



## Prebiotics: Clinical Applications, Types, Sources and Definition

Joshua Cript\*

Department of Nutrition, Yeni Yuzyil University, Istanbul, Turkey

\*Corresponding Author's E-mail: [cript.yein@tuk.ac.in](mailto:cript.yein@tuk.ac.in)

**Received:** 17-Mar-2023, Manuscript No. IRJM-23-92094; **Editor assigned:** 20-Mar-2023, PreQC No. IRJM-23-92094 (PQ); **Reviewed:** 03-Apr-2023, QC No. IRJM-23-92094; **Revised:** 26-Jun-2023, Manuscript No. IRJM-23-92094 (R); **Published:** 03-Jul-2023, DOI: 10.14303/2141-5463.2023.46

### Abstract

The microbes in your gut break down a group of nutrients called prebiotics. In recent years, there has been a growing interest in how they affect human health as a whole. Short chain fatty acids are released into the blood circulation as a result of their degradation, affecting not only the gastrointestinal tract but also other distant organs. They can feed the microbiota in the intestinal tract. Both galacto oligosaccharides and fructo oligosaccharides belong to a significant class of prebiotics that have a positive impact on human health. Scientists are attempting to industrially produce prebiotics because foods naturally contain low amounts of galacto and fructo oligosaccharides. Prebiotics appear to be fascinating candidates for promoting human health as a replacement or in conjunction with probiotics due to their safety, health benefits, and advantages in production and storage over probiotics. Prebiotics are covered in detail in this review, including the important role they play in human health.

**Keywords:** Prebiotics, Gut micro biota, Shortchain fatty acids, Fructo oligosaccharides, Galacto oligosaccharides

## INTRODUCTION

The human gastrointestinal tract is home to a wide variety of microorganisms, or gut macrobiotic. The human colon contains between  $10^{10}$  and  $10^{12}$  live microorganisms per gram. Human health depends on the microbial communities that live in the stomach, small, and large intestines. The large intestine is home to the majority of these microorganisms, which are mostly anaerobes (Flint, et al., 2012).

## LITERATURE REVIEW

Microbial balance can be affected by some endogenous factors, like mucin secretions, but the majority of the energy needed for growth comes from food. Particularly, carbohydrates those are not digestible. Prebiotics, or non-digestible dietary substances, are fermented by beneficial intestinal microbes, which derive their energy for survival from breaking down indigestible prebiotic binds. Prebiotics can thus selectively affect the microbiota in the gut. The intestine's metabolism and integrity, on the other hand, are influenced by the gut microbiota. In addition, they are able to suppress pathogens in healthy individuals by inducing some immunomodulatory molecules that have antagonistic

effects against pathogens and are produced by *Bifidobacterium* and *Lactobacillus* genera lactic acid (Morowvat, et al., 2015).

## DISCUSSION

### Types of pre biotics

Inulin and fructo oligosaccharide, also known as oligofructose, fall under this category. Their structure is a fructose linked linear chain with (21) links. They typically contain terminal glucose units linked by (21). FOS has a DP of less than 10, whereas inulin has a DP of up to 60.

Previously, some studies suggested that fructans could selectively stimulate lactic acid bacteria (Ernot, et al., 2009).

However, recent studies have demonstrated that the chain length of fructans is an important factor in determining which bacteria are able to ferment them. As a result, fructans can promote other bacterial species either directly or indirectly (Howlett, et al., 2010).

## Galacto-Oligosaccharides

The lactose extension product Galacto Oligosaccharides (GOS) are divided into two subgroups:

- The GOS that has an excessive amount of galactose at C3, C4, or C6, and
- The GOS that is made from lactose through enzymatic trans-glycosylation. This reaction mostly produces a mixture of tri to pentasaccharides and galactose linked *via* (6), (3), and (4) linkages. This kind of GOS is likewise named as trans-galacto-oligosaccharides or TOS (Bindels, et al., 2015).

*Lactobacilli* and *Bifidobacteria* can be greatly stimulated by GOSs. Infant *bifidobacteria* have been found to be highly incorporated with GOS. GOS also stimulates *Enterobacteria*, *Bacteroidetes*, and *Firmicutes*, but to a lesser extent than *bifidobacteria*. There are some GOSs got from lactulose, the isomer of lactose. GOSs derived from lactulose are also regarded as prebiotics.

## Starch and glucose derived oligosaccharides Resistant Starch (RS)

This is a type of starch that can't be broken down by the stomach. By producing a high level of butyrate, RS can improve health; therefore, it has been suggested to be included in the category of prebiotics. Different gatherings of *Firmicutes* show the most noteworthy joining with a high measure of RS. *Ruminococcus bromii*, *Bifidobacterium adolescentis*, and to a lesser extent *Eubacterium rectale* and *Bacteroides thetaiotaomicron* were all found to be capable of degrading RS *in vitro*. However, in the absence of *R. bromii*, RS degradation is impossible in mixed bacterial and fecal incubations. Polydextrose is an oligosaccharide derived from glucose. It is composed of glucan with numerous glycosidic linkages and branches. It has been suggested, but not proven, that it can stimulate *bifidobacteria*.

## Mechanisms of prebiotic change in the gut microbiota

Prebiotics are able to alter the composition and function of the microorganisms that live in the gut by providing them with energy. In phylogeny, distant bacterial species share the capacity to consume a particular prebiotic frequently. Additionally, a functional metagenomics method recently reported it. In this approach, genes for the breakdown of several prebiotics in a heterologous host, such as *E. coli*, are identified from a metagenomic library of the human microbiota (Johnson, et al., 2013).

FOS, GOS, and Xylooligosaccharides (XOS) can be fermented by clones from a variety of species, including *Firmicutes*, *Actinobacteria*, and *Bacteroidetes*. Some other studies, on the other hand, say that some species can break down a certain prebiotic. *Bifidobacterium sp.* fermentation of starch and fructans are illustrations in this regard. The length of the chain is another important factor in determining which species are capable of fermenting a particular prebiotic. For instance, only a small number of species are capable of fermenting inulin (DP 60), whereas a large number of microorganisms are

capable of degrading FOS (DP 10).

Cross feeding, or the fermentation of a complex prebiotic's byproduct as a substrate for another microorganism, can occur from time to time. *Ruminococcus bromii*, for instance, is capable of breaking down resistant starches, and several species can make use of the fermentation products of this reaction. At the same time, some products might affect other species in a negative way (Costabile, et al., 2012).

Additionally, prebiotics can alter the gut's environment. It has been demonstrated that a one unit change in the gut pH from 6.5 to 5.5 can contribute to a change in the composition and population of the gut microbiota. As was previously mentioned, the majority of the fermentation products of prebiotics are acids, which lower the pH of the gut. The pH modification can change the number of inhabitants in corrosive touchy species, like *Bacteroids*, and advance butyrate arrangement by *Firmicutes*. This cycle is called butyrogenic impact.

## Security of prebiotics

It is assumed that prebiotics do not cause severe or life threatening side effects. Oligosaccharides and polysaccharides cannot be broken down by enzymes in the intestines. They are shipped to the colon to be matured by the stomach microbiota. As a result, prebiotics osmotic effects account for the majority of their side effects. As a result, prebiotic recipients may experience flatulence, bloating, cramping, and osmotic diarrhea. The development of their side effects is influenced by the chain length of prebiotics. Surprisingly, shorter chain prebiotics may cause more side effects. Shorter inulin molecules, which ferment more quickly and are primarily metabolized in the proximal colon, may account for this phenomenon. In contrast, those with longer chains ferment later and more slowly in the distal colon. In addition to the chain length, the prebiotic dose may have an impact on its safety profile (Al-Sheraji, et al., 2013).

For instance, low doses of prebiotics (2.5-10 g/day) and high doses (40-50 g/day) of prebiotics can result in osmotic diarrhea and flatulence, respectively. It should be noted that in order for prebiotics to exert their beneficial effects on human health, a daily dose of 2.5-10 g is required (Prapulla, et al., 2000). This indicates that prebiotics can have mild to moderate side effects at therapeutic doses. The majority of available prebiotics have doses ranging from 1.5 to 5 g per serving (Mohkam, et al., 2016).

## CONCLUSION

Developing effective and diverse prebiotics for the modification of the microbiota hemostasis appears to be very difficult due to the diversity of the gut microbiota in various populations, countries, and even individuals based on various dietary regimens. Prebiotics, on the other hand, appear to be a more convenient option in this regard due to their much simpler production and formulation processes and lack of cold chain

requirements for transportation and storage. Prebiotics negligible side effects are another significant benefit.

As a result, as a standardized approach, designing particular, population specific prebiotics based on the resident gut microbiota of each community may ultimately contribute to the reduction of certain disorders in each society. This idea has the potential to put an end to the major debates about prebiotics and could be included in future prebiotics guidelines from the WHO or FAO.

## ACKNOWLEDGEMENT

None

## CONFLICT OF INTEREST

None

## REFERENCES

1. Flint HJ, Scott KP, Louis P, Duncan SH (2012). The role of the gut microbiota in nutrition and health. *Nat Rev Gastroenterol Hepatol.* 9:577-558.
2. Morowvat MH, Nezafat N, Ghasemi Y, Zare MH, Mohkam M (2015). Probiotic potential of five lactobacillusstrains isolated from traditional Persian yoghurt in fars province, iran: Viewing through the window of phylogenetics. *Biosci Biotechnol Res Asia.* 12:1265-1272.
3. Ernot DC, Boileau TW, Bauer LL, Middelbos IS, Murphy MR, et al. (2009). *In vitro* fermentation profiles, gas production rates, and microbiota modulation as affected by certain fructans, galactooligosaccharides, and polydextrose. *J Agric Food Chem.* 57:1354-1361.
4. Howlett JF, Betteridge VA, Champ M, Craig SA, Meheust A, et al. (2010). The definition of dietary fiber discussions at the ninth vahouny fiber symposium: Building scientific agreement. *Food Nutr Res.* 54:5750.
5. Bindels LB, Delzenne NM, Cani PD, Walter J (2015). Towards a more comprehensive concept for prebiotics. *Nat Rev Gastroenterol Hepatol.* 12:03-310.
6. Johnson CR, Combs GF, Thavarajah P (2013). Lentil (*Lens culinaris* L.): A prebiotic rich whole food legume. *Food Res Int.* 51:107-113.
7. Costabile A, Fava F, Roytio H, Forssten SD, Olli K, et al. (2012). Impact of polydextrose on the faecal microbiota: A double blind, crossover, placebo controlled feeding study in healthy human subjects. *Br J Nutr.* 108:471-481.
8. Al-Sheraji S, Ismail A, Manap M, Mustafa S, Yusof R, et al. (2013). Prebiotics as functional foods: A review. *J Funct Foods.* 5:1542-1553.
9. Prapulla S, Subhaprada V, Karanth N (2000). Microbial production of oligosaccharides: A review. *Adv Appl Microbiol.* 47:299-343.
10. Mohkam M, Nezafat N, Berenjjan A, Negahdaripour M, Behfar A, et al. (2016). Role of *Bacillus* genus in the production of value added compounds. In *Bacilli and Agrobiotechnology*. Springer international Publishing. Basel, Switzerland. 1-33.