



Elucidating genomic instability and its outcomes as cancer origin

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ABSTRACT

Increased propensity of alterations in the genome during the life cycle of cells is called as genomic instability. It is a major cause of oncogenesis. There are four major mechanisms that control the genome instability while the normal cells divide. These mechanisms are DNA replication of high precision and accuracy in S-phase, mitosis involving precise chromosome separation, correct repair of infrequently occurring DNA damage, and cell cycle development in synchronized manner. This briefly throws light on processes at molecular level that play significant role in preventing oncogenesis through genomic instability.

Keywords: DNA, RNA, Genes, Instability, Cancer, Implications.

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INTRODUCTION

Genomic instability as a major driving force of tumorigenesis. In normal circumstances, healthy somatic cells undergo cell division to form exactly same duplicate genome that equally divides to form daughter cells containing same genetic material as parent cells. Abnormally high number of errors in cell division results in various nature of genome alterations and aberrations in the daughter cells [1-4]. Some of these important alterations include specific genes mutations, gene amplifications, rearrangements or deletions of chromosome segments, entire chromosome gain or loss etc. Increased frequency of alterations in genome sequence may impair cell division cycles, uneven cell growth and death, and ultimately cancer. As stated earlier, genomic instability is defined as higher chances and tendency of genomic alterations in cell division process. Here, genomic instability results due to failure of parental cells to duplicate the genome accurately and for-

mation of daughter cells with inaccurate distribution of the genomic material. The process of cell division in normal tissues proceeds with high-fidelity, regulated tightly to avoid neoplasm and cancer initiation. at the molecular level process of oncogenesis can be viewed as a series of cell divisions that involves accumulation of genomic alterations. A pre-cancerous cell formation from a normal cell can be seen as result of alteration(s) of vital genes in a progenitor cell. Not all pre-cancerous cells may lead to cancer, however add on genomic alterations can allow their further growth to initiate cancer. Consequently, increased number of neoplastic cells can consolidate to a clinical stage that can be diagnosed as cancer. Further genetic alterations among the cancer cells can result in subpopulations of cells with even more aggressive properties [5-10]. Thus, the accumulation of genome with altered sequences is a triggering factor and an impetus for tumorigenesis. During neoplastic transformation and progression, genetic changes occur and accumulate in distinct subsets of cell populations, establishing a critical point in this model of tumorigenesis. Thus, heterogeneity observed in cancer can be attributed to the diverse genetic background among the cancer cells.

Mechanisms of genomic stability

Major mechanisms used to maintain genomic integrity. Since uncontrolled cell growth results in cancer, and tumorigenesis is triggered by the accumulation of genomic alterations during cell, it becomes imperative to understand how genomic stability is preserved during cell divisions and tumorigenesis is averted during normal tissue growth. Genomic stability during normal cell division process follows four mechanisms: (i) DNA replication of high precision and accuracy in S-phase, (ii) mitosis involving precise chromosome separation and distribution

among daughter cells (iii) correct repair of infrequently occurring DNA damage in all phases of cell cycle, and (iv) checkpoint control with progress of cell cycle. Other mechanism(s) can be considered as outcome of genomic instability and may aid in development of cancerous cells. Such mechanisms include apoptosis (programmed cell death) and senescence (loss of cells ability to grow and divide). In all four mechanisms numerous molecular processes are involved. For example, in the S-phase, the entire genomic DNA duplication is an accurate process with high fidelity occurring only once for a cell and only once per cell cycle. Genomic instability is evident with any tendency for errors in this process [11-14].

The major mechanisms to minimize genomic alterations in association with DNA replication are as following. (i) proofreading activities by DNA polymerases and High-fidelity of base-pairing. (ii) Mismatch repair machinery mainly in repeat DNA sequences, mismatched bases, and replication slippage resulting in secondary DNA structures (iii) Timely resolution of slowed down replication forks. Various forms of replication blockages often pause or even collapse DNA replication forks. Timely re-start of replication process ensures duplication of the genome in entirety and minimizes the likelihood of further genome alterations. Proteins of homologous recombination and other DNA repair processes are required for this process. (iv) Maturation of Okazaki fragments. While DNA synthesis proceeds, multiple Okazaki fragments represent duplicated lagging strand. RNA primer and a short DNA segment (i.e. a segment) at the 5' - end of each Okazaki fragment is a synthesized by a low-fidelity DNA polymerase. The DNA segments and the RNA primers are removed before the ligation of Okazaki fragments. Here, genomic alterations may results with dysfunction in Okazaki fragment maturation. (v) Replication licensing mechanisms to ensure that the entire genome is duplicated completely once and only once per cell cycle [15-19]. The assembly of pre-replication complex at the site of replication origin before S-phase probably controls this regulation. (vi) Newly synthesized DNA is re-assembled into chromosomes in co-ordinated manner. (vii) Other critical mechanisms for accurate replication include exact duplication of epigenetic signatures on the newly synthesis DNA and chromatin telomere maintenance.

Interrelating genomic stability with cancer

It is significant to note that the outcome of the DNA repair varies in fixing genomic instability. Rearrangements of genome segments or alterations on the DNA sequence may take place while execution of some of the repair processes to fix DNA double helix chemical damages. This type of repair is commonly called as 'error-prone' repair. Noticeably, it may lead to genomic instability, although it can prevent further genomic alterations otherwise arising from the initial DNA damage [20-24]. In contrast, 'error-free'

repair processes may not only preserve the original genome structure, but also fix the chemical damage to the DNA, an example is the repair of DNA DSBs. The 'error-free' homologous recombination repair of DSB is less likely to cause genomic alterations. Conversely, the non-homologous end-joining pathway carry high risk of mutations and/or genome rearrangements, hence 'error-prone'. Nonetheless, the basis of this classification is relative risk to produce errors. Accordingly, it is to be remembered that the 'error-free' repair sometimes undeniably causes errors and the 'error-prone' repair does not always produce errors [26-30].

Cell cycle progression is co-ordinated by Checkpoints. The progression of the cell cycle is highly coordinated since the cell division is conducted in an orderly, systematic and logical manner. Significant propensity for genomic alterations is evident with premature entry of a cell into the next cell cycle phase [31-35]. Checkpoints at every phase of the cell cycle are built to ensure smooth progression from one phase to the next with minimum risk of genomic alteration. Removal of risk factors (such as spindle abnormality prior to anaphase, DNA damage in G1/S/G2 phase, etc.) by delaying the entry into the next phase reduces the risk of genomic alterations. In addition, severely damaged or high risk cells from the dividing pool are eliminated by cell cycle checkpoints that effectively trigger some processes (e.g. mitotic catastrophe, apoptosis, and senescence) [36-41].

CONCLUSION

The relationship between genomic instability and cancer is complex and almost every major aspect of cell and molecular biology is involved. In this review, we collect nine review articles to cover few aspects related to DNA replication, DNA damage response and repair, and to exemplify their implications in cancer therapy. The specific topics are restart of stalled replication forks, replication licensing, maturation of Okazaki fragments, RecQ and Blm helicases in resolving stalled replication forks, RAD9 checkpoint protein in tumorigenesis, microRNA regulation of p53, epigenetic regulation of DNA damage repair, DNA repair polymorphism and cancer risk, and synthetic lethality and viability in the context of tumorigenesis and therapy. Although the cell cycle checkpoints and regulation of mitosis are integral parts of the genome stability maintenance system, reviews in these aspects are not included due to space limitation.

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