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| Table 1.Studies reflecting the impact of diet on gut microbiota diversity and the association with health status. |
| **No** | **First Author****Year** | **Population****(n)** | **Type of study**  | **Population characteristics** | **Type of diet characteristics**  | **Microbiota****assessment****technique** | **Findings** |
|  | Tandon, D., *et al,* 2018(81) | n=80 | CT | Healthy individuals living in Western IndiaAge:18-55Normal weight, excluded: heavy smokers and alcohol consumption, no medication during last month, major illness in last 3 months, no grapefruit juice, xanthine-containing products, tobacco-containing products or alcohol within 48 hours prior to day 01 of study.FFQ applied | simple and complex carbohydrates (i.e. rice, wheat, sorghum and millet) and fibre-rich components (i.e. fruits, vegetables, whole grains, sprouts, etc.)  | 16S rDNApyrosequencing (V3-V4region)Illumina technology | 95 % *Bacteroidetes* (median abundance 71.5%), *Firmicutes* (18.7%), *Proteobacteria* (3.8%), and *Actinobacteria* (0.6%) *Prevotella*-dominated community ;*Sutterella* and *Succinivibrio* dominant *in Proteobacteria* phylum.negative correlation (p-value < 0.1) between *Prevotella* and other bacterial species constituting the microbial community positive correlation (p-value < 0.1) between the patterns of abundances of. *Dorea*, *Blautia*, *Roseburia*, *Ruminococcus*, *Bacteroides*, *Paraprevotella*, *Faecalibacterium*, and *Collinsella.* |
|  | Liao, M., *et al*, 2018(82) | n=134 | CT | Chinese isolated Yao population (n=47), and ethnic populations from the same rural area (Zhuang: n =28 and the major ethnic Han: n=59)No antibiotics or probiotics in the six months before the sampling dates; | Diet pattern of Yao group slightly different than the other two groups: Yao: frequent consumption of grains, plant oil, vegetables, starches; moderate fruits, pickled foods, meat, fish, eggs; less frequent: milk, seafood, yogurt, fried food, smoked food, nuts, mushrooms.more people in the Yao group regularly had breakfast compared to the other two groups (P = 0.002)   | 16S rDNApyrosequencing (V3-V4region) | Dominant *Bacteroides* and *Prevotella* in all groups;Lower abundance of *Prevotella* correlated with low alcohol consumption;Great alcohol intake, higher abundance of *Bacteroides;**Megamonas* more abundant in the fecal microbiota of the Han group, compared to the Zhuang (p=0.048) or Yao group (p<0.001);*Succinivibrio,* more abundant in the fecal microbiota of the Yao group compared to the Han group (p = 0.054) and the Zhuang group (p = 0.187). |
|  | Jain, A., Li, XH.,Chen, WN., 2018(83) | n=16 |  | Healthy Indians (n=11) and Chinese (n=5);ages 22–35;no gastrointestinal disorder, no antibiotics or laxatives use, 3 months before the trial. | Indian: whole wheat, rice, lentils, legumes, green vegetables, fruits and dairy products; whole grains, ghee, white flour, and fast food are also substantially included in the Indian diet. Chinese: high animal fat and protein consumption, besides carbohydrate (rice, noodles, beans, refined grains, white flour, peanut oil, sea food, fish, meat, lard).  | 16S rDNApyrosequencing (V4 region)Illumina technology | Major phyla in both groups*: Firmicutes*, *Actinobacteria*, *Bacteroidetes and Proteobacteria**Bacteroidetes* (*p* = 0.001) and *Prevotella* (*p* = 0.002) significantly dominant in Indians as compared to Chinese;*Prevotella copri-*potential biomarker of diet |
|  | Li, H., *et al.,* 2018(84) | n=24 |  | Healthy Chinese herdsmen (Tibet) from 3 regions with different levels of urbanization;Age:39-16no antibiotics 3 months before the trial, no pregnant women. | Traditional herdsmen(TH) -main food: Zanba (∼50% high-fiber food), vegetables (potato, cabbage), few fruits consumption, animal food (beef, mutton);Semi-urban herdsman(SUH)- main food: Zanba, noodle, rice; occasional consumption of animal food (beef, mutton, eggs), vegetables (potato, cabbage, radish, lettuce), occasional consumption of fruits (apple, banana);Urban herdsman (UH)- main food (noodles, rice), often consumption of animal food (beef, mutton, pork, eggs), various vegetables and fruits . |  | Majoy phyla*:* *Bacteroidetes* (54.7%), *Firmicutes* (37.3%), *Tenericutes* (3.0%), *Proteobacteria* (2.4%), and *Actinobacteria* (2.1%) Abundance of *Prevotella:* TH (45,86%); SUH (36,14%), UH (18,59%);UH: dominance of *Bacteroides* (19.48 %);*Prevotella* gradually decreased with the degree of urbanization (from TH to SUH to UH), while *Bacteroides*, *Faecalibacterium*, *Blautia*, *Collinsella*, *Ruminococcus*, *Coprococcus,* and *Dorea*, increased with the degree of urbanization.  |
|  | Deschasaux, M., *et al*., 2018 (64) | N= 2,084  |  |  Dutch (n=439), Ghanaians (n=367), Moroccans (n=280), Turks(n=197), African Surinamese (n=443), and South- Asian Surinamese(n=358 ).  | Moroccans/Turks : high fiber consumption, red meat, olive oil, fast food, sweets;Surinamese low fiber consumption, chicken, rice/noodles, sugary drinks;Dutch: processed meat, coffee, alcohola ‘prudent/healthy’ pattern (for example, fish, fruit, vegetables, legumes)  | 16S rDNApyrosequencing (V4 region) | Major phyla: *Firmicutes Bacteroidetes, Actinobacteria,* and Proteobacteria. Dominant genera: *Prevotella*, *Faecalibacterium*, and *Bacteroides* average abundance of *Prevotella* in Moroccans/Turks (23.6%) and *Bacteroides* in South-Asian Surinamese (12.5%)  ‘trade-off ’ between the abundance of *Prevotella* OTUs (operational taxonomic units ) (mainly *P. copri*; higher in Moroccans, Turks, and Ghanaians) and *Bacteroides* OTUs (higher in Surinamese)Clostridiales (*Oscillospira*, *Ruminococcus bromii*, *Coprococcus)* higher in Dutch. |
|  | Sandberg, J., *et al.,* 2018(85) | n=99 | 3-day randomized crossover intervention  | Healthy men and women with BMI < 28 kg/m2 between 50 and 70 years old from Swedenno antibiotics or probiotics 3 weekes before33 subjects grouped in three groups: subjects with highest *Prevotella/Bacteroides* ratios, “HP”, n = 12; subjects with lowest *Prevotella/Bacteroides* ratios, “LP”, n = 13; and subjects with high abundance of both measured bacteria, HPB, n = 8. | barley kernel bread (BKB) and white wheat bread (WWB) consumed three times/day (100 g potentially available starch per day in the first 2 days)day 3: half of the daily intake (i.e., 50 g available starch) | 16S rRNA quantitative PCR. |  BKB intervention lowered the blood glucose responses to the breakfast independently of *Prevotella/Bacteroides* ratios (P < 0.01). HP group : lower insulin response and lower IL-6 concentrations compared with the LP group (P < 0.05).  HP and HPB groups: lower hunger sensations compared to the LP group (P < 0.05).*Prevotella* and *Bacteroides* at baseline did not stratify metabolic responders and non-responders to barley DF intervention. |
|  | Qian, L., et al. 2018(86) | n=29 |  | Chinese people between 45-65 years old;No chronic gastrointestinal diseases; no antibiotics, lipid-lowering agent, probiotics and prebiotics within the past six weeksHigh fat diet (HFD) group (≥40% of dietary calories came from fat) or low-fat diet (LFD) group (<40%).HFD: n=15LFD:n=14 | High fat and low fat diet | 16S rDNApyrosequencing (V3-V4 region) | HFD group *Prevotella (Paraprevotella)* and *Abiotrophia* unclassified genus of S24-7 (family level) of *Bacteroidetes*, *Gemmiger*, *Akkermansia* and *Rothia*, *LFD group : Bacteridaceae*, *Bacteroides* and *Clostridium XVIII*  |
|  | Kushugulova, A., *et al*., 2018(87) | n=84 |  | Kazakh male and female healthy subjects (n=26) and metabolic syndrome (MetS) (n=58) patients aged 25–75 years, Comparison with microbiomes of the European control samples (MetaHIT)No antibiotics intake 3 months before;FFQ applied;Stool samples were collected twice: once in summer (August) and once in winter (January)  | Subjects received synbiotic (yoghurt containing six probiotic species, collagen, pectin and inulin): n=43Subjects receiving controls: yoghurt without supplements: n =41  |  | *Actinobacteria, Proteobacteria, Firmicutes* and *Bacteroidetes* in all samples;More than 1% of *Blautia*, *Bifidobacterium*, *Ruminococcus,* *Bacteroides*, *Eubacterium*, *Faecalibacterium*, *Prevotella*, *Streptococcus* and *Clostridium;**Prevotella-* rich enterotype (71%) for Kazakh people, compared to Danish people (26%);no significant changes in the microbiome under synbiotic treatment compared with placebo., |
|  | Kashtanova D.A. et al., 2018(88) | n=92 |  | Caucasian participants (Moscow and Moscow Region) aged 25 to 76 years , men and women, no clinical cardiovascular or other chronic diseases ; but with the possible presence of cardiovascular risk factors ;Not treated with any drugs (for at least 6 months)  | food frequency questionnaires applied | 16S rDNApyrosequencing (V3-V4 region);Illumina technology | Obesity was associated with higher *Serratia* (adj. *p* = 0.003) and *Prevotella* (adj. *p* < 0.0003) in relative abundance. Abdominal obesity was associated with higher abundance of *Serratia* (adj. *p* = 0.004) and *Prevotella* (adj. *p* = 0.0008) and lower levels of *Oscillospira* (adj. *p* = 0.0005). Glucose metabolism disturbances were associated with higher *Blautia* (adj. *p* = 0.0007) and *Serratia* (adj. *p* = 0.003) prevalence *Serratia* and *Prevotella* genera were more abundant among participants with obesity, high blood pressure and impaired glucose metabolism. |
|  | Haro *et al*., 2018(33) | n=106 | prospective, randomized, controlled trial (5 years) | male patients with coronary heart disease (CHD)obese people with Metabolic Syndrome(MetS-OB):n=33obese people withoutMetS: n=32 nonobesepeople without MetS:n=41 | Mediterranean and low-fat diet (LF) |  | Baseline: Higher *Firmicutes/Bacteroidetes* ratio in the MetS-OB group than in the NonMetS-NonOB group (low *Prevotella, Bacteroides*) MD, LF diet increased levels of *Prevotella*, *Bacteroides* in MetS-OB group after 2 yearsLow *B/F* rationo significant microbiota changes after the dietary intervention. In the NonMetS-NonOB and NonMetS-OB groups. |
|  | Hjorth *et al*., 2018(35) |  | Randomized controlled intervention (6 months)  | Danish participants with increased waist circumference (n=181);1st group : New Nordic Diet (NND) :n=622nd group:control diet :n=119 | New Nordic Diet (NND) high in dietary fiber, whole grain, fruit andVegetables or a control diet Average Danish Diet (ADD)  | 16S rDNApyrosequencing | NND associated with high *P/B* ratio and larger body fat lossLow *P/B* ratio-no difference in body loss. |
|  | Kumbhare,S.V., *et al*, 2017(89) | n=99 | Observational study | Indian (n=47) and Finnish children (n=52), 13–14-year-old;no indications of infections during the sampling time and with a medication history of no antibiotic consumption for three months preceding sample collection  | Typical Indian or Finnish diet;No information about dietary habits | 16S rRNA bacterial gene sequencing (V4 region)qPCR | *Firmicutes*, *Actinobacteria, Bacteroidetes, Proteobacteria* and *Verrucomicrobia* as the most dominant phyla in both Finnish and Indian children;*Bifidobacteriaceae* (34%) and *Lachnospiraceae* (32%) in Finnish;*Veillonellaceae* (29%), *Bifidobacteriaceae* (23%) and *Prevotellaceae* (21%) -the most dominant bacterial family in Indian children ;Genera *Prevotella* and Megasphaera predominant in Indian whereas *Bifidobacterium* and *Blautia* dominant in Finnish. |
|  | Li, J., *et al*, 2017(63) | n=192 |  | Han Chinese(n=48), Kazaks(n=48), Uyghurs (n=96), any clinical symptoms and not used any antibiotics for one month. | no precise information of food/nutrient uptake  | 16S rRNA bacterial gene sequencing (V1 V3 region)qPCR | Kazaks and Uyghurs (Muslim populations) dominated by the *Prevotella* enerotype and the HANs dominated by the *Bacteroides* type. The eneterotypes Bacteroides and Prevotella with functional gene differences between the two enterotypes : B type exhibited higher abundances at GH92 and GH20, which are associated with animal glycan, while the P type exhibited significantly higher abundance at GH13, which is associated with starch and glycogen  |
|  | Lan, D., *et al*, 2017(90) | n=208 |  | healthy Tibetans from 6 different regions;age: 0.7 to 86 years ;indigenous residents with no bowel or metabolic diseases nor take any antibiotics or probiotics within three months before sampling dates.  | Traditional Tibetan diet:high consumption of fried wheaten food, red meat, and fermented dairy products with low quantities of vegetables and fruits  | 16S rRNA bacterial gene sequencing (V4 region) | Bacteroidetes (60.00%), Firmicutes (29.04%), Proteobacteria (5.40%), and Actinobacteria (3.85%);Prevotellaceae the most abundant 42.86%; bacterial profiles in Tibetan guts varied significantly with increasing altitude, BMI, and age, and facultative anaerobes were rich in Tibetan guts. |
|  | Shankar, V., *et al* 2017(29) |  | No information | healthy preadolescentand adolescent male volunteers from Egypt (Giza) and teenagers from Midwest region of the USA (Ohio) n=42Egipt :n=28USA: n=14No antibiotic/ probiotic intake for at least 3 months prior to sample collection. | Egyptians consuming a Mediterraneandiet and U.S. teenagers fed a typical Western diet. | 16S rDNApyrosequencing (V4 region)qPCRIllumina technology  |  *Prevotella; Megasphaera, Eubacterium, Mitsuokella, and Catenibacterium* Presence of *Succinivibrio and Treponema* Levels of short-chain fatty-acids (propionic, acetic butyric)  Aminoacids, but higher levels of tryptophan and glycine; levels  bile acids, taurine, choline. levels  |  *Bacteroides Ruminococcus,* *Coprococcus, and Blautia* Aminoacids (7 of 9, especially lysine)  Lower levels of tryptophan and glycine;  bile acids, taurine, choline. |
|  | Nakayama, J., *et al*., 2017(13) |  | Observational study | Children from rural and urban Philippines (Baybay city and Ormoc city) n=43Rural: n=24; urban: n= 19Age: 7-9  | **Urban**: fast-food (4 times/week), higher consumption of confectionary such as biscuit and sweetened pastry, meat and fats. | 16S rDNApyrosequencing | **Rural** *Prevotella (P.copri)* correlated with carbohydrates, vitamin A and β-carotene from fruits (green mango, banana)  S*uccinivibrio*  | **Urban** *Bacteroides* correlated with high intake of fat   *Ruminococcaceae*  |
|  | Girard, C., et al.,2017(91) | N=59 |  | healthy Inuit participants (n=26) and residents from Montreal (Canada) (n=33) ,who had not taken antibiotics in the previous 3 months.  | Dietary information in 2 categories: Inuit diet (individuals who consumed traditional Inuit food at least twice a week) and Western diet (individuals who only occasionally or never ate traditional Inuit food);The Western diet category included individuals from both Montreal and Nunavut who consumed traditional Inuit food infrequently or never. traditional Inuit diet low in carbohydrates and rich in animal fats and protein (marine mammals, such as caribou, muskox, seal, whale, and fish) but in the last hundreds of years shift toward processed store-bought foods  | 16S rDNApyrosequencing | *Prevotella* spp., were enriched in Montrealers and among the Inuit consuming a Western diet;lower *Prevotella* strain diversity in Nunavut participants consuming an Inuit diet than in those consuming a Western diet (*P* < 0.05).  |
|  | Fernández-Navarro, T., *et al*., 2017(92) | n=68 | cross-sectional study  | 27 men and 41 women, aged from 19 to 67 years old | Diet assessed through FFQ;Cluster I: higher intake of sucrose and lower intake of fiber and total animal protein was observed in individuals from cluster;Cluster II was characterized by a profile with a higher intake of oils and fats, sweetened foods and sauces and lower intake of fruits, dried fruits, and fish, representative of a Western pattern  | Fast Real-Time PCR System  | Cluster analysis of body mass index, fat mass, glucose, LDL/HDL ratio, leptin, MDA and CRP classified the subjects into two groups :cluster I (*n* = 38) and cluster II (*n* = 26).  levels of the intestinal *Bacteroides-Prevotella-Porphyromonas* group were lower in the cluster and linked to a higher pro-oxidant and pro-inflammatory status, whose individuals also had lower intake of fruits, dried fruits, and fish. levels of *Lactobacillus* group and acetate concentrations were directly related with the grade of obesityhigher intake of fat and oils and sweetened foods, suggestive of consuming a highly palatable diet, was associated with the presence of a chronic pro-inflammatory and pro-oxidant status linked to overweight and obese subjects from cluster II  |
|  | Chen, T., *et al.*, 2017(51) | n=6 |  | healthy Chineseages 18 to 50, no history of gastrointestinal disease, no antibiotic usage within the previous 6 months.  | 24 h dietary recall, normal dietary pattern and life style, no excessive alcohol drink during the study. Fresh stool samples provided Two groups: D1(n=2)-no difference in fermentation profiles between Arabinoxylans from sorghum bran (SAX) and corn arabinoxyan (CAX);D2 as a large difference in profiles coupled with a high initial rate of fermentation for SAX.  | 16S rRNA bacterial gene sequencing (V1 V3 region)qPCR | Microbiota of D1 was dominated by *Prevotella* (38.7%,)  D2 by *Bacteroides* ( 25.0%);D1 fermented all three fibers with similar high total SCFA production;Compared to FOS ,CAX and SAX produced similarly high levels of propionate and low levels of butyrate;same levels of acetate produced by the three fibers;D2 *Bacteroides* enterotype : CAX structure was slower fermenting and initially produced less total SCFAs, though by 24 h reached the same high level as SAX.rapid initial rise in SCFAs of SAX was contributed by higher acetate and butyrate production;The *Prevotella*-dominated microbiota produced 2–3 times more propionate than the *Bacteroides*-dominated microbiota;α-Diversity decreased significantly during fermentation in D1 and increased in D2;higher fiber utilizing capacity in the *Prevotella* enterotypes . |
|  | De Moraes, A.C.F., et al., 2017(93) | n=268  | cross-sectional study  | Healthy Brazilian subjects, 35 to 65 years and body mass index (BMI) <40 kg/m2 ;omnivore: n=100; lacto-ovo-vegetarians:n=102 strict vegetarians :n=66 | FFQ appliedstrict vegetarian (no consumption of animal products); lacto-ovo-vegetarian (consumption of dairy products and/or eggs) omnivore (consumption of animal products more than once a month  | 16SrRNA sequencing, V4 region  | predominance of *Firmicutes* and *Bacteroidetes* 111 participants were assigned to *Bacteroides*, 55 to *Prevotella,* and 102 to *Ruminococcaceae* enterotype.;Strict and lacto-ovo-vegetarians had lower BMI (23.1 ± 4.1 and 24.4 ± 3.9 vs. 26.4 ± 4.7 kg/m2, respectively, *p* < 0.001) and LDL-c values (99 ± 31 and 101 ± 27 vs. 112 ± 29 mg/dL, respectively, *p* = 0.005) than omnivores ;*Prevotella* cluster contained higher amount of strict vegetarians individuals than the other enterotypes (40.0 vs. 20.7 and 20.6, *p* = 0.04). P.-type had similar anthropometric profile but a lower mean LDL-c concentration than the *Bacteroides* enterotype (96 ± 23 vs. 109 ± 32 mg/dL, *p* = 0.04). better cardiometabolic profile *for Prevotella* enterotype, *Eubacterium ventriosum* (r BMI = −0.33, *p* = 0.03, and r HDL-c = 0.33, *p* = 0.04), *Akkermansia* (r 2h glucose = −0.35, *p* = 0.02), *Roseburia* (r BMI = −0.36, *p* = 0.02 and r waist = −0.36, *p* = 0.02), and *Faecalibacterium* (r insulin = −0.35, *p* = 0.02) abundances were associated to better cardiometabolic profile. f  |
|  | Marungruang, N., et al., 2017(94)  | n=51 | CT | Non-smoking healthy volunteers from Sweden, i.e., over-weight or obese but without any known medical condition  risk individuals (*n* = 47), between 51 and 72 years old and with a BMI of 25–33 kg/ m2 Twenty-three subjects completed the multifunctional diet arm and 24 completed the control diet intervention. Thus, results from 47 completers (12 men and 35 women)   | 8-week intervention;Two groups: multifunctional diet (MFD) with potential ability to modulate different biomarkers related to the inflammatory tonus and cardiometabolic risk or a control diet (CD)foods and/or meals with anti-inflammatory potential in that they promote low acute glycemic responses, are rich in polyphenols and/or specific dietary fiber with prebiotic action, are rich in omega 3 fatty acids such as oily fish and rapeseed oil, or with anti-oxidative and anti-hyper- cholesterolaemic effects, e.g., soybeans and almonds  | 16S rRNA bacterial gene sequencing (V3 V4 region) | No significant alterations of the gut microbiota composition at phylum or genus taxonomic levels ;increased abundance of *Prevotella copri* in the MFD group as compared to the control group. *Treponema* correlated positively with blood pressure. In contrast, *Faecalibacterium* showed a negative association with blood pressure, while *Bilophila* appeared to associate with a negative blood lipid profile.  |
|  | De Moraes , A.C., et al., 2017(95) | n=268 | Cross-sectional study | non‐diabetic individuals (54.2% women, mean age 49.5 years) 35–65 years old,  | stratified according to dietary type: strict vegetarian (n=66), lacto-ovo-vegetarian(n=102), and omnivore (n=100). | 16SrRNA sequencing, V4 region  | greatest abundant phyla were *Firmicutes* (40.7 ± 15.9%) and *Bacteroidetes* (39.5 ± 19.9%) ;strict vegetarians: higher *Prevotella* abundance and *Prevotella/Bacteroides* ratio than the other groups. lower proportion of *Faecalibacterium* than lacto‐ovo‐vegetarians, and both vegetarian groups had higher proportions than did omnivores ;*Succinivibrio* and *Halomonas* from the *Proteobacteria* phylum overrepresented in omnivore ;worse lipid profile; higher values of anthropometric data, insulin in the omnivorous group. |
|  | De Filippo, C., *et al.* 2017(19) |  | Observational study | Healthy children living in urban and rural Burkina Faso (BR) and Italy n=37Rural:n=11Urban:n=26Age :2-8 years;No antibiotic/probiotic intake in the last 6 months,Not been hospitalized in theprevious 6 months. | **Rural BR**: vegetarian, rich in fibers, low in fat, animal protein, and simpleSugars (indigenous cereals :millet, and sorghum; legumes :Niebè; vegetables :Néré, black-eyed peas, and baobab leaves; fruits: mango, papaya, and bananas; fermented products.**Urban BR**: African diet of cereals (millet, sorghum, rice, soya)and legumes (Niebè), but also bread, milk and dairy productssuch as cheese and yogurt, eggs, fruit juices, snacks, sweet bakery products and different kinds of meat and fish, including frozenfish no more than three times per week.**Italian**: typical Western diet, high in starch, simple sugars, animal protein, and fat andlow in fiber (Cereals and starchy component; legumes: beans, peas, vegetables :carrot, potatoes, fennel, tomato, zucchini; Fruit: apple, pear, peach, grapes, bananas, tangerine; Milk and milk derivatives :cow's milk, mozzarella, parmesan, cheese; Oil and fats :Extra virgin olive oil and butter; Meats, meat derivatives, fish; Egg and derivatives; peanuts, sugar and honey, snacks ). | 16S rDNApyrosequencing (V5-V6region)  | **Rural** Ratio *Bacteroides*/*Firmicutes* *Prevotella* (*P. copri, P. stercorea* and*P.melaninogenica), Xylanibacter*)*Treponema, Succinivibrio**Lachnospiraceae incertae sedis*, *Roseburia*, and*Dorea* Levels of short-chain fatty-acids (propionic, valeric, butyric).  | **Urban** *Bacteroides, Bifidobacterium*  *Prevotella (*almost absent)  *Alistipes,**Barnesiella, Bilophila* Levels of short-chain fatty-acids (especially butyric acid).dg |
|  | Haro *et al*., 2016(33) |  | prospective, randomized, opened, controlled trial  | Obese patients (men) from SpainN=20Age:20-75 years old | a Mediterranean diet and a low-fat, high-complex carbohydrate diet (LFHCC diet). | 16S rDNApyrosequencing | LFHCC diet increased the *Prevotella* and decreased the *Roseburia* genera, whereas the Med diet decreased the *Prevotella* and increased the *Roseburia* and *Oscillospira* genera   |
|  | Gutiérrez-Díaz *et al*., 2016 (34) |  | Transversal study | adults with non-declared pathology (n=31), (23 females, 8 males; with a mean age of 42.1 ± 10.9 years old).  | Mediterranean diet | 16S rDNApyrosequencing | Mediterranean diet score (MDS) was directly associated with the abundance of phylum *Bacteroidetes*, family *Prevotellaceae* and genus *Prevotella* and inversely related to the phylum *Firmicutes* and the genus *Ruminococcus*;Higher concentrations of faecal propionate and butyrate in subjects with higher MDS.  |
|  | Borgo F., *et al*., 2016(36) |  | Observational case control study  | Obese and normal weight Italian children (n=61)Obese group (n=28):15 females and 13 males Normal-weight group (n=33) | No information about the type of diet higher dietary intakes of energy of obese children | DGGE analysis;16S rDNApyrosequencing  | *Bacteroides/Prevotella* group weresignificantly less abundant in obese children;no significant differences in the Bifidobacterium spp. Lactobacillus spp., and Enterobacteriaceae between the two groups.  |
|  | Wang, Y, *et al.,* 2016(40) |  | randomized, single-blinded, controlled crossover trial (5 weeks) | Male and female subjects (n=19) | 1. a wheat and rice (WR) based control;
2. 3 g low molecular weight (LMW) barley β-glucan (288 kDa);
3. 5 g LMW barley β-glucan (292 kDa);
4. 3 g high molecular weight (HMW) barley β-glucan (1,349 kDa)
 | 16S rDNA pyrosequencing (V4 region);Illumina sequencing of 16S rRNA genes  | 5 g LMW β-glucan and 3 g LMW β-glucan did not alter the gut microbiota composition;3 g/d HMW β-glucan increased Bacteroides and Prevotella, but decreased Dorea.*Bacteroides, Prevotella,* and *Dorea* composition correlated (*P* < 0.05) with shifts of CVD risk factors, including body mass index, waist circumference, blood pressure, as well as triglyceride levels.  |
|  | Li, K., *et al*., 2016(96) | n=68 |  | Healthy Tibetan and Han individuals;four groups: 1. 13 native Tibetan herders living at an altitude of more than 4800 m; 2) 13 native Tibetan peasants living at an altitude of 3600 m; 3) 12 individuals of the Han population who migrated to a high altitude and lived in Lhasa (3600 m) for over 20 years; and 4) 30 citizens of a low-altitude Han population who lived in the Chinese hinterland (Chengdu, Sichuan Province) at an altitude of about 500 m.

Age range:35–55 years old, normal weight no history of gastrointestinal disease, liver disease, hypertension, or diabetes.  | Traditional diets | 16S rRNA V1–V3 regions  | relative abundance of *Prevotella* of the Tibetan microbiome compared to Han stool enriched in *Bacteroides*, even both groups were living at the 3600 m altitude;Tibetan herders living at 4800 had flora enriched in butyrate-producing bacteria, possibly in response to the harsher environment  |
|  | Gomez, A. et al., 2016(16) | n=57 |  | African individuals (BaAka hunter-gatherers and Bantu) inhabiting Dzanga Sangha Protected Areas (DSPA), Central African Republic Comparison with US American gut microbiota | Diet based on consumption of fibrous tubers, such as bitter manioc root and other highly fibrous starches, such as wild yams , high consumption of high quantities of *Gnetum africanum* (koko) leaves  | 16S rRNA variable region (V1-V3).  | Dominance of Firmicutes and Bacteroidetes ;Bantu :5:1 Firmicutes: Bacteroidetes ratio, BaAka :1:1 ;BaAka microbiota: abundance of Prevotellaceae, Treponema, and Clostridiaceae, while the Bantu gut microbiome is dominated by Firmicutes. ;Other characteristic taxa of BaAka microbiota over Bantu were *Sutterella*, *Anaerovibrio*, and unclassified members of the Clostri- diaceae and Cyanobacteria ;Enrichment of *Faecalibacterium* and lactic acid bacteria (*Leuconostoc*, *Lactococcus*) in the Bantu ;Metabolite signature in BaAka : lipids (40.8% of all metabolites), carbohydrates (19%), sterols (18.9%), phosphates (8%), organic acids (7.9%), amino acids and amines (3.3%), and bile acids (1.7%) ;Coprostan-3-ol, the main conversion product from cholesterol metabolism in the distal colon : most abundant metabolite (15.6% ± 10.6%) *Prevotella*, unclassified Clostridiaceae, and *Treponema* significantly depleted in US Americans; western-like features in the Bantu, including an increased abundance of predictive carbohydrate and xenobiotic metabolic pathways. abundance of predicted virulence, amino acid, and vitamin metabolism functions, as well as dominance of lipid and amino-acid-derived metabolites in BaAka hunter-gathereres. |
|  | De Filippis *et al*., 2016(12) |  | Cross-sectional study | Healthy vegetarians (n=51), vegans (n=51) and omnivores (n=51) from different cities in Italy | Typical vegetarian, vegan or omnivore diet | 16S rDNApyrosequencing | Vegetarians and vegans had a high-level adherence to the Mediterranean Diet.*Lachnospira* and *Prevotella* linked to high-level adherence to Mediterranean Diet;*L-Ruminococcus* positively associated to omnivore diet;*Prevotella* was the only Bacteroidetes having positive correlations with SCFA;Urinary TMAO levels were significantly lower in vegetarian and vegan compared to omnivores.  |
|  | Balfegó, M., et al., 2016(97) | n=35 | Randomized trial |  drug-naïve patients with type 2 diabetes  | type 2 diabetes standard diet (control group: CG), or a standard diet enriched with 100 g of sardines 5 days a week (sardine group: SG) for 6 months.  |  | no significant differences in glycemic control between groups ; decreased plasma insulin and homeostasis model of assessment - insulin resistance after 6 months;both interventions decreased phylum *Firmicutes* (SG and CG: P = 0.04) and increased *E. coli* concentrations (SG: P = 0.01, CG: P = 0.03) SG decreased *Firmicutes/Bacteroidetes* ratio (P = 0.04) and increased *Bacteroides-Prevotella* (P = 0.004) compared to baseline.  |
|  | Kelly, N.T, et al., 2016(98) | n=112 | Epidemiological study |  biracial participants from the Bogalusa Heart Study (BHS) (35% black and 65% white) of residents from Bogalusa, Louisianan=55-high lifetime CVD risk profile n=57 with low lifetime CVD risk profile  | No information about dietary habits. | 16S rDNA V4 region  | microbial richness was consistently associated with decreased lifetime CVD risk profile;genera *Alloprevotella* (P=2.96×10-6), *Prevotella 7* (P=7.95×10-5) and *Paraprevotella* (P=6.48×10-4) associated with CVD risk;Within the Firmicutes phylum, four taxa associated with lifetime CVD risk: two genera from the Lachnospiraceae family, *Tyzzerella 4* (P=1.51×10-4) and *Tyzzerella* (P=4.39×10-4), and two genera from families Veillonellaceae and Erysipelotrichaceae, *Megamonas* (P=4.18×10-5) and *Catenibacterium* (P=1.51×10-4) ;*Prevotella 2* and *Prevotella 7* were associated with increased lifetime CVD risk, *whereas Alloprevotella* was associated with decreased lifetime CVD risk  |
|  | Kang, C., et al., 2016(54) | n=12 | Clinical trial | Healthy chinese subjects enrolled in Third Military Medical University in Chongqing.  | controlled feeding trial;6-weeks 0, 5, 0 and 10 mg/d capsaicin (CAP) from chili powder.  | 16S rRNA bacterial gene sequencing (V3 V4 region) | Dietary CAP increased the Firmicutes/Bacteroidetes ratio and *Faecalibacterium* abundance, accompanied with increased plasma levels of glucagon-like peptide 1 (GLP-1) and gastric inhibitory polypeptide (GIP) and decreased plasma ghrelin level.;*Bacteroides* enterotype (E1) and *Prevotella* enterotype (E2);higher fecal *Faecalibacterium* abundance and butyrate concentration after CAP interventions than those in E2 subjects.  |
|  | Pedersen , H.K., et al., 201656) | n=291 | Cohort study | 291 normoglycaemic and middle-aged Danish MetaHIT individuals as previously reported1, as well as 75 Danish type 2 diabetes patients 75 type 2 diabetes patients and 277 out of the 291 of the non-diabetic individuals  | No information about dietary patterns | 16S rRNA bacterial gene sequencing (V3 V4 region) | *Prevotella copri* and *Bacteroides vulgatus* may directly impact host metabolism., as theyare identified as the main species driving the association between biosynthesis of increased levels of branched-chain amino acids (BCAAs) and insulin resistance  mice fed a high-fat diet, and found that a challenge with *P. copri* led to increased circulating serum levels of BCAAs, insulin resistance and an aggravation of glucose intolerance  |
|  | De Vadder, F, et all., 2016(75) | No information |  | Rodentsmice, aged 12–14 weeks and Male Sprague-Dawley rats (Charles River), aged 6–8 weeks  | daily gavage for 7 days with live P. copri strain DSM18205 Sodium succinate (Sigma) or FOSs (Orafti P95, kindly donated by Beneo) were incorporated into the diet at 5% w/w (succinate) or 10% w/w (FOS).  | 16S rRNA bacterial gene sequencing (V1 V2 region) | Conventional mice colonized with the succinate producer Prevotella copri exhibited metabolic benefits, which could be related to succinate-activated IGN;Prevotella improved glucose metabolism, by increased glucose tolerance  |
|  | Cao, C.C., et al., 2016(99) | n=30 |  | healthy American, Indian, and Jamaican women ;aged 28.3 6 0.8 years old  | Isotope infusion with [guanidino-15N2]arginine, [5,5-2H2]citrulline, and [15N2]ornithine and given oral [U-13C6]arginine in the fasting and postprandial states.  | 16S rRNA bacterial gene sequencing (V3 V5 region) | three dominant stool community types : *Prevotella, Bacteroides,* and *Bacteroides* with *Clostridium*Indian women had increased mean relative abundances of Prevotella (42%) compared to American and Jamaican women (7% and < 1%, P = 0.03) which were associated with diet, impaired intestinal absorptive capacity, and arginine flux. fasting state, Indian women had lower citrulline flux than did American and Jamaican women *Bacteroides* was dominant in the American and Jamaican (38% and 14% (P = 0.03) ;more than half of the American samples lacked *Prevotella* completely. *Prevotella* was found at greater mean relative abundances in the Indian cohort (42%) than in the American (7%) or Jamaican (<1%) cohorts (P = 0.03)  |
|  | Gutiérrez-Díaz, I., et al., 2016(34) | n=31 | Transversal study | adults with non-declared pathology (23 females, 8 males; with a mean age of 42.1 ± 10.9 years old).  | FFQ Mediteraneean Diet  | 16S rRNA  | Mediteraneean Diet Score (MDS ) associated with a higher abundance of Bacteroidetes (p = 0.001), Prevotellacea (p = 0.002) and Prevotella (p = 0.003) and a lower concentration of Firmicutes (p = 0.003) and Lachnospiraceae (p = 0.045). subjects with MDS ≥ 4, higher concentrations of faecal propionate (p = 0.034) and butyrate (p = 0.018)  |
|  | Zhang, J., et al. ,2015(100) | N=314 | **Cohort study** | Healthy young adults from China ( 7 ethnic groups (that is, the Bai, Han, Kazakh, Mongol, Tibetan, Uyghur and Zhuang )18 and 35 years old145 urban and 169 rural residents  |  | 16S rRNA bacterial gene sequencing (V5 V6 region) | *Firmicutes*, *Bacteroidetes*, *Proteobacteria* and *Actinobacteria* most dominant phyla (73.47, 14.13, 5.83 and 3.36% of the total sequences )*Prevotella*, *Xylanibacter* enriched in rural individuals; *Lactobacillus, Methanobrevibacter, Methanosphaera* *Methanobacterium* more abundant in the rural Mongol individuals than in urban. |
|  | Greenhill, A.R., et al.,2015(101) | N=115 |  | people living a subsistence life- style in rural areas of Papua New Guinea 2 to 66 years,  | Traditional lifestyle  | everse transcrip- tion-quantitative PCR (RT-qPCR)  | Most abundant bacteria, present in more than 92% of samples.  *: Clostridium leptum* subgroup (log10 9.3±0.7), *Prevotella spp (*log10 9.0±0.9), *C. coccoides* group (log10 8.9±0.7) and *Atopobium* cluster (log10 8.1±0.8) average number of *Prevotella spp.* was significantly greater than average number of *Bacteroides fragilis* group (log10 6.8±0.9)  |
|  | La-ongkham O., et al. 2015(102) | N=60 |  | 60 healthy Thai children (aged 8–11 years)  | Typical food The children from NE had significantly higher consumption frequency of meat (chicken and beef), a wide variety of carbohydrate sources (noodle, fermented rice and sweet potato) including vegetables and fruit, while in CT, there was a significant preference for rice, breakfast cereal and cow milk.  | qPCR  | higher abundance of lactobacilli, *Clostridium coccoides*–*Eubacterium rectale*, *Clostridium leptum*, *Prevotella* and *Bacteroides fragilis* in children from the NE region. the consumption frequency of vegetables showed a moderately positive correlation coefficient of 0.42 and 0.34 to the *Lactobacillus* group (*P* = 0.001) and the *Prevotella* group (*P* = 0.008) a diet of fish and beef showed a moderately negative correlation coefficient of −0.41 (*P* = 0.001) and −0.33 (*P* = 0.09) to *Bifidobacterium* spp.  |
|  | Dehingia, M., et al.., 2015(62) | N=193 |  | healthy volunteers belonging to 15 different ethnic groups from four different states of India ;20–35 years, who had not taken antibiotics within three months prior to sample collection  | Traditional Indian dietThe staple food of all the ethnic groups was rice with variation in consumption of vegetables, fish, meat, legumes, whole grains, fruits and tubers. The tribes from Manipur and Sikkim consume relatively higher quantity of fermented foods such as fermented bamboo shoot, fermented soy bean, fermented mustard seeds and leaves, along with some dried and smoked fish and meat in each servings. The Sikkim tribes consume more milk products in their diet compared to the others.  | 16S rRNA bacterial gene sequencing (V3 V4 region) | Geography and diet had significant effect on GBP of the Indian tribes which was dominated by *Prevotella*.A comparison with the worldwide data revealed that GBP of the Indian population was similar to the Mongolian population (Mongolia) major bacterial phyla detected were *Firmicutes, Bacteroidetes* and *Actinobacteria* *Faecalibacterium*, *Eubacterium*, *Clostridium*, *Blautia*, *Ruminococcus* and *Roseburia* were found to be core genera in the representative populations of the world  |
|  | Karl, J.P., et al., 2015(103) | N=77 |  |  over- weight Chinese adults aged 25–55 y  | 23-week intervention;a 9-wk weight-loss intervention phase (phase 1) : 3–4 cans of a custom-made precooked porridge/d which consisted of a variety of whole grains and traditional Chinese medicinal plant foods limited amounts of fruit, vegetables, and legumes during phase 1 2 supplemnets: a powdered blend of bitter melon and oligosaccharides, a powdered blend of prebiotic soluble and fermentable fibers,  a 14-wk maintenance phase (phase 2) : high-fiber, low-meat (,50 g/d) diet.  |  | Prevotella and Bacteroides had strongest associations with fecal menaquinone content(vitamin K forms ). The strongest and most consistent relations were between Prevotella spp. and MK5 and MK11–MK13, between Bacteroides spp. and MK9 and MK10, and between Escherichia/Shigella spp. and MK8.  |
|  | Tap, J., et al., 2015(104) | n=19 | Clinical trial | healthy young adults (nine males, 10 females, aged from 19 to 25 years) with no history of gastrointestinal problems completed the study.  | Subjects were randomly assigned to receive each meal plan during the 5 days with a 2-week washout period: 10 subjects followed a first round of 10 g dietary fibre per day for 5 days, followed by 2-week washout, then a second round of 40 g per day for 5 days, followed by a 7 days washout sequence. Nine other volun- teers followed the exact same sequence but with 40 g per day in the first round and 10 g per day in the second round  | 16S rRNA bacterial gene sequencing (V3 V4 region) | Higher microbiota richness was associated with higher microbiota stability upon increased dietary fibre intake. High microbial richness was also associated with high proportions of Prevotella and Coprococcus species and high levels of caproate and valerate(*P* < 0.05).  |
|  | Martínez, I., *et al* 2015(11) | N=62 | Observational study | People from rural Papua-New Guinea (PNG: 2 groups) and from urban USA (Nebraska)rural: n=40; 2/3 womenAge: 17-50 yearsurban: n=22; mean age: 27 years old | **Rural (PNG):** carbohydrate-based diet (staple foods: sweet potato, taro, and plantain; banana, cassava, yam, and sago; leafy green vegetables, fruits and legumes); pork and fish are consumed less frequently (twice weekly)**Urban ( USA):** westernized omnivorous diets. | 16S rDNApyrosequencing (V5-V6region) |  **Rural**   *Prevotella* *Firmicutes (Staphylococcus, Eubacterium, Erysipelotrichaceae, Incertae sedis, Clostridium senso stricto, Sarcina, Enterococcus, Lactobacillus);* *Faecalibacterium; Blautia; Clostridium XIVb, XIVa, and IV;**Ruminococcus; Lachnospiraceae Incertae sedis; Gemella; Turicibacter; Phascolarctobacterium)* *Proteobacteria (Enterobacteriaceae,Helicobacteriaceae ).*  | **Urban**  *Bacteroides,* *Parabacteroides,* *Alistipes*, *Odoribacter*, and *Barnesiella* *Bifidobacterium;* *Bilophila, Aquabacterium,**and Acidovorax.* |  |
|  | Nakayama, J., *et al*., 2015(15) |  | Observational study | Children living in different countries from Asia (China, Japan, Taiwan, Thailand, Indonesia)n=303age: 7-11  | Carbohydrate-rich diet: rice and wheat (noodles, dumplings, steamed bread) in China, Indonesian and Thai children eat rice more frequently than Chinese and JapaneseSoybeans (tempeh), sweet potatoesin Indonesia. | 16S rDNApyrosequencing (V6-V8region) | *Prevotella* enterotype (*P.copri, P.stercorea*) in Indonesia and Thailand (Khon Kaen)*Bacteroides/Bifidobacterium* in China, Japan, Taiwan. |
|  | Ferrocino *et al*., 2015(32) |  | Cross-sectional study | Healthy omnivore (n = 51), ovo-lacto-vegetarian (n = 51) or vegan (n=51) from 4 different cities in Italyequal portions of men and women aged 18–55. | Typical omnivore, lacto-vegetarian or vegan diet | 16S rDNApyrosequencing (V3-V9region) | *Prevotella micans*, *B. vulgatus* and *Faecal bacterium prausnitzii* characteristics of theovo- lacto-vegetarian group ;*Prevotella copri* characteristic of the omnivore subjects. |
|  | De Filippis, F., et al., 2016(12) | N=153 |  | Healthy omnivore (n = 51), vegetarian (n = 51) or vegan (n=51) from 4 different cities in Italy  | Typical omnivore, lacto-vegetarian or vegan diet Total food and beverage consumption was assessed by means of a 7-day weighed food diary, level of adherence to the Mediterranean dietary pattern was assessed  |  | 88% of the vegans, 65% of the vegetarians and also 30% of the omnivores showed high MD adherence rates. Bacteroidetes phylum was more abundant in vegans and vegetar- ians compared with omnivores (p<0.05); accordingly, higher Firmicutes: Lachnospira and Prevotella associated to plant-based diets and negatively associatied with the omnivore diet (p<0.01)faecal levels of acetic, pro panoic and butanoic acids (and corresponding esters) strongly correlated with the consumption of fruit, vegetables, legumesValerate and caproate concentrations were linked to consumption of protein- rich animal foods and fat (p<0.05) Ruminococcus positively associated to omnivore diets Bacteroidetes ratios were found in most of the omnivores Prevotella was the only Bacteroidetes having positive correlations with SCFA ( p<0.05) Urinary TMAO levels were significantly lower in vegetarian and vegan (p<0.0001) compared with O subjects L-Ruminococcus strongly correlated with TMAO  |
|  | Kovatcheva-Datchary *et al*., 2015(21) |  | Randomized cross-over study (3 days) | Healthy Swedish subjects (n=39);6 men, 33 women 50–70 yearsBMI normal to slightly overweight (BMI 18–28 kg/m2), fasting plasma glucose % 6.1 mmol/l, non-smoker, overall healthy, and no known metabolic disorders or food allergies. Anti-hypertensive medications and prescription-free painkillers without any anti-inflammatory action were accepted.  | 1st group: 100 g of barley kernel-based bread (BKB) three times a day2nd group : 100 g of white wheat bread (WWB) three times a day  | 16S rDNApyrosequencing qPCRShotgun Metagenome Analysis  | High *Prevotella/Bacteroides* ratio in responders than non-responders after BKB. Abundance of *P.copri* in responders.mean blood glucose and serum insulin responses measured on day 4 after a standardized breakfast were improved following BKB compared with WWB in the total group  |  |
|  | Kovatcheva-Datchary *et al*., 2015(21) |  |  | Germ –free mice 3 experiments:1. adult Swiss Webster and C57BL/6 male mice (Taconic),7 days
2. C57BL/6 male mice/4 weeks;7 days
3. 10- to 12-week-old GF Swiss Webster male mice on a chow diet
 | chow diet (low in fat and protein and high in dietary fibers) with live or heat-killed control *P. copri* (five mice per group). high-fat diet (4 weeks) and gavaged with live *P. copri* or media control (for 7 days). inoculation with single gavage of 108 CFU *P. copri* strain DSM18205 and/or *B. thetaiotaomicron* strain ATCC 29148 or the isogenic *B. thetaiotaomicron* mutant strain (BT1686-89)  |  | standard chow diet (low in fat and protein and high in dietary fibers) improved glucose tolerance following treatment with live human feces-derived *P. copri* (DSM 18205) compared with heat- killed *P. copri* Similar colonization of both bacteriaBi-colonization lower levels of both bacteriamice mono- colonized with *P. copri* had high cecal levels of succinate and no propionate production; mice mono-colonized with *B. thetaiotaomicron* hadhigh cecal levels of propionategerm-free mice transplanted with microbiota from responder human donors exhibited improved glucose metabolism and increased abundance of Prevotella and liver glycogen content compared with germ-free mice that received non-responder microbiota. |
|  |  Hu *et al*.2015(38) |  | Cross-sectional study |  obese Korean adolescents (n=67) normal adolescents (n=67) 13 - 16 years old | No information about dietary patterns  | 16S rDNApyrosequencing (V3-V9region) | no difference in the Firmicutes-to-Bacteroidetes (F/B) ratio higher *Prevotella* levels in obese than in normal weight childrenhigher levels of *Bacteroides* in normal weight children*Prevotella* and *Bacteroides* associated with BMI*Prevotella* positively associated with triglycerides and high-sensitive C-reactive protein  |
|  | Haro, C.,et al., 2015(58) | n=20 | prospective, randomized, opened, controlled trial  | 20 obese patients (men) within the Coronary Diet Intervention With Olive Oil and Cardiovascular Prevention (CORDIOPREV)  | Med diet (35% fat, 22% monounsaturated) and the LFHCC diet (28% fat, 12% monounsaturated).  | 16S rDNApyrosequencing (V3-V9region) | LFHCC diet increased the *Prevotella* and decreased the *Roseburia* genera, Med diet decreased the *Prevotella* and increased the *Roseburia* and *Oscillospira* genera (*P* =.028, .002, and .016, respectively).  abundance of *Parabacteroides distasonis* (*P* =.025) and *Faeca- libacterium prausnitzii* (*P* = .020) increased after long-term consumption of the Med diet and the LFHCC diet changes in the abundance of 7 of 572 metabolites found in feces, ( amino acid, peptide, and sphingolipid metabolism), could be linked to the changes in the gut microbiota.  |
|  | Wu *et al.* 2014 (60)[1] |  | cross-sectional study |  vegans (n=15) and omnivores (n=6) from urban USA | Vegan or omnivorous diet for 6 months | 16S rDNApyrosequencing (V1-V2region) | No significant differences in bacterial community composition in the two groups;increased levels of cometabolites among vegans and increased levels of lipids and amino acids among omnivores;no significant effect on the levels of faecal SCFAs in the two groups. |
|  | Ruengsomwong *et al*., 2014(31) |  | Clinical trial | Thai healthy non- vegetarians (n=6) aged between 53-78 yearsThai healthy vegetarians (n=7) aged between 42-61 years  | Non-vegetarian : red meat (only pork), white meat such as fish and chicken and eggs.50 % consumed yoghurt and milk.Thai fruits on a daily basis Vegetarian:all the subjects consumed yoghurt and milk and thai fruits ona daily basis. | PCR-DGGE Analysis  | Abundance of *Prevotella,* *C. coccoides-E. rectale* group, and Enterobacteriaceae in the vegetarian group;Higher number of *Prevotella* species in the vegetarian group than non-vegetarian;Higher numbers of *Bacteroides*, the *C. coccoides-E. rectale* group, and *Bifidobacterium* in non-vegetarians;higher number of *Bacteroides* in the non-vegetarians. |
|  | Schnorr, S.L., *et al.,* 2014*.*(14) |  | Observational study | People from rural Tanzania (Hazda hunter gatherers) and from urban Italy (Bologna)n= 43rural: n=27 (aged 8–70 years ) urban: n= 16 (aged 20–40 years) | **Rural (Tanzania):** wild foods: meat,honey, baobab, berries and tubers.**Urban (Italy)**: Mediterranean diet: abundant plant foods, fresh fruit, pasta, bread and olive oil; low-to-moderate amounts of dairy, poultry, fish and red meat, carbohydrates came from easily digestible starch (54%) and sugar (36%) while very little was derived from fibre-solubleor insoluble fibers (10%). | 16S rDNApyrosequencing (V4 region)qPCR | **Rural:** Dominant: *Firmicutes, Bacteroidetes* Absence of *Actinobacteria* and *Bifidobacterium* *Prevotella, Eubacterium, Oscillibacter, Butyricicoccus, Sporobacter,*  *Succinivibrio Treponema* Unclassified *Bacteroidetes, Clostridiales* and*Ruminococcaceae*Propionate levels **Urban:**High *Bifidobacterium, Bacteroides, Blautia, Dorea.* High butyrate levels |
|  | Fernandes, J., et al., 2014(105) | N=94 |  | Healthy lean individuals (n=52) and overweight or obese individuals (n=42) | 3-day diet records | 16S rDNApyrosequencing  | OWOB participants had higher faecal acetate (P=0.05), propionate (P= 0.03), butyrate (P=0.05), valerate (P= 0.03) and total short chain fatty-acid (SCFA; P= 0.02) concentrations than LN.No significant differences in Firmicutes to *Bacteroides/Prevotella* (F:B) ratio between groups*Bacteroides/ Prevotella* negatively correlated with SCFA (P = 0.002)F:B ratio positively correlated with SCFA (P< 0.0001). |
|  | Zhu, L., et al., 2014(106) | N=22 | cross-sectional pilot study  |  constipated obese children (n=8) and control obese children (n=14) | 3-day diet history supplemented by a 24 h dietary recall ;Food Frequency Questionnaire  | *16S rRNA gene V4 –V5 pyrosequencing.*  | 31.68% *Prevotellaceae (Prevotella copri, P. disiens*, and *P. corporis)**genus)* in control group and2.78% in constipated subjects;*Lachnospiraceae* and *Ruminococcaceae* (*Firmicutes)* increased in the constipated patients Significantly decreased abundance in *Prevotella* and increased representation in several genera of *Firmicutes* were observed in constipated patients compared with controls. *Lactobacillus* and *Bifidobacteria* were not decreased in the microbiomes of the constipated patients.These alterations in the fecal microbiome of constipated patients suggested that a novel probiotic treatment includ- ing certain *Prevotella* strains may be more effective than conventional probiotic products incorporating *Lactobacillus* or *Bifidobacterium* species *Prevotellaceae* was the only family significantly decreased in the constipated patients  |
|  | Vitaglione *et al.,* 2014(37) |  | placebo-controlled randomized controlled trial (8 weeks) | healthy and overweight/obese Italian subjects (n=80)low intake of fruits andvegetables and sedentary lifestyle;subjects randomly assigned by the dietitian to the WG or the control group. | WG subjects included in their diet 70 g/d (3 biscuits/d) of WG product, whereas control subjects included 1 package (33 g) of crackers and 3 slices of toasted bread (w27 g).  | 16S rDNApyrosequencing (V4 region)qPCRIllumina technology | WC subjects: increase in *Prevotella*Positive correlation of fecal FA and the abundance of *Bacteroidetes*inflammatory TNF-a and a trend toward reduced IL-6 after 8 wk, as well as an increase of the anti-inflammatory IL-10after 4 wk of WG consumption. |
|  | Mejıa-Leon *et al*., 2014(41) |  | cross-sectional case-control study  | Mexican children (n=29)Children with Type 1 diabetes (T1D) (n=21)Healthy controls (n=8)7 - 18 years old | No information about dietary patterns | 16S rDNA pyrosequencing (V4 region); |  newly diagnosed T1D cases- high levels of *Bacteroides* control group –dominance of *Prevotella.* Children with T1D treated for 2 years –same levels of *Bacteroides* and *Prevotella* as the control group.  |
|  | Matijasic, B.B., et al., 2013 (66) | n=60 |  | 60 healthy individuals living in Slovenia ( 31 vegetarian participants (11 lacto- vegetarians and 20 vegans) and 29 omnivore participants.) Age: 1.5–67 years old, regular dietary type for at least 1 year before this research  | FFQ Participants divided into groups: vegetarian(lacto- vegetarians, vegans)omnivores | V3 16S rRNA  | vegetarian diet was associated with higher ratio (% of group-specific DNA in relation to all bacterial DNA) of Bacteroides–Prevotella, Bacteroides thetaiotaomicron, Clostridium clostridioforme and Faecalibacterium prausnitzii, but with lower ratio (%) of Clostridium cluster XIVa. higher concentration and ratio of Enterobacteriaceae in female participants (p \ 0.05 and p \ 0.01) and decrease in Bifidobacterium with age (p \ 0.01)  |
|  | Fernandez-Raudales, D., et al., 2012(107) | N=64 | randomized, double-blind trial.  | Male participants (20–45 y of age) with a body mass index (BMI) ranging from 25–44  | 500 mL per day low glycinin soymilk (LGS, 49.5% β-conglycinin/6% glycinin), conventional soymilk or or bovine milk (M, 0% β-conglycinin/0% glycinin).  |  |  total bacteria increased in all treatmnets over time (p< 0.001) Bacteroides-Prevotella (p=0.001), Bifidobacterium, and Lactobacillus(p< 0.001) increased in LGS and M;Bifidobaterium significantly reduced in lGS (p=0.003) and S (p< 0.001)  |
|  | Queipo-Ortuno,M.I.,et al 2012 (108) | N=10 | randomized, crossover, controlled intervention study (4 weeks) | healthy male volunteers  | red wine, the equivalent amount of de- alcoholized red wine, or gin for 20 d each.  | 16S rDNApyrosequencing (V2-V3regions) | Increase in *Enterococcus, Prevotella, Bacteroides, Bifidobacterium, Bacteroides uniformis, Eggerthella lenta, and Blautia coccoides–Eubacterium rectale* groups (P , 0.05) systolic and diastolic blood pressures and triglyceride, total choles- terol, HDL cholesterol, and C-reactive protein concentrations de- creased significantly (P , 0.05)  |
|  | Grzes ́kowiak, L., 2011(109) | N=75 |  | Malawian 6-month-old infants (n 44) were compared with Finnish infants (n=31)  | breast-fed and having an age-appropriate diet typical for each area  | 16S rDNApyrosequencing | Bifidobacteria were dominant at 6 months of age in all of the infants, although in greater proportions in Malawian (70.8%) than in Finnish infants (46.8%; P < 0.001). Additional distinctions in bacterial group composition comprised Bacteroides-Prevotella (17.2% vs 4.7%; P < 0.001) and Clostridium histolyticum (4.4% vs 2.8%; P 1⁄4 0.01), respectively. The species Bifidobacterium adolescentis, Clostridium perfringens, and Staphylococcus aureus were absent in Malawian but detected in Finnish infants.  |
|  | Wu, G.D., 2011(60) | N=10 | controlled-feeding study (10 days) | US hospitalized individuals  |  diet information collected from 98 healthy volunteers using two questionnaires that queried recent diet (“Recall”) and habitual long-term diet (food frequency questionnaire; “FFQ”).  | 16S rDNApyrosequencing | *Bacteroidetes* and *Actinobacteria* positively associated with fat intake and negatively with fibre;*Prevotella* positively associated with carbohydrate-based diet (self-reported vegetarian: 27% *Prevotella* enterotype versus 10% *Bacteroides* enterotype; P = 0.13). long-term diet is particularly strongly associated with enterotype parti- tioning.  *Firmicutes* and *Proteobacteria* positively associated with fibre intake and negatively correltaed with fat intake;  |
|  | Zhang, J., et al., 2011110) | N=64 |  | healthy Mongolian adults with nohistory of gastrointestinal-related disease ;volunteers lived a typical modern lifestyle in Ulan Bator(n=36) volunteers living in a pasturing area (Khentii) (n=12)  | Typical dietFFQ applied | 16S rDNApyrosequencing | 4 phyla dominant: *Bacteroidetes, Firmicutes, Proteobacteria and Actinobacteria* (contributing 55.56%, 39.53%, 2.68% and 0.85% of the total amount of sequences**)**Prevotella the most abundant36.31% of the total number of sequences dominance of Bacteroidetes (55.56%) and a low Firmicutes to Bacteroidetes ratio (0.71).;*Prevotella*, *Solobacterium*, *Succinivibrio*, *Escherichia coli*/*Shigella* group, *Olsenella*, *Oribacterium* and *Lactobacillus*- abundant in Khentii residents,;*Bacteroides*, *Oscillibacter*, *Roseburia*, *Alistipes*, *Coprococcus*, *Parabacteroides*, Subdoligranulum, Barnesiella, Odoribacter, Parasutterella, *Butyricimonas, Coprobacillus, Victivallis, Anaeros- porobacter* and *Akkermansia* -abundant in Ulan Bator residents.   |
|  | De Filippo et al. (2010)(19) | n=30 |  | healthy children: male (n=9) ; female (n=6)living in a village from Burkina Faso, healthy children : male (n=9) ; female (n=6) living in the urban area of Florence, Italy ;1–6 y of age, had not taken antibiotics or probiotics in the 6 mo before the sampling dates, and had not been hos- pitalized in the previous 6 mo  | BF diet consists mainly of cereals (millet grain, sorghum), legumes (black-eyed peas, called Niébé), and vege- tables, so the content of carbohydrate, fiber and nonanimal protein is very highItalian diet: typical western diet high in animal protein, sugar, starch, and fat and low in fiber.   | 16S rDNA pyrosequencing (V5; V6 region); | BF children showed a significant enrichment in Bacteroidetes and depletion in Firmi- cutes (P < 0.001), with a unique abundance of bacteria from the genus Prevotella and Xylanibacter ;short-chain fatty acids (P < 0.001) in BF than in EU children.;Enterobacteriaceae (Shigella and Escherichia) were significantly underrepresented in BF than in EU children (P < 0.05)  |
|  | Costabile A., et al., 2010(111) | n= 32 | Dietary intervention study (double- blind, randomised, placebo-controlled cross-over )  | healthy volunteers (aged 20 – 42 years old); women: 14men: 18 | Group 1: very- long-chain inulin extracted from artichoke (VLCI) 10g/d for 3 weeks3 weeks washout period2nd group: the placebo (10g/d of maltodextrin) for 3 weeks, and then after a 3-week washout, they consumed VLCI (10g/d) for another 3-week  |  | faecal bifidobacteria and lactobacilli significantly higher upon VLCI ingestion compared with the placebo. *Bacteroides–Prevotella* numbers significantly reduced ;No significant changes in faecal SCFA concentrations  |
|  | De Palma , G., et al., 2010(112) | n=62 |  | 24 untreated CD patients;18 treated CD patients 20 healthy children ;No antibiotics at least 1 month before to the faecal sampling.  | normal-gluten containing diet, gluten-free diet for at least 2 years  |  | *Bacteroides*-*Prevotella* group proportions were more abundant (P < 0.050) in untreated CD patients than in controls. Levels of IgA coating the *Bacteroides*-*Prevotella* group were significantly reduced (P < 0.050) in both CD patients in comparison with healthy controls ;*Bifidobacterium*, *Clostridium histolyticum*, *C. lituseburense* and *Faecalibacterium prausnitzii* group proportions were less abundant (P < 0.050) in untreated CD patients than in healthy controls.  |
|  | Prieto  *et al*., 2018(39) |  |  | Germ-free mice (male Swiss Webster mice) (n=26)6 week old | 1. Standard diet(SD) for 12 weeks
2. High-fat diet with butter (BT) (n = 9)
3. High-fat diet with extra virgin olive oil (EVOO) (n = 9)
 | 16S rDNA pyrosequencing( V3–V4 region).  | High levels of *Prevotella* inSD diet, inversely correlated with total cholesterol;High levels of *Sutterellaceae*, *Marispirillum* and *Mucilaginibacter dageonensis* in EVOO diet;High levels of *Desulfovibrio* in BT diet. |