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DNA Profiling in Identification of Mutational Signatures

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Editorial

Cancer and causes of mutation

Cancer is designated as unhindered cell growth. Gene mutations can initiatemalignancy by increasing the rate of cell division or preventing usual controls on the system, like cell cycle arrest or apoptosis. As per earlier established studies, it is well known that the primary cause of cancer is some unwanted changes in the structure of DNA that are else considered as mutations. Mutations causing cancer can be due to a number of reasons including the lack of fidelity of the DNA replication machinery, disclosures to the mutagen, enzymatic DNA alteration, and faulty repair of DNA that consequences a certain fingerprint on DNA damage. Every living cell of the human body retains somatic mutations all through life.

Definition of mutational signatures

Somatic mutations exist in all cells and occur throughout life. They are the consequence of multiple mutational processes, including the intrinsic slight infidelity of the DNA replication machinery, exogenous or endogenous mutagen exposures, enzymatic modification of DNA, and defective DNA repair. Diverse mutational processes produce exclusive combinations of mutation types, designated "Mutational Signatures".

These mutational signatures otherwise considered as fingerprints support in understanding cancer development and prevention. All-embracing analyses have revealed several mutational signatures in human cancer kinds. Nevertheless, previous researches were not adequate to identify all probable mutational signatures [1].

Mutational signatures identification by DNA profiling

Mutations are of numerous categories like single nucleotide mutations or deletion or insertion of a chain of nucleotides subsequent in genetic changes. These changes can act as mutational signatures to be identified by molecular fingerprinting/DNA fingerprinting. The major significance is having a prevalent database of reference mutational signatures ever. About 50% of the mutational signatures have recognized explanations; however, this source could find more causes and recognize cancer development well. Definite mutational signatures, or molecular fingerprints, disclose the cancer response to drugs [2].

Forthcoming prospective

Many future aspects are present using a DNA profiling technique. Accumulation of mutational signatures from model systems, exposed to known mutagens or disturbances of the DNA maintenance machinery and assessment with those found in human cancers. Other is the association of the causes of mutational signatures with other biological characteristics of each cancer through varied methods extending from molecular profiling to epidemiology. Jointly, the researchers will develop the cancer etiology understanding with possible suggestions for prevention and management.

Mutational signatures can reveal sources of cancer drivers

Mutational signatures support to classify mutational processes acting on the genome. As per some of the research it indicates, some regions are more vulnerable to disruption by some mutagenic processes than others are. There is a strong association between mutational processes and driver mutations [3,4].

References

1. https://www.sciencedaily.com/releases/2020/02/200205132330.html
2. Hanane Omichessan, Gianluca Severi and Vittorio Perduca. "Computational tools to detect signatures of mutational processes in DNA from tumours: A review and empirical comparison of performance." *PloS One* 14 (2019): e0221235.
3. Daniel Temko, Ian P.M. Tomlinson, Simone Severini and Benjamin Schuster-Böckler, et al. "The effects of mutational processes and selection on driver mutations across cancer types." *Nat Commun* 9 (2018): 1-10.
4. Stephen Henderson, Ankur Chakravarthy, Xiaoping Su and Chris Boshoff, et al. "APOBEC-mediated cytosine deamination links PIK3CA helical domain mutations to human papillomavirus-driven tumor development." *Cell Rep* 7 (2014): 1833-1841.

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