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## **Omic or Multi-Omics Approach can Save The Mankind**

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The publication of the first draft of human genome, has led to the explosion of high throughput technologies including genomics, epigenomics, transcriptomics, proteomics, and metabolomics aiming to characterize the various biological molecules (DNA, RNA, proteins, and metabolites). These high throughput technologies collectively called as omics revolutionized medical research in the last two decades [1]. The advent of next generation sequencing (NGS) reduced the time and economic cost of traditional sequencing and has led to the emergence of genomics as the first discipline of omics. Following the emergence of genomics, a number of projects such as The Cancer Genome Atlas (TCGA), 1000 Genome Project (1KGP), and the International Cancer Genome Consortium have been accomplished [2, 3]. These projects contributed significantly to the understanding of genetic variations in different cancers, for instance, TCGA produced over 2.5 petabytes of big data. Furthermore, the big data produced by these mega projects has been made publicly available to the clinicians and researchers to fast-track the diagnosis and prognosis of complex rare diseases. In developed countries, a multi-omics approach has been applied holistically to the clinical practice for the diagnosis and prognosis of various cancers and rare Mendelian diseases [4].

The use of multi-omic approach has been adopted in different clinical laboratories throughout the globe particularly in the developed countries and has led to the emergence of precision medicine. Advancement in multi-omics dramatically improved the clinical outcomes and classical trend of “one-size-fits-all” has been shifted to a personalized approach. The multi-omics approach is now commonly correlated with the clinical phenotypes of specific patient to precise diagnosis and prognosis regimens. The multi-omics approach enabled the understanding of complex molecular mechanisms of human diseases and

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identified potential pharmacological targets and biomarkers. In the developed countries, advanced laboratories mostly now rely on multi-omics approach to holistically characterize the disease profile of an individual patient. Multi-omics approach now enables the oncologist to think that each tumor is different and needs to be treated on the basis of its specific molecular characteristics. Furthermore, the molecular dysfunction of each tumor needs to be studied and treated accordingly.

The multi-omics approach decoded the molecular dysfunctional signatures of various multisystem disorders [5]. Biological processes are highly dynamic and involves a number of interactions such as genome, epigenome, transcriptome, proteome, metabolome, and ionome. Therefore, it is imperative, to apply a holistic multi-omics approach to comprehend or decipher a specific multisystem disorders [6]. A number of studies clarified the concept that in comparison to single-omic analysis, multi-omics added significantly to the understanding of various complex multi-system disorders [7, 8]. Multi-omics approach involving transcriptomic, proteomic and epigenomic was applied to postmortem human brains to decipher the molecular signatures of Alzheimer's disease [9].

Omics can help in determining the mutational landscape of various rare genetic diseases and cancers of Pakistan's population as they differ from rest of the world. For instance, single-nucleotide gene polymorphisms (SNPs) in the synuclein alpha (SNCA) gene has been associated with increased risk of Parkinson's disease (PD) [10, 11]. The association of SNCA with increased risk of PD is a well-established fact, however SNCA polymorphisms were absent in Pakistani PD patients [12]. Furthermore, there are many other rare diseases in Pakistani population with a different mutational landscape from the western population, however due to the lack of functional use of omics in Pakistan these mutational differences still need to be detected/investigated. Identifying the mutational landscape of various rare genetic diseases and cancers of Pakistan's population can help improve the treatment and outcomes as well as can help drive the clinicians and researchers to develop precise treatment regimens.

Decoding the genomes of emerging viruses was not possible before the advent of multi-omics technologies. In comparison with Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV), the genome of severe acute SARS-CoV2 was decoded within a month and the data has been made publicly available due to the technological advancements in omics. The exponential growth of publicly available SARS-CoV2 sequencing data aided tremendously in its vaccine development by different companies across the world. With such fast track

sequencing and identification, it was made possible to design and implement a robust diagnostic kit around the world. Omics is now being implied to carry out surveillance and detect variants as COVID-19 is progressing. World has moved quickly to mitigate the spread of the virus using the tools of Omics [13, 14]. Overall, omics armed the world dealing with this pandemic successfully and will better prepare the community for similar challenges in the future. Single genetic testing hampered the cancer research and detection of other rare genetic diseases. However, the emergence of NGS as multiscale, robust, and high throughput testing enhanced the diagnostic outcomes [15]. To overcome the common use of traditional testing for various genetic diseases, one of our previous report introduced the use NGS for the diagnosis and screening of  $\beta$ -Thalassemia in Pashtun Family using the entire *HBB* gene [16]. Integration of Omics can fast-track the screening and diagnosis of infectious, genetic and metabolic diseases and cancers.

Currently, multi-omics technologies are flourishing, however these technologies are still not adopted by the clinicians in developing countries due to various factors such as economic cost, turnaround time, analyzing and interpreting the big data, lack of communication and collaboration between academia and clinicians. Keeping in view the integrative utility of multi-omics in cancers and rare diseases, it is important to train the clinicians to understand the importance of multi-omics approach.

In addition to rare genetic diseases, and cancers, Omics also contributed greatly in the surveillance and monitoring of antimicrobial resistance (AMR). Traditional culture based detection of AMR bacteria hampered the diagnosis and treatment regimens. Omics can quickly identify microbes and its antibiotic resistant properties through 16S rRNA gene region or metagenome shotgun sequencing [17]. Omics has led to a paradigm shift and has made it possible to quickly explore gut microbiomes [18, 19], identify useful microbes and eventually use microbes in a beneficial manner. Omics can also identify harmful microbes and will arm the humanity to devise suitable measures against such microbes. Antibiotic resistant microbes' identification using genome sequencing has made it all possible to provide quick, accurate, precise and effective treatments. Although the current pandemic has exposed several limitations in the developing countries in implementing such technologies due to lack of local availability of critical reagents and equipment, genomics is still becoming a popular choice in the diagnostic, treatment and prognostic arena. In summary, it is clear that Omics is beginning to bring a paradigm shift and enabling the scientist to personalize

treatments, improve crops and its productivity, tackle microorganism in a better manner, improve animal's health, productivity and efficiency.

The alarmingly high prevalence of genetic diseases in Pakistan mostly due to consanguineous marriages [20] can be mitigated effectively through better genetic counseling by incorporating various applications of omics. In conclusion, integration of omics can bring significant improvement in the human health of developing nations and can revolutionize agriculture and livestock sector thereby improving the country's economy.

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