Gut microbiota remodelling during anti-IL-23 and anti-IL-17 therapy in psoriasis patients: a single centre observational study

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Background and aim: The gut-skin axis (GSA) is crucial for understanding the pathogenesis of psoriasis, since it is characterized by specific dysbiotic signatures of both the gut and skin microbiota. Gut dysbiosis may alter skin homeostasis through the IL-23/IL-17 axis, which is involved also in psoriatic comorbidities, such as inflammatory bowel disease[1].Targeting this pro-inflammatory pathway could be one of the therapeutic options, and anti-IL-23 or anti-IL-17 monoclonal antibodies (mAbs) are indeed effective systemic treatments for moderate to severe psoriasis[2]. This study aims to *i)* evaluate gut microbiota variation in psoriasis patients before, during, and after systemic anti-IL-23 or anti-IL-17 mAbs therapy; *ii*) assess clinical outcomes such as Psoriasis Area Severity Index (PASI), Dermatology Life Quality Index (DLQI), and Investigator's Global Assessment (IGA) at the baseline and during the follow-up visits.

Methods: Stool samples were collected from a cohort of informed consent naïve psoriatic patients (n = 43) at baseline (T0), after 16 (T16) and 52 (T52) weeks of anti-IL-23 or anti IL-17 mAbs treatment. Microbial DNA was isolated (QIAmp® PowerFecal® Pro DNA Kit). Gut microbiota composition was analysed using 16S rDNA sequencing of the V3-V4-V6 hypervariable regions, processed with the MicrobAT software and the Ribosomal Database Project (RDP), and assessed with MicrobiomeAnalyst for alpha- and beta-diversity. Clinical endpoints were statistically analysed as well.

Results: Preliminary data confirm an altered Bacillota (formerly Firmicutes)/Bacteroidetes [B(F)/B] ratio at T0, indicative of intestinal dysbiosis. Both the treatments not only improve the condition but also shift the B(F)/B ratio, increasing species within the Bacteroidetes phylum and enhancing microbiota biodiversity. Besides microbiota changes, both the treatments improve PASI, IGA, and DLQI scores compared to the baseline.

Conclusion: These results demonstrate a progressive increment in gut biodiversity and a normalization of the ratio of B(F)/B in both the patient groups. This pilot study underscores the potential role of biologics in the GSA homeostasis, as the restoration of gut microbiota may support clinical outcomes in psoriasis treatment. Moreover, multicentric studies and gut microbiota analysis on a larger scale could pave the way to better comprehend the relationship between psoriasis and microbiome and lead to personalized, microbiota-targeted therapeutic strategies.

Bibliography:

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