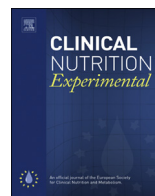




ELSEVIER

Contents lists available at ScienceDirect

## Clinical Nutrition Experimental

journal homepage: [http://  
www.clinicalnutritionexperimental.com](http://www.clinicalnutritionexperimental.com)

## Perinatal nutrition: How to take care of the gut microbiota?

Izaskun García-Mantrana <sup>a, 1</sup>, Bibiana Bertua <sup>b, 1</sup>, Cecilia Martínez-Costa <sup>b, \*\*</sup>,  
Maria Carmen Collado <sup>a, \*</sup><sup>a</sup> Department of Biotechnology, Institute of Agrochemistry and Food Technology, National Research Council (IATA-CSIC), Valencia, Spain<sup>b</sup> Department of Paediatrics, University of Valencia, Paediatric Gastroenterology and Nutrition Section, Hospital Clínico Universitario de Valencia, Valencia, Spain

## ARTICLE INFO

## Article history:

Received 22 November 2015

Received in revised form 12 February 2016

Accepted 14 February 2016

Available online 24 February 2016

## Keywords:

Nutrition

Microbiome

Perinatal

Mode of delivery

Lactation

## SUMMARY

Perinatal and postnatal nutritional environments can result in long-lasting and/or permanent consequences that may increase the risk of chronic diseases in adulthood. The impact of perinatal nutrition on infant microbiome development has been increasingly gaining interest, however scarce information can be found about nutrition on maternal microbiome. The infant microbiome plays an essential role in human health and its assembly is determined by maternal offspring exchanges of microbiota. Microbial colonization runs in parallel with the immune system maturation and has a decisive role in intestinal physiology and regulation. This process is adversely affected by several practices, including caesarean section, antibiotics, and infant formula, which have been related to a higher risk of non-communicable diseases. Limited research has been performed to assess whether nutritional status and diet lead to changes in the maternal microbiota and thus affect the infant microbial colonization process during the critical frame of life. Early microbial colonization has a decisive role on human health, and alterations in this process have been lately associated with specific diseases in the future. The aims of this review are, firstly, to update nutritional recommendations for the perinatal period and, secondly, to analyse the influence of both maternal microbiome and nutrition on infant gut microbiota development.

\* Corresponding author. IATA-CSIC, Av. Agustín Escardino 7, 49860 Paterna, Valencia, Spain. Tel.: +34 963900022.

\*\* Corresponding author. Paediatric Gastroenterology and Nutrition Section, Hospital Clínico Universitario de Valencia, Spain. Tel.: +34 963864170.

E-mail addresses: [Cecilia.Martinez@uv.es](mailto:Cecilia.Martinez@uv.es) (C. Martínez-Costa), [mcolam@iata.csic.es](mailto:mcolam@iata.csic.es) (M.C. Collado).<sup>1</sup> Both authors contributed equally to this work.

## 1. Microbiome, diet and human health

Recent research has revealed the importance of our gut microbiome for an optimal health status. The overuse of antibiotics, unbalanced diets, caesarean-sections (C-section) deliveries, excessive hygiene, and continuous stress are permanently changing our microbiome [1–3]. There is a clear relationship between what we eat and the balance and diversity of the community of bacteria we harbour, which has repercussions on our health status. Therefore, balanced diets would promote a well-structured microbiota. It is known that a long-term diet is able to affect the gut microbiota composition and activity, however, it is still unclear if the microbiota changes and responds to short-term interventions [4]. Disturbances in the microbiota composition and reduction in microbial diversity have been described as strong risk factors for the development of life-style diseases such as allergies, diabetes, obesity and metabolic syndrome, and irritable bowel syndromes [5]. It has also been reported that reduced microbial diversity and functional richness are related to alterations in the metabolism and a prolonged low-grade inflammation state [5,6]. Dietary intervention improved low gene richness and clinical phenotypes, although it seemed to be less efficient for inflammation variables in individuals who presented lower gene richness from the beginning.

Recently published studies reported that animal-based diets increased bile-tolerant bacteria while decreasing bacteria able to metabolize dietary plant polysaccharides [4]. Consequently, there are significant differences in microbiota between people who follow a Western-type diet and those who follow a more ancestral diet and lifestyle. In fact, the more balanced is the diet, the more diverse is the microbiota. Specific dietary components may promote disorders in the gut microbiota, which can be involved in the pathogenesis of many disease states [7].

Some studies suggest that high microbial enterotypes ratios have been strongly associated with several dietary components related to protein and animal fat-sources (*Bacteroides*), compared to carbohydrate-related diets (*Prevotella*) [8,9]. Other experts, however, did not find this relation [7]. An alternative study [10] demonstrated that vegetarians diets were related to less trimethylamine N-oxide (TMAO) levels from dietary L-carnitine – present in red meat – compared to animal and omnivorous diets using a microbiota-dependent mechanism. This study reported a relationship between elevated serum and plasma levels of TMAO and the presence of specific microbes, significantly increasing the risk of developing atherosclerosis.

In contrast to excessive dietary compounds, a recent study [11] focused on the influence of undernutrition, particularly amino acid deficiency, in gut microbiota composition leading to intestinal inflammation. Another study suggested that kwashiorkor disease in twins was related to a specific response of the gut microbiome [12].

Additionally, geography has a strong influence on the composition of gut microbial populations, probably due to lifestyle. It has been examined how gut microbes differ in the human population through the characterisation of faecal samples from 531 healthy Amerindian, Malawian and USA metropolitan inhabitants. It was reported significant differences in the microbial diversity between USA and the other two countries [13]. This study revealed that differential microbial traits were also evident in early life, suggesting that it would be needed to take into account specific factors as life period, diet and nutrition, physiological variations, and also, the impact of Westernization [13]. Additional studies [14] have demonstrated the Carbohydrate Active enzyme (CAZyme) profile shifts according to geography and is age-specific according to the 448 human gut microbiome databases analysed from nine geographies including Europe, America, Asia and Africa. This study revealed a core 89 CAZyme families present across 85% of the gut microbiomes analysed suggesting a more precise understanding of the role of carbohydrate active enzymes in human diet and nutrition.

Download English Version:

<https://daneshyari.com/en/article/2690444>

Download Persian Version:

<https://daneshyari.com/article/2690444>

[Daneshyari.com](https://daneshyari.com)