Identification of unique gene expression profiles in older women with youthful appearing skin

Anne Lynn S. Chang,[1] Robert Spitale,[1] Eduardo Torre,[1] Rui Li,[1] Dale Kern,[2] Helen Knaggs[2]

[1] Stanford University School of Medicine [2] NuSkin International, Provo UT

BACKGROUND

The genetics and epigenetics of healthy skin aging into older age are not well understood.

While age-related gene expression profiles exist, the question of what intrinsic mechanisms may control the rate at which individuals age is not well-explored.

OBJECTIVES

To identify gene expression profiles of older women with visibly youthful skin.

METHODS

Stanford IRB approval

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Enrolled 118 females of European descent:
Aged 18-93 years, Fitzpatrick Skin Type I/II
Exclusion criteria : individuals who had used anti-aging medications or had undergone cosmetic procedures excluded.

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Punch biopsies of the skin on the sun-protected arm and sun-exposed cheek.

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Covariates included cumulative sun exposure and smoking history.

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Skin samples subjected to 3'-end sequencing for expression quantification ("3-seq").

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Skin appearance rated for skin aging parameters by a dermatologist blinded to chronological age.

METHODS

DISCUSSION AND CONCLUSIONS

These data suggest that intrinsic skin aging can occur at different rates.

These findings represent a unique molecular profile of healthy skin aging that may be used to assess the efficacy of topical agents or oral supplements to retard or reverse the skin aging process.
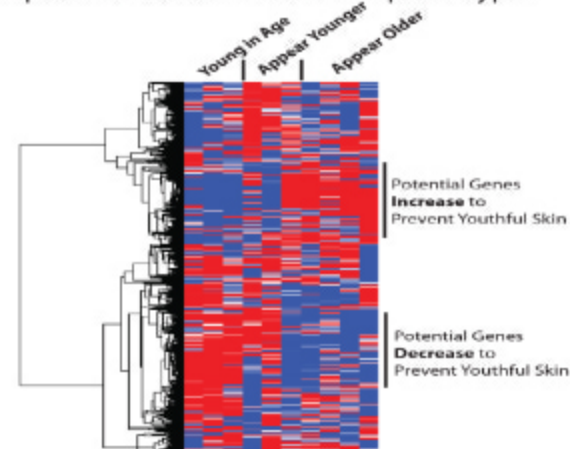
Candidate skin aging genes identified include novel pathways for future study.
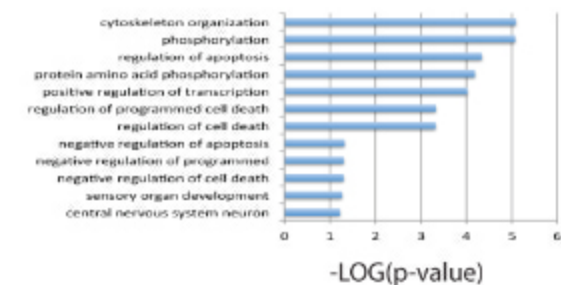
FUNDING

RESULTS

Unbiased clustering: distinct gene expression signature of >300 genes characteristic of older women with youthful appearing skin compared to women without this phenotype.

Gene ontology (GO) terms of genes most significantly altered in young-appearing skin include cytoskeletal organization and phosphorylation

BP_FAT Gene Analysis in DAVID