BRIEF-COMUNICATION

Interaction between food pyramid and gut microbiota. A new nutritional approach

Daniela O **MAGRO**[1], Carina **ROSSONI**[2], Rogerio **SAAD-HOSSNE**[3] and Andrey **SANTOS**[1]

[1] Universidade Estadual de Campinas, Faculdade de Ciências Médicas, Campinas, SP, Brasil.
[2] Instituto of Environmental Health, Faculty of Medicine (ISAMB), Universidade de Lisboa, Lisbon, Portugal. [3] Universidade Estadual Paulista, Faculdade de Medicina, Departamento de Cirurgia, Botucatu, SP, Brasil.

HIGLIGHTS

- Integration between food pyramid and gut microbiome.

- Negative and positive effects of food on the gut microbiome using the food pyramid.

- SCFA-s-producing bacteria and their effects on the gut microbiome.

ABSTRACT — The food pyramid is a pre-established nutritional education tool. The integration between the intestinal microbiome, food groups, and SCFA-producing bacteria, which benefit from the ingestion of these foods, has the potential to further improve and innovate healthy eating. The diet-microbiome interaction needs to be incorporated into nutrition science, and the food pyramid might assist in this interaction and nutritional learning. Against this context, this brief communication proposes through the food pyramid, the interactions between the intestinal microbiota, food groups, and SCFAs-producing bacteria.

Keywords — Microbiota; food pyramid; nutrition.

Corresponding author:
Andrey Santos. Email: andreysts@gmail.com

INTRODUCTION

The food pyramid emerged in the United States in 1992[1] and was adapted for the Brazilian population by Philippi et al. in the late 1990s[2]. The food pyramid is used as an instrument for the nutritional guidance of individuals and population groups, respecting their eating habits and the different regional and institutional realities. Its original purpose was to convey two main ideas: variety and proportionality, both by images and by the size of the food group[2]. However, it is still very focused on nutrients and not on foods.

This food and nutrition education tool has been widely used to emphasize in the population the importance of increasing consumption of grains, vegetables, and fruits, as part of a healthy diet to prevent the development of chronic diseases.

Similarly, the last 15 years have seen unprecedented progress in microbiome research and the first attempts to clinically manipulate the gut microbiota to treat and prevent these diseases[3].

The role that the microbiota plays in intestinal function and in maintaining the health of the host depends on a balance between potentially pathogenic bacteria and numerous non-pathogenic microorganisms, which are distributed in four major phyla in the human intestine: bacteroidetes and firmicutes which correspond to 90% and proteobacteria and actinobacteria[4].

Thus, the usual dietary pat-

terns are associated with the composition of the individual's intestinal microbiota, although significant changes in the proportions of macronutrients (carbohydrates, proteins, and fats) and fibers (<25 grams/day) may induce changes in bacterial diversity and in the production of nutrients derived from bacterial metabolism[5]. It is assumed that low fiber intake in western societies induces depletion of the gut microbiota and subsequent increases in the rates of chronic diseases such as obesity, cardiovascular disease, type 2 diabetes, colon cancer[5], and more recently inflammatory bowel diseases[6]. Fibers are classified as soluble and insoluble and have different properties.

Soluble fiber dissolves in water, forming viscous gels, and is fermented by colonic bacteria. Highly fermentable fibers with high solubility and viscosity include beta-glucans and pectin. They are found naturally in whole grain such as oats and barley (ß-glucans) and fruits such as apples (pectin). Non-viscous soluble fibers that are fermented by the gut microbiota include inulin, gum acacia, resistant starch, polydextrose, and corn fiber[7]. Fructans of the inulin type, are found naturally in agave (a type of succulent plant), artichokes, asparagus, bananas, chicory root, garlic, onions, and leeks. Resistant starches (legumes, seeds, raw and cooked potatoes, green bananas, and whole grains) and polydextrose are not absorbed in the small intestine, as their physical and chemical characteristics make them inaccessible to α-amylase[8].

Insoluble fibers do not dissolve in water, do not form gels and their fermentation is limited[9]. Water-insoluble fibers have rapid gastric emptying. Cellulose is poorly fermented by intestinal bacteria, however, its presence in food accelerates intestinal transit and reduces the time of colonic bacterial fermentation of undigested foods[9].

Prebiotic fibers are ingredients selectively fermented by colonic bacteria that result in specific changes in the composition and/or activity of the intestinal microbiota. This generally refers to a fiber's ability to increase the growth of *Bifidobacterium* and *Lactobacillus*, which contribute to improving intestinal barrier function, mucus production and host immunity, reducing subpopulations of potentially pathogenic bacteria (*Clostridium and Enterococcus species*), acid production of short-chain fatty

acids (SCFAs), acetate, propionate and butyrate, and anti-inflammatory action[3,9,10].

Resistant starch and soluble fibers such as beta glucan and pectin ferment the three SCFAs while fructans ferment butyrate, and cellulose stimulates acetate production[10].

Butyrate is considered the most beneficial in terms of colonic health as it is the preferred energy source for colonic epithelial cells and promotes cell differentiation and proliferation. Butyrate-producing bacteria, mainly *Eubacterium rectale, Roseburia spp, Faecalibacterium Prausnitzii*, and *Akkermansia muciniphila*, are associated with reduced inflammation[7].

Against this context, this brief communication proposes through the food pyramid, the interactions between the intestinal microbiota, food groups, and SCFAs-producing bacteria (FIGURE 1).

The first level of the pyramid is represented by the group of cereal, tubers, and roots. These foods are mainly a source of resistant starch, flavonoids, and polyphenols whose function for the gut microbiota is to increase the SCFAs (acetate, propionate, and butyrate), reduction of intestinal permeability, decrease the lipopolysaccharides (LPS) and endotoxemia[3,7,8].

The second level of the pyramid is represented by the group of vegetables and fruits. The functions these foods in the gut microbiota are increasing production of SCFAs bacteria (mostly acetate and butyrate respectively), maintaining intestinal mucosal integrity, improving insulin sensitivity and anti-inflammatory properties. Furthermore, there is a decreased risk of certain cancers and reduced endotoxin-bearing Proteobacteria levels[3].

The third level of the pyramid includes the group of plant (beans, peas, and lentils) and animal proteins (milk and dairy products, meat, fish, and eggs). The plant beans provide resistant starch to intestinal bacteria, increasing butyrate and decreasing the levels of serum pro-inflammatory cytokines[11]. The milk and dairy products produce Lactobacillus and Bifidobacterium that might suppress the growth of pathogens[4]. The high concentrations of animal protein increase the populations of pathogens such as *Escherichia coli* and the lower concentrations of dietary protein decrease butyrate-producing bacteria[12]. The ideal is the daily adequacy of plant and animal proteins.

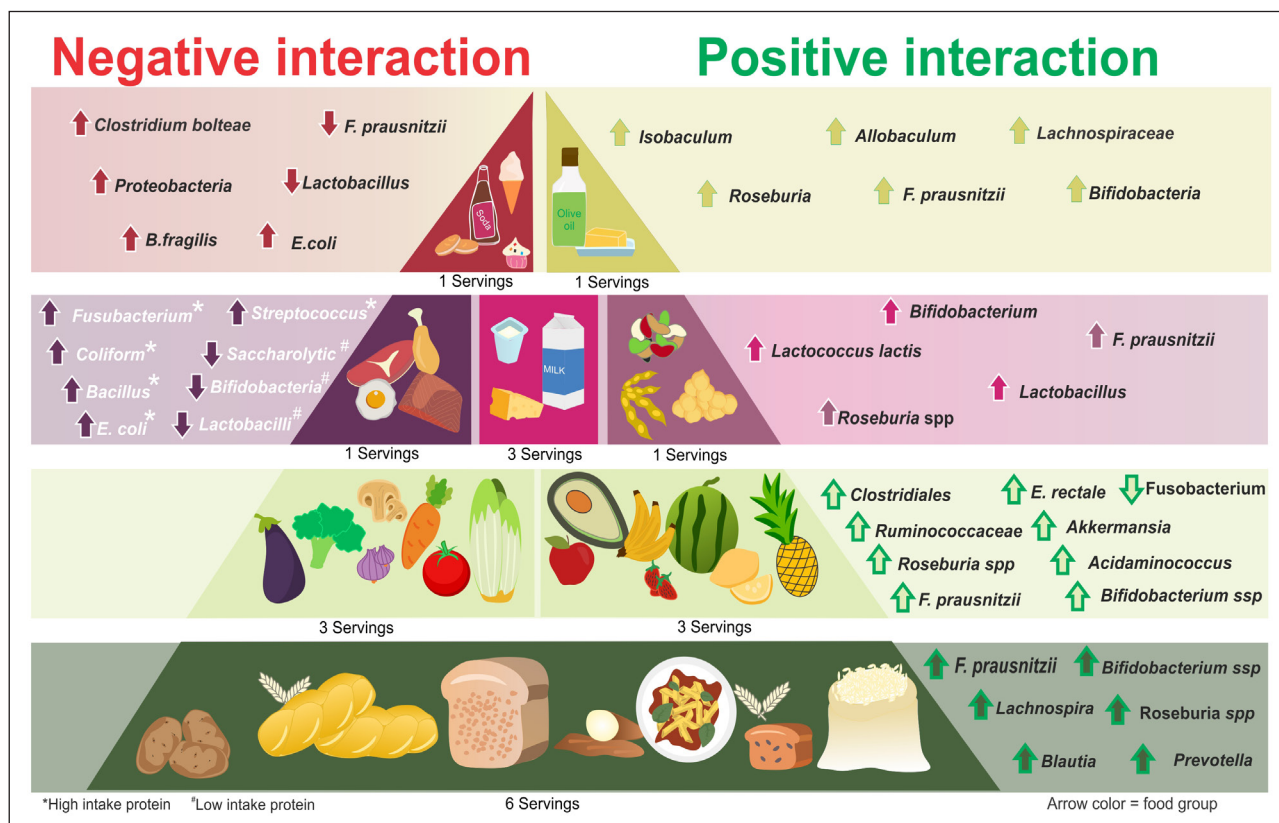At the top of the pyramid are the groups of

FIGURE 1. Food pyramid and gut microbiota.

fats, sugars, and ultra-processed foods. These foods should be consumed in moderate amounts. High consumption of saturated fat reduces bacterial abundance, diversity, and richness, and increases body mass index (BMI) and insulin resistance[13]. However, polyunsaturated fatty acids (PUFA), and fish and olive oil, increase the gut microbiota diversity, SCFA production, and reduce inflammation and intestinal permeability when consumed in limited amounts[14].

Both high sugar and processed and ultra-processed foods reduce diversity bacterial, increase gut permeability, and inflammatory properties[7]. The most recent dietary guideline for the Brazilian population warns to avoid ultra-processed foods and increase natural and minimally processed foods[7]. TABLE 1 shows the main foods, the bacteria they produce and their role in the microbiome.

The food pyramid is a pre-established nutritional education tool. The integration between the intestinal microbiome, food groups, and SCFA-producing bacteria, which benefit from the ingestion of these foods, has the potential to further improve and innovate healthy eating. The diet-microbiome interaction needs to be incorporated into nutrition science, and the food pyramid might assist in this interaction and nutritional learning.

Authors' contribution
The overall conceptualization of studies included in this work was done by Magro DO and Santos A. Magro DO, Rossoni C, Saad-Hossne R and Santos A wrote the paper, which was reviewed and edited by all the authors.

Orcid
Daniela O Magro: 0000-0002-8180-6254.
Carina Rossoni: 0000-0002-6494-4639.
Rogerio Saad-Hossne: 0000-0002-8166-0304.
Andrey dos Santos: 0000-0003-2922-3032.

TABLE 1. The main foods, the bacteria they produce and their role in the microbiome.

Food	Nutrient	Bacteria	Function	References
Potato	Resistant starch and polyphenols	Bifidobacteria, *Faecalibacterium prausnitzii* and Lachnospira	Increases the SCFA, reduction of intestinal permeability and endotoxemia	(8)
White rice	Resistant starch	Blautia, *Faecalibacterium prausnitzii*	Antimicrobial activity; SCFA synthesis; lowering blood glucose	(15)
Whole grains	Flavonoids, ferulic acids	Bifidobacterium and butyrate producers (Eubacterium rectale, Roseburia faecis, and Roseburia intestinalis)	Increased fecal acetate and total SCFAs; anti-inflammatory effects	(7)
White bread	Resistant starch	Increased Bifidobacterium,	Increases propionate, butyrate, and glucagon-like peptide-1 (GLP-1); decreases lipopolysaccharide (LPS)	(15)
Fruits	Resistant starch, flavonoids	Increased *Faecalibacterium prausnitzii*, Akkermansia muciniphila, Ruminococcaceae, Clostridiales, and Acidaminococcus. Inversely associated with Fusobacterium	Increasing production of SCFAs, maintaining intestinal mucosal integrity, improving insulin sensitivity and anti-inflammatory properties	(3)
Vegetables	Metabolized glucosinolates, generating chemopreventive isothiocyanates	Increased Bacteroides, *Bacteroides thetaiotaomicron*	Decreased risk of certain cancers	(11)
Raw vegetables	Resistant starch	Clostridium and Bacillus. Might increase the diversity of bacteria	Alleviate the symptoms of gluten related diseases	(11)
Banana and garlic	Resistant starch and Inulin	Increased Bifidobacterium	Promoted satiety, and reduced body weight	(7)
Mushrooms	Fiber, polysaccharides, heteroglucans, peptidoglucans, proteoglucans, and vitamins	Increased Bacteroides, Lactobacillus, Roseburia, Prevotella, *Faecalibacterium prausnitzii* and Bifidobacterium	Increases SCFA-producing bacteria. Reduced endotoxin-bearing Proteobacteria levels	(3, 11)
Animal protein	Amino acids from dietary protein can be used for protein synthesis by gut microbes. The undigested protein and amino acids are mainly fermented into various bacteria metabolites, such as SCFA, hydrogen sulfide, and ammonia	High concentrations of dietary protein increase the populations of pathogens Escherichia coli, Fusubacterium, Coliforms, Streptococcus and Bacillus. Lower concentrations of dietary protein decrease butyrate-producing bacteria including Lactobacilli, Bifidobacteria and Saccharolytic	Some of these bacterial metabolites can be transported inside colonocytes and exert beneficial or deleterious effects on these epithelial cells depending on their toxic potential and concentration in the lumen. Lower dietary protein decreased substrate is available for E. coli proliferation. However, when the concentration of protein in the diet is too low to meet the basic requirement for the host, it can increase the abundance of potential pathogens and decrease the population of prebiotics	(12)
Dried legumes (beans, seeds, lentils)	Resistant starch	Ruminococcus spp and Bifidobacterium spp	Resistant starch has been reported to increase SCFA production. Phytic acid improves the composition of cecal organic acids, microbiota, and mucins, and it may decrease the levels of serum pro-inflammatory cytokines	(11)
Milk and dairy products	Proteins, lipids, carbohydrates, amino acids, minerals and vitamins	Lactobacillus and Bifidobacterium	Suppresses the growth of pathogens	(4)
Fish and Olive oil	Omega 3 and Omega 9	Roseburia, *Faecalibacterium prausnitzii*, Bifidobacteria	Increases the SCFA, reduction of IL17, inflammation reduction via reducing intestinal permeability and endotoxemia	(14)
High fat	Total fat	Increased Blautia, reduction of bacterial abundance, diversity, and richness, increase Clostridium bolteae, reductium *Faecalibacterium prausnitzii*,	Increased BMI, insulin resistance	(13)
Fat	n–6/n–3 PUFA proportion at 3/1 to 11/1 (polyunsaturated fatty acids)	Increased Allobaculum, Isobaculum, Proteobacteria, and Lachnospiraceae	Low levels of triglycerides, decreasing or preventing adipose tissue fat accumulation, insulin resistance, inflammation, hypertension, atherosclerosis, obesity, cardiovascular diseases (CVD), and type 2 diabetes mellitus (T2DM)	(14)
Fat (PUFA)	PUFA (Polyunsaturated fatty acids) (safflower, sesame, pumpkin seed, rice bran, human milk, olive, peanut, wheat germ and hemp)	Increased *Faecalibacterium prausnitzii*, and Lactobacillus	Increased gut microbiota diversity, increases SCFA production, reduction of BMI and T2DM	(14)
Ultra-processed Foods	Food additives, enriched with salt, sugars, saturated fats, and hydrogenated fat	Reduction of Lactobacillus, increases the populations of pathogens	Reduced diversity, increased gut permeability, inflammatory properties	(13)
High sugar diet	Glucose and fructose	Modifies the ratio of Proteobacteria and Bacteroidetes	Reduced diversity, increased gut permeability, promotes metabolic endotoxemia, development of metabolic dysregulation	(13)

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RESUMO – A pirâmide alimentar é uma ferramenta pré-estabelecida de educação nutricional. A integração entre microbioma intestinal, grupos de alimentos e bactérias produtoras de ácidos graxos de cadeia curta (AGCC), que se beneficiam da ingestão de carboidratos fermentáveis, tem o potencial de melhorar e inovar ainda mais a proposta de alimentação saudável. O conceito dieta-microbiota intestinal pode ser incorporado à ciência da nutrição, e a pirâmide alimentar pode auxiliar nessa interação nutricional. Diante desse contexto, esta breve comunicação propõe, por meio da pirâmide alimentar, a ampliação do conhecimento entre a microbiota intestinal, grupos alimentares e bactérias produtoras de AGCC.

Palavras-chave – Microbiota; pirâmide alimentar; nutrição.

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