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Perturbation of Neonatal Microbial Gut Community by Peripartum Antibiotics in Wistar Rats Lead to Decreased Weight Gain

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Abstract

Cross talk between a mammalian host and its intestinal microbiota plays a role in immune mediated diseases such as allergies, asthma, type 1 diabetes, as well as in obesity and auto immune diseases. Over the past decades, a significant increase of these diseases in young children in the developed world has been documented. In Western countries the pattern of initial colonization of the gut during the first days of life has changed dramatically. Among factors potentially modulating initial colonization, the use of antibiotics is particularly important. Antibiotics are frequently administered orally to either mothers or young children to treat or prevent bacterial infections not necessarily related to the gastrointestinal system. This has adverse effects on the commensal gut microbial community, as it disrupts the intricate balance between specific bacterial groups within this ecosystem, potentially leading to dysbiosis.

We hypothesized that modulation of community composition and function induced by peripartum antibiotics affects intestinal microbial composition and general health of the offspring.

To address this, 33 pregnant Wistar rats were dosed by oral gavage with either amoxicillin (AMX), vancomycin (VAN) or water (CON) daily from 8 days before delivery until weaning of the offspring. Significant lower weightgain of the offspring of antibiotic treated dams compared to the control were observed. The antibiotic treated dams had significantly larger caecum size and higher caecal pH as well as spleen size than control animals. Offspring were dissected at different time points and significant changes in liver, spleen and epididymal fat were measured between groups. Composition of the gut microbiota, alpha diversity, caecum short chain fatty acid levels, caloric contents of faeces, bile salt levels, acute phase protein haptoglobin in blood, social and locomotive behavior as well as gene expression of tight junction proteins are currently being analyzed .