



PSORIASIS

## **METAGENOMIC ANALYSIS OF THE HUMAN GUT MICROBIOME IN NON-TREATED PLAQUE PSORIASIS PATIENTS**

*Ignacio Dei-cas<sup>(1)</sup> - Florencia Giliberto<sup>(2)</sup> - Alberto Penas Steinhardt<sup>(3)</sup>*

*Psoriasis Bsas, Dermatology, Buenos Aires, Argentina<sup>(1)</sup> - Laboratorio De Distrofinopatías, Facultad De Farmacia Y Bioquímica-uba Inigem, Conicet-universidad De Buenos Aires, Buenos Aires, Argentina<sup>(2)</sup> - Laboratorio De Genómica Computacional, Dto. Ciencias Básicas-universidad Nacional De Luján, Luján, Argentina<sup>(3)</sup>*

**Introduction:** Psoriasis is a chronic, immune-mediated inflammatory skin disease. Gut microbiota is implicated in the maturation of the host immune system and in many metabolic pathways. Dysbiosis has important functional consequences and is implicated in many diseases.

**Objective:** The aim of this study was to investigate whether there were differences in gut microbiota in psoriasis patients vs non-psoriasis controls and between psoriasis severity groups.

**Patients and methods:** 55 untreated plaque psoriasis patients (28 with mild disease and 27 with moderate to severe disease defined by PASI and BSA  $\geq 10$  and IGA  $\geq 3$ ) and 27 non-psoriasis healthy controls matched to moderate to severe psoriasis patients by sex, age and BMI were included. Fecal microbial diversity and composition were analyzed using the Illumina MiSeq sequencing platform by targeting the hypervariable V3-V4 regions of the 16S rRNA gene. Bioinformatic analysis was performed.

**Results:** Biodiversity (alfa diversity) did not differ between psoriasis patients and non-psoriasis controls. Comparing the principal phyla detected, we found that psoriasis patients differ from non-psoriasis controls in the observed community structure, but only differences in the relative abundances of Firmicutes and Bacteroidetes were significant ( $p < 0.05$ ). The linear discriminant analysis (LDA) effect size (LEfSe) method revealed that the genus *Faecalibacterium* and *Blautia* were higher in psoriasis patients and *Bacteroides* and *Paraprevotella* in non-psoriasis controls ( $p < 0.05$ , LDA score  $> 2$ ). According to psoriasis severity, we found that severe psoriasis patients had lower biodiversity than mild psoriasis patients ( $p: 0.049$ ). No differences for beta diversity were found.

**Conclusion:** These results demonstrated that there were differences in gut microbiota in patients with psoriasis. Thus, the role of the gut microbiome in psoriasis pathogenesis and





the associated immune response merits further study.

