



ORIGINAL ARTICLE

Breastfeeding increases microbial community resilience^{☆,☆☆}

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KEYWORDS

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Abstract

Objective: Since the present group had already described the composition of the intestinal microbiota of Brazilian infants under low social economic level, the aim of the present study was to analyze the microbial community structure changes in this group of infants during their early life due to external factors.

Methods: Fecal samples were collected from 11 infants monthly during the first year of life. The infants were followed regarding clinical and diet information and characterized according to breastfeeding practices. DNA was extracted from fecal samples of each child and subjected to PCR-DGGE analysis.

Results: The results revealed a pattern of similarity between the time points for those who were on exclusive breastfeeding or predominant breastfeeding. Although there were changes in intensity and fluctuation of some bands, the DGGE patterns in the one-year microbial analysis were stable for breastfeeding children. There was uninterrupted ecological succession despite the influence of external factors, such as complementary feeding and antibiotic administration, suggesting microbiota resilience. This was not observed for those children who had mixed feeding and introduction of solid food before the 5th month of life.

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59**PALAVRAS-CHAVE**Aleitamento materno;
Microbiota intestinal;
Análise de
dendrograma;
Resistência
microbiana;
Alimentação;
Antibiótico

Conclusion: These results suggested an intestinal microbiota pattern resilient to external forces, due to the probiotic and prebiotic effects of exclusive breastfeeding, reinforcing the importance of exclusive breastfeeding until the 6th month of life.

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Aleitamento materno aumenta a resiliência da comunidade microbiana**Resumo**

Objetivo: Como nosso grupo já havia descrito a composição da microbiota intestinal de neonatos brasileiros em baixo nível socioeconômico, o objetivo deste estudo foi analisar alterações estruturais da comunidade microbiana deste grupo de neonatos no início de sua vida devido a fatores externos.

Métodos: Amostras fecais foram coletadas mensalmente de 11 neonatos durante o primeiro ano de vida. Os neonatos foram acompanhados com relação a informações clínicas e nutricionais e caracterizados de acordo com práticas de amamentação. O DNA foi extraído das amostras fecais de cada criança e submetido a análise através da técnica de Reação em Cadeia da Polimerase – Eletroforese em Gel de Gradiente Desnaturante (PCR-DGGE).

Resultados: Os resultados revelaram um padrão de similaridade entre seus próprios pontos temporais em indivíduos em aleitamento materno exclusivo ou predominante. Apesar de variações na intensidade e flutuação de algumas bandas, o padrão DGGE na análise microbiana de um ano foi estável em crianças em aleitamento materno. Houve sucessão ecológica ininterrupta apesar da influência de fatores externos, como alimentação complementar e administração de antibióticos, sugerindo resiliência da microbiota. Isso não foi observado nas crianças com alimentação heterogênea e introdução de alimentos sólidos antes do quinto mês de vida.

Conclusão: Nossos resultados sugerem um padrão de microbiota intestinal resiliente a forças externas, devido a efeitos probióticos e prebióticos do aleitamento materno exclusivo, reforçando a importância do aleitamento materno exclusivo até o sexto mês de vida.

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Introduction

The intestinal microbiota is an important key in health and disease.¹ It is well known that the intestinal microbiota compositions of newborns and children are influenced by birth,² diet,³ geographic region, and environmental influences.^{4,5}

New methods in *16S rRNA* sequencing^{6,7} are rewriting the understanding about the relationship between bacteria and human host, and the use of these methods for characterizing the intestinal microbiota of infants and children living in developed countries has received increasing attention.^{3,8} However, few studies conducted in developing countries have corroborated the global observation of inter-individual variability,^{4,9} despite the differences in intestinal microbiota composition. All these findings may contribute to the worldwide understanding of how a geographic region and its environmental contamination influence or do not influence the intestinal microbiota establishment.

The authors previously described the microbiota composition of a group of children living at a low socioeconomic level in Brazil, characterized by low rates of *Staphylococcus* in early ages¹⁰ and a high abundance of *Escherichia* at the 12th month of age.⁵ However, information about how the microbial community structure changes in the short term due to external factors was missing.

Denaturing gradient gel electrophoresis (DGGE)¹¹ has demonstrated the dynamics of the diversity in the intestinal microbial community can be assessed to determine microbial structural differences between environments¹² and their changes over time.¹³ The present study analyzed the microbial community structure of this group of children monthly during their first year of life, using DGGE.

Material and methods**Subjects and samples**

A group of 11 children living at a low socioeconomic level was analyzed, as previously described.^{5,10} The infants were vaginally delivered at the University Hospital of the University of São Paulo (HU-USP). Information concerning the socioeconomic condition of the family and sanitary conditions was collected monthly, during medical appointments. The child's diet was monitored regularly, concerning the period of lactation and timing of the introduction of new foods. The occurrence of infections, health complications, and medication uses were recorded. Fecal samples were collected from babies on the first 2 days, the 7th day, and every month up to the 12th month of life. The mothers were instructed to collect the fecal sample immediately after elimination

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