

A Short Note on Biomarkers of Aging and Their Applications

Park Geon Hyung^{*}

Department of Geriatrics, Seoul University, Seoul, South Korea

<u>ISSN: 2329-884</u>7 Journal of

Aging Science

ABOUT THE STUDY

Biomarkers of aging are biomarkers that can assess functional potential at a later age better than chronological age. In other words, the biomarkers of aging would give a true "biological age", which may vary from the chronological age. Verified biomarkers of aging allow test interventions to extend lifespan because changes in biomarkers are observed throughout the organism's lifespan. Although maximum lifespan would be a means of validating biomarkers of aging, it would not be a practical means for long-lived species such as humans because longitudinal studies would take far too much time. Ideally, biomarkers of aging should assess the biological process of aging and prevent disease, minimize the amount of injury to be tested in the organism, and measure reproduction over a short period of time compared to the organism's lifespan.

Although hair becomes gray with age, gray hair cannot be called an aging biomarker. Similarly, skin wrinkles and other common changes seen with aging are no better indicators for future activity than over time. Bio gerontologists have continued their efforts to find and verify the biomarkers of aging, but so far success has been limited. CD4 and CD8 memory T cells and innocent T cell levels were used to provide better estimates of life expectancy in middle-aged mice. Advances in big data analysis have allowed the development of new types of "aging clocks". The epigenetic clock is a promising biomarker of aging and can accurately predict human chronological age. Basic blood biochemistry and cell counts can also be used to accurately estimate age over time. Subsequent studies of the hematological clock on large datasets from populations in South Korea, Canada, and Eastern Europe have demonstrated that biomarkers of aging can be population-specific and predict mortality. It is also possible to estimate human chronological age using a transcriptomic clock.

Applications of aging biomarkers

The main mechanisms identified as potential biomarkers of aging are DNA methylation, loss of histones, and histone modification. Uses for biomarkers of aging are ubiquitous and identifying the physical parameter of biological aging allows humans to identify our true age, mortality and morbidity. The change in physical biomarker should be proportional to the change in the age of the species. Therefore, once the biomarker of aging is established, humans will engage in research into extending life expectancy and finding timelines for the emergence of potential genetic diseases.

One of the applications of this search is to determine the biological age of an individual. DNA methylation uses the structure of DNA at different stages of life to determine age. DNA methylation is the methylation of a cysteine in the CG or CpG region. The Hyper methylation of this area is associated with reduced transcriptional activity and is the opposite of Hypermethylation. In other words, the more "tightly" held the DNA region, and then more stable and "younger" the species are. By examining the properties of DNA methylation in tissues, it was found that it is almost zero for embryonic tissues, which can be used to detect the acceleration of age and the results can be reproduced in tissue. Another major benefit is the role played by the pleiotropic P53 gene in the control of metabolic homeostasis and age-related obesity and diabetes.

Correspondence to: Dr. Park Geon Hyung, Department of Geriatrics, Seoul University, Seoul, South Korea, E-mail: geonhy@gmail.com Received: 01-Feb-2022, Manuscript No. JASC-22-15879; Editor assigned: 03-Feb-2022, PreQC No. JASC-22-15879 (PQ); Reviewed: 15-Feb-2022, QC No. JASC-22-15879; Revised: 17-Feb-2022, Manuscript No. JASC-22-15879 (R); Published: 23-Feb-2022, DOI: 10.35248/2329-8847.22.S10.002. Citation: Hyung PG (2022) A Short Note on Biomarkers of Aging and Their Applications. J Aging Sci. S10: 002.

Copyright: © 2022 Hyung PG. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.