Developing a Method to Evaluate Skin Aging Using Proteomics Technology

Tran, Minh (School: HUS High School for Gifted Student)
Hoang, Lam (School: High School for Gifted Students, Hanoi University of Science)

Background: Skin aging is a natural biological process that was cause by a comprehensive combination of intrinsic and extrinsic factors. This process varies a lot among individuals and often being accelarated from mid-40s onward. To reduce premature skin aging, studies have been conducted to indentify biomarkers for skin health mornitoring and precision skin care. In this study, we attemped to develope a non-invasive method for skin aging assessment via tape-stripping coupled with proteomic profiling. Method: The study was conducted on 39 female participants with aged from 20-30s and 50-60s. Stratum corneum layer of the skin were collected using D-squame tapes from both upper arm and dorsal hand. Proteomics analyses were performed using LC-MS/MS systems, followed by downstream analyses with various bioinformatic methods. Results: A total of 3,551 proteins were identified from LC-MS/MS analysis. Among that, 188 and 230 differentially expressed proteins (DEPs) were found to be associated with natural aging and photoaging, respectively. These markers were used to generate natural aging and photoaging indices, which effectively distinguished the two age groups and sampling locations. Single geneset enrichment analysis identified several biological pathways, which was showed to be associated with skin aging accelleration, significantly altered among groups such as hyaluronan metabolism and DNA damage response. Using public database, we also identified potential biomarkers as indicators for retinols usages. Conclusion: This study offers a study non-invasive tool for assessing skin aging at a molecular level. By successfully distinguish natural aging and photoaging, these results provide a scientific structure for evaluating the efficacy of cosmetic treatments.

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