CHARACTERIZATION OF THE GUT MICROBIOME IN PREGNANCY

Saraiva, M.A.[1], Dobbler, P.C.T[1] , Perdomo, J.R[1] , Corso A.L.[2], Silveira, R.C.[2] , Procianoy, R.S.[2] , Roesch, L.F.W.[1]

Institution: [1] Universidade Federal do Pampa, *Campus* São Gabriel - Centro Interdisciplinar de Pesquisas em Biotecnologia – CIP-Biotec
[2] Universidade Federal do Rio Grande do Sul/Hospital de Clinicas de Porto Alegre

Abstract

Microorganisms from the digestive tract play an important role for the human healthy status. They contribute to proper functioning of the intestine, modulate the immune system, help to digest non-digestible dietary components and protect against pathogens of the intestinal epithelium. During pregnancy, many physiological changes occur, which in turn might cause changes in intestinal microbial communities. The objective of this study was to map the composition of microbial communities in the digestive tract of healthy pregnant women in order to identify the main microbial phyla present. For this preliminary study, fecal samples collected in late pregnancy from nine women were analyzed. Mothers analyzed gave birth after a term pregnancy; they were not subject to antibiotic therapy, did not suffer from diabetes, did not use corticoids and had natural (vaginal) delivery. Samples were collected at the Hospital de Clinicas de Porto Alegre, mixed with glycerol and frozen at -80 °C until microbial DNA extraction. Total DNA was extracted, and the 16S rRNA gene was amplified and sequenced using Ion Torrent-PGM platform. The sequence analysis followed the protocol suggested by the Brazilian Microbiome Project (http://www.brmicrobiome.org). A total of 124,189 high quality sequences were obtained and classified at phylum level. Bacteroidetes (59.1%, ± 28%), Firmicutes (33%, ± 25%) and Proteobacteria (5% ± 3%) were the most abundant phyla found in mothers who delivered their babies after term gestation. Tenericutes, Actinobacteria, Chloroflexi, Elusimicrobia, Fusobacterium, Lentisphaerae, Spirochaetes, Synergisteres and Verrucomicrobia were also found in all samples but in relative abundance smaller than 1%. These results highlighted the high microbial interpersonal variation among individuals and showed the existence of an established and dominant group of phyla present in the digestive tract of pregnant women.

Key words: Human microbiome, digestive tract, Next Generation Sequencing

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