

Aging in Humans and Role of DNA Methylation

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Received: July 29, 2018; **Published:** September 27, 2018

Keywords: Aging; DNA Methylation; Forensic

Aging is a gradual and indubitable phenomenon occurs in human life which is affected by many factors such as genetics, environment, lifestyle, smoking, alcohol, and disease [1]. During aging, alteration of gene expression, cellular structures, and telomeres in humans occurs. Biochemical alterations like DNA methylation are closely associated with aging in humans [2]. It is a result of an enzymatic process in which -CH₃ group is bound to DNA at CpG site [3,4]. Modifications in DNA methylation are categorized into two types (a) hypomethylation and (b) hypermethylation [5]. Hypomethylation in cancerous cells is because of deprivation of methylation from the repetitive regions of the concerned genome and it is also associated with the loss of imprinting and instability of chromosomes [5,6]. Hypermethylation occurs when there is enhance in methylation of cytosine (C) and adenosine (A) moieties in DNA [6]. When cytosine (C) is followed by guanine (G) nucleotide and separated by one phosphate atom then that area is recognized as CpG site and DNA methyltransferases (DNMTs) are the enzymes which act as catalysts in this reaction [3]. A large frequency of CpG sites clustered in a region is called as CpG islands. These are recognized as areas having G +C content > 50%, length > 200 base pairs, and observed/expected CpG ratio of 0.6 approximately [7]. When hypermethylation of CpG islands takes place in the promoter regions of tumor-suppressor genes, it directly causes carcinogenesis. Another definition which is equally relevant, important, and related to DNA methylation is demethylation [8]. Demethylation is the loss of a -CH₃ group from a molecule. Demethylation is helpful in the mechanisms of many diseases and epigenetic reprogramming of genes [9]. Epigenome-wide association study (EWAS) shows the significance of DNA methylation in the biological research area. This process is a valuable tool to foretell human age, complex disorders such as diabetes, rheumatoid arthritis, stroke, metabolic diseases and also helpful in forensic science [3]. The significance of prediction of age can be rationalized by the following concepts: (1) in the area of forensic science when investigating a suspect, based on blood, hair left at the crime spot (2) for verifying several theories associated with biological aging (3) in understanding the cell differentiation and ontogeny (4) in diagnosing age-linked disorders such as cancer, metabolic disorders etc. (5) in foretelling the onset and levels of several diseases [10-13]. For future perspectives, many attempts can be created to improve the age prediction accuracy in humans and to discover the other biological processes. In addition to this, the most changeable span of an individual in its whole lifespan can be found out. By these parameters, the accuracy of age prediction in youngsters [14] as well as older people can be made which will help in measuring the quality of life (QoL) in the aging population [15,16]. The authors think that all these efforts can be helpful in clinical and forensic areas.

Financial Support and Sponsorship

Nil.

Conflict of Interest

None.

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Volume 6 Issue 10 October 2018

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