesis. In this scientific era where innumerable studies are undergoing with so much old and new literature there is need to metaanalyse the literature before publishing the results. Metaanalysis of studies help us to determine the uncertainity, increase statistical power and help in decision making.

The members of editorial board will uphold their responsibilities to shield the quality of scientific research and record. All the procedures will be carried out in a fair manner and to highest ethical standards. No article shall be published under any incentive or influence. Lastly, I take this opportunity to request you all to come forward and contribute scientific material and share clinical experiences for benefit of readers. I congratulate Editor in Chief and editorial team members for

the excellent job done and wish them all a great success in their endeavour of bringing out a useful journal.

References

1. Cancer-World Health organization
2. Plummer M, de Martel C, Vignat J, et al. (2016) Global burden of cancers attributable to infections in 2012: a synthetic analysis. Lancet Glob Health; 4(9): e609-616.
3. Stewart BW, Wild CP, editors. World cancer report 2014. Lyon: International Agency for Research on Cancer; 2014.
4. Ettinger DS, Wood DE, Akerley W, et al. (2015) Non-Small Cell Lung Cancer, Version 6.2015. J Natl Compr Canc Netw; 13(5): 515-524.
5. Ma R, Gong J, Jiang X (2017) Novel applications of next-generation sequencing in breast cancer research. Genes and diseases; 4(3): 149-153.

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