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Commentary

Cancer Genome and Its Treatment

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DESCRIPTION

A group of diseases known as cancer are caused by Genetic mutations that change cell function and lead to uncontrolled development and malignancy. These abnormalities can include DNA mutations, rearrangements, deletions, amplifications, and the addition or deletion of chemical markers, among other variations. Cells may produce aberrant quantities or misshaped proteins that do not function normally because of these alterations. The combination of various genetic changes work together to promote cancer. Acquired genetic variations are the main cause of most malignancies. But, in about 5% of cases, the person inherited a variation that significantly raises their risk of causing a cancer.

Unfortunately, some cancers are more difficult to assess because looking at their genomes would involve invasive, uncomfortable biopsies or surgeries where very little amounts of the cancer tissue are taken for analysis. Because repeated biopsies are simply not possible, this also makes it more challenging for clinicians to monitor how treatment for some cancers is progressing. Instead of directly sampling the tumour, recent advancements now enable the detection of circulating tumour DNA (or ctDNA) in the blood of patients. Cancer cells release some of their DNA into the bloodstream as they rapidly divide and die. These ctDNA fragments can now be found and sequenced in the bloodstream independently from the patient's normal DNA using current diagnostic procedures known as “liquid biopsies”.

Advancements in high-throughput genomic technologies present new chances to positive effect and cure cancer. Many upcoming sequencing and data analysis studies from the last ten years have allowing to map the genetic landscapes of different cancer types, and single cell analyses are illuminating tumour heterogeneity. Innovative new technologies such as spatial omics can provide previously unattainable insight into the microenvironment and spatiotemporal tumour architecture. In this aspect, the following subjects are covered in the special issue's review and experimental and clinical studies:

- Whole genome sequencing
- Individual cell genomics
- Signatures of mutations
- Epigenomics
- Tumor progression
- Techniques for data analysis, bioinformatics, and machine learning
- Heterogeneity of the tumour-circulating tumour cells
- Medical precision
- Interactions between tumour microenvironments
- Immunology computation

Environmental variables can lead to somatic mutations. For instance, the DNA C base can change to a T base as a result of the sun's harmful UV radiation, which can result in the development of tumours. By comparing the sequences from a patient's sample and a sample of their tumour, these can be found using whole genome sequencing. Several additional environmental factors, such as smoking, viral infections, or the random alterations that take place when a cancer is quickly spreading, can also produce modifications to the cancer genome, which are detectable.

Treatment of cancer genome

Refining treatment: The right move of treatment for the patient can be determined using some genetic variations which are found in the cancer genome. The possibility that a person will respond to given treatment can vary depending on several variants.

For example, EGFR-inhibitor medicines work well on tumours with specific EGFR gene variants but not on tumours without those variants. Hence, based on the genetic information from their tumour, two persons with the same diagnosis of breast cancer may receive different therapy.

The major obstacle for targeted cancer therapy remains to be treatment resistance. Patients understand the resistance mechanisms in multiple ways. Expect new treatment paradigms to grow as new resistance mechanisms are identified. To develop the profession, creative biomarker studies are required, but they must consider factors as tumour heterogeneity, the risks and expenses of invasive biopsies, and patient comfort. In order to reduce the number of tumour biopsies, patient discomfort, expense, and inconvenience, non-invasive biomarkers and

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advanced technologies should be explored. They include the utilisation of circulating tumour cells and cytokines.