ABSTRACT

Psoriasis is a chronic, immune-mediated inflammatory skin disease. Its pathogenesis is associated with dysregulated cooperation among keratinocytes, innate and adaptive immune cells, coupled with environmental triggers, including microbiota.

The aim of our study was to describe the microbiota composition in psoriasis and explore the role of bacteria and fungi in the pathogenesis of this disease.

We used a mouse model of psoriasis induced by topical application of imiquimod (IISI) in both germ-free (GF) mice and conventional (CV) mice with microbiota manipulated by administration of a mixture of broad-spectrum antibiotics (ATB). ATB treatment markedly changed the intestinal but not the skin bacterial diversity and led to higher resistance to IISI in CV mice. Metronidazole was the most effective antibiotic, alleviating IISI symptoms in CV, but not in GF mice. This confirms that the effect of metronidazole on IISI was microbiota-dependent.

Additionally, we characterized the microbiota composition of psoriatic lesions and unaffected skin in psoriatic patients compared to healthy controls, as well as the impact of different sampling approaches on uncovering cutaneous microbiota composition. We observed significant differences in α- and β-diversities when comparing identical samples sequenced on V1V2 and V3V4 regions of 16S rRNA. Sampling methods, i.e. swab, scraping, and biopsy, uncovered similar α-diversity, but each method revealed some specific bacterial and fungal species. For the first time, we showed a psoriasis-specific co-occurrence pattern between bacterial and fungal species. We also found elevated serum levels of intestinal fatty acids binding protein in psoriatic patients, suggesting intestinal barrier disruption.

Our results emphasize the importance of microbiota composition, as well as the integrity of intestinal barrier in the pathogenesis of psoriasis. It is still unclear whether the observed co-occurrence pattern has etiological significance or is secondary to the disease.

Keywords: psoriasis, skin microbiota, mouse model of psoriasis, sequencing