ABSTRACT BOOK ABSTRACTS



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GLOBAL SKIN HEALTH

AGING-RELATED CHANGES IN THE SKIN MICROBIOME: THE POTENTIAL ROLE OF SKIN BACTERIA IN THE AGING PROCESS

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Introduction & Objective: Skin aging is associated with changes in cutaneous physiology as wrinkles, flaky skin and xerosis and might be associated with skin microbiome change. The big interest in the field of skin microbiome lead us to think about a possible change on skin microbiome associated to aging.

Materials and methods: Skin microbiota was evaluated between two different age groups of 37 healthy Japanese women, i.e. younger adults of 21–37 years old and older adults of 60–76 years old, using bacterial 16S rRNA gene Next Generation Sequencing and data mining.

Results: The analyses revealed that the bacterial richness was significantly higher in the older than the younger group on cheek and forehead. The diversification of skin microbiota in older women consisted mainly in 16 species frequently detected in humid environments as oral cavity. At present, their biological is largely unknown on skin. However, it is intriguing that the prevalence of these bacteria on skin has been recently reported as a signature of atopic dermatitis, a skin disorder presenting altered epidermal maturation and immune function. The diversification of the skin microbiota was also largely due to the reduction of the most predominant genus Cutibacterium in the older older group, in correlation with the decrease sebum level. Bioinformatics mining of C. acnes genomes confirmed that the majority of C. acnes strains is capable of triglyceride breakdown via one specific triglyceride lipase encoded gene that is absent from other major skin commensals (Staphylococcus and Corynebacterium sp.).

Conclusion: These recent data open new opportunities in diagnostic and anti-aging care through mimicking the presence of a "young skin microbiome signature" by adding prebiotics or promoting the innate immune defences to prevent the development of oral bacteria on the skin could be explored.





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