

## Maternal Dysbiosis Alters Offspring Gut Microbiota and the Etiopathogenesis of Neurodevelopmental

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### Abstract

It has been demonstrated that maternal infections and/or inflammation cause dysbiosis, with an increased risk of neurodevelopmental disorders such as Autism in children. Therefore, we hypothesized that prenatal maternal antibiotics (ABX) use could induce long-term gut microbiota and immunological effects on the offspring, which leads to increased susceptibility and severity of the dysbiotic and immunological response. Our studies aimed to investigate the long-term alterations in the offspring and how these are influenced by the acute treatment of pregnant dams. A broad-spectrum ABX-cocktail consisting of (vancomycin, ampicillin, and neomycin), or vancomycin alone, was administered ad-lib orally to elicit a dysbiotic environment. To determine the long-term effects, we analyzed the gut microbiota of offspring and their immune responses in the periphery and the brain of C57BL/6J mice during infancy, early adolescence, and adulthood. We first performed 16s rRNA sequenced, then analyzed computationally predicted metabolic pathways. Next, serum and brain cytokine levels were determined. ABX treatment can have several adverse effects on the gut microbiota, including reduced diversity, altered metabolic activity, and immune function. We show that the maternal ABX treatment significantly alters the gut microbiota diversity, composition, and potential metabolic pathways from infancy well into adulthood. Lower levels of chemokines and inflammatory cytokines in offspring. In conclusion, this study shows that the gut microbiome is altered by maternal ABX treatment, and the extent of the alteration is determined by the ABX regimen, age, and sex of offspring.