PSORIASIS

UNEXPLORED DIVERSITY AND STRAIN-LEVEL STRUCTURE OF THE SKIN MICROBIOME ASSOCIATED WITH PSORIASIS.

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Introduction: The cutaneous microbiota plays a crucial role in the physiology of the skin, for example by restricting harmful microorganisms or by modulating or enhancing immune responses against invaders. It is therefore unsurprising that skin diseases like psoriasis are associated with alterations (dysbiosis) in the skin microbiome. Such alterations may contribute to the pathogenesis of psoriasis as keratinocytes - which are exposed to and sense the skin microbiome - trigger immune responses in psoriasis.

Objective: To characterize the microbiome of psoriasis patients both in affected and in unaffected skin sites in terms of strain-level structure and diversity.

Materials and Methods: 28 psoriasic patients (PASI 2-35) who had not undergone antibiotics of topical treatments for the previous 3 months and 1 week respectively and with at least one of the four samples not affected by psoriasic plaques were enrolled. Swab samples from the olecranon skin area and retroauricular crease were obtained and processed via high-resolution new generation shotgun metagenomics, a promising technique successfully employed in characterizing the gut microbiome in type-2 diabetes, inflammatory bowel diseases and obesity, and which can overcome the limitations of PCR-based surveys used in most skin microbiome studies. Functional genomic features associated with unaffected and diseased skin were also investigated.

Results: Psoriasic ear sites showed a decreased species richness ($p = 0.008$). Members of the genus Staphylococcus were significantly more abundant on diseased skin compared to unaffected skin ($p = 0.023$), but overall no strong specific biomarker associated with psoriasis was identified. At finer strain-level analyses, strain heterogeneity colonization and functional variability were observed.

Conclusions: These results suggest that diversity and strain-level variations may characterize psoriasic microbiome. This study may provide a baseline for further high-resolution analyses in relation to the pathogenesis of psoriasis.