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Changes in Skin Microbiome Diversity According to the Age of Xian Women

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Abstract : Skin is the largest organ of the human body and can provide the diverse habitat for various microorganisms. The ecology of the skin surface selects distinctive sets of microorganisms and is influenced by both endogenous intrinsic factors and exogenous environmental factors. The diversity of the bacterial community in the skin also depends on multiple host factors: gender, age, health status, location. Among them, age-related changes in skin structure and function are attributable to combinations of endogenous intrinsic factors and exogenous environmental factors. Skin aging is characterized by a decrease in sweat, sebum and the immune functions thus resulting in significant alterations in skin surface physiology including pH, lipid composition, and sebum secretion. The present study gives a comprehensive clue on the variation of skin microbiota and the correlations between ages by analyzing and comparing the metagenome of skin microbiome using Next Generation Sequencing method. Skin bacterial diversity and composition were characterized and compared between two different age groups: younger (20 – 30y) and older (60 - 70y) Xian, Chinese women. A total of 73 healthy women meet two conditions: (I) living in Xian, China; (II) maintaining healthy skin status during the period of this study. Based on Ribosomal Database Project (RDP) database, skin samples of 73 participants were enclosed with ten most abundant genera: Chryseobacterium, Propionibacterium, Enhydrobacter, Staphylococcus and so on. Although these genera are the most predominant genus overall, each genus showed different proportion in each group. The most dominant genus, Chryseobacterium was more present relatively in Young group than in an old group. Similarly, Propionibacterium and Enhydrobacter occupied a higher proportion of skin bacterial composition of the young group. Staphylococcus, in contrast, inhabited more in the old group. The beta diversity that represents the ratio between regional and local species diversity showed significantly different between two age groups. Likewise, The Principal Coordinate Analysis (PCoA) values representing each phylogenetic distance in the two-dimensional framework using the OTU (Operational taxonomic unit) values of the samples also showed differences between the two groups. Thus, our data suggested that the composition and diversification of skin microbiomes in adult women were largely affected by chronological and physiological skin aging.

Keywords : next generation sequencing, age, Xian, skin microbiome
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