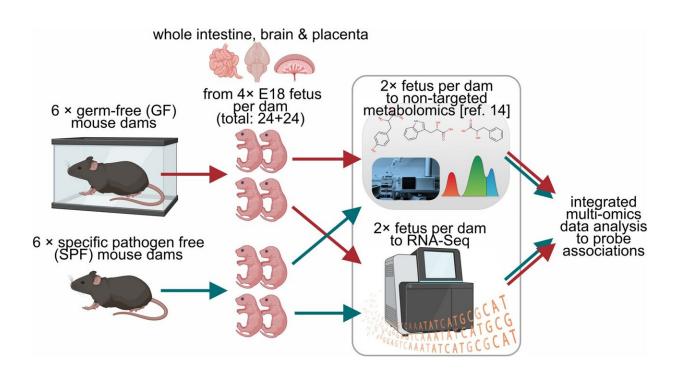


## Study shows maternal microbiota can affect fetal development

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Experimental design. Figure created with Biorender.com. Credit: *BMC Biology* (2023). DOI: 10.1186/s12915-023-01709-9

In a Finnish study, significant differences in the gene activity of the fetal intestine, brain and placenta were identified, depending on the microbes in the mother's body and the compounds produced by them. The findings indicate that maternal microbes are important to her offspring's development and health.



The microbiota of the mother, or dam, is thought to be important for the development and health of her offspring. However, so far little is known about how interactions with the microbiota begin and what the mechanisms of action are.

<u>A collaborative study</u> carried out at the Universities of Helsinki, Eastern Finland and Turku investigated how the maternal microbiota affects fetal development by comparing the fetuses of normal and germ-free mouse dams living in a sterile environment. The researchers measured gene expression and the concentrations of small-molecular compounds, or <u>metabolites</u>, in the fetal intestine, brain and placenta. The research has been published in *BMC Biology*.

"The effects of the dam microbiota and the metabolites it produces on fetal development have not been previously investigated in such a comprehensive manner," says Mikael Niku, the principal investigator of the study from the Faculty of Veterinary Medicine, University of Helsinki.

"Our study sheds light on the significance of the microbiota and the mechanisms by which the microbiota affects individual development and pregnancy. We identified previously unknown compounds in the fetus, which are likely to be microbial, and which can be important for individual development."

The researchers demonstrated that there were considerable differences in <u>gene expression</u> in the intestine, brain and placenta of the fetuses of germ-free and normal mouse dams.

In the gut, genes associated with the immune system and host-microbe interactions were less active in the fetuses of germ-free dams. There were significant differences in the expression of genes in the brain associated with the development and functioning of the nervous system.



In the placenta, there were differences in the expression of several important genes that regulate pregnancy.

The differences were more extensive in male fetuses, indicating that they may be more sensitive to the effects of the maternal microbiota, at least in mice.

The researchers discovered that the expression of many important genes was associated with the concentration of metabolites likely to be modulated by the maternal <u>microbiota</u>. These metabolites were absent in the fetuses of germ-free dams, or occurred at least at significantly lower concentrations.

"It would appear that such microbial products are likely to affect the development of the intestine and brain as well as the functioning of the placenta. Many of these metabolites are previously unknown," Niku says.

The group is now investigating the occurrence of microbial metabolites in other mammals: piglets and calves, as well as in the meconium and amniotic fluid samples of babies.

Today, deficiencies in the host–microbe interactions of the early stages of life caused by, for example, an unbalanced environment or antibiotics, may predispose the offspring to dysfunction in the <u>immune system</u>, such as inflammatory bowel diseases and allergies.

"Our research helps us understand the origin of such disorders, making it potentially possible in the future to enhance their prevention and treatment," Niku says.

**More information:** Aleksi Husso et al, Impacts of maternal microbiota and microbial metabolites on fetal intestine, brain, and



## placenta, *BMC Biology* (2023). DOI: 10.1186/s12915-023-01709-9

## Provided by University of Helsinki

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