Prebiotic Potential of Dietary Beans and Pulses

Subjects: Endocrinology & Metabolism | Microbiology | Food Science & Technology Contributor: Ravinder Nagpal , Saurabh Kadyan , , Bahram Arjmandi , Prashant Singh

Dietary pulses, including dry beans, lentils, chickpeas, and dry peas, have the highest proportion of fiber among different legume cultivars and are inexpensive, easily accessible, and have a long shelf-life. The inclusion of pulses in regular dietary patterns is an easy and effective solution for achieving recommended fiber intake and maintaining a healthier gut and overall health. Dietary pulses-derived resistant starch (RS) is a relatively less explored prebiotic ingredient. Several in vitro and preclinical studies have elucidated the crucial role of RS in fostering and shaping the gut microbiota composition towards homeostasis thereby improving host metabolic health.

| aging | beans | fiber | gut health | lentils | microbiota | microbiome | prebiotic |
|--------|-----------|--------|------------|---------|------------|------------|-----------|
| pulses | resistant | starch | | | | | |

1. Introduction

Pulses are valuable dry grains from leguminous crops. Domesticated around 10,000 years ago, pulses have been consumed as a key staple food crop, especially in developing nations, thus providing a primary means of protein and energy ^[1]. However, the past century has witnessed a change in the eating habits of the population, especially the decline of the pulse consumption in the daily diet and a surge in the chronic disease rates ^[2]. Based on a posteriori and a priori dietary patterns, consumption of whole grains and legumes/pulses are linked with longevity and better cardiovascular, metabolic, and cognitive health ^[3]. On the contrary, diets rich in refined grains, red meat, and sugar have been associated with an increased risk of mortality and adverse cardiometabolic outcomes ^[3].

Although there are numerous pulse varieties available worldwide, Food and Agriculture Organization (FAO) has listed 11 main types, namely beans, broad beans, Bambara beans, chickpeas, lentils, cowpeas, peas, pigeon peas, vetches, lupins, and other "minor" pulses ^[4]. Among them, lentils (*Lens culinaris* L.), beans (*Paseolus vulgaris* L.), chickpeas (*Cicer arietinum* L.), and peas (*Pisum sativum* L.) are the most frequently consumed pulses worldwide ^[5]. Pulses possess superior nutritional properties and harbor various bioactive compounds, viz., fermentable fibers, bioactive peptides, and phytochemicals ^[6]. The high nutritional value of pulses is attributed to their high-quality protein and soluble and insoluble dietary fiber ^[7]. The daily intake of dietary fiber at a level of 14 g/1000 kcal or above has been proposed to confer health benefits in human cohorts ^[8]. Still, a developed nation like the United States is far from achieving this level, and the magnitude of the gap is nearly 50–70% shortfall ^[9]. To address this shortfall, supplementation of diets with pulses could be one promising strategy as the total fiber content in pulses can range up to 30 g/100 g dry weight (peas: 14–26 g; lentils: 18–20 g; chickpeas: 18–22 g;

beans: 23–32 g), with insoluble fiber being the major sub-component (peas: 10-15 g; lentils: 11-17 g; chick-peas: 10-18 g; beans: 20-28 g) ^[4].

Starch is the major carbohydrate in pulses accounting for nearly 50% portion of carbohydrates ^[10]. Certain starches present in the raw and/or cooked pulses exist in the form of dietary fiber instead of available carbohydrates. This is due to the partial or complete modification in the starch structure during heat processing of foods leading to the formation of resistant starch (RS). RS remains un-digested in the upper-gastrointestinal tract and reaches the large intestine, where it is metabolized by intestinal microbes into a wide range of metabolites, which helps in the maintenance of optimal human health ^[11]. Past studies have also proven the prebiotic potential of RS in improving the post-prandial glycemic and insulinemic responses, increasing satiety, reducing cholesterol and stored fat, and promoting weight loss, making it an apt ingredient, especially for the management of gut-associated metabolic disorders ^{[12][13][14][15]}. Hitherto, studies assessing the human health benefits of RS were confined to RS derived from cereals and tubers, with little to no focus given on RS derived from pulses. Recently, efforts were made in researchers' lab to isolate and purify starches from 18 pulses which were evaluated for their functional properties in order to promote their use as superior food ingredients in industry ^[16]. Owing to the superior sensory property of selected pulse RS compared to traditional fibers like whole cereals, fruit fibers, etc., the supplementation of this functional ingredient in diet could act as a beneficial nutritional intervention for the control of metabolic diseases ^[17].

Nowadays, it has been widely popularized that the human gastrointestinal (GI) tract is a frontline mediator system wherein the intestinal bacteria aid in the digestion of dietary constituents of consumed foods and synthesizes low molecular weight bioactive molecules, which ultimately exerts a crucial role on human health and well-being ^[18]. The human gastrointestinal tract contains nearly 10¹⁴ microorganisms belonging to over 1000 species and has a bacterial genomic content of approximately 100 times over compared to the human genome ^[19]. About 95% of the total microbes present in the human body are colonized in the GI tract. The GI tract is the home of bacteria, eukaryotes, and archaea and is collectively known as gut microbiota ^[20]. Several factors such as the morphology of the gut, nutrient availability, pH, and presence or absence of oxygen are responsible for the variation in gut microbiota composition and growth of certain microbial taxa specific to different regions of the gut. The most common gut bacteria are associated with the four major phyla, with the most abundant being Firmicutes (65%), followed by Bacteroidetes (25%), Proteobacteria (8%), and Actinobacteria (5%). Moving down the taxonomic hierarchy, the GI tract harbors three main groups of extremophile anaerobes *Clostridium coccoides* group (or *Clostridium cluster XIVa*), *Clostridium leptum* group (or *Clostridium cluster IV*), and *Bacteroides* ^[21]. The gut microbes, together with their metabolites produced as a result of the degradation of different substrates, provide a range of immune, metabolic and neurobehavioral functions to host health.

Gut microbiota is dynamic in nature and changes continuously during the lifespan of an individual ^[22]. During the aging process of an individual, dynamic changes occur in behavioral, environmental, biological, and social processes. Genomic instability, epigenetic alterations, and telomere attrition are primary indicators of aging, resulting in cellular senescence, problems in nutrient sensing, and mitochondrial-related dysfunctions, which further negatively impact intercellular communication and exhaustion of stem cells ^[23]. Thus, the aging-associated decline

in the cellular functions and immune system responses leads to chronic low-grade inflammation and increased gut permeability, thereby marking the onset of various gastrointestinal disorders, cardiometabolic disease, muscle frailty, cognitive decline, and gut dysbiosis ^[24]. Aging-associated problems are further aggravated by the ill effects of western diets rich in fat and sugars, which may increase the propensity towards gut dysbiosis ^[25]. The maintenance of a healthy and diverse gut microbiota that coevolves with our lifespan is a principal factor in the amelioration of various age-related diseases. Earlier studies by researchers' group indicated that the severity of gut dysbiosis is higher in older cohorts than the young ones ^[26].

2. Resistant Starch and Human Health

Starch is a dietary carbohydrate that is commonly found in everyday food. It is the second most abundant chemical compound in the plants after cellulose. Chemically, starch is composed of two monosaccharide molecules that are amylose (linear chain) and amylopectin (branched chain). These molecules are linked together with alpha 1-4 and/or alpha 1-6 glycosidic bonds. Based on physical and physiological properties, starch can be classified into three categories, namely rapidly digestible starch, slowly digestible starch, and resistant starch (RS) ^[27]. Englyst and coworkers (1982), in an in vitro study, found that some portion of the starch remained undigested even after enzymatic treatment. Further studies confirmed that these starches were undigested by the amylases in the small intestine and enter the colon, where it is utilized by gut microbial communities. They named this starch fragment "resistant starch" ^[28]. The digestibility of the starch in the small intestine is primarily affected by the structure of the starch molecule and the ratio of amylose to amylopectin. Chemically, RS has a relatively low molecular weight (12 KDa) and has a linear structure made up of α -1,4-D-glucan moieties obtained from the retrograded amylose fraction ^[17].

Resistant starch is further subdivided into five types depending upon its structural features. RS type 1 (RS1) is physically inaccessible starch and has the most complex structures as it is frequently found entrapped within protein matrix or non-starch components of the plant cell wall (e.g., whole grains or pulses) ^[11]. Compared to RS1, the cellular structure is absent in RS type 2 (RS2). The RS type 2 possesses native, uncooked, and semicrystalline starch granules having a B- or C-type polymorph (e.g., high-amylose starch, raw potato starch) ^[11]. The RS type 3 (RS3) is obtained by retrogradation process upon cooking and cooling of starch-containing foods. Its resistance to digestion could be due to lower activity of pancreatic α -amylases toward starch double helices as against fully gelatinized starch molecules (e.g., retrograded high amylose maize starch) ^[29]. The RS type 4 (RS4) is the starch-modified through chemical processes such as esterification, crosslinking, hydroxypropylation, acetylation, and phosphorylation ^[30]. The functional groups block the site of action of starch digestive enzymes, which confers resistance of RS4 to digestion. The RS type 5 (RS5) is defined as the starch obtained by complex formation between high amylose starch with the lipids, which further increases the enzyme resistance of high amylose by preventing granule swelling during cooking ^[17].

Resistant starch possesses many desirable functional and health-promoting properties ^[27]. An overview of the effect of resistant starch derived from the pulses on the health outcome of humans and rodents is summarized in **Figure 1**. RS fermentation in the lower GI tract produces different starch oligomers and SCFAs. SCFAs are

actively involved in reducing the risk of diabetes, cancer, obesity, and other cardiovascular diseases ^{[8][9][25]}. Among them, acetate, propionate, and butyrate have been extensively studied for their health benefits. Acetate is the major SCFA that is produced to the tune of 65% in the colon resulting in significant drops in pH. Thus, it helps in the inhibition of various pathogenic microorganisms and indirectly aids in the absorption of minerals such as calcium, iron, and sodium Butyrate, on the other hand, provides energy to colonocytes, possesses anti-inflammatory properties, protects against colon cancer, and plays a key role in gut homeostasis as well as maintaining the integrity of epithelium ^[31]. Butyrate is also responsible for lower levels of glycolysis and glycogenolysis (Ashwar et al., 2017). Propionate is another important metabolite that is partially absorbed via portal veins and reaches the liver. It is then metabolized as a glucogenic substrate resulting in inhibition of pathways leading to reduced 3-hydroxy-3-methylglutaryl co-enzyme A (HMG-CoA) activity and suppression of acetyl-CoA reductase, thereby imparting reduction in blood plasma cholesterol levels ^[32]. The serum cholesterol-lowering effect of RS was demonstrated in rats when they were fed a cholesterol-free diet ^[33].



Figure 1. Illustration depicting the effects of resistant starches (RS) derived from dietary beans and pulses on host (rodent and human) health. ↑: increased; ↓: decreased.

3. Benefits of Dietary Beans and Pulses on Gut Health

The recent advances linking the role of dietary fibers in ameliorating different disease states have led to increased interest in pulse-based foods. Various types of fibers present in pulses include long-chain soluble and insoluble polysaccharides, resistant starch, and galactooligosaccharides. In addition, these components can act as prebiotic precursors, which are digested by beneficial microorganisms in the gut. The consumption of pulses in the diet has been linked to the reduction in serum cholesterol, increased satiety, and low post-prandial blood glucose levels, thus mitigating the risk of different metabolic diseases like cardiovascular diseases, obesity, diabetes, etc. ^{[34][35]}. In fact, several meta-analyses concluded that daily pulse intake of approximately 2/3 cups could significantly lower total and LDL cholesterol ^[36]. The low glycemic response of pulse is associated to the physical barrier between the starch and digestive enzymes by the intact cell wall of whole pulses after cooking. Furthermore, pulse consumption is closely associated with reducing blood pressure and providing protection against reactive oxygen species due to the presence of high levels of polyphenols ^[37].

In the last few years, more research has been directed towards pulses which could be a sustainable source of plant protein compared to animal protein to feed the growing population and to simultaneously address the food insecurity problems ^[4]. Additionally, whole pulses being rich in plant-based protein and dietary fibers underpins the hypothesis of their positive effects on the gut microbiota. Table 1 summarizes the influence of consumption of pulses in various forms-cooked, flour, meals, or supplemented in the diet, on the gut microbiota changes in rodents and humans. А study on pulse flour exhibited improved arowth of genera Bifidobacterium, Faecalibacterium, Clostridium, Eubacterium, and Roseburia along with enhanced butyrate and acetate production ^[38]. Several studies have reported that the incorporation of pulses in the diet increases the abundance of Prevotella, Dorea, and Ruminococcus flavefaciens, and decreased abundance of Ruminococcus gnavus in mice models [18][39][40][41][42]. Prevotella is a genus possessing a large spectrum of glycoside hydrolases and is known for its ability to produce SCFAs following the carbohydrates fermentation ^[39]. The species Ruminococcus flavefaciens had been found to decrease in overweight (BMI: 25.0-29.9) and obese (BMI: >30.0) subjects [43]. The abundance of *Ruminococcus gnavus*, a mucolytic species, has been linked to an increase in gut-barrier pathologies in subjects with obesity and inflammatory bowel disease [41]. Another positive effect of pulse intake is the increased prevalence of Akkermansia muciniphila in the gut, which is often categorized as nextgeneration probiotics [8][44]. Interestingly, this bacterium is also mucolytic but has an inverse correlation with R. gnavus [45]. Majority of the studies reported herein demonstrated a decrease in the ratio of Firmicutes to Bacteroidetes. This reduction in the ratio of two major phyla has been associated with the amelioration of obesity, possibly due to altered energy extraction from carbohydrates metabolism in the colon [46]. Among the Bacteroidales, the members representative of the pulse-based diets includes Muribaculaceae (S24-7), Rikenellaceae and B. acidifaciens [18]. Lentil consumption was found to be associated with increased prevalence of *Roseburia* in mouse feces [40]. *Roseburia* is involved in butyrate production and has negative correlation with several diseases such as colitis and Crohn's disease [47]. Although these studies revealed beneficial effects of pulses in positively modulating the gut microbiome, the impact on different gut genera is complex, which may be dependent upon many variables, such as pulse type, dose, age, status of cohorts, duration of the study and the sequencing methodology adopted.

Table 1. Effect of dietary pulses on gut microbiota-related changes in rodents and humans.

| Pulse-Type | Cohort | State of Cohort | Age | Dose | Duration of Study | ley Shifts in Gut Microbiota | Outcome | References |
|----------------------------|--------|--|----------------|---------|---------------------------------------|--|--|------------|
| Cooked chickpeas | Human | Healthy | 18–65 years | 200 g/d | 3 weeks | Phylum Bacteroidetes Genus Megasphaera Clostridium I, II, IV, XI clusters Species Faecalibacterium prausnitzii Subdoligranulum Clostridium histolyticum, Clostridium lituseburense groups | Reduction in pathogenic and putrefactive gut bacteria species in cohorts Less intestinal colonization by armonia- producing bacterial species | 600 |
| Cooked pinto beans | Human | Healthy; Pre- metabolic syndrome | 18–51 years | 130 g/d | 12 weeks + 4 weeks run-in | Species Peptostreptococcus productus Eubacterium limosum | High propionate production Lower serum total cholesterol, LDL, and HDL | (42) |
| Cooked navy bean powder | Human | Colorectal cancer survivors (overweight and obese) | 47–81 years | 35 g/d | 28 days | Species Clostridium sp., Lachnaspira sp., Coprococcus sp. Bacteroides fragilis Anaerostipe sp. | Boost in microbial richness compared baseline for colorectal cancer survivors but had no effect on their diversity | 50 |

| Pulse-Type | Cohort | State of Cohort | Age | Dose | Duration Key Shifts in Gut Microbiota of Study | Outcome | References |
|--|------------------------|--|--|---------------|--|---|---------------|
| Cooked navy beans (incorporated in meals and snacks) | Human | Colorectal cancer survivors (overweight and obese) | NB: 60.9 ± 11.0 years Control: 65.50 ± 3.07 years | 35 g/d | 4 weeks | Thirty and twenty-six significant metabolite differences in stool samples from baseline and control, respectively Navy bean- derived metabolites (247/560) including N- methylpipecolate, 2-aminoadipate, piperidine, and varillate Abundance of ophthalmate increased by 5.25 fold | 53 |
| Beans, chickpeas, peas, or lentils-based foods | Human | Healthy | 57 ± 6.3 | 150 g/d | 4 months | Reduction in total cholesterol and LDC by 8.3% and 7.9% | [<u>52</u>] |
| Dolichos lablab L. (standardized extract) | Mice (C57BL/6 male) | IBS model | 7 weeks | 100–400 mg/kg | 15 days | Minimized weight loss with no effect on food intake Attenuated | 53 |

| Pulse-Type | Cohort | State of Cohort | Age | Dose | Duration of Study | ey Shifts in Gut Microbiota | Outcome | References |
|----------------------------------|------------------------|-----------------|------------|---------------|----------------------|---|--|------------|
| | | | | | | | induced colonic scores • Reduced mast cell count, TNF-q in the colon • Reduced visceral pain-related behaviors • Dose-dependent reduction of c- Fos expression in the brain | |
| Chickpea supplemented diet | Mice (C57BL/6 male) | Healthy | 5 weeks | 200 g/kg diet | 3 weeks | Family Clostridiaceae (feces only) | Enhanced colon crypt mucus content and mucin mRNA expression | [41] |
| | | | | | | i Peptococcaceae Genus Provincella | Improved expression of epithelial tight junction proteins | |
| | | | | | | t Dorea | Enhanced metagenomic | |
| | | | | | | Species Ruminococcus flavefaciens | tunctions (e.g., † butanoate metabolism; † | |
| | | | | | | 1 Bifidobacterium pseudolongum | biosynthesis) | |
| | | | | | | Parabacteroides distansonis Undefined on in the Ruminoconcour panus (coreal only) | Increased SCFAs production | |

| Pulse-Type | Cohort | State of Cohort | Age | Dose | Duration of Study | ey Shifts in Gut Microbiota | Outcome | References |
|--|--------------------------|---------------------|------------|--|----------------------|--|---|------------|
| | | | | | | i Lactococcus i Turicibacter | Enhanced taxa richness in the cecum | |
| Cooked white and dark red kidney beans | Mice (C57BL/6 male) | DSS induced colitis | 5 weeks | BD + 20% beans | 3 weeks | | Enhanced acetate, butyrate, and propionate production Increased colon crypt height, and MUC1 and Relmg mRNA expression Reduced serum levels of IL-17A, TNF-α, IFN-γ, IL- 1β, and IL-6 | (42) |
| Cooked Navy bean or black bean | Mice (C57806 male) | Healthy | 4 weeks | Supplementation @20% to the basal diet | 3 weeks | Genus Prevotella Prevotella S24-7 undefined genera within the Clostridiales order and Coriobacteriaceae family (BB only) Oscillospira, Ruminococcus Coprococcus Lactococcus, | Enhanced SCFAs production and expression of receptors GPR- 41, 43, 109 Increased crypt length, epithelial cell proliferation, goblet cell number, crypt mucus level, and mucin mRNA | 29 |
| | | | | | | : Streptococcus | expression | |

Common beans, chickpea, and lentils have been shown to exert positive effects in the modulation of the colonic microenvironment in animal models ^{[18][39][40][42]}. These include enhancement of (i) crypt mucus content and mucin mRNA expression; (ii) expression of epithelial tight junction proteins; (iii) crypt length, epithelial cell proliferation, and goblet cell number; (iv) SCFAs levels (acetate, propionate, and butyrate); (v) expression of G protein-coupled receptors in the intestine; (vi) reduced pro-inflammatory cytokines in the serum. Increased expression of G protein-coupled receptors in the colon is related to sensing high SCFA production by gut microbes which are implicated in adipose tissue metabolism and appetite regulation ^[57]. The benign role of whole pulse consumption in the modulation of human gut microbiota and metabolite profile have also been explored in the past by researchers using clinical trials ^{[48][49][50][51][52]}. Some of these include reduction in pathogenic and putrefactive gut bacteria species; increase in *Bacteroidetes* and *Faecalibacterium prausnitzii*; decreased total serum cholesterol, LDL- and HDL-cholesterol; boost in microbial richness, and significant change in metabolite profile (e.g., ophthalmate) in colorectal cancer survivors.

| Pulse-Type | Cohort | State of Cohort | Age | Dose | Duration of Study Ke | y Shifts in Gut Microbiota | | Outcome | References | for |
|-----------------|------------------------|------------------------------------|------------|-------------------|-------------------------|---|---|---|--------------|------------|
| | | | | | - | 1 rc4-4 1 Coprobacillus | | Reduced serum endotoxin concentration | | 101 |
| | | | | | | 1 Parabacteroides 1 Aldercreutzia | | Enhanced apical junctional complex | | |
| | | | | | | L unassigned members o Peptococcaceae, Erysipelotrichaceae, Clostridiaceae, Mogibacteriaea Rikenellaceae families | ae, Peptostreptococcaceae, Christensenellaceae, and | components (occludin, JAM- A, ZO-1, and E- | | lon. The |
| | | | | | | Species | | cadherin) | | icicioic, |
| | | | | | | t Ruminococcus flavefaciens | | | | digested |
| | | | | | | Ruminococcus gnavus | | | | romisina |
| | | | | | | L Clostridium perfringens (NB only) | | | | 0 |
| | | | | | | : undefined species in the Lachnospiraceae family (BB only) | | | | |
| Cranberry beans | Mice (C57BL/6 male) | Healthy and DSS induced colitis | 5 weeks | BD + 20% beans | 3 . weeks | Family | | In healthy cohorts: • Increased cecal SCFAs, colon | <u>(54</u>) | t can be |
| | | | | | | Lactobacillaceae | | crypt height, crypt goblet cell | | cereals, |
| | | | | | | L Clostridiaceae | [58] | mucus content | | nd Toch |
| | | | | | | L Peptococcaceae | | Enhanced | | .110 10511 |
| [<u>6</u>] | | | | | | i Peptostreptococcaceae | [<u>59]</u> | expression of Muc1, Klf4, | | y weight |
| | | | | | | L Rikenellaceae | | Relmβ, and Reg3y | | the RS |
| | | | | | | L Pophyromonadacea | | | | n of the |
| | | | | | | Genus | | In diseased cohorts: | | n or the |

geraunzeu starch post-cooking and cooling is usually associated with the increased content of resistant starch in the cooked pulses ^[60]. Still, the amount of RS in raw, baked, and boiled pulses differ significantly, and it is a function of its intrinsic factors (e.g., amylose to amylopectin ratio, crystallinity, granular structure) and external factors (e.g., processing methods employed, storage period and conditions ^[13]. In brown lentils (*Lens culinaris*, Medikus), RS content was further increased by the addition of lipids, resulting in the formation of amylose-lipid complexes (RS5 type) ^[61].

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| Pulse-Type | Cohort | State of Cohort | Age | Dose | Duration of Study | Key Shifts in Gut Microbiota | Outcome | Reference | es |
|----------------|----------------------------|-----------------|------------|-----------------------|----------------------|--|--|-----------|--------------|
| | | | | | | L Peptococcaceae | | | |
| L | | | | | | : Christensenellaceae - Genus | | | asir; |
| | | | | | | † Allobaculum | | | ore |
| | | | | | | ↑ Sutterella (II) ↑ rc4 4 (of Peptococcaceae), | | | CI3 |
| | | | | | | r RF32 (of Alphaproteobacteria) | | | 21.7 |
| | | | | | | 1 Oscillospira | | | |
| | | | | | | L Dorea | | | |
| | | | | | | : Lactococcus | | | |
| | | | | | | : Streptococcus | | | |
| | | | | | | • Species | | | |
| | | | | | | t B. acidifaciens | | | |
| | | | | | | t B. pullicaecorum | | | |
| | | | | | | LR. gnavus | | | n Cl |
| | | | | | | L M. schaedleri | | | <u>ا</u> ن ر |
| | | | | | | LC. methylpentosum | | | |
| | | | | | | | | | 10^{-2} |
| Cooked red len | ils Mice (C57Bl/6 male) | Healthy | 5 weeks | 20% w/w basal diet | 3 weeks | • Phylum | Improved fecal microbiota q- | [40] | ±0 |
| | | | | | | † Firmicutes | diversity | | |
| | | | | | | : Bacteroidetes | Abundance of | | |
| | | | | | | • Family | SCFA producing bacteria | | ; Ho |
| | | | | | | 1 Parabacteroides | | | ~~ · |

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 1.

| 2 ^{Pulse-Type} | e Cohort | State of Cohort | Age | Dose | Duration of Study | Key Shifts in Gut Microbiota | Outcome | References | 1 |
|-------------------------|-------------------|-----------------|-------|--------------|----------------------|--|---|------------|---------|
| 2 | | | | | | Genus Coprococcus | Increased mRNA expression of SCFA receptors | | - |
| | | | | | | t Dorea | (GPR 41,43), tight | | |
| 2 | | | | | | 1 Roseburia | junction proteins (E-cadherin, | | es in |
| | | | | | | 1 Turicibacter | Zona Occulden-1 Claudin-2) | | əlvst |
| | | | | | | t Prevotella | | | Jugot |
| | | | | | | t Unknown genus belonging to the Lachnospiraceae family | | | |
| 2 Chickpea, le | entil, Mice | Obese | 3-4 | 40% w/w diet | 17 | • Phylum | Three fold | (8) | rick |
| bean | nu (CS/BL/6 male) | | weeks | | weeks | 1 Bacteroidetes | elevation of bacterial count in | | non |
| | | | | | | : Firmicutes (statistically significant in bean and lentil diet) | the cecum | | е |
| | | | | | | Species | 2.2–5 fold increase in | | al |
| | | | | | | 1 Akkermansia muciniphila (bean and lentil fed diet only) | Bacteroidetes to Firmicutes ratio | | 040. |
| | | | | | | | Reduced lipid accumulation in | | |
| 3 | | | | | | | adipose tissue | | |
| | | | | | | | Decreased subcutaneous and visceral fat mass compared to high-fat control | | nal |
| | | | | | | | but greater compared to a | | |
| 3 | | | | | | | low-fat control | | o fecal |
| 3 | mentau | υιριομα | ະເພດະ | | III I. <i>1</i> - | | but greater compared to a low-fat control | ບອເ | 01 |

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| QPulse-Type | Cohort | State of Cohort | Age | Dose | Duration of Study | tey Shifts in Gut Microbiota | Outcome | References | uono: |
|-------------------|--------------------------|---|------------|-------------------|----------------------|--|---|------------|---|
| | | | | | | | 108 differential metabolites identified related to pulse types | | , |
| Whole mun bean | g Mice (C57BL/6 male) | Diet-induced obesity (1 w HFD feeding) | 4 weeks | HFD + 30% bean | 12 weeks | Phylum Bacteroidetes Firmicutes | Reduction in hepatic steatosis Reduction in body weight gain. | [44] | nd i-64, 1 |
| | | | | | | Family Lachnospiraceae | fat accumulation, and adipocyte size | | |
| J | | | | | | 1 Ruminococcaceae 1 unassigned member of Lachnospiraceae • Genus | Significant a- and b- diversity Ameliorated insulin resistance | | ro .tion of |
| | | | | | | 1 Blautia 1 unassigned member of Muribaculaceae | and glucose tolerance • Normalization of HFD-induced gut | | .1039/c |
| З | | | | | | 1 Turicibacter 1 Akkermansia 1 Bactericides | microbiota dysbiosis | | |
| | | | | | | 1 Bilfidobacterium | | | nt to tbio.20 |
| | | | | | | : Mucispirillum : Ruminiclostridium | | | |
| Δ | | | | | | i unassigned member of <i>Ruminococcaceae</i> | | | |

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