ABSTRACT BOOK ABSTRACTS



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AUTOIMMUNE BULLOUS DISEASES

THE IMBALANCE OF GUT MICROBIOTA AND ITS CORRELATION WITH PLASMA INFLAMMATORY CYTOKINES IN PEMPHIGUS VULGARIS PATIENTS

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Introduction: Pemphigus vulgaris (PV) is an autoimmune disease characterized by the presence of IgG autoantibodies against desmoglein-3 and also cellular immune disorder characterized by alterations in cytokine production. The past two decades witmessed the role of gut microbiota on the development of immune system as well as autoimmune diseases. However, there was no data about the gut microbiota in pemphigus vulgaris previously.

Objective: This study was designed to investigate whether the gut microbiota was altered in pemphigus vulgaris patients, compared to healthy controls, and its correlation with plasma inflammtory cytokines.

Methods: Fecal bacterial diversity was analyzed in 18 pemphigus vulgaris patients and 14 age- and gender- matched healthy people, by using hypervariable tag sequencing of the V3-V4 region of the 16S rRNA gene. The levels of 21 inflammatory markers and Th1/Th2/Th17/Treg-related cytokines were assessed in the plasma by luminex screening system.

Results: We identified abundant genus 14 differentially taxa. At level. Lachnospiracea_incertae_sedis and Coprococcus were declined, however the Collinsella, Granulicatella, Flavonifractor, Escherichia/Shigella, Abiotrophia and Coprobacillus were increased in PV. The chemokine and cytokine profiles indicated that the plasma level of C5a, YKL-40, IL-2R, IL-6, IL-8, IL-7, IL-1β, IL17A, IL-5, IL-21 were significantly increased in PV. Flavonifractor were positively correlated with C5a, YKL-40, IL-6, IL-8, IL-7, IL-1β, IL17A, IL-21. Lachnospiracea incertae sedis and Coprococcus were negatively correlated with IL-17A.

Conclusion: Our study is consistent with the hypothesis that pemphigus vulgaris patients have gut microbial dysbiosis which might contibute to the disorder of immune system and the development of the disease.





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