

Alteration in intestinal microbiota tied to T1DM susceptibility

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(HealthDay)—Individuals with islet autoimmunity have alterations in intestinal microbiota, according to a study published online June 19 in *Diabetes*.

Aimon K. Alkanani, from the University of Colorado Denver in Aurora, and colleagues conducted high-throughput sequencing of bacterial 16S rRNA genes in subjects with islet [autoimmunity](#) living in the United States.

The researchers found that after adjustment for gender, age, autoantibody presence, and [human leukocyte antigen](#), gut microbiomes of seropositive individuals were different from those of autoantibody-free first-degree relatives (FDRs) with respect to the abundance of four taxa. Compared with healthy controls with no family history of autoimmunity, subjects with autoantibodies, seronegative FDRs, and

new-onset [type 1 diabetes](#) patients had different levels of the Firmicutes genera *Lactobacillus* and *Staphylococcus*. In seropositive subjects with multiple versus one autoantibody there were trends toward increased and reduced abundances of the Bacteroidetes genera *Bacteroides* and *Prevotella*, respectively. The gut microbiomes of autoantibody positive individuals and seronegative FDRs clustered together, but were distinct from those of new-onset patients and healthy negative controls. In seropositive versus seronegative FDRs there were no differences in biodiversity.

"Our data raise the hypothesis that alterations in the structural composition of the intestinal microbiota are associated with type 1 diabetes progression," the authors write. "Identifying bacteria and immune pathways associated with early [diabetes](#) may lead to a new class of immunotherapies to modulate the [gut microbiota](#) and prevent islet destruction."

More information: [Abstract](#)
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