

# Oral microbial activity may help identify autism in children

Hicks SD, et al. *Autism Res.* 2018;doi:10.1002/aur.1972.

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Steven D. Hicks

Gene expression activity within oral microbial communities may be altered in children with autism spectrum disorder, findings published in *Autism Research* revealed.

These results suggested that changes in the bacteria within a child's mouth may provide biomarkers for identifying autism.

Although prior research has revealed disrupted gut-brain signaling in autism spectrum disorder, almost all studies of the ASD microbiome have focused on the lower gastrointestinal (GI) tract, **Steven D. Hicks, MD, PhD**, from the department of pediatrics at Pennsylvania State University College of Medicine, and colleagues explained.

“We conducted this research to examine whether intestinal microbiome disruption in patients with autism extended to the oropharynx,” Hicks told *Healio Psychiatry*.

The investigators identified changes in the salivary microbiome collected via cheek swab of 180 children with ASD, 60 with non-autistic developmental delay and 106 typically developing children. The authors sequenced and quantified RNA from actively transcribing microbes across the three groups and compared differences between autistic children with and without GI disturbances, according to a press release.

After examining microbe activity in the saliva of 346 children aged 2 to 6 years, the researchers detected 12 groups of microbes that differed in those with autism or developmental delay.

“These microbes had unique patterns of energy metabolism, particularly metabolism of lysine (a neurotransmitter precursor),” Hicks said. “Most importantly, the microbial patterns displayed diagnostic utility for distinguishing children with autism from peers with typical development or developmental delay without autism.”

Hicks and colleagues also identified 28 groups of microbes that distinguished autism patients with and without GI disturbance, further supporting that the gut-brain axis plays a role in ASD.

The results showed that five microbial ratios distinguished ASD from typically developing children with a 79.5% accuracy, three distinguished ASD from non-autistic developmental delay with a 76.5% accuracy and three distinguished ASD children with/without GI disturbance with an 85.7% accuracy. Examination of taxonomic pathways via the Kyoto Encyclopedia of Genes and Genomes microbial database revealed significant differences within energy metabolism and lysine degradation.

These findings indicated that GI microbiome disruption in ASD extends to the oropharynx, according to the researchers.

“The take home message for clinicians is that saliva microbial profiles show surprising diagnostic potential for autism spectrum disorder,” Hicks told *Healio Psychiatry*. “This technology may soon be paired with other objective, molecular measures to provide a rapid and accurate adjunct for autism diagnosis.” – *by Savannah Demko*

**Disclosures:** Hicks is a coinventor of preliminary patents that are licensed to Quadrant Biosciences, Inc and reports consulting for Motion Intelligence, Inc. Please see the study for all other authors’ relevant financial disclosures.



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