



HAL
open science

Maternal gut microbiome alteration has enduring effects on offspring's metabolic programming and neuroendocrine plasticity

Patricia Parnet

► **To cite this version:**

Patricia Parnet. Maternal gut microbiome alteration has enduring effects on offspring's metabolic programming and neuroendocrine plasticity. 46ème Colloque de la SNE, Sep 2024, Nice, France. hal-04665899

HAL Id: hal-04665899

<https://hal.inrae.fr/hal-04665899v1>

Submitted on 31 Jul 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Abstract SNE 2024

2500 caractères max, spaces included

Maternal gut microbiome alteration has enduring effects on offspring's metabolic programming and neuroendocrine plasticity

Rastelli Marialetizia¹, Catherine MICHEL², Isabelle Grit², Patricia Parnet², Sebastien G. Bouret¹

Development and plasticity of Neuroendocrine Brain , UMR-S 1172, Lille Neuroscience and Cognition Center (LiNCog), Université de Lille, CHU de Lille, INSERM

Nantes Université, INRAE, UMR 1280, PhAN, IMAD, F-44000 Nantes, France

The alarmingly high prevalence of obesity and type 2 diabetes, particularly in children, highlights the need to better understand the mechanisms involved in the development of these pathological conditions. Previous studies showed that alterations in the maternal nutritional environment disrupt the development of hypothalamic circuits with enduring metabolic consequences in the offspring. Recent evidence also linked maternal gut microbiome with offspring's brain development and behavior. Nevertheless, whether the maternal gut microbiome (mGM) affects the development of offspring's hypothalamic circuits with short- and long-term consequences on hypothalamic function remains unknown. Here, we examined the consequences of impairment of mGM on physiological and neurodevelopmental outcomes in the offspring. To this aim, we developed a mouse model of maternal dysbiosis during gestation and lactation by administering a cocktail of large spectrum antibiotics (ABX) in dams. The aim was to target critical phases of the hypothalamic development, that include embryonic neurogenesis, postnatal circuit formation and hypothalamic barriers maturation. We first validated the model by confirming that during gestation, lactation and up to weaning the abundance of gut bacteria was markedly reduced in ABX-treated dams compared to controls. Maternal body weight during gestation, litter size or litter sex ratio were not affected by the treatment. A battery of metabolic tests were performed to examine the consequence of maternal dysbiosis on the offspring's metabolic regulation. mGM alteration slows pre-weaning offspring body weight gain. However, the offspring of antibiotic-treated dams (off_ABX) display a catch-up growth between weaning and adulthood, mainly due to an increase in longitudinal growth. At adulthood, male off_ABX develop metabolic alterations. Adult female off_ABX exhibit delayed puberty onset, but no metabolic impairments. In addition, preliminary results suggest that off_ABX present neuroanatomical changes of the blood-hypothalamic barrier in the median eminence, which is at the crossroad between the brain and the periphery and plays a crucial role in regulation of metabolism. Together, these results support the hypothesis that mGM contributes to the development of the neuroendocrine hypothalamus with both short- and long-term consequences on metabolic regulation and reproductive functions in the offspring associated with structural changes of the blood-hypothalamic barrier