Synopsis of Original Research Paper

Development of molecular marker for aging based on epigenetic changes of skin cells

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With the aim of developing molecular markers that can be applied to quantitatively assess skin cell ageing, we planned to carry out genomic analysis of skin epidermal cells sampled from a large number of subjects. Here we focused on the 'epigenetic clock', a method to estimate human ages based on methylation status of the genomes. Although various epigenetic clocks have been developed for various organs for people in Western countries, these are expected to have large errors if applied to the Japanese skin data. So, it is necessary to collect original epigenetic data and develop a formula for estimating ages suitable for Japanese skin tissue. The resulting age estimator is expected to be of use not only in the cosmetology field, but also in various fields such as forensic medicine and physical anthropology. As this study has been significantly delayed from its original plan and is still ongoing, the main results of the study will be published elsewhere in the future. In this paper, we present the results of verification experiments on each technical element that was required to complete this research. Specifically, we report the evaluation of sampling methods that allow samples to be taken without contact between the subject and the experimenter, a comparison of the collection efficiency of five different sample types, and the results of trial measurements of bacterial flora that is possibly associated with aging. After several trial experiments, we have achieved a situation where we can use these technologies consistently. The collection and analysis of samples for this study is currently underway. In the near future, the main objective of this study -the development of ageing markers for skin- should be achieved.