

Altered gut microbiome seen in patients with active lupus

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(HealthDay)—The microbiome of patients with systemic lupus

erythematosus (SLE), particularly those with increased disease activity, has reduced taxonomic complexity, according to a study published online Feb. 19 in the *Annals of the Rheumatic Diseases*.

Doua Azzouz, Ph.D., from the New York University (NYU) School of Medicine in New York City, and colleagues obtained matched blood and [fecal samples](#) from 61 [female patients](#) with SLE. Fecal 16S rRNA analyses were performed, and sera were profiled for antibacterial and autoantibody responses. Findings were validated in two independent cohorts.

The researchers found that in patients with SLE, the microbiome showed decreased species richness diversity compared with controls; the most pronounced reductions in taxonomic complexity were seen for those with a high SLE disease activity index (SLEDAI). An overall fivefold greater representation of *Ruminococcus gnavus* (*RG*) of the *Lachnospiraceae* family was seen in patients with SLE; reciprocal contractions of a species with putative protective properties were also seen in individual communities. There was a correlation for gut *RG* abundance with [serum antibodies](#) to only one of eight *RG* strains tested. There was a direct correlation for anti-*RG* antibodies with SLEDAI score and antinative DNA levels, and there were inverse correlations with C3 and C4. Individuals with active nephritis had the highest levels of serum anti-*RG* strain-restricted antibodies in the discovery cohort; this finding was replicated in the validation cohorts.

"Our analyses provide the first evidence that lupus is associated with intestinal outgrowths of *RG*, an obligate anaerobic species," the authors write.

NYU has filed intellectual property related to this study.

More information: [Abstract/Full Text](#)

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