Transcriptional profiling to identify genes controlling human skin aging

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BACKGROUND

➢Human skin aging occurs at different rates, with some individuals showing less effects of aging than others, despite environmental insults

OBJECTIVE

➢To identify gene expression profiles which associate with normal human aging

➢To identify gene expression profiles which associate with exceptionally youthful skin aging

METHODS

➢IRB approved protocol

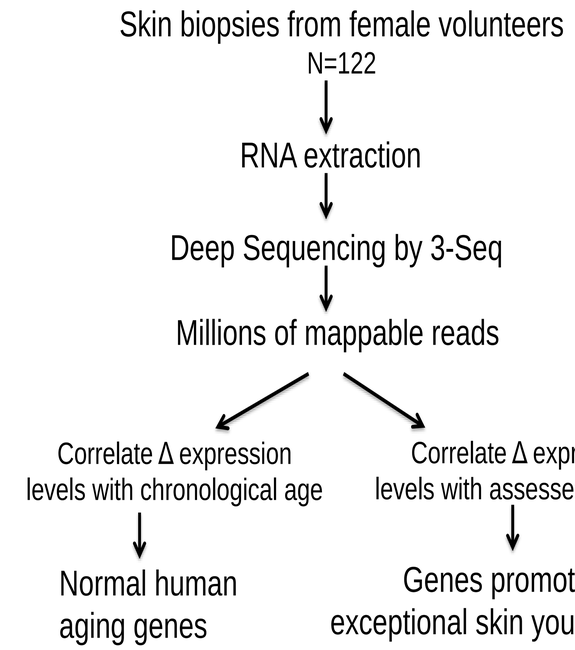
➢Inclusion criteria:

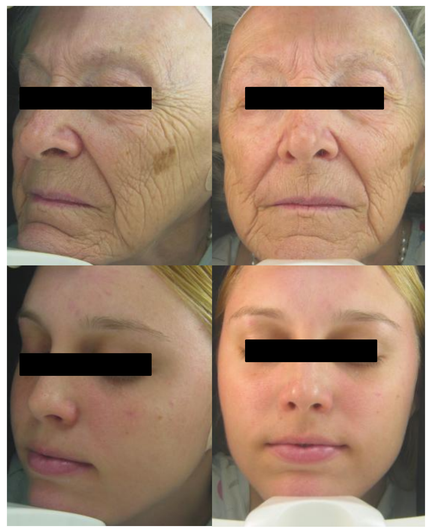
- female volunteers from Northern California
- aged ≥ 18 years old
- Fitzpatrick skin type I or II
- in general good health as assessed by the investigator

➢Exclusion criteria:

- prior use of prescription medications to improve the appearance of aging skin
- Prior facial cosmetic procedures
- dermatologic conditions on the face
- use of self-tanner two weeks prior to enrollment

STUDY DESIGN





Additional clinical parameters to be assessed:

➢ Association with fat accumulation

➢ Association with biomarkers of oxidative stress

RESULTS

➢ Skin aging assessments by dermatologist raters blinded to chronological ages have identified the top 10 individuals with skin youthfulness

➢ The remaining 112 individuals will form the basis of normal aging gene expression profiles from the 3rd to the 9th decade of life

LIMITATIONS

This study is limited by sample size.

CONCLUSIONS

➢ While this study is still in progress, identification of master regulators may lead to novel pathways which promote healthy skin aging

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