Microbial Composition of the Initial Colonization of Newborns

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The compositional development of the intestinal microbiota in early life has attracted considerable research interest during the past decade after the association of gut colonization patterns with the risk of noncommunicable diseases has been recognized. To date, intestinal dysbiosis has been linked to conditions ranging from inflammatory or immune-mediated diseases, such as atopic disease, type I diabetes, inflammatory bowel disease, and necrotizing enterocolitis, to overweight and obesity. It is plausible, although not thoroughly proven, that perturbations in gut colonization play a causal role in the development of disease [reviewed in 1]. Epidemiological data demonstrate that aberrant gut microbiota composition in early infancy may precede the development of atopic disease, obesity, infantile colic, or necrotizing enterocolitis. Further corroboration for a causal connection between early gut microecology and the risk of disease has been obtained from both experimental animal models and epidemiological studies linking factors which are known to disrupt early gut colonization, such as cesarean section delivery [2] or early antibiotic exposure [3], to increased disease risk. Elucidating the origin and composition of the intestinal microbiota in the neonatal period and early infancy may, therefore, be of high clinical importance.

Neonates and infants acquire their indigenous gut microbes from other humans and predominantly from the mother. During delivery, the neonate receives a colonizing inoculum of maternal vaginal microbes including Lactobacillus, Prevotella, and Sneathia species [4]. Early colonization patterns of infants born by cesarean section delivery differ significantly from those of vaginally born individuals, and long-term differences in gut microbiota composition, immune development, and disease risk have been reported between subjects born vaginally or by cesarean section [1].

It has recently been suggested that human gut colonization may begin prior to birth [1, 5].
Accumulating evidence suggests that the placenta and amniotic fluid harbor a sparse but distinct microbiota, which may be the source of the microbes detected in meconium. We have recently reported that species belonging to *Bacteroides, Lactobacillus, Prevotella*, and *Peptostreptococcus* are detectable in both amniotic fluid and meconium [5]. Experimental animal studies have provided evidence to suggest that bacteria introduced in the maternal gut are transported to the amniotic fluid and fetal gut. The details and significance of intrauterine gut colonization remain to be determined.

After birth, the most important modulator of gut colonization is breast milk. Initial neonatal gut microbiota characterized by *Escherichia coli*, enterococci, streptococci, and *Clostridium* species is rapidly followed by anaerobic *Bifidobacterium* and *Bacteroides* species. Breastfed neonates and infants typically harbor an intestinal microbiota dominated by bifidobacteria, which may be detectable already during the first days of life. The predominance of bifidobacteria in breastfed neonates may be explained by human milk oligosaccharides, which selectively promote the growth of specific bifidobacteria and particularly *B. longum* subsp. *infantis*. Interestingly, human milk also contains live microbes, which may colonize the neonatal gut. The neonatal gut microbiota shares features with the maternal milk microbiota already during the first days of life [5], but the significance of the bacteria in human milk to infant health is currently not known.

Disturbances in neonatal gut colonization are often detected as a result of cesarean section delivery, prematurity, antibiotic exposure, or formula feeding. The same exposures have also been associated with increased disease risk, which, therefore, may at least in part be attributable
to intestinal dysbiosis (Fig. 1). Supporting healthy gut colonization by reducing cesarean section rates, prudent use of antibiotics, and promotion of breastfeeding, as well as prebiotic or probiotic supplementation in high-risk individuals, may have a significant impact on child health and deserves rigorous scientific research efforts.

References

3 Turta O, Rautava S: Antibiotics, obesity and the link to microbes – what are we doing to our children? BMC Med 2016;14:57.