

Tracing Microbial Origins of Skin Aging Biomarkers via Metabolomics

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The human skin, the body's largest organ, protects against external insults and reflects overall health¹. Aging causes molecular changes characterized by specific metabolites, providing insights into skin aging. However, the skin's chemical pool can include both microbial- and host-derived metabolites². This study aimed to identify whether age-related metabolite markers (n=206) in the skin of northern Mexican subjects (n=75) originate from the host or microbes to better understand skin aging mechanisms³. Our methodology consisted of an unconventional approach that predicted the microbial skin community through metabolites. We mined public microbial metabolomic datasets⁴ to identify putative links between these key metabolites and their potential microbial producers. On the other hand, 16S rRNA skin datasets along metadata (n=498) from the American Gut Project⁵ were reanalyzed to determine the bacteria correlated with age in various anatomical sites. We concordantly identified 37 bacterial genera on human skin whose abundance correlated with age and links to the production of metabolites. A gender-specific skin microbe-metabolite landscape was noted. Four genera—*Streptomyces*, *Pseudomonas*, *Bacteroides*, and *Staphylococcus*—emerged as candidates driving the production of age-associated metabolites globally. Our findings provide compelling new insights into the dynamic interplay between the skin microbiota and metabolome during aging.

References

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