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Cancer Genomics Research-Opportunities and Challenges

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Cancer Genomics

Though a large number of genetic alterations that determined the development & progression of several types of cancer have been identified through research studies, few types of tumors have not been deeply characterized. Knowledge gained from the foregoing genomic studies might be useful to define the full set of driver mutations and other alterations to DNA and RNA in many cancers through new technology. Studies that relate to the genetic information from normal tissue and tumors rom the same patient allow the researchers to discover the changes in the genome that may drive the cancer.

Currently the other opportunities in the genomic research will be helpful in expanding the use of genomic methods to investigate on the molecular basis of clinical phenotypes. These approaches help the researchers to identify the changes in genes that may distinguish aggressive cancers from indolent ones, for example. Similarly, these approaches could be used to study the molecular basis and response to a given therapy, and mechanisms of resistance to the treatment.

The wealth of the emerging data from the studies of cancer genome is increasing and integrated with the patients' medical history and clinical data. These integrated results are used in the development and more tailored approaches in diagnosing the cancer and treatment, to improve methods of predicting the cancer risk, prognosis, and response to treatment.

Genomic tools are also essential in analysing the results from the clinical trials.

Comprehensive analysis of genomic cancer has exposed a great diversity abnormalities found in the genome within the cancers of a single type. Moreover, the recurrent genetic alterations within these single type cancers are often involved in the small percentage of cases only. Identifying those genetic changes initiate the cancer development and helps in discovering the rare genetic alterations that drive the challenges in the field of cancer genomics.

The other challenge is acquiring a high-quality biological sample needed for genomic studies, particularly for types of tumor that are unusual or rare, or those cannot be treated primarily by surgery.

Developing the cell lines and animal models that incarceration the diversity of cancer in human is also an unmet need. Rare cancer subtypes models may be non-existent or underrepresented, and there are no models for many recurrent genetic lesions in human cancer.

Analysing and managing the vast amounts of data involved in the genomic studies are the additional challenges. In this his area of research, it requires an efficient bioinformatics infrastructure and increasingly involves the contributions of data from cross-disciplinary teams.

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