The Effect of Dietary Types on Gut Microbiota Composition and Development of Non-communicable Diseases

Martin Soldan , Lubica Argalasova * , Lucia Hadvinova , Bonzel Galileo , Jana Babjakova

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Review

The Effect of Dietary Types on Gut Microbiota Composition and Development of Non-Communicable Diseases

Martin Soldán, Ľubica Argalášová *, Lucia Hadvinová, Bonzel Galileo † and Jana Babjaková

Institute of Hygiene, Faculty of Medicine, Comenius University in Bratislava, Špitálska 24, 813 72 Bratislava, Slovakia; soldan9@uniba.sk (M.S.); lucia.hadvinova@fmed.uniba.sk (L.H.); bonzel1@uniba.sk (B.G.); jana.babjakova@fmed.uniba.sk (J.B.)
* Correspondence: lubica.argalasova@fmed.uniba.sk
† Diploma student at the Institute of Hygiene, Faculty of Medicine, Comenius University in Bratislava, Špitálska 24, 813 72 Bratislava, Slovakia.

Abstract: The importance of diet shaping the gut microbiota is well known and may help with improving the overall health of an individual. Many other factors also have an influence, such as genetics, age, exercise, antibiotic therapy, or tobacco use. The purpose of this review is to summarize how three distinct dietary types (plant-based diet, Mediterranean diet, and Western diet) affect the composition of gut microbiota and the development of non-communicable diseases (NCDs). PubMed, Web of Science and Scopus databases were used for searching papers with an emphasis on keywords ''dietary pattern'', ''gut microbiota'' and ''dysbiosis''. Plant-based diet and Mediterranean diet promote the production of beneficial bacterial products, and more microbial diversity and therefore are generally considered healthy dietary types. On the other hand, the Western diet is a typical example of an unhealthy approach to nutrition which leads to an overgrowth of pathogenic bacteria. Moreover, understanding the impact of diet on the modulation of gut microbiota may give rise to new therapeutical strategies.

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Introduction

The gut microbiota is a dynamic complex of microorganisms located in the gastrointestinal tract of humans [1]. It includes *Bacteria, Archaea,* viruses, protists and the relationship between microorganisms and the human host is mutually symbiotic and beneficial [2]. Representing a pivotal part of human body, gut microbiota plays significant role in nutrition and its physiology [3]. It is often times suggested to be a superorganism [4]. So far 2,172 species have been identified, with 12 distinct phyla. The majority of isolated species, 93,5% were *Proteobacteria*, *Actinobacteria, Firmicutes and Bacteroidetes* [5]. *Firmicutes* make up 65% of the total gut bacteria, *Bacteroidetes* 23%, *Actinobacteria* 5% and the fourth most represented phyla are *Proteobacteria* [6].

Diet is an essential factor for maintaining healthy status and preventing non-communicable diseases (NCDs). NCDs contain cancer, cardiovascular diseases, cognitive or metabolic impairments and they represent the majority of cases of mortality all around the world. It is suggested that diet has a great influence on the gut microbiota formation, which participates in the pathogenesis of NCDs [7,8]. Therefore, the aim of this review is to assess the relationship between 3 dietary types (plant-based diet, Mediterranean diet and Western diet) and the bacterial composition of the gut.

The purpose of this review is to summarize how three distinct dietary types (plant-based diet, Mediterranean diet, and Western diet) affect the composition of gut microbiota and the development of non-communicable diseases (NCDs). PubMed, Web of Science and Scopus databases were used for searching papers with an emphasis on keywords ''dietary pattern'', ''gut microbiota'' and ''dysbiosis''.

1. Composition of Gut Microbiota in the Gastrointestinal Tract

The distribution, quantity and type of microorganisms vary through the digestive tract. Only a little number of species appear in the stomach and small intestine. The majority populate the colon, which is located at the distal part of the digestive tract [9]. This is due to different physiology, pH, accessibility of substrates, oxygen partial pressure, flow rate of digestion and host secretions [10]. At least 700 different bacterial species are present in the human mouth cavity [11]. More than 94% is comprised of 6 phyla, *Bacteroidetes, Firmicutes, Fusobacteria, Actinobacteria, Proteobacteria and Spirochaetes.* The distribution of bacteria is modified by saliva, soft and hard tissue surfaces. More essentially, the hard surface of the tooth enables the formation of biofilms, which establish a steady environment for the bacterial growth [12]. In oesophagus, the most abundant genus is *Streptococcus* [13]. It is suggested that healthy stomach microbiota is mostly formed by *Prevotella, Veillonella, Streptococcus, Haemophilus* and *Rothia.* In addition, *Bacteroidetes, Firmicutes, Fusobacteria, Actinobacteria* and *Proteobacteria* were also found [14]. People, who tested positive for *Helicobacter pylori* had this bacterium as the most represented. However, the presence of *Helicobacter pylori* does not affect the microbial diversity of stomach [15].

The small intestine microbiota is less diverse and numerous than in the colon, with a biological mass of 10^3-10^7 microbial cells per gram of intestinal tissue, mainly because of lower pH, pancreatic peptides, bile acids or quicker transit time. It is assumed, that the most abundant phyla are *Proteobacteria* and *Firmicutes*, which can withstand these factors [16]. Anaerobic conditions of the colon provide a good environment for anaerobic microorganisms to grow [17]. The most represented bacterial phyla are *Bacteroidetes* and *Firmicutes,* which together make up 90% of the total bacteria population [18]. During life, the ratio between *Bacteroidetes* and *Firmicutes* varies, which can implicate the health of an individual. In terms of density, dominant bacterial genera, *Bacteroides, Bifidobacterium, Eubacterium, Clostridium, Propionibacterium, Peptostreptococcus and Ruminococcus* account for 10^9 of bacterial cells/gram of colon tissue [19]. There are also pathogenic bacteria present in the colon, namely *Escherichia coli, Vibrio cholerae, Bacteroides fragilis, Salmonella enterica* and *Campylobacter jejuni* and they form around 0.1% of the total bacterial population [20].

2. Function of Gut Microbiota

Gut microbiota has the ability to break down dietary fibre (oligosaccharides, polysaccharides, pectin, lignin, and resistant starches). By doing so, it generates short-chain fatty acids (SCFA), namely acetate, butyrate and propionate [21,22]. SCFA are absorbed in the gastrointestinal tract (GIT) and represent a valuable source of energy for host cells [23]. SCFA also has a variety of different effects, for example regulation of gene expression, apoptosis, chemotaxis, activation of gluconeogenesis and possibly regulation of appetite or its importance in the correct function of epithelial cells in the GIT [24–26]. Acetate was reported to be involved in the production of IgA by intestinal B-cells and IgA plays a crucial role in the toleration of gut bacteria and fighting against pathogenic bacteria [27]. Essential vitamins are yet another critical product of gut bacteria, such as vitamin K and several vitamins from the B group [28]. Furthermore, the gut bacteria can break down primary bile acids, transforming them into secondary bile acids, which can be reabsorbed [29]. The gut microbiota is also associated with the activation of polyphenols. After the activation, polyphenols are absorbed in the portal system [30].

It has been discovered that gut microbiota is connected to the brain. The axis between the gut and brain is a two-way communication, which is made of a network linking the central, autonomic, enteric nervous system and the hypothalamic pituitary adrenal system. It has been claimed that the axis affects multiple mechanisms, such as satiety and digestive functions, also behaviour and mood can be influenced, because the gut microbiota is able to modulate the serotoninergic system [31,32].

3. Factors Influencing the Gut Microbiota

The gut microbiota is at early stages of life influenced by the mother's microbiota, but various factors shape it later in life, for instance infections, the immune system, diet or the use of medication. Genetics play an essential role in the formation of gut microbiota and several bacterial species are heritable, such as *Actinobacteria* and *Firmicutes*. This can be demonstrated in monozygotic and dizygotic twins. Both types of twins, when sharing the same environment show differences, but the difference between the gut microbiota of monozygotic twins is smaller [33]. Age is another important factor in gut microbiota composition. In infants, the gut microbiota lacks diversity when compared to adults. There is a large influx of bacteria until about 3 years of age when the gut microbiota starts to develop the adult characteristics [34]. This can be justified by the transition from a diet based on milk into a solid diet [35]. In adult humans, the structure and function of gut microbiota stay stable, but events such as diseases and antibiotic treatments may cause an alteration by changing bacterial composition and transferring genes of antibiotic resistance [1,36,37]. In the elderly population (over 65 years old), bacterial diversity is lower than in adults and the facultative anaerobic bacteria grow at the expense of useful bacteria [38].

Alcohol, smoking and exercise represent other determinants in shaping the gut microbiota. Alcohol promotes dysbiosis through two mechanisms: a change in gut microbiota composition and a reduction of nutrient absorption. Smoking as a risk factor acts in many ways. For instance, by modifying pH, oxygen levels and production of acid in the gastrointestinal tract. Tobacco is also an immunosuppressant. Exercise can enhance the diversity of gut microbiota and is even suggested as a remedy to dysbiosis-related chronic illnesses. However, it is difficult to prove the beneficial effects of exercise on the gut microbiota of athletes, since most of them have a distinct diet [39–45].

Diet and geography are important factors involved in the diversity of gut microbiota [46]. When comparing industrialized and non-industrialized countries, there is a greater *Bacteroidetes* to *Firmicutes* ratio [44]. Another division is by using enterotypes. Enterotype 1, characterized by an abundance of *Bacteroides*, enterotype 2, rich in *Prevotella* and enterotype 3, where *Firmicutes* are large in number, especially *Ruminococcus* [47]. Highers altitudes suit anaerobic bacteria and during cold environmental stress, there is a change in *Bacteroidetes* versus *Firmicutes* ratio, in favour of *Firmicutes* [48,49].

4. Diseases Related to Gut Microbiota

Dysbiosis is a term, that indicates the change and imbalance of the gut microbiota composition, which can lead to various illnesses [50]. Gastrointestinal diseases, for example Irritable bowel syndrome (IBS) are affected by gut microbiota by many mechanisms. There is a disruption in the gut-brain axis, changed motility of GIT, raised visceral sensitivity and intestinal barrier function is also modified [51]. In terms of gut bacteria composition of IBS patients, *Bifidobacterium* and *Faecalibacterium* populations were reduced. On the other hand, *Proteobacteria*, *Bacteroides* and *Lactobacillacae* were in higher numbers in contrast to the control group [52]. Inflammatory bowel disease (IBD) consists of Crohn's disease and ulcerative colitis [53]. Numerous changes in the gut microbiota of IBD patients have been reported, namely a higher abundance of *Candida tropicalis*, *Escherichia coli*, and a decrease in *Firmicutes*, *Bacteroidetes* or *Faecalibacterium prausnitzii* in comparision with the control group [44,54,55]. The pathogenesis of colorectal cancer (CRC) is characterized by a greater number of pathogenic bacteria. For example, *Bacteroides fragilis* and *Escherichia coli* promote a chronic inflammation of intestinal tissue, which can lead to the development of CRC [56].

The gut microbiota possesses multiple mechanisms, that can affect the development of obesity, such as modulating appetite, energy absorption, inflammation or fat storage [57]. It was believed, that *Bacteroidetes/Firmicutes* ratio changes during the pathogenesis of obesity, however this has been recently proven untrue, as there is no microbiological connection to human obesity [58]. Dysbiosis of the gut microbiota is a factor connected to the pathogenesis of Diabetes mellitus (DM), both type 1 and type 2 [59]. To be more specific, type 1 DM patients exhibit a higher abundance of *Ruminococcus* and *Bacteroides*, with a lower proportion of *Prevotella* and *Clostridium* as opposed to the control group. Similarly to obesity, in type 2 DM there is a drop in *Akkermansia* and *Bifidobacterium* amounts [60–62].

Furthermore, type 2 DM represents a good environment for the growth of opportunistic pathogens, for example *Escherichia coli* or *Clostridium symbiosum* [63].

It is suggested that the gut-brain axis might be associated with neuroinflammation, a process, that leads to the loss of neurons, which is typical for Alzheimer disease (AD) and Parkinson disease (PD). PD patients had a higher abundance of *Enterobacteriaceae* and reduced populations of *Prevotellaceae.* AD is influenced by pathogenic bacteria like *Mycobacterium tuberculosis*, *Staphylococcus aureus* or *Salmonella spp.* [64,65]. Pathogenic bacteria also seem to be involved in the pathogenesis of depression and anxiety disorders, namely *Enterobacteriaceae* and *Desulfovibrio* [66]. Autism spectrum disorder (ASD) is another neurological disability, in which the dysbiosis of gut microbiota is suggested to be involved, but the evidence is conflicting [67].

In addition, gut bacteria are also affiliated with other diseases, for example cardiovascular disorders (by producing SCFA), and autoimmune disorders like multiple sclerosis or rheumatoid arthritis (by altering immune responses) [68,69].

Table 1. Effect of dietary types on gut microbiota composition.

Dietary type	Reference	Studies	Sample	Main findings
Plant-based	Sidhu et al (2023) [76]	12 interventional studies	583 participants, 21-61 years old, men and women healthy, obese, with rheumatoid arthritis and cardiovascular risk	↑*Ruminococcaceae* and ↓ *Bacteroidaceae* in individuals following plant-based diet, *Coprococcus* and *Faecalibacterium* increased in vegans and decreased in vegetarians
Plant-based	Trefflich et al (2020) [78]	16 cross-sectional studies	1229 participants, 498 omnivores, 389 vegetarians and 342 vegans, 18-72 years old (except for 1 study), men and women	↑ *Bacteroidetes*, ↓ *Proteobacteria* and ↑ *Verrucomicrobia* in vegans compared to omnivores, *Firmicutes* levels were similar, ↑ *Actinobacteria* in vegetarians
Mediterranean	Kimble et al (2023) [73]	34 studies in total, 17 randomized control trials, 17 observational (3 prospective and 14 cross-sectional	4526 participants 22- 95 years old, majority healthy, others with a medical condition	↑ *Bacteroidetes* and ↓ *Firmicutes* in individuals, following Mediterranean diet, also ↑ *Faecalibacterium prausnitzii*

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Western	Wolters et al (2019) [87]	15 studies in total, 9 cross-sectional observational studies, 6 randomized control trials	From 9 to 531 participants (cross-sectional observational studies), from 20 to 88 participants (randomized control trials), mean age 8.1-63.3 years old, 10 studies included men and women, 2 only men and 3 only women	↓ of total bacteria in individuals following diet high in monounsaturated fatty acids (MUFA), ↑ *Firmicutes* and ↓ *Bacteroidetes*, increase in *Prevotella*, *Enterobacteriaceae*, *Parabacteroides* and *Turicibacter* populations

5. The Effect of Diets on Gut Microbiota Composition

Plant-based diets are comprised of fruits, vegetables, seeds, nuts, legumes, whole grains and herbs [70]. There are multiple forms of plant-based diets, which differ in restricted components. Flexitarians rarely consume meat, while pescatarians eat fish and seafood as their only sources of meat. Ovolactovegetarians exclude meat products, but consume dairy or eggs and lastly, vegans have a diet, where every component is plant-based [71]. The idea of the Mediterranean diet is based on the diet of countries located near the Mediterranean Sea [72]. It is mostly a plant-based diet with olive oil as a main source of fat. In terms of animal products, the consumption is moderate [72,73]. The Western diet is often considered an unhealthy diet and is defined by excessive consumption of processed and refined foods, simple sugars, sweets or animal fats. In addition, consumption of fruits, vegetables, nuts and whole grains is insufficient [6,74,75] (Table 1, 2).

In 2023, there was a systematic review done by Sidhu et al. about **plant-based diet** influence on the composition of gut microbiota and the benefits of plant-based diet in inflammatory and metabolic disorders. They included randomized control trails, non-randomized control trails and pre-post interventions, that highlighted the impact of plant-based diet on gut microbiota. Systematic review consisted of 12 interventional studies, that were incorporated with a total of 583 participants, aged between 21 and 61 years old, both men and women. In terms of health status, participants were healthy, obese, rheumatoid arthritis patients and individuals with cardiovascular risk. They followed a plant-based diet for certain amount of time, ranging from 5 days to 13 months. A higher abundance of *Ruminococcaceae* and a decreased population of *Bacteroidaceae* were revealed in individuals following plant-based diets. However, differences between vegan and vegetarian diet have been discovered. Vegans had *Coprococcus* and *Faecalibacterium* in higher numbers. On the other hand, in vegetarians these bacteria populations decreased. It has been also found that rheumatoid arthritis patients improved after following the plant-based diet together with patients with cardiovascular disorders, whose lipid profiles and blood pressures were more optimized. The positive outcomes might be related to metabolic products like SCFA or TMAO (Trimethylamine N-oxide) [76]. SCFA, which are produced by the degradation dietary fibres and carbohydrates, play an important role in immune, metabolic, and neural systems [25]. Consumption of vegetables and fruits affect levels of SCFA highly [76]. Elevated TMAO level is associated with inflammation and metabolic diseases, mainly obesity and diabetes. Plant based diet has been also shown to decrease levels of TMAO [77] (Table 1, 2).

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Trefflich et al. published a systematic review related to the relationship between gut microbiota composition and vegan or vegetarian diet in comparison to omnivores. 16 studies were included in the final review with cross-sectional design. Apart from 1 study they consisted of men and women of age between 18 and 72. Total number of participants were 1229, out of which were 498 omnivores, 389 vegetarians and 342 vegans, which followed a vegetarian or vegan diet for more than a month. Vegans had higher levels of *Bacteroidetes* in contrast to omnivores, *Firmicutes* levels were similar. An increase in *Actinobacteria* populations in vegetarians also have been reported. In vegans, a decrease in *Proteobacteria* and an increase in *Verrucomicrobia* have been found, both compared to omnivores [78]. In addition, Losno et al. investigated the composition of adult gut microbiota and compared vegans with omnivores. They found, that *Bacteroidetes* were in higher numbers in vegans when compared to omnivores. Within *Bacteroidetes*, vegans exhibited an increase in *Prevotella*, but *Bacteroides* results were conflicting. On the other hand, *Bifidobacteria* and *Enterobacteria* were less abundant in the vegan population when compared to omnivores. Interestingly, also lower abundance of *Staphylococcus, Streptococcus and Corynebacteria* were present in a group following a vegan diet [79] (Table 1).

Kimble et al. assessed the effect of **Mediterranean diet** on gut bacteria diversity, abundance and its metabolic products. The systematic review evaluated 34 studies with a total of 4526 participants aged 22 to 95 years old. The majority of participants were healthy, but individuals with other medical conditions were also included. 17 studies were observational and the other 17 were randomized control trials. In terms of observational studies, 3 were prospective and 14 were cross-sectional studies. Regarding to bacterial diversity, an increase in *Bacteroidetes* and a decrease in *Firmicutes* populations in those, who followed the Mediterranean diet have been reported. Moreover, a higher abundance of *Faecalibacterium prausnitzii* has been found [73]. Three fundamental elements of the Mediterranean diet are fibre, extra virgin olive oil (EVOO) and polyunsaturated fatty acids (PUFA) [72]. It has been demonstrated that consumption of EVOO leads to an expansion of *Lactobacillus* and reduced growth of pathogenic bacteria [80]. Similarly, PUFA has also an impact on anti-inflammatory processes with its cardioprotective properties [6,72]. PUFA ω-3 has a beneficial effect on *Bifidobacterium* growth. On the other hand, ω-3 have an opposite effect on *Faecalibacterium* populations [6,81]. In terms of fibre, it is metabolized by gut bacteria and SCFA are synthetised, which have anticancer and cardioprotective properties [72]. Similarly to plant-based diet, TMAO levels are also decreased [82]. In addition, this diet has also a positive role in reducing the risk of the development of diabetes mellitus and other metabolic disorders [83]. So et al. conducted a systematic review and a meta-analysis, where they analyzed the impact of dietary fibre on the composition of gut microbiota but did not identify any alteration of the alpha diversity. However, an increase in *Bifidobacterium* and *Lactobacillus* has been discovered [84]. Other beneficial effects are attributed to a decreased oxidative state, inflammation and positive impact on metabolic health represented by increased levels of *Eubacterium rectale* and *Clostridium leptum*, bacteria producing short-chain fatty acids, raising levels of *Bacteroides, Bifidobacteria* and *Faecalibacterium prausnitzii species*, and lower levels of *Blautia species* and *Firmicutes* [85] (Table 1, 2).

Health consequences of the **Western diet** are numerous, such as dyslipidemia, insulin resistance, systemic inflammation, overactivation of sympathetic and renin-angiotensin systems or altering the gut microbiota [75]. A major effect of the Western diet on the gut microbiota is due to a high consumption of processed and ultra-processed foods. It has been discovered that various factors like acellular nutrients, artificial sweeteners and emulsifiers can have a negative impact on the gut microbiota and thus promote dysbiosis [86]. Another important part of the Western diet is the excessive consumption of fats. Wolters et al. conducted a systematic review of the impact of fat on the composition of gut microbiota. They incorporated a total of 15 studies, out of which 9 were cross-sectional observational studies and 6 randomized control trials. The number of participants varied, cross-sectional studies included from 9 to 531 participants, randomized control trials from 20 to 88. 10 studies included men and women, 2 only men and 3 only women with mean age ranging from 8.1 to 63.3 years. Individuals followed a high-fat diet for 3 weeks up to a year. A reduced number of bacteria has been observed in individuals following the diet high in monounsaturated fatty acids

(MUFA), however *Prevotella*, *Enterobacteriaceae*, *Parabacteroides* and *Turicibacter* populations have grown. The ratio between *Bacteroidetes* and *Firmicutes* was also changed, with an increase in *Firmicutes* and decreased levels of *Bacteroidetes* [87] (Table 1).

Other components of the Western diet might also have effects on gut microbiota, for instance refined carbohydrates, red meat and salt. A high-salt diet leads to a decrease in SCFA production and a reduced *Lactobacillus* abundance [6,88]. On the other hand, consumption of red meat leads to an increase in TMAO production [76]. The pathogenesis of CRC is highly influenced by the disproportionate consumption of red meat and processed meat. Dysbiosis of the gut microbiota might play a role in the CRC pathogenesis, namely an increased volume of *Escherichia coli*, *Streptococcus bovis*, *Bacteroides fragilis* and *Fusobacterium nucleatum*, which can create inflammation or alter the oncogenes and tumor-supressing genes [89]. Added sugars might also modulate the gut microbiota. An increase in *Firmicutes* among *Bacteroidetes/Firmicutes* ratio has also been described in connection to the consumption of sweetened beverages [90]. Negative effects on insulin metabolism are associated with higher levels of *Clostridium bolteae and Blautia*, which are linked with the consumption of mainly short fatty acids (SFA) in the diet [87] (Table 1, 2).

Table 2. *Firmicutes/Bacteroidetes* ratio, SCFA and TMAO production change with different dietary types.

	Plant-based diet	**Mediterranean diet**	**Western diet**
***Firmicutes/Bacteroidetes* ratio**	↓ (Trefflich et al., 2020) [78]	↓ (Kimble et al., 2023) [73]	↑ (Wolters et al., 2019) [87] (Ramne et al., 2021) [90]
SCFA production	↑ (Sidhu et al., 2023) [76]	↑ (Merra et al., 2020) [72]	↓ (Miranda et al., 2018) [88]
TMAO production	↓ (Beam et al., 2021) [77]	↓ (De Filippis et al., 2016) [82]	↑ (Sidhu et al., 2023) [76]

Conclusions

Plant-based diet and Mediterrean diet are rich in fibre and are linked to an increase in production of SCFA and lowering TMAO levels, which both have a great impact in improving cardiovascular and metabolic diseases. Moreover, there is an overall decrease in inflammation of the body. Mediterranean diet is also typical for its PUFA and EVOO content, which multiply the cardioprotective effect. Both dietary types also have a positive influence on bacterial diversity of the gut. In the contrary, the Western diet is characterized by high consumption of processed and ultra-processed food, fats, salt and red meat. As a result, it leads to lower levels of SCFA and higher levels of TMAO, an increase of the cardiovascular risk, insulin resistance, systemic inflammation or development of CRC. Bacterial diversity is reduced, which is linked to overgrowth of pathogenic bacteria.

Current scientific literature acknowledges plant-based diet and Mediterranean diet as healthy forms of diet compared to the unhealthy Western diet. It is a big challenge to further evaluate the relationship between dietary types and gut microbiota composition, since diet seems to be significant factor influencing it. Additionally, a healthy gut can prevent and improve the outcome of various NCDs, therefore targeting dysbiosis may provide valuable therapeutical effects.

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