



PSORIASIS

MICROBIOME COMMUNITY ANALYSIS IDENTIFIES IMBALANCE BETWEEN PROPIONIBACTERIUM AND CORYNEBACTERIUM AS CHARACTERISTICS OF PSORIATIC LESION

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Background: Several studies have investigated cutaneous microbiota in patients with psoriasis. However, the psoriasis-specific microbes are still undetermined, and the correlation between cutaneous microbiota and clinical features remains unclear.

Methods: Using quantitative PCR and high-throughput sequencing targeting on V3-V4 of 16S rRNA, we assayed the profiles of cutaneous microbiota in 116 health controls(NN), 72 psoriatic lesions(PP) and 53 unaffected skins(PN). We also investigated the correlation of psoriasis-specific taxa with clinical characteristics.

Results: Psoriatic lesion shows more bacterial load and less taxonomic diversity. Propionibacterium and Corynebacterium are identified as psoriasis-specific taxa. There is an imbalance between Propionibacterium(Pr) and Corynebacterium(Cr) in psoriatic skins. ROC analysis identifies the ratio of Cr/Pr+Cr as a signature for distinguishing PP from PN and NN (AUC>0.70). Proportion of Propionibacterium shows significant correlation with abnormality of skin capacitance (CAP) as well as transepidermal water loss (TEWL); Corynebacterium was associated with severity of local lesions.

Conclusions: We determine the abnormality of microbiota in psoriatic lesion characterized by higher bacterial load and imbalance between Propionibacterium and Corynebacterium. Our results suggest that the interaction between cutaneous microbiota and psoriatic lesion may play an important role in maintenance and exacerbation of psoriasis.

