Intro

Autistic Spectrum Disorder (ASD) is a severe neurodevelopmental disorder that is primarily characterized by abnormal behavioral symptoms: social interaction impairment, stereotyped behavior, and restricted interests. With its prevalence increasing dramatically over the past decades, ASD now affects 1 out of 59 children in the United States. According to national census data on handicapped individuals, China also has an increased prevalence with ASD first on its list of top mental disabilities.

Accumulating evidences demonstrates that gastrointestinal (GI) symptoms, such as gaseousness, diarrhea, and constipation, often co-occurred with ASD core symptoms in children with ASD. Moreover, recent studies have shown that changes in gut microbiota can modulate the gastrointestinal physiology, immune function, and even behavior through the gut-microbiome-brain axis. Thus, these co-occurring gastrointestinal symptoms have prompted researchers to examine the gut microbial composition of ASD children and determine their potential role in promoting and reflecting ASD symptoms.

Abstract

Autism Spectrum Disorder (ASD) is a severe neurodevelopmental disorder. To enhance the understanding of the gut microbiota structure in ASD children at different ages as well as the relationship between gut microbiota and fecal metabolites, we first used the 16S rRNA sequencing to evaluate the gut microbial population in a cohort of 143 children aged 2–13 years old. We found that the α-diversity of ASD group showed no significant change with age, while the TD group showed increased α-diversity with age, which indicates that the compositional development of the gut microbiota in ASD varies at different ages in ways that are not consistent with TD group. Recent studies have shown that chronic constipation is one of the most commonly obvious gastrointestinal (GI) symptoms along with ASD core symptoms. To further investigate the potential interaction effects between ASD and GI symptoms, the 30 C-ASD and their aged-matched TD were picked out to perform metagenomics analysis. We observed that C-ASD group displayed decreased diversity, depletion of species of Sutterella, Prevotella, and Bacteroides as well as dysregulation of associated metabolism activities, which may involve in the pathogenesis of C-ASD. Consistent with metagenomic analysis, liquid chromatography-mass spectrometry (LC/MS) revealed some of the differential metabolites between C-ASD and TD group were involved in the metabolic network of neurotransmitters including serotonin, dopamine, histidine, and GABA. Furthermore, we found these differences in metabolites were associated with altered abundance of specific bacteria. The study suggested possible future modalities for ASD intervention through targeting the specific bacteria associated with neurotransmitter metabolism.

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