Next-generation sequencing in clinical oncology: Transforming cancer treatment.

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Cancer, a multifaceted disease, has long posed numerous challenges for medical researchers and practitioners. Its complexity arises from the diversity of types and subtypes, each with unique genetic signatures. However, the advent of next-generation sequencing (NGS), also known as high-throughput sequencing, is revolutionizing the field of oncology, shedding new light on the genetic intricacies of various cancers and transforming the approach to cancer treatment. Next-generation sequencing is a term used to describe a number of different modern sequencing technologies, including Illuming's sequencing by synthesis, Ion Torrent's semiconductor sequencing, and Pacific Biosciences' single-molecule real-time sequencing, among others. These advanced technologies allow us to sequence DNA and RNA much more quickly and cheaply than older methods like Sanger sequencing, dramatically enhancing the detailed study of genomes [1].

NGS platforms work by simultaneously sequencing millions of small fragments of DNA or RNA. Sophisticated computer programs then piece together these fragments by looking for areas of overlap. This advanced technology enables us to sequence an entire human genome within a single day. The application of NGS in oncology is incredibly valuable for diagnosing, classifying, and managing cancer. Traditionally, cancers were classified by their tissue of origin. However, NGS technology allows us to reclassify them based on their genetic profile, a far more effective approach. For instance, breast cancers can be divided into subtypes based on the presence or absence of certain gene mutations, which gives more information about prognosis and guides targeted treatment strategies [2]. NGS also enables us to identify genetic mutations across a broad spectrum of cancer-related genes, making it a powerful tool for diagnosing cancer. For example, a patient with lung cancer can be tested for EGFR mutations, ALK rearrangements, and other potential genetic changes that could be driving their cancer, all in one test.

The most profound impact of NGS in oncology lies in its ability to facilitate personalized cancer treatment, also known as precision oncology. By sequencing a patient's tumor, clinicians can gain detailed insights into the genetic mutations driving a patient's cancer. This knowledge can then guide the selection of targeted therapies that specifically inhibit the function of the mutated genes. Additionally, NGS can help predict a patient's response to specific treatments and identify those at risk of aggressive disease or relapse. For instance, chronic lymphocytic leukemia (CLL) patients with a TP53 mutation have a poor response to standard chemotherapy and are often directed towards alternative treatments. NGS plays a crucial role in monitoring minimal residual disease (MRD), the small number of cancer cells that may be left after treatment and could lead to relapse. NGS is highly sensitive and can detect MRD that would be missed by traditional imaging or laboratory tests [3].

Moreover, as tumors evolve, they can develop resistance to treatments. NGS can help identify new mutations that arise during treatment, which can drive this resistance. By tracking these changes, clinicians can adapt treatment strategies to overcome resistance and improve patient outcomes. Despite the enormous potential, there are challenges to the widespread adoption of NGS in clinical oncology. These include the high cost of sequencing, the complexity of data analysis and interpretation, and the need for robust databases to match identified mutations with targeted treatments. Additionally, ethical and legal issues related to genetic data handling must also be addressed [4].

However, the future of NGS in oncology is undeniably promising. With the rapid pace of technological advancements and decreasing sequencing costs, the use of NGS in routine cancer care is becoming increasingly feasible. Furthermore, the development of liquid biopsy techniques, which detect genetic material from tumors in a blood sample, opens the door to non-invasive cancer diagnosis and monitoring, further expanding the potential applications of NGS. next-generation sequencing is poised to usher in a new era in oncology, one where cancer treatment is tailored to the genetic makeup of an individual's tumor. While challenges remain, the promise of NGS in enhancing our understanding of cancer and improving patient outcomes is a testament to the potential of this powerful technology [5].

References

1. Postemsky PD, Bidegain MA, Lluberas G, et al. Biorefining via solid-state fermentation of rice and sunflower by-products employing novel monosporic strains from Pleurotus sapidus. Bioresour Technol. 2019;289:121692.
2. Yasui M, Oda K, Masuo S, et al. Invasive growth of Aspergillus oryzae in rice koji and increase of nuclear number. Fungal Biol Biotechnol. 2020;7(1):1-5.

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3. Lee DE, Lee S, Jang ES, et al. Metabolomic profiles of Aspergillus oryzae and Bacillus amyloliquefaciens during rice koji fermentation. Molecules. 2016;21(6):773.
4. Postemsky PD, Bidegain MA, Lluberas G, et al. Biorefining via solid-state fermentation of rice and sunflower by-products employing novel monosporic strains from Pleurotus sapidus. Bioresour Technol. 2019;289:121692.
5. Yasui M, Oda K, Masuo S, et al. Invasive growth of Aspergillus oryzae in rice koji and increase of nuclear number. Fungal Biol Biotechnol. 2020;7(1):1-5.

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