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Commentary

Metagenome-wide association study reveales disease-specific landscape of the gut microbiome of systemic lupus erythematosus: a constellation of dysbiosis and inflammation

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Abstract

This commentary evidences the role of dysbiosis in patients with systemic lupus erythematosus (SLE). It was shown that specific Streptococcus spp. may exert a pathogenic role by empowering the gut inflammation, especially through the observation of a correlation with acylcarnitine. Nonetheless, geographical differences should be carefully taken into account since genetic, dietary and other lifestyle habits may influence the composition of gut microbiota. More in-depth investigations of this possible association are soon expected.

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Keywords- Autoantibody; Lupus; Gut; Mirobiota; Streptococcus; Genetic-Environment Interplay; Autoimmunity; Diet; Microbiome

I. INTRODUCTION

The intriguing relationship existing between the microbiota and the development of autoimmune diseases still requires to be elucidated. The disruption of the delicate balances among the bacterial species is at the basis of the dysbiosis observed in patients with systemic lupus erythhematosus (SLE) (1). Among the many questions that deserve an answer, certainly it would be interesting to understand whether these changes occur in the stages preceding the development of the disease, or whether they are an epiphenomenon, or a pathogenic mechanism by which the disease develops and maintains itself. Indeed, it was already shown that gut microbiota could play an important role in SLE pathogenesis. Zhang et al. observed in a murine lupus model a marked depletion of Lactobacilli and an increase of *Lachnospiraceae* compared to age-matched healthy controls in young, female lupus-prone mice (2). Hevia and colleagues investigated the presence of gut dysbiosis in SLE patients in remission (SLEDAI score lower than 8) in absence of any immunosuppressant or glucocorticoid treatment during the previous months. A relatively higher abundance of Bacteroidetes was identified in the SLE group. Moreover, a significantly lower *Firmicutes/Bacteroidetes* ratio in SLE individuals compared with healthy controls was detected (3). The high prevalence of Bacteroidetes has been confirmed in the study conducted by Johnson and colleagues, in lupus-prone SNF1 mice with more severe disease (4).

The paper by Tomofuji et al. (5) found an increase of *Streptococcus intermedius* and *Streptococcus anginosus* in patients with SLE.

The microbial pathways related to sulfur metabolism and flagella assembly were altered in the patients with SLE. The authors confirmed the presence of dysbiosis in patients with SLE and observed that there were two metabolites that were more abundant (acylcarnitine and isocitric acid) and significantly positively correlated with *Streptococcus intermedius*.

II. CONCLUSIONS

In conclusion, the presence of these *Streptococcus spp*. should deserve further researches. Indeed, these bacteria are not innocent bystanders (6): in rare circumstances they are known to provoke even severe diseases including endocarditis. The correlation with an inflammatory molecule such as acylcarnitine supports this hypothesis. Nevertheless, the results should be detailed since genetic and dietary habits could influence the outcome of the microbiological analysis. The authors themselves suggest that only some species have the same directional effects between the studies, suggesting that effects of geography, lifestyle and even analytic methods cannot not be rejected.

AUTHORS CONTRIBUTION

CP conceptualized and wrote the manuscript.

CONFLICT OF INTEREST

The author declares no conflict of interest.

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