***In Silico* Analysis of Gene Interaction Networks for Personalized Skin Aging Therapy**

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**Background and aims.** Skin aging is a multifactorial biological process influenced by both genetic and environmental factors. Single nucleotide polymorphisms (SNPs) are known to influence gene expression and biological pathways related to skin structure and function. In recent years, senolytic compounds have gained attention for their ability to selectively eliminate senescent cells; however, their application in personalized skin aging therapy remains limited. This study aimed to construct a gene interaction network by analyzing SNP-related genes and to screen potential senolytic compounds, thereby contributing to the development of personalized therapeutic strategies for skin aging.

**Methods.** The study included 2,386 senolytic compounds obtained from the Selleck Chem L1200 library, along with aging-related skin targets collected from the Ageing Clusters, GEO Datasets, and HGNC databases. The applied methods consisted of constructing a gene interaction network to identify therapeutic targets and potential senolytic compounds for the treatment of skin aging, analyzing genes affected by single nucleotide polymorphisms (SNPs) in Asian skin, performing molecular docking of compound–target complexes using AutoDock Vina and AutoDock4, and conducting molecular dynamics simulations of the selected complexes using GROMACS.

**Results.** The gene interaction network identified ten target genes, among which TNF, IL6, and MMP9 were specifically associated with SNPs found in Asian skin. Furthermore, K517 (GSK2606414), K1329 (CP 43), and K1720 (AMG-47a) were identified as promising senolytic compounds for the treatment of skin aging due to their strong binding affinities with the investigated targets. The TNF–K517 complex satisfied evaluation parameters in molecular dynamics simulation after 100 nanoseconds.

**Conclusion/Discussion.** The study highlighted three SNP-related genes and identifies promising senolytic compounds through *in silico* methods. TNF–K517 demonstrated stable binding, suggesting its potential application in personalized therapy for skin aging.

**References.**

1. Hahnel E, Lichterfeld A, Blume-Peytavi U, Kottner J. The epidemiology of skin conditions in the aged: A systematic review. *J Tissue Viability*, 2017; 26(1): p. 20-28.
2. Tsitsipatis, D.,  Martindale JL, Ubaida-Mohien C, et al., Proteomes of primary skin fibroblasts from healthy individuals reveal altered cell responses across the life span. *Aging Cell*, 2022; 21(5): p. e13609.
3. Khojah H, Ahmed SR, Alharbi SY, et al., Skin anti-aging potential of Launaea procumbens extract: Antioxidant and enzyme inhibition activities supported by ADMET and molecular docking studies. *Saudi Pharmaceutical Journal*, 2024; 32(7): p. 102107.
4. Yang H, Zhang Q, Zhang B, Zhao Y, Wang N. Potential Active Marine Peptides as Anti-Aging Drugs or Drug Candidates. *Mar Drugs*. 2023;21(3):151.
5. Papaccio F, Ramasamy TS, Gunawardena TN, et al. Focus on the contribution of oxidative stress in skin aging. *Antioxidants (Basel)*. 2022;11(6):1163.