

Bacteria A Benefit Cell

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Mini Review

Before birth, microbiota does not exist in the human body, and microorganisms start to adapt in several locations in the body after birth. The microflora in the intestinal tract takes a long period to be formed. After they formed, human body get benefits from these microbiota and the important benefit the immune system supports, disposal of waste gastrointestinal, development metabolism and resistance the body against the pathogenic microorganisms [1-7].

Microbiota in the intestinal play a major benefit to the human health, the forming of these microbiota depended on the type of nutrients and lifestyle, and these reflected on the impact of formed microbiota on the body energy and metabolism [8-12]. Study the reflect of the food type on the intestinal microbiota were determined by several studies, López-Nicolás et al. [13] studied the effect of fruit juices pine bark extract (PBE) on the intestinal microbiota and they found that the pure phenolic compounds such as gallic acid had a high antimicrobial effect on *Staphylococcus aureus* and *Escherichia coli*.

A study on the effects of lactose or inulin on constipated elderly patients of measured microbiota composition, the results show considerable interindividual variations that inulin increased bifidobacteria significantly and decreased enterococci in number and enterobacteria in frequency. Where the individuals consuming lactose, increase in fecal counts of enterococci and decrease in lactobacilli. Further, clostridia were detected. Total bacterial counts remained unchanged [14]. The dynamic mutual relations between the intestinal microflora and colon cancer risk can be modified by dietary components and eating behaviors. Composition of intestinal microbiota can be influenced by several dietary components.

Dietary modifiers the numbers and types of microbes and have been reduced colon cancer risk experimentally by generating bioactive compounds from food components. Further, gastrointestinal microbiota can impact both sides of the energy balance equation [15]. On the other hand, dieting affect the intestinal microbiota, several studies sought the relationship between the nutrient types and the composition of the intestinal

microbiota, and the consequent of that on the human health and his activities. The determine of chronic soy consumption on modified gut microbiota activities, the results showed high concentrations of is flavones and their gut microbiota metabolites in the plasma, urine, and feces in the high-soy diet consumer compare to who consumed the low-soy diet [16].

In a study of dietary types to clarify some compounds etiologic role in colon cancer. The results showed that consuming a mixed Western diet was more able to hydrolyze glucuronide conjugates, and more microbially degraded bile acids compare with the vegetarians, seventh-day Adventists, Japanese and Chinese [17]. The probability of the effect of trans galacto oligo saccharides and a placebo on the composition and activity of the intestinal microbiota were determined in samples of males and females, and the concluded of this work confirmed that trans galacto oligo saccharides do not beneficially change the composition of the intestinal microflora, and After the ingestion of both placebo and trans galacto oligo saccharides number of bifidobacteria increased in intestinal microbiota [18].

Instead of the effect of the nutrient on the composition of microbiota, some factors had a side effect on the composition of macrobiotic. One of the most important factors is using the antibiotics; several studies investigate and determine the frequency and change of intestinal microbiota after a course of antibiotic treatment [19-21]. To study the effect of amoxicillin and vancomycin in the composition of microbiota randomized samples were measured to detect the changes in microbiota; the results showed that vancomycin reduced microbiota diversity and decrease gram-positive bacteria [22].

The antibiotics ciprofloxacin, clindamycin, vancomycin, amoxicillin, clarithromycin, and lansoprazole were studied as tream of long period antibiotic treatments. The conclusion of these studies improved the side effect of reduction and changes of the intestinal microbiota, facultative anaerobes and Enterobacteria increased after treatments with the antibiotics amoxicillin, clarithromycin, and lansoprazole, The influence of the intestinal microbiota differ

to the different antimicrobial agents in different ways, the effect in microbiota depends on several factors for example the agent spectrum, the dosage and duration of treatment [23- 25].

Moreover, treatment with chemotherapy has a side effect on the microbiota including changes in their composition and their population, recently several studies investigated the effect of chemotherapy on the intestinal microbiota, 5-fluorouracil therapy influence in methane produces by methanogenesis which reverse association with diarrhea and positive association with constipation, the intestinal microbiota have been toxicity during the therapy [26].

Further, the impact of chemotherapy treatment on the composition of the microbiota extended to the composition of the human milk microbiota, a recent comparing study on the microbiota composition in cancer patient mothers and healthy mother's milk showed that the genera *Bifidobacterium*, *Eubacterium*, *Staphylococcus* and *Cloacibacterium* were depleted, where the genera *Acinetobacter*, *Xanthomonadaceae* and *Stenotrophomonas* were decreased [27].

The gut microflora plays a major role to repair the intestinal homeostasis and integrity. In a survey of intestinal microflora, bacteremia, mucositis, chemotherapy-induced diarrhea, chemotherapy-induced mucositis, radiotherapy-induced mucositis to evaluate the function of gut microflora in the pathogenesis of gastrointestinal mucositis, authors found that Patients who receiving cytotoxic and radiation therapy exhibit marked changes in intestinal microflora, with most frequently, decrease in *Bifidobacterium*, *Clostridium cluster XIVa*, *Faecalibacterium prausnitzii*, an increase in *Enterobacteriaceae* and *Bacteroides*, and they concluded that gut microflora can play a major role in the pathogenesis of mucositis by the changing of intestinal barrier function, innate immunity and intestinal repair mechanisms [28].

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