

Vaginal Microbiota Can Keep Newborns Healthy Throughout their Life

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Abstract

Babies are born either by normal deliveries (through vaginal canal), or by C-sections. Those who are born through vaginal canal during labour they get exposed to the microbiota (mostly beneficial) which is quite stable during pregnancy.

The various species colonize the skin, oral cavity, and gut which help in developing the immune system in new born even from neonatal stages. The babies which are born by C-section miss this opportunity and due to lack of immune system they are unable to fight infections. In addition to vulnerable to infections, epidemiological studies suggest that it is associated with higher risk of developing asthma, food allergy, type 1 diabetes, and obesity during infancy.

An impaired immune system in later life due to the lack of exposure to maternal bacteria that would occur during the standard birthing process, they may have health problems throughout their life.

Keywords: Vaginal canal • Asthma • Diabetes • Oral cavity

Introduction

Human microbiota plays a vital role in maintaining health during whole life span of individuals. The vaginal microbiome plays an important role in maternal and neonatal health. However if the natural balance of types of organisms is disturbed, it may be dangerous to the health and can even produce serious diseases.

It has been shown that internal and external microbiota on human is influenced by a wide variety of factors such as, geographical connotations, socioeconomic status, diet, exercise, environment, religion, genetic and hereditary factors, ethnicity, psychological stress, migration, yoga and exercise chronic illnesses and immunological. In addition to these factors we believe that circadian regulatory mechanism in the pineal-hypothalamic-pituitary-gonadal axis is also operative and has a pivotal role in quality and quantity of microbiota in human body.

Endocrine physiology of human female changes 3 times in her life time viz., at menarcheal age, during pregnancy and at the time of menopause. Therefore, the vaginal microbiota population is highly dynamic. In recent years our understanding of vaginal bacterial community composition and structure has significantly broadened as a result of investigators using identification of population by nucleic acid sequence analysis using modern methodology (Figure 1).

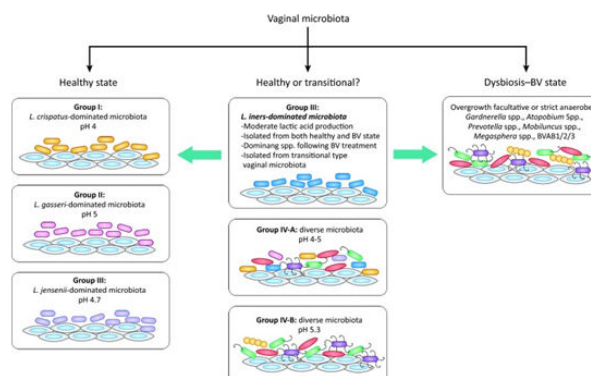


Figure1: Showing the dynamism of vaginal microbiota.

The vaginal microbiota refers to the bacterial communities present in the female reproductive tract; a healthy vaginal microbiota is characterized by resilience and stability, whereas an unstable microbiota could be prone to invasion by pathogenic bacteria and dysbiosis. The vaginal microbiota resembles that of the cervix and is physiologically dominated by *Lactobacillales*, but *Clostridiales*, *Bacteroidales*, and *Actinomycetales* are also regularly detected. Bacterial community differences and shifts are almost exclusively detected between different *Lactobacillus* strains without any negative impact on pregnancy outcomes. During pregnancy, microbial richness and diversity are reduced along with an increased bacterial load [1]. At the same time, the prevalence of potential pathogens like microbial species of urea plasma and mycoplasma is reduced. The taxonomic composition of the microbial community of the vagina remains stable during pregnancy with an increase of the microbial diversity before birth of the healthy infant at term. These data lead to the conclusion that the composition of the vaginal microbiota is tightly regulated during pregnancy and that the switch to the non pregnant situation precedes and maybe even triggers birth. For healthy newborns and their subsequent healthy life depend on the microbiota composition in vagina during child bearing age, during pregnancy and post pregnancy periods.

Vaginal Microbiota during Reproductive-Age

Studies have shown that the development of the microbiota in the developing foetus begins in utero. This “seeding” from the mother to newborn may serve as an early inoculation process for the development of immune system in the new born; the long-term health outcomes of newborns is partially depends on it. Furthermore, specific disturbances of the vaginal microbiota have been involved in complications of pregnancy. It is observed that a woman’s birth mode, that is, the method through which she was delivered by her mother, is an important early life factor in determining how a woman’s vaginal microbiota is initially seeded and transitions into adulthood. Thus, any differences in the composition of vaginal microbiota attributable to birth mode must persist through known hormonally-driven transitions in the microbiota during early childhood and puberty, including the longitudinal dynamics observed among reproductive-age women in menstruation and pregnancy [2].

Reproductive-age women with *Lactobacillus*-dominated vaginal microbiota are at lower risk for bacterial vaginosis, which reduces the likelihood acquisition and development of abnormal pregnancy outcomes. While there are a number of studies on demographic and behavioural risk factors for BV in adult women, less is known about the early risk factors for BV. At present, it is understood that the healthy vaginal microbiota is dominated by *Lactobacillus* species, while BV is characterized by a relatively low abundance of *Lactobacillus* spp. accompanied by *Polymicrobial anaerobic* overgrowth, including species

such as *Gardnerella vaginalis*, *Prevotella spp.*, *Bacteroides spp.*, *Mobiluncus spp.*, and *Mycoplasma hominis*.

Microbiota during Pregnancy

Despite the critical role of the human microbiota in health, the understanding of microbiota compositional dynamics during and after pregnancy is incomplete. During pregnancy vaginal microbiota dynamics is significantly different when ethnicity is considered. For example, Caucasians have decreased variation of the microbiota during the progression of pregnancy between different subjects, while African-American women show quite more divergence between different individuals. Most women experienced a post delivery disturbance in the vaginal community characterized by a decrease in *Lactobacillus* species and an increase in diverse anaerobes such as *Peptoniphilus*, *Prevotella*, and *Anaerococcus* species [3]. These findings have important implications for predicting premature labour, a major global health problem, and for understanding the potential impact of a persistent, altered postpartum microbiota on maternal health, including outcomes of pregnancies following short inter pregnancy intervals. Regardless of ethnicity, the vaginal microbiota just after birth dramatically changes and becomes less *Lactobacillus*-dominated. There is also greater biodiversity of species, irrespective of the original microbial make-up.

There are many influences on vaginal microbiota stability during pregnancy, such as the absence of menstrual flow, no cyclic hormonal alterations, the absence of vaginal and/or cervical secretions that are associated with the usual reproductive cycle, but also altered sexual activity during pregnancy. Most of these factors contribute to the resilience of the vaginal microbiota. In pregnancy, such imbalances in the vaginal microbiome are associated with an increased risk of post-abort infection, early, and late miscarriage, histological *chorioamnionitis*, *postpartum endometritis*, preterm premature rupture of membranes (PPROM) and preterm birth. Overall data points to a preponderance of *Lactobacillus acidophilus* and *Lactobacillus gasseri*, while *Lactobacillus iners*, *Lactobacillus crispatus* or *Lactobacillus jensenii* are observed less frequently. The relationship between Bacterial vaginitis and preterm birth in particular has profound implications since children who are born prematurely have higher rates of cardiovascular disorders, respiratory distress syndrome, neurodevelopmental disabilities and learning difficulties compared with children born at term, along with increased risk of chronic disease in adulthood. Also, preterm birth complications are estimated to be responsible for 35% of the world's annual neonatal deaths [4].

Studies that have observed vaginal microbiota have been quite helpful for diagnosing abnormal states, even achieving prediction of outcomes when pursuing assisted reproduction. Current data suggest that the state of vaginal microbiota at the moment of embryo transfer may affect pregnancy outcome. The other part depends on the various activities and factors unique to the labour and birth environment that may influence the microbiota of women and newborns. During the labour and birth process

i.e. route of birth, antibiotics used, and the nursing procedures matters how strong the newborn's immune system develops. Vaginal Microbiota and Preterm Birth: The relationship between bacterial vaginitis and preterm birth in particular has profound implications since children who are born prematurely have higher rates of cardiovascular disorders, respiratory distress syndrome neurodevelopmental disabilities and learning difficulties compared with children born at term, along with increased risk of chronic disease in adulthood. Also, preterm birth complications are estimated to be responsible for 35% of the world's annual neonatal deaths [5].

Post delivery

Most women experienced a post delivery disturbance in the vaginal community characterized by a decrease in *Lactobacillus* species and an increase in diverse anaerobes such as *Peptoniphilus*, *Prevotella*, and *Anaerococcus* species. This disturbance was unrelated to gestational age at delivery and persisted for up to 1 y. These findings have important implications for predicting premature labour, a major global health problem, and for understanding the potential impact of a persistent, altered postpartum microbiota on maternal health, including outcomes of pregnancies following short inter pregnancy intervals.

Conclusion

Babies born by Cesarean section (C-section) are more likely to develop metabolic and chronic disorders, including celiac disease, diabetes mellitus, obesity, food allergy, and asthma, in early childhood, compared to those born by vaginal delivery. Microbes from vaginal fluids colonize the skin, oral cavity, and gut of babies as they are born through vaginal canal. This early microbial exposure and colonization influences development of the immune system and affects metabolism and immune function later in life. The early-life microbiota is now being recognized as a major influence on long-term human health and development.

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