Intestinal dysbiosis associated with Systemic Lupus Erythematosus. By A. Hevia[1], C. Milani[2], P. López[3], A. Cuervo[4], S. Arboleya[1], S. Duranti[2], F. Turroni[2§], S. González[4], A. Suárez[3], M. Gueimonde[1], M. Ventura[2], B. Sánchez[1], and A. Margolles[1]. *[1]Instituto de Productos Lácteos de Asturias (IPLA), Consejo Superior de Investigaciones Científicas (CSIC), Villaviciosa, Asturias, Spain, [2]Laboratory of Probiogenomics, Department of Life Sciences, University of Parma, Italy, [3]Immunology Area, Department of Functional Biology, University of Oviedo, Asturias, Spain, [4]Physiology Area, Department of Functional Biology, University of Oviedo, Asturias, Spain, §Current address: Alimentary Pharmabiotic Centre and Department of Microbiology, Bioscience Institute, National University of Ireland, Western Road, Cork, Ireland.*

Systemic Lupus Erythematosus (SLE) is the prototypical systemic autoimmune disease in humans, characterized by the presence of hyperactive immune cells and aberrant antibody responses to nuclear and cytoplasmic antigens, including characteristic anti-dsDNA antibodies(1). Although growing evidence suggests that the gut microbiota might impact disease symptoms and progression (2), how and why this microbial community influences SLE physiology remains to be elucidated. We performed a cross-sectional study in order to know if an SLE-associated gut dysbiosis exists in patients without active disease. A representative group of 20 SLE patients, considering strict inclusion and exclusion criteria, was recruited and we used an optimized Ion Torrent 16S rRNA gene-based analysis protocol to decipher the fecal microbial profile of these patients (3), and compare it with that of age and sex-matched 20 healthy control subjects. We found diversity to be comparable using Shannon's index. However, we saw a significantly lower *Firmicutes*/*Bacteroidetes* ratio in SLE individuals (median 1.97) than in healthy subjects (median 4.86) ($p<0.002$). A lower *Firmicutes*/*Bacteroidetes* ratio in SLE patients was corroborated by quantitative PCR analysis. Notably, a decrease of some *Firmicutes* families was also detected. This dysbiosis is reflected, by *in silico* functional inference, in an overrepresentation of oxidative phosphorylation and glycan utilization pathways in SLE microbiota, as well as ion channels and ion-coupled transporters. This is the first report describing an SLE-associated intestinal dysbiosis. Our results suggest that a targeted modulation of the intestinal microbiota could have an influence on SLE physiology.

FIGURE 1. Principal Component Analysis using the 16S rRNA profiles and the phylum (A) and family (B) level. Presence/absence of SLE was further included as metadata. (HD: healthy control, closed circles; LS: SLE, open triangles).

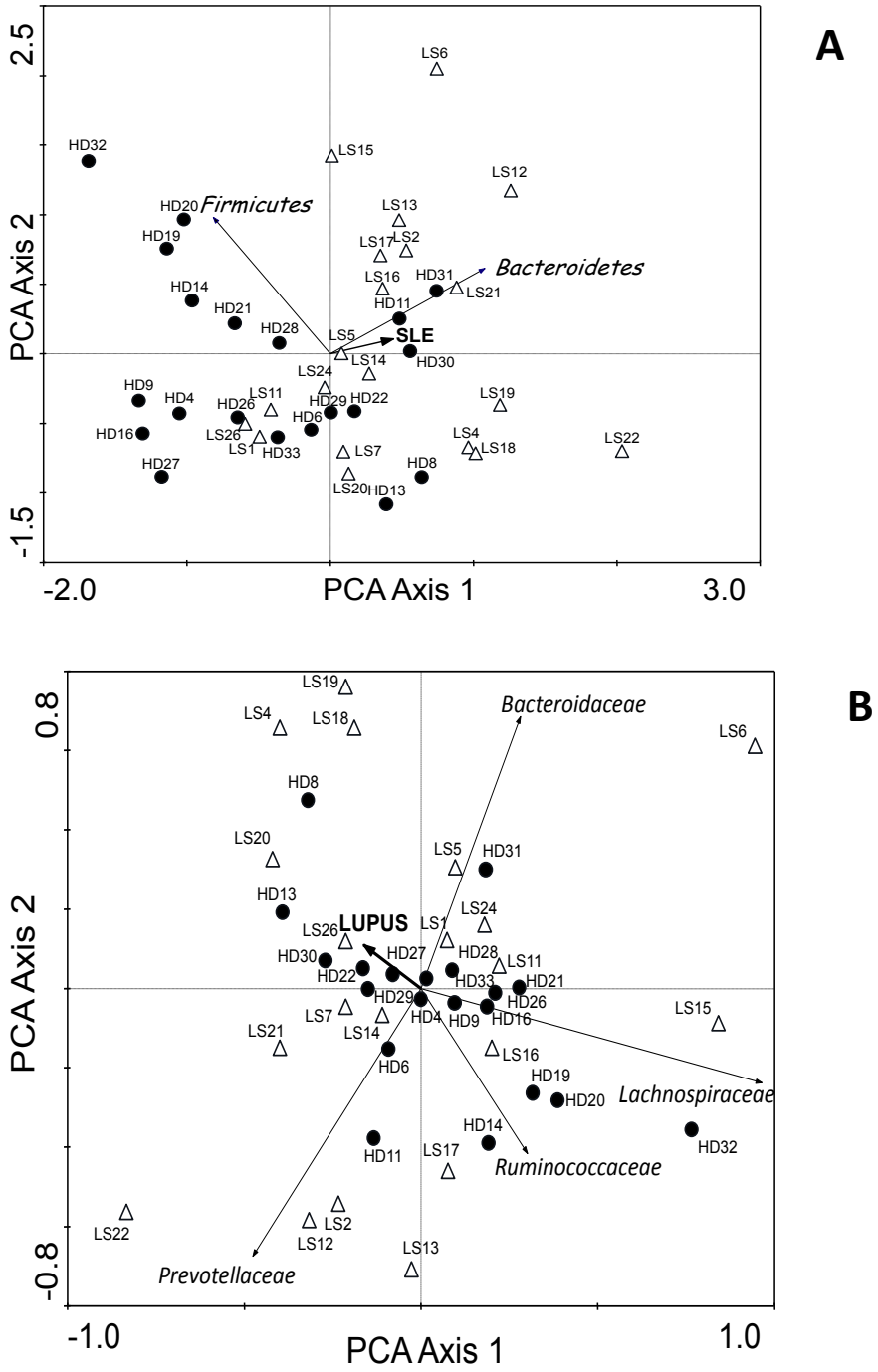
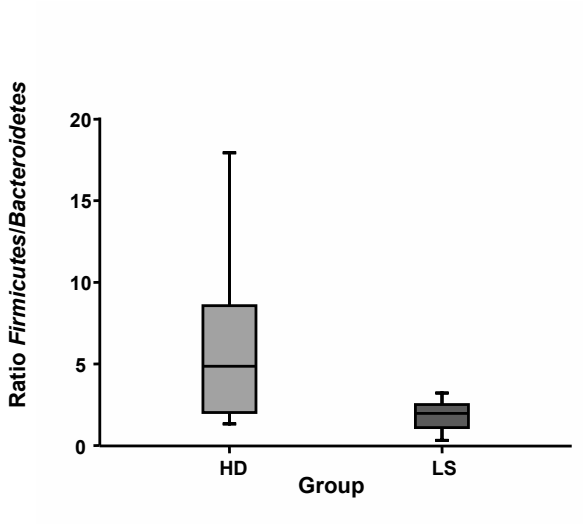


FIGURE 2. Box plot of *Firmicutes*/*Bacteroidetes* ratios (median ± IQR) in SLE patients (LS codes) vs. healthy controls (HD codes). Ratios are significantly different ($P < 0.002$).



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