

1. Disordered intestinal microbes are associated with the activity of Systemic Lupus Erythematosus

期刊年卷: CLINICAL SCIENCE. 2019 Mar 14. pii: CS20180841.

DOI: 10.1042/CS20180841.

IF2018 = 5.237

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文章简介

系统性红斑狼疮 (systemic lupus erythematosus, SLE) 是一种多发于青年女性, 累及多脏器的自身免疫性炎症性疾病, 常伴有面颊疹、关节炎、光敏感性和肾炎。在抗磷脂抗体阳性患者中有着显著的发病率和死亡率。**裘宇容教授团队揭示了 SLE 患者肠道菌群及其相关代谢途径与正常人存在明显的异常, 该成果发表在《Clinical Science》。**该研究采用基于 16SrRNA 高通量测序技术对每个粪便样本的微生物组成进行研究, 通过不同手段的生信分析, 为我们揭示了肠道菌群与系统性红斑狼疮之间的关系。**这些紊乱的细菌及相关代谢通路可能为研究 SLE 发病机制, 寻找 SLE 诊断或疾病动态监测生物标志物提供新的思路和方法。**

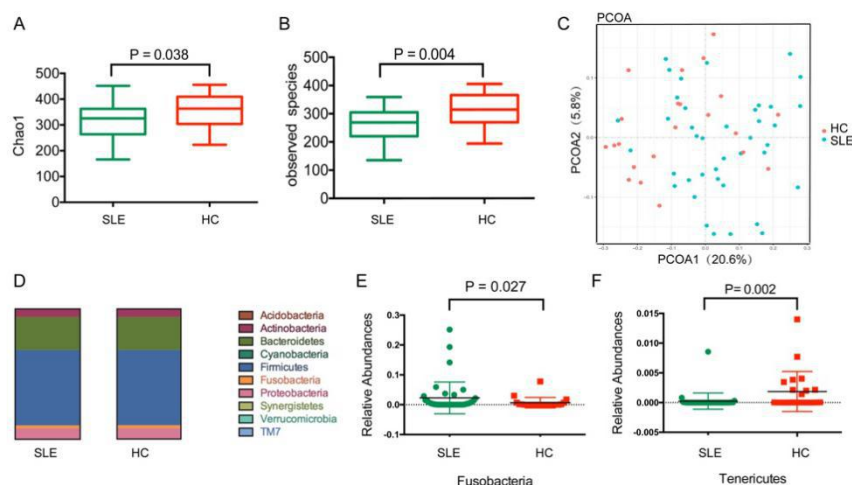


Fig. The different microbial diversity between SLE patient group and healthy controls. A-B. Significantly different richness of α -diversity between the gut microbiota of SLE and HC. C. Principal coordinate analysis illustrating the grouping patterns of SLE and HC group based on the unweighted UniFrac distances. Each closed circle represented a sample. Distances between any pair of samples represented their dissimilarities. D. The average relative abundances of the predominant bacterial taxa at the phylum level in the SLE patients and HC group. E-F. The significantly different phyla in SLE patients compared to healthy controls. HC, healthy controls; SLE, Systemic lupus erythematosus patients.