



THE PROBLEM OF OBESITY AND ITS RELATIONSHIP WITH THE INTESTINAL MICROBIOTA

Isabella Amanda Marinho Costa*	University Center of Rio Grande do Norte, Rua São João Del Rey, 2951, Nova Parnamirim- Brazil. *Corresponding Author
Yasmim Bárbara Ribeiro de Freitas	University Center of Rio Grande do Norte, Rua Claudino Coelho, 32, Centro, São José do Campestre - Brazil.
Priscylla Kelly Rocha Pinheiro Abrantes	Federal University of Rio Grande do Norte, Rua dos Laranjais, 18, Nova Parnamirim, Parnamirim- Brazil.
Rosiane Gabriela Neves Pereira	University Center of Rio Grande do Norte, Avenida Maria Lacerda Montenegro, 1010, Nova Parnamirim- Brazil.

ABSTRACT Obesity is a disease that affects millions of people. Day after day science can find answers that demonstrate how this disease manages to evolve. The objective of this research is to analyze the current scenario involved in the high prevalence of obesity and the factors related to the intestinal microbiota responsible for the increase in obesity rates. The methodology used was the literature review. It is concluded that the bacteria that make up the intestinal microbiota are able to modulate the metabolism of intestinal cells, contributing to the increase in weight.

KEYWORDS : Obesity, Microbiota, Health, Nutrition.

INTRODUCTION

Obesity is a nutritional disorder in which an excess of body weight gain is evidenced. According to Mustillo et al (2003), the high worldwide prevalence of this epidemic is alarming, given that different age groups are affected.

The studies by Ventura et al (2009), describe that intestinal microbiota is considered an ecosystem formed by a rich diversity of microorganisms, essential for the proper functioning of the human organism.

According to Tanaka et al (2009), the intestinal microbiota is acquired in each individual during the postnatal period, being made up of a wide range of bacteria, which assist in the absorption of nutrients.

Another form of acquisition is the mother's natural milk, which is a relevant source of microorganisms that participate in the composition of the babies' intestinal microbiota.

Study by Wang et al (2016), highlight that more than 100 million microorganisms participate in the formation of this microbiome.

According to Ludwig et al (1999), among the determining factors for the high prevalence of obesity, fatty and hypercaloric food stands out, through the intake of mainly processed foods.

Because of the relevance of obesity and the associated factors, the hypothesis that the composition of the intestinal microbiota interferes with the progression of obesity has recently been raised.

METHODOLOGY

The research was bibliographic using databases from Google Scholar, Scielo, Science Direct, Capes and PubMed Journals, from the years 2013 to 2018.

General search terms, such as "intestinal microbiota", "obesity" and "intestinal microbiota and obesity" were used.

RESULTS

The total number of publications found in the databases searched for the period between 2013 and 2018: For the research descriptor "intestinal microbiota", 82400 papers; for obesity, the research resulted in 21,100 publications; while for "intestinal microbiota and obesity" 3110 publications were found.

Considering the high prevalence rates of obesity in the contemporary world population, the understanding of factors related to its cause and progression are of great value, as they allow and identification of strategies and measures that can be taken for both effective prevention and early treatment.

Factor 1: Individual habits contribute to a differential composition of the intestinal microbiota. The World Health Organization recommends regular physical activity. According to Galle et al (2019), considering that most obese individuals are sedentary, the lack of physical activity also influences the composition of the intestinal microbiota.

Factor 2: According to Jbilo (2005), studies point out that genetic and environmental factors comprise the causes of obesity, in which physiological and metabolic disorders are observed in the affected individual's body. The bodily mechanisms that control the balance between food intake and energy expenditure are deregulated, affecting and altering intestinal cells.

Factor 3: The functions of the intestinal microbiota, highlighting the control of digestion and absorption of nutrients and the secretion of substances responsible for transmitting information to the immune, vascular and nervous systems of the mucosa.

CONCLUSIONS

The study found that the composition of the intestinal microbiota is related to a higher prevalence of obesity.

Genetic, psychosocial and environmental factors are also determining factors for a greater predisposition to obesity in the world population, including the Brazilian population.

Understanding the factors related to the differential composition of the intestinal microbiota in obese individuals is of great value, encouraging further studies on the subject, since a better quality of life for affected individuals is desirable.

REFERENCES:

1. Aiello, M. A., and Leuzzi, F. (2010), "Waste Tyre rubberized concrete: Properties at fresh and hardened state." *Journal of Waste Management*, ELSEVIER.
2. Gallè, F., Valeriani, F., Cattaruzza, M. S., Ubaldi, F., Spica, V. R., & Liguori, G. (2019). Exploring the association between physical activity and gut microbiota composition: a review of current evidence. *Ann Ig*, 31(6), 582-589.
3. Jbilo, O., Ravinet-Trillou, C., Arnone, M., Buisson, I., Bribes, E., Péleraux, A., ... & Casellas, P. (2005). The CB1 receptor antagonist rimonabant reverses the diet-induced obesity phenotype through the regulation of lipolysis and energy balance. *The FASEB journal*, 19(11), 1567-1569.

4. Mustillo, S., Worthman, C., Erkanli, A., Keeler, G., Angold, A., & Costello, E. J. (2003). Obesity and psychiatric disorder: developmental trajectories. *Pediatrics*, 111(4), 851-859.
5. Tanaka, S., Kobayashi, T., Songjinda, P., Tateyama, A., Tsubouchi, M., Kiyohara, C., ... & Nakayama, J. (2009). Influence of antibiotic exposure in the early postnatal period on the development of intestinal microbiota. *FEMS Immunology & Medical Microbiology*, 56(1), 80-87.
6. Ventura, M., Turrioni, F., Canchaya, C., Vaughan, E. E., O'Toole, P. W., & van Sinderen, D. (2009). Microbial diversity in the human intestine and novel insights from metagenomics. *Frontiers in Bioscience*, 14(1), 3214-3221.
7. Wang, J., Gao, Y., & Zhao, F. (2016). Phage-bacteria interaction network in human oral microbiome. *Environmental microbiology*, 18(7), 2143-2158.
8. Ludwig, D. S., Majzoub, J. A., Al-Zahrani, A., Dallal, G. E., Blanco, I., & Roberts, S. B. (1999). High glycemic index foods, overeating, and obesity. *Pediatrics*, 103(3), e26-e26.