

Mode of delivery alters infants' gut microbiota and this may impact respiratory health in first year of life

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New research being presented at this year's European Congress of Clinical Microbiology & Infectious Diseases (ECCMID) in Amsterdam, the Netherlands (13-16 April), suggests that mode of delivery influences the development of the microbial composition of the gut (i.e. the gut microbiota) in infants, independently of a mother's use of antibiotics. This, in turn, may affect infants' respiratory health during the first year of life.

The prospective Microbiome Utrecht Infant Study (initiated by the Spaarne Gasthuis hospital in Hoofddorp in collaboration with the University Medical Centre Utrecht, the Netherlands) involving 120 infants, found that children born by [caesarean section](#) (C-section) had a delay in the normal development of their [gut microbiota](#), and a higher abundance of potentially [harmful bacteria](#), compared to infants delivered vaginally—which could be the mechanism driving the increased risk in respiratory infections.

Over 1000 different types of bacteria live in the gut, where they elicit important functions for health, for example helping to digest food, stimulating the development of the immune system, and protecting against infection.

After birth, infants become colonised by an increasing diversity of gut microbes until a relatively stable state is reached. The pace and pattern

by which infants acquire their [gut microbiome](#) is thought to have a substantial impact on health in later life. Disruption of the normal development of the gut microbiome has been linked with a range of diseases including irritable bowel disease, asthma, allergies and cancer.

Previous research indicates that early life microbiota development is influenced by mode of delivery, although it has been suggested that this depends mostly on maternal antibiotic exposure.

To assess the independent effects of mode of delivery, Marta Reyman, from the Wilhelmina Children's Hospital, Utrecht, the Netherlands, and colleagues analysed the gut microbiota development in 46 C-section and 74 vaginally delivered infants using stool samples collected 10 times during their first year of life. Antibiotic administration to mothers undergoing a C-section was postponed until after clamping of the umbilical cord. Maternal stool samples were also examined 2 weeks after delivery.

Analyses showed that gut microbiota composition differed significantly between C-section and vaginally delivered infants in the first year, which was most pronounced shortly after birth. This was accompanied by measurable faecal seeding (transfer of maternal vaginal microbes) from mother to child in vaginally delivered infants, but not in children born by C-section.

In infants born by C-section, the gut microbiota was less stable and the development of the health-promoting bacterial species *Bifidobacterium* spp. was delayed compared to vaginally delivered children. Additionally, infants born by C-section had much higher levels of potential pathogenic gut bacteria, irrespective of length of hospital stay after birth, feeding type, and antibiotic use.

Interestingly, the researchers also found that the gut microbiota early in

life was associated with the total number of respiratory infections over the first year.

"Our findings suggest that mode of delivery affects the developing infant gut [microbiota](#), independent of a mother's use of antibiotics during birth. Compared to vaginally delivered [infants](#), children born by C-section have different trajectories of bacterial colonisation, which could have implications for their future [respiratory health](#)", says Marta Reyman, who is the Ph.D. student on this study. "Further research and larger studies will be needed to fully understand the consequences of these changes. The insights gained might help to design strategies to prevent health-related problems following birth by C-section."

The major limitation of this study is the use of 16S rRNA based sequencing, which does not allow annotation of bacteria on species level, or generate results based on genetic content of microbial communities.

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