EUKARYOTIC AND PROKARYOTIC MICROBIOTA INTERACTIONS

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Abstract

The nature of the relationship between the communities of microorganisms making up the microbiota in and on a host body has been increasingly explored in recent years. Microorganisms, including bacteria, archaea, viruses, parasites, and fungi, have often long co-evolved with their hosts. In human, the structure and diversity of microbiota vary according to the host’s immunity, diet, environment, age, physiological and metabolic status, medical practices (e.g. antibiotic treatment), climate, season, and host genetics. The recent advent of next generation sequencing (NGS) technologies enhanced observational capacities and allowed for a better understanding of the relationship between distinct microorganisms within microbiota. The interaction between the host and their microbiota has become a field of research into microorganisms with therapeutic and preventive interest for public health applications. This review aims at assessing the current knowledge on interactions between prokaryotic and eukaryotic communities. After a brief description of the metagenomic methods used in the studies analysed, we summarise the findings of available publications describing the interaction between the bacterial communities and protozoa, helminths, and fungi, either in vitro, in experimental models, or in humans. Overall, we observed the existence of a beneficial effect in situations where some microorganisms can improve the health status of the host, while the presence of other microorganisms has been associated with pathologies, resulting in an adverse effect on human health.

Keywords: Microbiota, mycobiota, interactions, host, NGS, metagenomics, culturomics, metabarcoding
1. Introduction

Several microorganisms have been isolated from different body parts of living beings. The community of microorganism living within a body, referred to as “microbiota”, is made up of bacteria, archaea, fungi, protozoa, metazoa (mainly helminths) and viruses. Viruses, including giant viruses, have been found to be part of microbiota (1–3). The microbiota vary from one human to another and its composition and diversity may be influenced by interactions between host genetics, immune response, diet and the physiological and pathological(5) conditions of the environment (4). Other factors potentially influencing the bacterial intestinal microbiome include diet (animal proteins, fatty acids, carbohydrates, processed foods, dietary fibres) (6–8), age (4), stool consistency (9,10), physiological and metabolic status (11,12), medical practices (e.g. antibiotic treatments) (13), seasons (14) climate change (15), seasonal cycles (16) and the host’s genetic background (17–20). The core human microbiota is composed of at least 1,800 genera and up to 40,000 bacterial strains (21) that carry around 10 million non-human genes (22). Studies of human microbiota were carried out by Antonie van Leeuwenhoek at the end of the 17th century following his discovery of “animalcules” through the microscopic observation of human mouth scrapings (23). The microbiological application of DNA-based assays, nucleotide sequencing and matrix-assisted laser desorption ionisation time-of-flight mass spectrometry (MALDI-TOF-MS) considerably enhanced capacities to identify microorganisms (24,25).

The opportunistic and pathogenic nature of various microorganisms is increasingly reported in Inflammatory Bowel Disease therapy, fostered by the growing use of immunosuppressive therapies (26). To date, several studies have led to an enlargement of the bacterial microbiota repertoire which is critical to establishing the link between diseases and the bacterial species involved (27,28). While there are many studies on the isolation, identification and phenotypic and genomic characterisation of prokaryotic communities, few studies have aimed at describing eukaryotic communities and their influence on the bacterial microbiota. Studies have shown that Blastocystis protozoa are associated with a healthy digestive microbiota (14,29,30) while protozoa such as Giardia duodenalis (30,32), and Entamoeba histolytica (33) have been linked to dysbiosis situations. In addition, studies have suggested that the gut bacterial community structure is associated with a risk of P. falciparum infection (34) and also of severe malaria (35). The addition of Lactobacillus and Bifidobacterium probiotics to the gut microbiota has been advocated to reduce Plasmodium parasite density (35). A study reported that Enterobius vermicularis infection in children was associated with an increased gut microbial diversity, and
a higher relative abundance of Alistipes, and Faecalibacterium, whereas the quantity of Acidaminococcus, Megasphaera, Veillonella, and Fusobacterium was relatively low compared to the non-infected group (36). A lower diversity of mouse gut microbiota and an increase in the relative abundance of Lactobacillaceae has been observed following a Trichuris muris infection (37). The results of another study pointed out that Nematode infection triggers both qualitative and quantitative changes in the microbiota that can significantly alter the microbial metabolism and thus influence the host’s nutrition and immunity (38). It has been suggested that interactions between bacterial and fungal communities are involved in Clostridium difficile infection pathophysiology and in the persistence and recurrence of Clostridium difficile infections (39). Moreover, a study comparing fungal microbiota in the guts of healthy subjects and patients with Crohn’s disease highlighted a fungal community dysbiosis in the Crohn’s disease cohort, suggesting that fungi may be involved in the pathogenesis of inflammatory bowel diseases (40). While studies on the eukaryotic microbiota remain relatively scarce, this review aimed at assessing the current knowledge on interactions between the prokaryotic and eukaryotic communities, derived from studies based on microbial genomics, metagenomics, and/or culturomics approaches.

2. Methods
2.1 Literature search strategy

We searched for articles in PubMed and Web of Science. We used the following Mesh terms in PubMed by limiting articles to those on the microbiota (human, animal) and by publication date (20 March 2008 to 3 February 2020): (“parasites” [mesh Major Topic] or “protozoa” [All Fields] or “protozoan infections/parasitology” [Mesh terms] or “helminths” [Mesh major topic] or “helminthiasis/drug therapy” [Mesh terms] or “fungi” [Mesh major topic] or “mycobiome” [Mesh terms]) and (“Bacteria/microbiology” [Mesh major topic] OR “gastrointestinal microbiome” [Mesh terms]) and (“2008/03/20” [PDat]: “2020/02/03” [PDat] AND (“humans” [Mesh terms] OR “animals” [Mesh terms: noexp])). The search for articles on the Web of Science was carried out according to the keywords as follows: ((microbiota AND parasites AND host parasite interactions) OR protozoan infections AND metagenomics OR gastrointestinal microbiome)). The results of the search were refined by category and by date: (microbiology OR parasitology) AND publication years: (2016 OR 2011 OR 2017 OR 2009 OR 2015 OR 2008 OR 2012 OR 2018 OR 2013 OR 2014 OR 2010). We excluded these
categories of research: (biochemistry molecular biology OR virology OR immunology OR cell biology OR dentistry oral surgery medicine OR marine freshwater biology OR ecology OR public environmental occupational health) and [excluding] Web of Science categories: (food science technology OR pharmacology pharmacy OR biochemical research methods).

2.2 Data extraction

The selection of PubMed articles was compared to that of Web of science to eliminate duplicates in the bibliographic database, Zotero (www.zotero.org). We selected the articles obtained by the PubMed and Web of Science databases that refer to the community of prokaryotes and eukaryotes in the title and the text. These articles were included for drafting the review. Some articles come from their bibliographic references (see Figure 1 for details).
Figure 1: Flow diagram of the selection of articles and data extraction
3. Results

The search for articles corresponding to the MeSH terms used in the PubMed search database resulted in 387 articles. By focusing on animal and human microbiota and limiting research to the publication range to between 20 March 2008 and 3 February 2020, 378 articles were retained. The Web of Science search database generated 1,057 articles using the keywords mentioned above. By limiting the research to the domain of microbiology and parasitology and to the year of publication (2008–2018), 136 articles were retained. The evaluation of the title and text of 378 PubMed articles and 136 Web of Science articles involving the bacterial community in relation to protozoa, helminths and fungi resulted in 125 and 22 articles, respectively. The introduction of eligible articles by both search engines into the bibliographic database, Zotero (www.zotero.org), eliminated duplicates and 132 articles were retained. Considering reviews of the relationships between bacterial and protozoa, helminths, or fungal communities, 21 articles of interest were added to the bibliographic database and 153 articles were included for qualitative synthesis.

In this preliminary section, we will briefly describe the methods that were used to characterise the microbial communities in the articles analysed including: culture; qPCR; denaturing gradient gel electrophoresis (DGGE); cloned 16S rRNA amplicon; high-throughput sequencing of 16S rRNA amplicons (454 pyrosequencing); high throughput sequencing of 16S rRNA amplicons (Illumina); sequencing of 16S rRNA amplicons (Ion Torrent); whole metagenome shotgun sequencing (Illumina); and whole metagenome shotgun 454 sequencing.

3.1 Culturomics and culture-based methods

Culture-based methods are traditionally used for isolating bacteria from the digestive tract. The majority of bacteria cannot be cultivated in the conventional laboratory environment, resulting in an underestimation of the actual richness of species and an overestimation of the importance of the species that grow disproportionately well under standard laboratory conditions (41,42). Culture has enabled the development of new knowledge, which is important in the identification of antibiotic resistance, the study of virulence, genomic sequencing of microorganisms and the detection of organisms in low abundance, such as *Clostridium difficile*, by using selective growth media (42,43). “Culturomics” refers to the intensive culture of bacteria using different types of media and conditions (i.e. aerobic and anaerobic) and often adding nutrients to the culture media to mimic natural habitat conditions. Culturomics has contributed significantly to the discovery of new bacterial species (44).
3.2 Polymerase chain reaction

Quantitative real time PCR (qPCR) assays are commonly used to detect specific microorganisms. This tool can be used to detect all the members of a given taxon present in a sample, thus estimating the abundance of this taxon within the studied microbiota. qPCR requires primers and probes that are specific to a given taxon and allows quantification of the amplicons. However, it is prone to PCR biases, including amplification errors, formation of chimeric and heteroduplex molecules, and preferential amplification. Increasing the resolution requires a set of primers with different specific probes to target each taxon which can be amplified either within the same reaction (known as “multiplexing”), or separately. Multiplexing further complexifies the procedure and increases the time and cost required to obtain a relatively limited amounts of data (42).

3.3 Denaturing and temperature gradient gel electrophoresis (DGGE)

Denaturing and temperature gradient gel electrophoresis (DGGE) consists of separating DNA fragments on an electrophoresis gel containing a denaturing agent (such as urea, formamide) according to their physical-chemical properties into a series of bands whose characteristics can be compared between communities (42). The DGGE method has been widely used for the study of bacterial genetic diversity (45). However, it is limited by the lack of taxonomic resolution. It makes it possible to compare different community structures but cannot identify the taxa accounting for that difference (42). The DGGE method has the advantage, at a lower cost, of rapidly developing an image of the diversity and structure of microbial communities from several environmental samples. It has been used in the analysis of complex communities, in monitoring population dynamics, in the detection of sequence heterogeneities, in the comparison of DNA extraction methods yields, in the detection of clone banks, and in the determination of PCR and cloning biases (46,47). DGGE makes it possible to cut, re-amplify and sequence the bands to obtain taxonomic information (42,48,49).

DGGE assays are limited by the heterogeneous effectiveness of DNA extraction procedures (50), PCR biases (see before) (51), and potential contamination during DNA and PCR extraction (45). It has been noted that only fragments below 500 bp can be separated by DGGE, thus limiting sequence information. Furthermore, interpretation can sometimes be difficult as bands at similar positions do not necessarily correspond to identical sequences but may be sequences which share the same melting behaviour (52).
3.4 Sequencing of 16S rRNA amplicons or 16S metabarcoding

The 16S rRNA metabarcoding method is the most widely used method to analyse the bacterial microbiome. It uses the 16S rRNA gene barcode for taxonomic classification, which contains highly conserved regions, present in the majority of bacterial genomes, and hypervariable regions that allow taxa to be discriminated (42). The sequencing of the 16S rRNA gene is simplified and provides a high depth of taxonomic resolution (53).

The Sanger sequencing method can perform reads with lengths of more than ~1000 bp and a raw accuracy per base of up to 99.99%. High throughput shotgun Sanger genomic sequencing is useful for small projects from kilobase to megabase and the technology is likely to be excellent within a short period of time (54). Second generation DNA sequencing, using alternative DNA sequencing strategies, has been categorised using micro electrophoretic methods, hybridisation sequencing, real-time observation of single molecules, and cyclic network sequencing (55–59). Below, we list some technologies commercialised in the cyclic network sequencing category (e.g. 454 (used in the 454 Genome Sequencer, Roche Applied Science; Basel), Solexa Technology (used in the Illumina Genome Analyser (San Diego)), SOLiD platform (Applied Biosystems; Foster City, CA, USA), Polonator (Dover/Harvard) and the HeliScope Single Technology Molecule Sequencer (Helicos; Cambridge, MA, USA) (54).

Historically, as the first-generation sequencing commercially available system, the 454 Roche pyrosequencer provided long read lengths to obtain a highly informative 16S RNA fraction (60). The second-generation using cyclic-array strategies, has many advantages over Sanger sequencing, and can be summarised as follows: 1) the generation of sequencing characteristics obtained following the construction of a sequencing library, followed by in vitro clonal amplification, allows several choke points to be overcome; 2) sequencing through cyclic-array strategies provides a higher degree of parallelism than conventional capillary-based sequencing; 3) the cost of DNA sequence production can be reduced by adjusting the volume of the reagent from microlitres to femtolitres when immobilising array elements on a planar surface that can be processed by a single volume. Second-generation sequencing has, however, some disadvantages, including the length of the reads and raw precision which is lower when compared to Sanger sequencing (54).

Recently, sequencing technology has evolved to bench-top sequencers within the reach of small laboratories, namely the 454 GS Junior, the Ion Torrent Personal Genome Machine (PGM) and Proton, and the Illumina MiSeq and NextSeq 500. These bench-top sequencers offer multiple
advantages over large-scale sequencers. They can provide fewer reads per run and fewer bases per dollar. They are more adaptable, faster, and their low acquisition and operating costs make them affordable. The benchtop next-generation sequencers are described as being better suited for environmental microbiology studies given the generation of large amounts of sequence data with maximum yields of ~35 Mbp (454 GS Junior), ~2 Gbp (PGM Ion Torrent), ~10-15 Gbp (Ion Torrent Proton), ~10 Gbp (Illumina MiSeq), and ~100 Gbp (Illumina Next Seq 500) (53).

3.5 Whole genome shotgun (WGS)

Significant advantages of the WGS method have been reported in bacterial microbiome analysis studies. The WGS method has been suggested as an alternative to the 16S RNA sequencing method, which is a method used to sequence random DNA strands. The main advantages of the WGS method are that taxa can be more precisely defined at the species level. Noted that 16S RNA sequencing and the WGS method use distinct databases for taxa classification (61–64). Sequencing the entire genome of the shotgun has multiple advantages over the 16S amplicon method, including a higher sensitivity in the detection of bacterial species, an increase in the detection of diversity, and an increase in the prediction of genes. In addition, the increase in nucleotide sequence length, due either to long reads or to the assembly of contigs, has considerably improved the accuracy of species detection. Nevertheless, WGS is more expensive than the 16S rRNA amplicon sequencing method and requires more in-depth data analysis (65). It may also be necessary to sequence a high-coverage genome in order to identify and understand the genes of a bacterial taxon.

3.6 Impact of eukaryotes on bacterial communities

After this brief introduction to the methods that were used to characterise the microorganism communities in the studies we analysed, we will further detail the i) in vitro, ii) experimental, and iii) clinical data that is available on the interaction between bacterial communities and 1) protozoa, 2) helminth, and 3) fungi.

3.6.1 Impact of protozoa on bacterial community diversity

In this section, we describe the influence of protozoa (Cryptosporidium parvum, Giardia sp., Blastocystis sp, Entamoeba spp., Plasmodium yoelii, Leishmania infantum, Toxoplasma gondii, Trichomonas vaginalis, Cystoisospora) on bacterial diversity in humans and animals.

The presence of Cryptosporidium parvum has been described as upsetting the native intestinal microbiota in mice, with a taxonomic analysis showing an increased abundance of the phylum
Bacteroidetes, Porphyromonadaceae and Prevotellaceae in the infected groups (66). The presence of Giardia sp. has been associated with various changes in microbiota diversity. Several studies relating to the faecal microbiota in animal models or human cohorts have reported an increased abundance of the phylum Firmicutes among infected subjects (67–69). A highly heterogeneous description of the diversity of gut microbiota during Blastocystis sp. infection has been reported in various studies, although they all seem to conclude in favour of a beneficial impact on the gut microbiota (70–72). Divergences have been observed regarding the relative abundance of some species (e.g. Faecalibacterium prausnitzii, Prevotella), however some associations such as the negative association between Blastocystis spp. and Bacteroides in stool samples have been consistently reported (29,70–72). Entamoeba spp. infection has been shown to disturb the bacterial microbiota by increasing its diversity (73). However, given the variability of the tools used to study the microbiota, there are discrepancies regarding the abundance of some bacteria (e.g. Prevotella copri during Entamoeba spp. infection) (33,73). Other protozoa play a role in modulating the microbiota of bacteria. Thus, a reduction in the diversity of the microbiota has been described during infection with Plasmodium yoelii (35) and Leishmania infantum (74). The abundance of some bacterial genus of medical interest, such as Lactobacillus, increases during Toxoplasma gondii infections (35,75) and decreases during Trichomonas vaginalis infections (76). Similarly, Bifidobacterium abundance increases during Cystoisospora infections in cats (65) and decreases during Toxoplasma gondii infections in mice (75). A study has shown that Lactobacillus and Bifidobacterium, when used as a probiotic in mice infected with Plasmodium yoelii, resulted in decreased Plasmodium load (78).

### 3.6.2 Impact of protozoa on bacterial community structure

In this section, we will analyse the interactions between protozoa and the bacterial communities, in vitro and in vivo, from experimental or clinical studies (Table 1). We describe the impact of Giardia spp., Cryptosporidium parvum, Toxoplasma gondii, Plasmodium spp., Leishmania infantum, Cystoisospora spp., Blastocystis spp., Entamoeba spp., Dientamoeba fragilis, and Trichomonas vaginalis on the gut microbial community in vitro, in animals and in humans.

An in vitro study concerning the interaction between Giardia intestinalis and different lactobacilli demonstrated that both the Lactobacillus acidophilus NCC 2628 strain isolated from dog faeces and the probiotic Lactobacillus johnsonii La1 significantly inhibited the proliferation of G. intestinalis trophozoites (79).
In experimental studies, Barash et al. used cultivation-independent methods to evaluate microbial diversity and the impact of *Giardia* infection on the gut microbiota by infecting mice with *Giardia lamblia*. In this study, infection with *Giardia lamblia* was associated with an increase in *Proteobacteria* diversity and a decrease in *Firmicutes* and *Melainabacteria* diversity in the foregut and hindgut (80). The authors showed that the microbial structure due to *Giardia* associated-dysbiosis differed depending on the region of the gut. Thus, during giardiasis, the relative abundance of *Rhodocyclaceae* increased in the proximal small intestine, while an enrichment of *Moraxellaceae*, *Flavobacteriales*, *Comamonadaceae*, and *Bacteroidales* was observed throughout the small intestine, and *Clostridiaceae* were depleted across the intestinal tract (80). In contrast, germ-free mice who received *Giardia*-infected microbiota showed an increase in *Firmicutes*, associated with a decrease in *Phascolarctobacterium* (69). V4 region 16S metabarcoding with the Ion Torrent PGM™ platform showed an increase in *Catenibacterium*, *Pseudomonas*, and *Howardella* and a decrease in *Bacteroides* and *Pseudobutyrivibrio* following *Giardia duodenalis* infection in the gut bacterial communities of healthy dogs. The study of the structure and composition of gut microbiomes from healthy dogs and cats with or without *Giardia* infection and coccidia demonstrated an increase in *Roseburia* and a decrease in the abundance of *Subdoligranulum* following *Giardia cati* infection in cats. An increase in *Bifidobacterium*, *Olsenella*, *Megamonas*, *Geobacillus*, *Meiothermus*, *Bacillus*, *Camonas*, *Schlegelella*, *Chelatococcus*, *Silanimonas* was also associated with the presence of *Cystoisospora* in cats (77). The study of the disturbance of the faecal bacterial microbiota of mice infected with *Cryptosporidium parvum* by metabarcoding analysis showed that *Bacteroidetes*, *Prevotellaceae* and *Porphyromonadaceae* unclassified OTUs were over-represented in *C. parvum* infected mice, whereas distinct *Porphyromonadaceae* and unclassified *Bacteroidetes* OTUs were over-represented in the non-infected mice (66). Another study showed that severe *Cryptosporidium parvum* infection in mice was associated with an increased abundance of *Proteobacteria* and decreased abundance of *Firmicutes* (81). Regarding changes to the intestinal microbiota during *Toxoplasma gondii* ileitis, both metagenomic and quantitative PCR analyses of the intestinal bacterial microbiota in NOD2<sup>−/−</sup> mice and C57BL/6 wild type mice showed an increase in *Enterobacteria*, *Enterococci* and *Bacteroidetes/Prevotella* species during *T. gondii* ileitis. In particular, the total eubacterial load increased only in NOD2<sup>−/−</sup> mice (75). Furthermore, *Toxoplasma gondii* infection in mice led to an overgrowth of *Clostridia* spp. within the gut microbiota during the chronic stage of the disease, unrelated to the symptomatology (82). Regarding *Plasmodium* infection, Villarino et al. (35) used metagenomic analysis to show that the abundance of *Clostridiaceae*,...
Erysipelotrichaceae, Lactobacillaceae, and Peptostreptococcaceae increased in resistant (Jax and Tac) mice to Plasmodium yoelii, whereas the abundance of Bacteroidaceae, Prevotellaceae and Sutterellaceae increased in susceptible (NCI and Har) mice. In addition, these authors showed that the abundance of Lactobacillus and Bifidobacterium increased in mice resistant to Plasmodium yoelii and their use as probiotics decreased parasitic load. The study of Plasmodium chabaudi infection in mice showed an enhanced intestinal bacterial translocation during Plasmodium infection, promoting non-typhoidal Salmonella bacterial dissemination from the intestinal tract (83). Regarding Leishmania infantum, the metabarcoding analysis of the bacterial community within the midgut of one of its vectors, the sand fly Lutzomyia longipalpis, showed a progressive decrease in bacterial richness and Pseudomonadaceae abundance, whereas the abundance of Acetobacteraceae progressively increased following infection. The results of microbial community Fisher's linear discriminant analysis (LDA) showed that members of the Actinobacteria phylum (e.g. Tsukamurella, Tsukamurellaceae, Coprococcus, Porphyromonadaceae, Kocuria, Pigmentiphaga) were predominant in sand flies infected by L. infantum (74). In humans with Leishmania donovani complex associated with visceral leishmaniasis, 16S metabarcoding showed that Ruminococcaceae UCG-014 and Gastranaerophilales_uncultured bacterium were less abundant than in controls, and 18S rRNA metabarcoding showed an increase in Pentatrichomonas sp. and a decrease in Entamoeba sp. compared to controls. In the same subjects, a higher Blastocystis abundance was associated with a high bacterial diversity and a relatively low Escherichia-Shigella abundance. In addition, high Blastocystis abundance was associated with a relatively low Bacteroidaceae and high Clostridiales vadin BB60 abundance (84).

In one clinical study of Blastocystis spp. and intestinal bacterial microbiota interactions in cirrhotic patients with or without hepatic encephalopathy, 16S metabarcoding found a relatively high abundance of Alkaliphilus and Flavobacterium populations and a relatively low abundance of Veillonella and Streptococcus populations in Blastocystis-positive patients without hepatic encephalopathy (70). Another 16S metabarcoding study on the impact of Blastocystis colonisation on the diversity of human gut bacterial microbiota found an increase in the relative abundance of the genera Acetanaerobacterium, Acetivibrio, Coprococcus, Hespellia, Oscillibacter, Papillibacter, Sporobacter and Ruminococcus in patients colonised by Blastocystis spp. than in Blastocystis-free patients. At the class level, this study reported that Clostridia abundance increased whereas Enterobacteriaceae decreased in patients with Blastocystis spp. (71). A study carried out in Malian children colonised by Blastocystis has
shown similar results with higher microbiota diversity and more abundant beneficial bacteria. The phyla Firmicutes, Elusimicrobia, Lentisphaerae, Euryarchaeota and the species of Faecalibacterium prausnitzii (family Ruminococcaceae) and Roseburia sp. (family Lachnospiraceae) were associated with Blastocystis colonisation (85). In terms of Entamoeba spp., a prospective cohort study of clinical enteric infections, used qPCR detection to reveal a significantly higher level of Prevotella. copri in infants with diarrhoea due to Entamoeba histolytica, whereas the level of Bacteroides thetaiotaomicron was standard (33). The presence of Entamoeba dispar and/or E. histolytica was associated with a decrease in the relative abundance of Prevotella copri, an increase in Clostridiales Christensenellaceae, Elusimicrobiales Elusimicrobiaceae, and Spirochaetaceae Treponema, by 16S metabarcoding of the digestive microbiota in Pygmy hunter-gatherers and in the Bantu in Cameroon. Clostridiales and Ruminococcaceae displayed a significantly greater abundance in individuals with Entamoeba spp. (86). Some studies analysed the interaction between the simultaneous presence of multiple protozoa and the bacterial microbiota. One study aiming to assess the association between Blastocystis spp., Dientamoeba fragilis and intestinal bacteria, used qPCR and found a relative abundance of Bacteroides which was significantly higher in Blastocystis spp. and Dientamoeba fragilis negative groups compared to groups with a least one of these protozoa positive groups. The relative abundance of Clostridial cluster IV was significantly lower in the Blastocystis-positive/Dientamoeba-negative group compared with the Blastocystis-negative/Dientamoeba-positive group and the relative abundance of Clostridial cluster XIVa was higher in the Blastocystis-negative/Dientamoeba-negative group compared with the Blastocystis-positive/Dientamoeba-negative group (29). By studying the impact of Giardia duodenalis, Entamoeba spp. and Blastocystis hominis infections on the human gut microbiota using qPCR analysis, Lebba et al. found that Giardia spp. infection was associated with a dysbiotic condition explained by a slightly increase in Escherichia coli levels and increase in Bifidobacterium. Furthermore, Entamoeba spp/Blastocystis hominis were associated with a eubiotic condition described as a significantly higher Faecalibacterium prausnitzii-Escherichia coli ratio in the faecal bacterial community in people from Côte d’Ivoire (72).

The impact of protozoa on the composition and structure of the vaginal microbiota has also been studied using a similar approach. The relationship between vaginal bacterial community and Trichomonas vaginalis infection showed a decreased abundance in Lactobacilli and an increased abundance of Mycoplasma, Parvimonas, and Sneathia (76).
3.6.3 Influence of helminths on bacterial community diversity

In this section, we will summarise available data regarding the interactions between helminths and bacterial communities, in experimental or clinical studies.

According to experimental studies, *Trichiuris* spp. mono-infection has no impact on the diversity of the gut microbiota in the porcine colon (87,88), but when it comes to mixed infections, the data diverge: one study reported reduced bacterial diversity in children with a mixed infection involving *T. trichiura* and *Ascaris lumbricoides* (89), whereas others showed an increase in bacterial diversity among helminth-infected adults and children with *Trichuris*, hookworms and/or *Ascaris* (90,91). *Trichiuris* spp. infection has been associated in humans with an increased abundance of the *Prevotella* genus (89,90) but a significant reduction in their proportions of the microbiota in mice infected with *T. muris* (92). Likewise, clinical studies concerning the bacterial diversity of the gut microbiota report an enrichment of bacterial taxa among *Ascaris*-infected patients for some (91) and a reduced overall diversity during *Ascaris* spp. infection for others (89); however an experimental study on the analysis of the gut microbiota composition in pigs infected with *A. suum* showed a trend for increased microbial diversity (93). A higher abundance of *Prevotella* has also been observed with the presence of *Ascaris* spp alone or in combination with other helminths (93,94). Also, *Necator americanus* infection has been associated with an increased in the species richness but not in the bacterial diversity in patients with celiac disease (95). An increase in bacterial community diversity has also been found in mixed infections with *Leidynema appendiculatum*, *Hammerschmidtiiella diesingi*, *Thelastoma bulhoesi* in both *Periplaneta fuliginosa* and *Periplaneta americana* cockroach species (96). Similarly, bacterial community diversity was also higher in *Ovis aries* sheep infected by larval-stage *Haemonchus contortus* (97); after *Enterobius vermicularis* infection (36), and *Schistosoma mansoni* and *Schistosoma haematobium* infections (98) in children. The high abundance of *Proteobacteria* and lower abundance of *Firmicutes* has been observed in mixed *Leidynema appendiculatum*, *Hammerschmidtiiella diesingi* and *Thelastoma bulhoesi* infections in cockroaches (96). *Schistosoma mansoni* and *Schistosoma haematobium* infections in children showed a high abundance of *Firmicutes* and *Proteobacteria* (98). In addition, *Enterobius vermicularis* infection in children was associated with an increased abundance in *Bifidobacterium longum* and *Faecalibacterium prausnitzii* species, and was associated with greater bacterial community diversity (99).
3.6.4 Impact of helminths on bacterial community structure

The influence of Heligmosomoides polygyrus bakeri, Trichuris spp., Hymenolepis diminuta, Trichostrongylus retortaeformis, Toxocara cati, Leidynema appendiculatum; Hammerschmidtella diesingi; Thelastoma bulhoesi, Enterobius vermicularis, Ascaris lumbricoides, Necator americanus, Schistosoma haematobium on the microbiota of bacteria in the host (human or animal) has been described (Table 2). We found no in vitro studies aiming at dissecting the interaction between helminths and bacterial communities.

In experimental studies, Heligmosomoides polygyrus bakeri infection was associated with a significant increase in Lactobacillaceae abundance, using 16S rRNA Sanger sequencing and qPCR, in the ileum and with improved disease in an inflammatory bowel disease (IBD) mouse model (100). In Apodemus flavicollis, 454-pyrosequencing 16S V1V3 metabarcoding showed that Lachnospiraceae abundance increased in H. polygyrus infected mice and decreased in Syphacia spp. infected mice. In addition, Syphacia infection was associated with a decrease in of Firmicutes (Lactobacillus) OTUs, as opposed to H. polygyrus. An increase in the unidentified bacteria belonging to the phylum of Bacteroides (S24–7 OTUs) was observed in mice infected by Hymenolepis spp (101). Also, γ-Proteobacterial/Enterobacteriaceae and abundance of the bacteria of the Bacteroides/Prevotella group in the caecum, assessed via qPCR, was increased 14 days after Heligmosomoides polygyrus bakeri infection in mice (102). In an obese mouse model, Heligmosomoides polygyrus infection suppressed weight gain and increased the abundance of Firmicutes and Proteobacteria phyla, as was the case for Bacillus and Escherichia genera, in the gut bacterial community (103). In Schistosoma mansoni infected mice, gut bacterial diversity decreased, and Akkermansia muciniphila (phylum Verrucomicrobia) and Lactobacillales abundance increased compared to controls (104). Trichuris muris infection in mice decreased the bacterial diversity of the large intestine and an increase the relative abundance of Lactobacillaceae was observed. This alteration in the bacterial community structure resulted in greater abundance of Alistipes, Odoribacter, and Parasutterella, and a decrease in Allobaculum and Barnesiella (37). A further study using 454 pyrosequencing showed that Trichuris muris infection resulted in a decrease in the diversity and abundance of Bacteroidetes, namely Prevotella and Parabacteroides genera in the faecal bacterial communities in mice (105). Infection with the trematode Hymenolepis diminuta has been associated with a decrease in Actinobacteria and Tenericutes and an increase in Bacteroidetes (106). In another study, Hymenolepis diminuta infection produced a significant change in 48 OTUs, assessed via V4 region 16S metabarcoding, of the gastrointestinal bacterial
community of rats (107). The treatment of *H. diminuta* infection triggered an increase in the abundance of uncultured Bacteroidales family S24-7 and Ruminococcaceae and Mollicutes RF39 order. Also, the genera *Turibacter* and *Sutterella*, and Erysipelotrichaceae were significantly more abundant in non-infected rats (107). Illumina MiSeq V4 16S metabarcoding in rats showed that *H. diminuta* infection altered the *Firmicutes* species structure with an increase in *Clostridia* and a decrease in *Bacilli* (108).

Analysis of the duodenal microbiota of rabbits (*Oryctolagus cuniculus*) experimentally infected with *Trichostrongylus retortaeformis* by 454 pyrosequencing V3-V5 16S metabarcoding found an increase in *Leptospiraceae* and *Desulfobacteraceae*, and *Leptomena* and *Desulfocella*, whereas the abundance of *Porphyromonadaceae* and *Bacteroidaceae* was higher in controls (109).

Analysis of the intestinal microbiota in cats experimentally infected with *Toxocara cati* by Illumina MiSeq V3–V4 16S metabarcoding showed that i) *Firmicutes*, *Proteobacteria*, *Actinobacteria* and *Bacteroidetes* were abundant in all samples; ii) *Gammaproteo-Bacteria*, *Jeotgalicoccus*, and *Jeotgalicoccus psychrophilus* were less abundant in infected cats; whereas iii) there was a decrease in *Collinsella stercoris*, *Enterococcus cecorum*, *Ruminococcus gnavus*, *Dorea*, and *Lactobacillales* in non-infected cats (110).

In addition, 16S rRNA metabarcoding showed that *Ascaris suum* infection affects the microbial communities in the faecal and proximal colon of pigs. Significant changes in the abundance of *Prevotella* and *Faecalibacterium* and metabolic pathways have been observed following infection with *Ascaris suum*. A significant positive correlation was found between node connectivity of the operational taxonomic units assigned to *Proteobacteria* (especially the family *Alcaligenaceae*) and faecal acetate and propionate levels. However, the family *Porphyromonadaceae* was positively correlated with faecal egg counts (111). *Trichuris suis* experimental infection in pigs induced a decreased abundance of *Fibrobacter* and *Ruminococcus* and an increased abundance of *Campylobacter* in the colon microbiota, assessed using Illumina HiSeq 2000 16S metabarcoding (87). Another study on alterations in the porcine colon microbiota when experimentally infected with *Trichuris suis* showed a decreased abundance of *Ruminococcus*, *Oscillibacter* and *Succinivibrio* and an increased abundance of *Mucispirillum* and *Paraprevotella* using 16S metabarcoding and whole-genome shotgun (WGS) sequencing (88). The study of the gut bacterial community after therapeutic *Trichuris trichiura* infection of macaques with chronic idiopathic diarrhoea showed an increase the genus...
Streptophyta of the phylum Cyanobacteria using Illumina MiSeq V4 16S metabarcoding (112).

The Illumina MiSeq V3V4, V5V7 16S rRNA metabarcoding of the ovine gut bacterial community at different stages of Haemonchus contortus infection showed a relatively increased abundance of *Pseudomonas, Ochrobactrum, Escherichia/Shigella* and *Azotobacter* genera, at the egg stage; followed by *Achromobacter, Lentibacillus, Pseudomonas, Ochrobactrum, Kroppenstedtia, Dokdonella, Bacillus, Delftia, Oceanobacillus, Azotobacter, Pseudaminobacter* and *Candidatus Accumulibacter*, at the larval stage; and *Escherichia-Shigella, Pseudomonas; and Ochrobactrum* genera, at the adult stage (97). V3-V4 16S metabarcoding characterisation of the equine gut commensal flora when infected with low and high numbers of cyathostomin eggs, showed that the Methanomicrobia (class) and *Dehalobacterium* (genus) were more abundant in equines experimentally infected with lower egg counts compared to those infected with higher egg counts (113).

Regarding clinical studies, Illumina MiSeq V4-16S metabarcoding of the gut bacterial community of primary school children from Taiwan showed that *Enterobius vermicularis* infection was associated with increased gut bacterial diversity and mebendazole treatment was associated with a further increased gut bacterial diversity. Enterobiasis and mebendazole deworming were both associated with a relatively high abundance of *Bifidobacterium longum, Oscillospira sp., Faecalibacterium prausnitzii, Alistipes*. Mebendazole treatment induced a relative decrease in *Acidaminococcus intestini, Megasphaera elsdenii, Veillonella dispar, Fusobacterium varium; and a relative increase in Collinsella aerofaciens, and Streptococcus thermophilus* (36). 454 pyrosequencing V3V5 16S metabarcoding of the gut bacterial community in school children in Ecuador found no evidence for changes associated with *Trichuris trichiura* infection, but mixed *T. trichiura* and *Ascaris lumbricoides* infection was associated with a reduced bacterial diversity and a decreased proportional abundance of a few genera in the *Clostridia* class of *Firmicutes* (114). Another Illumina MiSeq V4 16S metabarcoding study found higher species richness and abundance of *Paraprevotellaceae, Mollicutes, Bacteroidales, and Alphaproteobacteria* in the gut bacterial community of Malaysian villagers infected with the soil-transmitted helminths, *Trichuris* spp., *Ascaris* spp., and hookworm (115). In patients with coeliac disease on a gluten free diet, 454 pyrosequencing V1V3-V3V5 16S metabarcoding of the intestinal microbiota showed that experimental *Necator americanus* infection was associated with significant increases in microbial species richness despite maintaining the bacterial composition of the intestinal flora (95). It has been reported by sequencing of the V3V4 region of the bacterial 16S rRNA with the Illumina MiSeq system that
the bacteria of *Verrucomicrobiae, Verrucomicrobiales, Verrucomicrobiaceae* and *Enterobacteriaceae, Lactococcus, Akkermansia* and a genus belonging to the *Enterobacteriaceae* and *Akkermansia muciniphila* had increased abundance in patients from Sri Lanka with intestinal helminths (*Ascaris, Trichuris, Hookworm*). However, *Leuconostocaceae* and *Bacteroidaceae* and *Bacteroides* were less common in patients infected with worms compared to those who were either not infected or under anti-helminthic prophylaxis (38). A study in Liberia and Indonesia, using Illumina MiSeq and 454 pyrosequencing V1 V3 16S of the gut microbiota metabarcoding showed that *Lachnospiraceae* were associated with the absence of soil-transmitted helminth (*Ascaris lumbricoides, Trichuris trichiura, Necator americanus*) infection, whereas 12 bacterial taxa were significantly associated with helminth infections, including *Olsenella*, the abundance of which significantly decreased after anthelmintic treatment. Successful anthelmintic treatment was associated with the presence of *Clostridium_IV, Turicibacter*, and *Collinsella*. *Akkermansia* and *Ruminococcus* were significantly associated with both infection at baseline and the prevention of parasite clearance (116). Illumina MiSeq V3V4 16S metabarcoding of the bacterial community in children’s guts showed that *Schistosoma haematobium* infection was associated with decreased abundance of *Firmicutes* and an increased abundance of *Proteobacteria*. In particular, the genus *Prevotella* was significantly more abundant in children infected with schistosomiasis (98). Another study on children from Côte d’Ivoire who were exposed to *Schistosoma mansoni* used 16S metabarcoding of the bacterial community and revealed that *Schistosoma mansoni* infection in children in Côte d’Ivoire was not associated with gut dysbiosis but *Fusobacterium* spp. abundance was positively correlated with the clinical efficacy of praziquantel treatment (117).

### 3.6.5 Impact of fungi on the diversity of bacterial communities

Like protozoa and helminths, fungi, also in the minority, play a crucial role in the interaction between prokaryotes and eukaryotes in the host.

The presence of the baker’s yeast *Saccharomyces* has been associated with an increase in the diversity of gut bacterial communities in human and animal models (118–121). Furthermore, a decrease in *Saccharomyces* spp. abundance has also been correlated with a decrease in bacterial diversity (122–124). Similarly, the ingestion of *Ganoderma lucidum* mycelium in mice with a high-fat diet displayed an anti-obesity effect that was associated with increased bacterial diversity (125). A non-statistically significant trend towards greater bacterial diversity and a
reduction in the richness of fungi has been observed between normal weight and obese children (120). In patients with chronic diseases, it has been observed that the increase in fungal microbiota diversity has very often resulted in a decrease in bacterial diversity, manifested by a decrease in the abundance of Bacteroidetes or Firmicutes (40,122,123,126–128). Infection with the microsporidia Paranoosema locustae was associated with a decrease in bacterial diversity in migratory locusts (129). Furthermore, Clostridium difficile colitis has been associated with a decrease in the diversity of fungal alpha (124). It was also noted in a study on the characterisation of fungi and bacterial microbiota in Rett Syndrome patients that a high abundance of Candida spp. was associated with an increased abundance of the Clostridia genus among the bacterial community, when using high-throughput sequencing of 16S rRNA (128). Furthermore, the existence of great fungal diversity in the Libellulidae Pantala flavescens, new symbiotic bacteria Leclercia sp., Oceanobacillus oncorhynchi, Methylobacterium extorquens has been described. The existence of an antibacterial activity of symbiotic fungi in the Pantala flavescens larvae has also been demonstrated (130). It is notable that a decrease in Malassezia abundance and a decrease in bacterial diversity have been seen in children with Hirschsprung disease and in Rett Syndrome patients (123,128). However, an increased abundance of Malassezia sympodialis associated with a decrease in bacterial diversity has been observed in children with inflammatory bowel disease (122). In the current literature, fungi are reported to influence the bacterial communities and tend towards a relatively healthy state. For instance, Saccharomyces spp. improves gastrointestinal discomfort and constipation, Ganoderma lucidum mycelium displays anti-obesity properties, and symbiotic fungi have antibacterial activity. All these fungal properties have been associated with the modulation of the diversity and structure of the host bacterial community (118,120,125,130,131).

3.6.6 Interactions between fungal and bacterial communities

Fungi are relatively numerous and ubiquitously colonize the living environment where they modulate the bacterial microbiota (Table 3). Hence, a growing body of evidence indicates that fungi may modulate the microbiota and play important roles in the physiology and immunity of the host (122). In the literature, studies of the interaction between fungus and bacteria mainly concern yeasts, including Candida albicans and the probiotics S. cerevisiae RC016 and Saccharomyces boulardii, filamentous fungi including Mucor circinelloides, macroscopic fungi, such as Ganoderma lucidum, and microsporidian enteropathogens.
The in vitro study of *Candida albicans* and *Clostridium difficile* interactions showed that the strictly anaerobic Gram-positive bacterium *C. difficile* can grow under aerobic conditions in the presence of *C. albicans*. In contrast *C. albicans* hyphal formation is inhibited by the presence of *C. difficile*, most probably due to p-cresol excretion (131). Another study on anaerobic bacterial/yeast interactions highlighted that the growth of *Bacteroides* was significantly enhanced in co-culture with *C. albicans* whereas the growth of *C. albicans* was affected neither by *B. fragilis* nor *B. vulgatus* co-culture, suggesting that *C. albicans* cells can serve as an additional nutrient source for the culture of bacteria in the anaerobic atmosphere of the gut (132).

An in vivo study, using a mouse model of obesity, showed through V3-V5 16S rRNA metabarcoding, that 4% to 8% water extract of the basidiomycete *Ganoderma lucidum* (WEGL) mycelium reduces the *Firmicutes*-*Bacteroidetes* and *Proteobacteria* ratio in high-fat diet mice. Treatment of high-fat diet-fed mice with 8% WEGL increased the abundance of the species *Parabacteroides goldsteinii*, *Bacteroides* spp., *Anaerotruncus colihominis*, *Roseburia hominis*, *Clostridium* spp., *Methylobacterium (Clostridium IV)*, *Clostridium* XIVa and XVIII, and *Eubacterium coprostanoligenes*, which were negatively correlated to obesity. Also, 8% WEGL increased the abundance of the species *E. coprostanoligenes*, *C. methylpentosum*, *P. goldsteinii*, *Bacteroides* spp., *A. colihominis*, *R. hominis* and *Clostridium* XIVa and XVIII in Chow diet mice (125). Other in vivo studies using mouse models have analysed the interaction between yeasts and the gut microbiota. Feeding with the probiotic *S. cerevisiae* RC016 was associated with a decrease of one logarithmic unit of *Enterobacteriaceae* in healthy mice compared with control mice using conventional culture methods (133). Moreover, some studies have revealed cooperation between the *Enterobacteriaceae* family and both *C. albicans* and *S. boulardii*, encouraging their gut colonisation and their effect on intestinal inflammation. The colistin-resistant *Escherichia coli* effect revealed the beneficial impact of *S. boulardii* and pathogenic effects of *C. albicans* on colitis severity in mice (134). Faecal microbiota transplantation can prevent fungal colonization of the gastrointestinal tract. In fact, experimental wild-type mice model is resistant to gut colonization by *Candida albicans*. Mice treated with β-lactam antibiotics (e.g. Ampicillin) experienced a dysbiosis in the gut microbiota which was beneficial to *Candida albicans* by colonising the digestive tract. Faecal microbiota transplantation effectively and immediately reduces *C. albicans* loads and prevents it from colonising the gastrointestinal tract of mice (135). Specific probiotics such as *Bifidobacterium* may also be of therapeutic interest by reducing the fungal load in *Candida albicans/Clostridium difficile*
infection models. In fact, the administration of _Candida albicans_ aggravates the severity of _Clostridium difficile_ infection by increasing gut inflammation. Unfortunately, the probiotic has no effect on the clostridium toxin in the faeces (136). Colonization by _C. albicans_ does not always have a deleterious effect, showing protective effects against lethal _C. difficile_ infections in mice models by acting on the cytokine IL-17A. The abundance of the beneficial bacteria _Bifidobacterium_ and _Akkermansia_ was significantly increased in mice colonised with _C. albicans_ (137). Another pathogenic opportunistic yeast, _Candida glabrata_, in an experiment using a colitis mouse model showed that the persistence of _C. glabrata_ in the gut is subject to remodelling its cell wall leading to an increase in chitin. Oral administration of chitin restored anaerobic bacteria including _Lactobacillus reuteri, Lactobacillus johnsonii, Bifidobacterium_ and _Bacteroides_ spp. and reduced aerobic bacteria such as _Escherichia coli, Enterococcus faecalis_, counters the effect of intestinal inflammation caused by colitis (138). The treatment of rats with _Saccharomyces cerevisiae_ fermentation prebiotic before stress leads to beneficial changes in the gut microbiota. Treating rats with yeast fermentate before exposure to heat stress resulted in changes in the relative abundance of _Bifidobacterium_ and _Allobaculum_, while _Acetanaerobacterium, Bacteroides, Eubacterium, Johnsonella, Lactococcus, Oscillospira, Roseburia_ and _Vallitalea_, substantially increased. (139). The usefulness of _Saccharomyces boulardii_ CNCM I-745 probiotics has been studied in other pathologies, through a controlled study of the lipid profile and the intestinal microbiota in a hypercholesterolemic hamster model. The abundance of the genus _Allobaculum_ increased and an unclassified genus in the family _Lachnospiraceae_, unclassified genus of _Desulfovibronaceaе, Oxalobacter_ and an unclassified genus in family F16 with the treatment of _Saccharomyces boulardii_ CNCM I-745 decreased with treatment of _Saccharomyces boulardii_ CNCM I-745. These genera g_CF231, _Allobaculum_, an unclassified _Lachnospiraceae_ and _Oxalobacter_ have been correlated with total plasma cholesterol (140). Elsewhere, a study investigated the effect of (3R, 30R)-astaxanthin on lipid metabolism and the gut microbiota in mice fed on a high-fat diet. Astaxanthin is produced from _Xanthophyllomyces dendrorhous_, a basidiomycete fungus. Supplementation with (3R, 3'R) -astaxanthin/X. dendrorhous on a high-fat diet prevented weight gain and decreased total cholesterol in the plasma and liver. Furthermore it regulated its intestinal microbiota optimising the _Bacteroidetes/Firmicutes_ ratio and increasing the abundance in _Verrucomicrobia_, particularly _Akkermansia_ (141). It has also been shown in a mouse model treated with the pathogenic fungus _Mucor circinelloides_ that the abundance of the bacterial genus _Bacteroides_ increases and the abundance of the bacteria _Akkermansia muciniphila_ decreases in these gastrointestinal tracts (142). The administration of mushrooms (Agaricus
*Bispora*) to pigs significantly reduced the *Salmonella typhymurium*-Lipopolysaccharide-induced inflammatory response at the alveolar macrophage level and positively modulated the metabolism of the pig microbiota by increasing the abundance of *Clostridial* taxa which are associated with improved intestinal health (143).

*In vivo* studies have also been carried out using insect models. The microbiota of healthy dragonfly (*Pantala flavescens*) larvae was analysed using culture-dependent methods and ITS barcoding for the fungi, and 16S barcoding for the bacterial symbionts; forty-eight fungal isolates were obtained, grouped in five classes (Leotiomycetes, Dothideomycetes, Eurotiomycetes, Sordariomycetes, Zygomycetes), were associated with a variety of symbiont bacteria, including *Sphingomonas*, *Methyllobacterium*, *Burkholderia*, *Pantoea*, *Enterobacter*, *Leclercia*, and *Serratia*, *Oceanobacillus* which were included in the *Proteobacteria* and *Firmicutes*. *Enterobacter* was the most abundant bacterial genus associated with these fungi (130). In honey bees (*Apis mellifera*), *Nosema ceranae* microsporidium infection was associated with a decreased abundance of *Alphaproteobacteria*, *Bifidobacterium* spp. and *Lactobacillus* spp., an increased abundance of *Gilliamella apicola*, and *Snodgrassella alvi* increased significantly in honeybees infected during the winter assessed using quantitative real-time PCR (qPCR) (144). *In vivo* insect models have also been used to study the impact of microsporidian parasites on the gut microbiota. Thus, in locusts (*Locusta migratoria*), infection with the microsporidian parasites *Paranosema locustae* alters the structure of the gut bacterial community, as assessed using 16S rRNA V4-V5 region pyrosequencing, by increasing the abundance of the genera *Citrobacter* (36%), *Lactococcus* (13.28%), and *Raoultella* (43%) (129).

In *Serinus canaria* birds, colonisation of the gastric mucosa by the opportunistic yeast *Macrorhabdus ornithogaster* was associated with the presence of *Lactobacillus* and *Candidatus Arthromitus*, assessed via 16S metabarcoding, whereas *Lactococcus*, *Pseudomonas*, *Acinetobacter*, *Lachnospiraceae*, *Propionibacterium* and *Weissella* were associated with uninfected birds (145).

The data on interactions between fungal and bacterial communities in humans remain scarce. Analysis of the diversity of bacterial and fungal communities in normal-weight and obese school-aged children showed the presence of *Eubacterium rectale*, *Saccharomyces cerevisiae*, *Candida albicans*, and *C. glabrata* in all subjects, whereas there was a significantly lower abundance of *Akkermansia muciniphila*, *Faecalibacterium prausnitzii*, *Bacteroides/Prevotella* Group, *Candida* spp., and *Saccharomyces* spp. in obese children, and *Debaryomyces hansenii* was found in two obese children (120). Another study using both 16S and ITS rRNA...
metabarcoding, analysed the impact of the antibiotic treatment of *Clostridium difficile* infection (CDI) on bacterial and fungal communities. It showed a relatively increased abundance of the *Pichiaceae* family (order of Saccharomycetales) in non-CDI patients and, in contrast, a relatively increased abundance of the *Ascomycota* phylum, the *Pleosporales* order, and the *Dothideomycetes* class in the patients with CDI. A relatively increased abundance of *Ascomycota* phylum and *Saccharomycetes* was observed in patients with CDI. The genera *Cadophora, Bandoniozyma,* and *Clitocybe* were more abundant in the non-CDI than in CDI patients (146). Another study looked at the effect of oral administration of *Saccharomyces boulardii* and its mode of administration on the intestinal microbial community in premature infants by 16S metabarcoding. The results showed that *Firmicutes* and *Proteobacteria* remained stable during the observation period. The oral administration of *Saccharomyces boulardii* had no significant influence on the bacterial community but the mode by which children were delivered changed the microbiota. *Bacteroides* and *Parabacteroides* were more abundant in children delivered vaginally compared to children born by Caesarean delivery on day 0. After two weeks of administration, the abundance of *Bacteroides* and *Parabacteroides* were higher in children delivered vaginally compared to children born by Caesarean section (121). In women treated for bacterial vaginosis, the effect of the antibiotic treatment was reduced by *Saccharomyces boulardii* prophylaxis, thus improving the colonic microbiota (147). Elsewhere, in patients with inflammatory bowel disease, a positive correlation was observed between the abundance of *Saccharomyces* and that of *Bifidobacterium, Blautia, Roseburia* and *Ruminococcus* using both ITS2 and 16S rRNA metabarcoding (122). Some studies have focussed on bacterial and fungal microbiota in patients with chronic inflammatory bowel disease. Patients with primary sclerosing cholangitis suffer from fungal microbiota dysbiosis, an alteration in composition and high biodiversity. An increased proportion of *Exophiala* and a decreased proportion of *Saccharomyces cerevisiae* has been observed among these patients. The signature of fungi dysbiosis is different when compared with patients with Irritable Bowel Disease. The bacteria-fungi correlation network highly affects the intestinal microbiota of patients with primary sclerosing cholangitis when compared to patients with Irritable Bowel Disease status. Gut fungi could therefore contribute to the pathogenesis of primary sclerosing cholangitis and could be considered as a new therapeutic target (148). Some species such as *Candida tropicalis, Serratia marcescens* and *Escherichia coli* have found to be associated with Crohn’s disease dysbiosis (127). Meanwhile, another study found that the genera *Candida, Debaryomyces, Saccharomyces, Malassezia, Sporobolomyces, Trichosporon, Wallemia,* unidentified *Filobasidiaceae,* and unidentified *Xylariale* as well as the genus *Enterococcus,*
Alicyclobacillus, and Lactobacillus was over-represented in patients with Crohn’s disease using 16S rRNA (MiSeq) and ITS2 (pyrosequencing) (40). The relative abundance of Bifidobacterium and several Clostridia including Anaerostipes, Clostridium XIVa, and Clostridium XIVb, as well as Erysipelotrichaceae Clostridium XVIII and Erysipelotrichaceae incertae sedis), Actinomyces, Eggerthella, Enterococcus, Escherichial/Shigella and Lactobacillus were higher in the Rett Syndrome patients compared with healthy controls when using high-throughput sequencing the V3-V5 regions of the 16S rDNA gene. The gut fungal community, analysed by sequencing the ITS1 region of the rRNA, revealed the most abundant genera in Rett Syndrome patients were Candida, Aspergillus and Trichosporon, whereas in healthy controls Penicillium, Malassezia, Debaryomyces, Mucor, Eremothecium, Pichia, and Cyberlindnera were the most abundant. The genus Candida was significantly more abundant in Rett Syndrome patients than in healthy controls (149). It has been reported, using MiSeq Illumina ITS-1 sequencing, that Candida species in the Hirschsprung disease group were composed of C. albicans, C. tropicalis, C. parapsilosis, and C. utilis while the Hirschsprung-associated enterocolitis group had a majority of C. albicans and low C. tropicalis. Ion Torrent 16S rRNA sequencing revealed a low proportion of Firmicutes and Verrucomicrobia and a higher proportion of Bacteroidetes and Proteobacteria in the Hirschsprung-associated enterocolitis group, when compared to the Hirschsprung disease group (123).

Food consumption has been associated with fungal abundance in the gut. An inverse association between Candida (fungus) and Bacteroides (bacteria) has been found. A higher abundance of Bacteroides has been observed in individuals whose diet is very high in protein, while Candida is more highly abundance in individuals who have recently consumed carbohydrates. Authors have also reported a positive correlation between Fusarium (fungus), Bryantella (bacteria) and Anaerostipes (bacteria), and Pichia (fungus) and Syntrophococcus (bacteria) (150,151).

4. Conclusions and perspectives

While the “One Health” concept acknowledges that human health is linked to animal health and to the environment (152,153), microbial community structures are dependent on interactions between each of their components. Studies addressing only one component, for instance the bacterial community, are limited by only providing a partial view of both the structure of micro-organism communities and the inter-kingdom interactions between communities of sympatric viruses, prokaryotes, and eukaryotes. The human and animal microbiota biotope includes the bacterial, viral, eukaryotic (protozoa and helminths) and fungal communities. These
communities of micro-organisms coevolve and maintain balanced relationships in the host. The relationship between prokaryotic and eukaryotic communities and their environment contributes to homeostasis and host health. This relationship is altered by the qualitative and quantitative modification of microbiota that are, among other factors, influenced by anti-infective treatments, genetic predisposition, and digestive and chronic diseases. Studies analysing the interaction between communities of prokaryotes and eukaryotes are scarce. However, large-scale controlled studies are needed to elucidate the mechanisms that explain variations in the diversity and abundance of the prokaryotic microbiota resulting from the presence of eukaryotes.

This review highlights that some bacteria, especially Lactobacillus sp., have been associated with the inhibition of infection by the protozoa Giardia duodenalis in vitro and Plasmodium falciparum in vivo. Infection of the intestinal protozoa has a qualitative and quantitative impact on the intestinal microbiota. Free-living amoebae maintain symbiotic relationships with most microorganisms such as virus, bacteria, fungi, and parasites. Several worms have been involved in alterations in bacterial communities. Infecting wild-type C57BL/6 mice with Heligmosomoides polygyrus bakeri significantly increased the abundance of the Lactobacillaceae family, but the clinical consequences of these changes in the intestinal flora have yet to be studied. Fungi can be used as a probiotic (EpiCor fermentate) to modulate the microbiota especially the bacterial community by improving gastrointestinal discomfort and constipation. Some studies have demonstrated that fungi are associated with modulation of the microbiota in chronic diseases as well as in cases of HIV and CDI infections.

The impact on host immunity and the metabolic potential of changes to the microbiota has not been addressed in this review.

The interaction between eukaryotes and prokaryotes resulted in modulation of the microbiota which led to the characterisation of the complexity of the microbiome. This interaction could play a significant role in the pathophysiology of various multifactorial chronic diseases. It is thus important to further study the structure and function of both prokaryotic and eukaryotic communities to better understand their interactions. The microbiota community structure has been characterised by the development of metagenomics/genomic and related culture methods. However, further research is warranted to bridge the knowledge gap on interactions between eukaryotes and prokaryotes.
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References

1. Virgin HW. The virome in mammalian physiology and disease. Cell. 2014 Mar 27;157(1):142–50.

2. Boyer M, Madoui M-A, Gimenez G, Scola BL, Raoult D. Phylogenetic and Phyletic Studies of Informational Genes in Genomes Highlight Existence of a 4th Domain of Life Including Giant Viruses. PLOS ONE. 2010 Dec 2;5(12):e15530.

3. Raoult D. TRUC or the Need for a New Microbial Classification. Intervirology. 2013;56(6):349–53.

4. Yatsunenko T, Rey FE, Manary MJ, Trehan I, Dominguez-Bello MG, Contreras M, et al. Human gut microbiome viewed across age and geography. Nature [Internet]. 2012 May 9 [cited 2018 May 4]; Available from: http://www.nature.com/doifinder/10.1038/nature11053

5. Lynch SV, Pedersen O. The Human Intestinal Microbiome in Health and Disease. Phimister EG, editor. N Engl J Med [Internet]. 2016 Dec 15 [cited 2018 May 4];375(24):2369–79. Available from: http://www.nejm.org/doi/10.1056/NEJMra1600266

6. Wu GD, Chen J, Hoffmann C, Bittinger K, Chen Y-Y, Keilbaugh SA, et al. Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes. Science [Internet]. 2011 Oct 7 [cited 2018 May 4];334(6052):105–8. Available from: http://www.sciencemag.org/cgi/doi/10.1126/science.1208344

7. David LA, Maurice CF, Carmody RN, Gootenberg DB, Button JE, Wolfe BE, et al. Diet rapidly and reproducibly alters the human gut microbiome. Nature [Internet]. 2014 Jan [cited 2018 May 4];505(7484):559–63. Available from: http://www.nature.com/articles/nature12820

8. Xu Z, Knight R. Dietary effects on human gut microbiome diversity. Br J Nutr [Internet]. 2015 Jan [cited 2018 May 4];113(S1):S1–5. Available from: http://www.journals.cambridge.org/abstract_S0007114514004127

9. Falony G, Joossens M, Vieira-Silva S, Wang J, Darzi Y, Faust K, et al. Population-level analysis of gut microbiome variation. Science [Internet]. 2016 Apr 29 [cited 2018 May 4];352(6285):560–4. Available from: http://www.sciencemag.org/lookup/doi/10.1126/science.aad3503

10. Vandeputte D, Falony G, Vieira-Silva S, Tito RY, Joossens M, Raes J. Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. Gut [Internet]. 2016 Jan [cited 2018 May 4];65(1):57–62. Available from: http://gut.bmj.com/lookup/doi/10.1136/gutjnl-2015-309618

11. Ley RE, Turnbaugh PJ, Klein S, Gordon JI. Human gut microbes associated with obesity. Nature. 2006 Dec;444(7122):1022–3.

12. Zhernakova A, Kuriolshikov A, Bonder MJ, Tigchelaar EF, Schirmer M, Vatanen T, et al. Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science. 2016 Apr 29;352(6285):565–9.

13. Francino MP. Antibiotics and the Human Gut Microbiome: Dysbioses and Accumulation of Resistances. Front Microbiol [Internet]. 2016 Jan 12 [cited 2018 May 5];6. Available from: http://journal.frontiersin.org/Article/10.3389/fmicb.2015.01543/abstract
14. Smits SA, Leach J, Sonnenburg ED, Gonzalez CG, Lichtman JS, Reid G, et al. Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania. Science [Internet]. 2017 Aug 25 [cited 2018 May 5];357(6353):802–6. Available from: http://www.sciencemag.org/lookup/doi/10.1126/science.aan4834

15. Liu K, Liu Y, Jiao N, Xu B, Gu Z, Xing T, et al. Bacterial community composition and diversity in Kalakuli, an alpine glacial-fed lake in Muztagh Ata of the westernmost Tibetan Plateau. FEMS Microbiol Ecol [Internet]. 2017 Jul 1 [cited 2020 Oct 12];93(7). Available from: https://academic.oup.com/femsec/article/93/7/fix085/3906652

16. Smits SA, Leach J, Sonnenburg ED, Gonzalez CG, Lichtman JS, Reid G, et al. Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania. Science. 2017 25;357(6353):802–6.

17. Zhernakova A, Kurilshikov A, Bonder MJ, Tigchelaar EF, Schirmer M, Vatanen T, et al. Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science [Internet]. 2016 Apr 29 [cited 2018 May 4];352(6285):565–9. Available from: http://www.sciencemag.org/lookup/doi/10.1126/science.aad3369

18. Goodrich JK, Waters JL, Poole AC, Sutter JL, Koren O, Blekhman R, et al. Human Genetics Shape the Gut Microbiome. Cell [Internet]. 2014 Nov [cited 2018 May 5];159(4):789–99. Available from: http://linkinghub.elsevier.com/retrieve/pii/S0092867414012410

19. Blekhman R, Goodrich JK, Huang K, Sun Q, Bukowski R, Bell JT, et al. Host genetic variation impacts microbiome composition across human body sites. Genome Biol [Internet]. 2015 Dec [cited 2018 May 5];16(1). Available from: http://genomebiology.com/2015/16/1/191

20. Goodrich JK, Davenport ER, Beaumont M, Jackson MA, Knight R, Ober C, et al. Genetic Determinants of the Gut Microbiome in UK Twins. Cell Host Microbe [Internet]. 2016 May [cited 2018 May 5];19(5):731–43. Available from: http://linkinghub.elsevier.com/retrieve/pii/S1931312816301536

21. Frank DN, Pace NR. Gastrointestinal microbiology enters the metagenomics era. Curr Opin Gastroenterol. 2008 Jan;24(1):4–10.

22. Li J, Jia H, Cai X, Zhong H, Feng Q, Sunagawa S, et al. An integrated catalog of reference genes in the human gut microbiome. Nat Biotechnol [Internet]. 2014 Aug [cited 2018 May 5];32(8):834–41. Available from: http://www.nature.com/articles/nbt.2942

23. PORTER JR. Antony van Leeuwenhoek: Tercentenary of His Discovery of Bacteria. BACTERIOL REV. :10.

24. Lagier J-C, Edouard S, Pagnier I, Mediannikov O, Drancourt M, Raoult D. Current and Past Strategies for Bacterial Culture in Clinical Microbiology. Clin Microbiol Rev [Internet]. 2015 Jan [cited 2018 May 5];28(1):208–36. Available from: http://cmr.asm.org/lookup/doi/10.1128/CMR.00110-14

25. Fournier P-E, Drancourt M, Colson P, Rolain J-M, Scola BL, Raoult D. Modern clinical microbiology: new challenges and solutions. Nat Rev Microbiol [Internet]. 2013 Aug [cited 2018 May 5];11(8):574–85. Available from: http://www.nature.com/articles/nrmicro3068
26. Dave M, Purohit T, Razonable R, Loftus EV. Opportunistic Infections Due to Inflammatory Bowel Disease Therapy: Inflamm Bowel Dis [Internet]. 2014 Jan [cited 2018 May 5];20(1):196–212. Available from: https://academic.oup.com/ibdjournal/article/20/1/196-212/4578889

27. Hugon P, Dufour J-C, Colson P, Fournier P-E, Sallah K, Raoult D. A comprehensive repertoire of prokaryotic species identified in human beings. Lancet Infect Dis [Internet]. 2015 Oct [cited 2018 May 5];15(10):1211–9. Available from: http://linkinghub.elsevier.com/retrieve/pii/S1473309915002935

28. Lagier J-C, Drancourt M, Charrel R, Bittar F, La Scola B, Ranque S, et al. Many More Microbes in Humans: Enlarging the Microbiome Repertoire. Clin Infect Dis [Internet]. 2017 Aug 15 [cited 2018 May 5];65(suppl_1):S20–9. Available from: http://academic.oup.com/cid/article/65/suppl_1/S20/4057577/Many-More-Microbes-in-Humans-Enlarging-the

29. O’Brien Andersen L, Karim AB, Roager HM, Vigsnæs LK, Krogfelt KA, Licht TR, et al. Associations between common intestinal parasites and bacteria in humans as revealed by qPCR. Eur J Clin Microbiol Infect Dis [Internet]. 2016 Sep [cited 2018 May 7];35(9):1427–31. Available from: http://link.springer.com/10.1007/s10096-016-2680-2

30. Iebba V, Santangelo F, Totino V, Pantanella F, Monsia A, Di Cristanziano V, et al. Gut microbiota related to Giardia duodenalis, Entamoeba spp. and Blastocystis hominis infections in humans from Côte d’Ivoire. J Infect Dev Ctries. 2016 Sep 30;10(9):1035–41.

31. Audebert C, Even G, Cian A, Blastocystis Investigation Group, Loywick A, Merlin S, et al. Colonization with the enteric protozoa Blastocystis is associated with increased diversity of human gut bacterial microbiota. Sci Rep. 2016 05;6:25255.

32. Beatty JK, Akierman SV, Motta J-P, Muise S, Workentine ML, Harrison JJ, et al. Giardia duodenalis induces pathogenic dysbiosis of human intestinal microbiota biofilms. Int J Parasitol [Internet]. 2017 May 1 [cited 2018 Dec 27];47(6):311–26. Available from: http://www.sciencedirect.com/science/article/pii/S0020751917300401

33. Gilchrist CA, Petri SE, Schneider BN, Reichman DJ, Jiang N, Begum S, et al. Role of the Gut Microbiota of Children in Diarrhea Due to the Protozoan Parasite Entamoeba histolytica. J Infect Dis [Internet]. 2016 May 15 [cited 2018 May 7];213(10):1579–85. Available from: https://academic.oup.com/jid/article-lookup/doi/10.1093/infdis/jiv772

34. Yooseph S, Kirkness EF, Tran TM, Harkins DM, Jones MB, Torralba MG, et al. Stool microbiota composition is associated with the prospective risk of Plasmodium falciparum infection. BMC Genomics [Internet]. 2015 Dec [cited 2018 May 7];16(1). Available from: http://www.biomedcentral.com/1471-2164/16/631

35. Villarino NF, LeCleir GR, Denny JE, Dearth SP, Harding CL, Sloan SS, et al. Composition of the gut microbiota modulates the severity of malaria. Proc Natl Acad Sci [Internet]. 2016 Feb 23 [cited 2018 May 7];113(8):2235–40. Available from: http://www.pnas.org/lookup/doi/10.1073/pnas.1504887113

36. Yang C-A, Liang C, Lin C-L, Hsiao C-T, Peng C-T, Lin H-C, et al. Impact of Enterobius vermicularis infection and mebendazole treatment on intestinal microbiota and host immune response. Mitreva M, editor. PLoS Negl Trop Dis [Internet]. 2017 Sep 25 [cited 2018 May 7];11(9):e0005963. Available from: http://dx.plos.org/10.1371/journal.pntd.0005963
37. Holm JB, Sorobetea D, Kiilerich P, Ramayo-Caldas Y, Estellé J, Ma T, et al. Chronic Trichuris muris Infection Decreases Diversity of the Intestinal Microbiota and Concomitantly Increases the Abundance of Lactobacilli. Allen IC, editor. PLOS ONE [Internet]. 2015 May 5 [cited 2018 May 7];10(5):e0125495. Available from: http://dx.plos.org/10.1371/journal.pone.0125495

38. Jenkins TP, Rathnayaka Y, Perera PK, Peachey LE, Nolan MJ, Krause L, et al. Infections by human gastrointestinal helminths are associated with changes in faecal microbiota diversity and composition. Serrano Ferron E, editor. PLOS ONE [Internet]. 2017 Sep 11 [cited 2018 May 7];12(9):e0184719. Available from: http://dx.plos.org/10.1371/journal.pone.0184719

39. Lamendella R, Wright JR, Hackman J, McLimans C, Toole DR, Bernard Rubio W, et al. Antibiotic Treatments for Clostridium difficile Infection Are Associated with Distinct Bacterial and Fungal Community Structures. Krajmalnik-Brown R, editor. mSphere [Internet]. 2018 Jan 10 [cited 2018 May 7];3(1):e00572-17. Available from: http://msphere.asm.org/lookup/doi/10.1128/mSphere.00572-17

40. Liguori G, Lamas B, Richard ML, Brandi G, da Costa G, Hoffmann TW, et al. Fungal Dysbiosis in Mucosa-associated Microbiota of Crohn’s Disease Patients. J Crohns Colitis [Internet]. 2016 Mar [cited 2018 May 7];10(3):296–305. Available from: https://academic.oup.com/ecco-jcc/article-lookup/doi/10.1093/ecco-jcc/jjv209

41. Eckburg PB, Bik EM, Bernstein CN, Purdom E, Dethlefsen L, Sargent M, et al. Diversity of the Human Intestinal Microbial Flora. Science [Internet]. 2005 Jun 10 [cited 2019 Aug 18];308(5728):1635–8. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1395357/

42. Costa M, Weese JS. Methods and basic concepts for microbiota assessment. Vet J [Internet]. 2019 Jul 1 [cited 2019 Aug 25];249:10–5. Available from: http://www.sciencedirect.com/science/article/pii/S1090023318303745

43. Lagier J-C, Edouard S, Pagnier I, Mediannikov O, Drancourt M, Raoult D. Current and Past Strategies for Bacterial Culture in Clinical Microbiology. Clin Microbiol Rev [Internet]. 2015 Jan [cited 2019 Aug 19];28(1):208–36. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4284306/

44. Lagier J-C, Hugon P, Khelaifia S, Fournier P-E, La Scola B, Raoult D. The Rebirth of Culture in Microbiology through the Example of Culturomics To Study Human Gut Microbiota. Clin Microbiol Rev [Internet]. 2015 Jan [cited 2019 Aug 19];28(1):237–64. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4284300/

45. Muyzer G, Smalla K. Application of denaturing gradient gel electrophoresis (DGGE) and temperature gradient gel electrophoresis (TGGE) in microbial ecology. Antonie Van Leeuwenhoek. 1998 Jan;73(1):127–41.

46. Muyzer G, Smalla K. Application of denaturing gradient gel electrophoresis (DGGE) and temperature gradient gel electrophoresis (TGGE) in microbial ecology. Antonie Van Leeuwenhoek. 1998 Jan;73(1):127–41.

47. Riemann L, Winding A. Community Dynamics of Free-living and Particle-associated Bacterial Assemblages during a Freshwater Phytoplankton Bloom. Microb Ecol. 2001 Oct;42(3):274–85.

48. Heuer H, Hartung K, Wieland G, Kramer I, Smalla K. Polynucleotide Probes That Target a Hypervariable Region of 16S rRNA Genes To Identify Bacterial Isolates Corresponding to
Bands of Community Fingerprints. Appl Environ Microbiol [Internet]. 1999 Mar [cited 2019 Aug 20];65(3):1045–9. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC91142/

Riemann L, Winding A. Community Dynamics of Free-living and Particle-associated Bacterial Assemblages during a Freshwater Phytoplankton Bloom. Microb Ecol [Internet]. 2001 Oct [cited 2019 Aug 20];42(3):274–85. Available from: http://link.springer.com/10.1007/s00248-001-0018-8

Theron J, Cloete TE. Molecular Techniques for Determining Microbial Diversity and Community Structure in Natural Environments. Crit Rev Microbiol [Internet]. 2000 Jan [cited 2019 Aug 21];26(1):37–57. Available from: http://www.tandfonline.com/doi/full/10.1080/10408410091154174

V. Wintzingerode F, Göbel UB, Stackebrandt E. Determination of microbial diversity in environmental samples: pitfalls of PCR-based rRNA analysis. FEMS Microbiol Rev [Internet]. 1997 Nov [cited 2019 Aug 21];21(3):213–29. Available from: https://academic.oup.com/femsre/article-lookup/doi/10.1111/j.1574-6976.1997.tb00351.x

Gelsomino A, Keijzer-Wolters AC, Cacco G, van Elsas JD. Assessment of bacterial community structure in soil by polymerase chain reaction and denaturing gradient gel electrophoresis. J Microbiol Methods [Internet]. 1999 Oct [cited 2019 Aug 21];38(1–2):1–15. Available from: https://linkinghub.elsevier.com/retrieve/pii/S0167701299000548

Sanschagrin S, Yergeau E. Next-generation Sequencing of 16S Ribosomal RNA Gene Amplicons. J Vis Exp JoVE [Internet]. 2014 Aug 29 [cited 2019 Aug 15];(90). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4828026/

Shendure J, Ji H. Next-generation DNA sequencing. Nat Biotechnol. 2008 Oct;26(10):1135–45.

Blazej RG, Kumaresan P, Mathies RA. Microfabricated bioprocessor for integrated nanoliter-scale Sanger DNA sequencing. Proc Natl Acad Sci U S A [Internet]. 2006 May 9 [cited 2019 Aug 24];103(19):7240–5. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1464327/

Gresham D, Dunham MJ, Botstein D. Comparing whole genomes using DNA microarrays. Nat Rev Genet [Internet]. 2008 Apr [cited 2019 Aug 24];9(4):291–302. Available from: http://www.nature.com/articles/nrg2335

Soni GV, Meller A. Progress toward Ultrafast DNA Sequencing Using Solid-State Nanopores. Clin Chem [Internet]. 2007 Nov 1 [cited 2019 Aug 24];53(11):1996–2001. Available from: http://clinchem.aaccjnls.org/content/53/11/1996

Shendure J. Accurate Multiplex Polony Sequencing of an Evolved Bacterial Genome. Science [Internet]. 2005 Sep 9 [cited 2019 Aug 24];309(5741):1728–32. Available from: http://www.sciencemag.org/cgi/doi/10.1126/science.1117389

Healy K. Nanopore-based single-molecule DNA analysis. Nanomed [Internet]. 2007 Aug [cited 2019 Aug 24];2(4):459–81. Available from: https://www.futuremedicine.com/doi/10.2217/17435889.2.4.459

Salipante SJ, Kawashima T, Rosenthal C, Hoogestraat DR, Cummings LA, Sengupta DJ, et al. Performance Comparison of Illumina and Ion Torrent Next-Generation Sequencing Platforms.
968 for 16S rRNA-Based Bacterial Community Profiling. Appl Environ Microbiol [Internet]. 2014
969 Dec [cited 2019 Aug 15];80(24):7583–91. Available from:
970 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4249215/

971 61. Kuczynski J, Lauber CL, Walters WA, Parfrey LW, Clemente JC, Gevers D, et al. Experimental
972 and analytical tools for studying the human microbiome. Nat Rev Genet [Internet]. 2011 Dec
973 16 [cited 2019 Aug 17];13(1):47–58. Available from:
974 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5119550/

975 62. Luo C, Rodriguez-R LM, Konstantinidis KT. A User’s Guide to Quantitative and Comparative
976 Analysis of Metagenomic Datasets. In: Methods in Enzymology [Internet]. Elsevier; 2013 [cited
977 2019 Aug 17]. p. 525–47. Available from:
978 https://linkinghub.elsevier.com/retrieve/pii/B978012407863500023X

979 63. Luo C, Rodriguez-R LM, Konstantinidis KT. MyTaxa: an advanced taxonomic classifier for
980 genomic and metagenomic sequences. Nucleic Acids Res [Internet]. 2014 Apr [cited 2019 Aug
981 17];42(8):e73. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4005636/

982 64. Sims D, Sudbery I, Iloff NE, Heger A, Ponting CP. Sequencing depth and coverage: key
983 considerations in genomic analyses. Nat Rev Genet [Internet]. 2014 Feb [cited 2019 Aug
984 17];15(2):121–32. Available from: http://www.nature.com/articles/nrg3642

985 65. Ranjan R, Rani A, Metwally A, McGee HS, Perkins DL. Analysis of the microbiome: Advantages
986 of whole genome shotgun versus 16S amplicon sequencing. Biochem Biophys Res Commun.
987 2016 Jan 22;469(4):967–77.

988 66. Ras R, Huynh K, Desoky E, Badawy A, Widmer G. Perturbation of the intestinal microbiota of
989 mice infected with Cryptosporidium parvum. Int J Parasitol. 2015 Jul;45(8):567–73.

989 67. Iebba V, Santangelo F, Totino V, Pantanella F, Monsia A, Di Cristanziano V, et al. Gut
990 microbiota related to Giardia duodenalis, Entamoeba spp. and Blastocystis hominis infections
991 in humans from Côte d’Ivoire. J Infect Dev Ctries. 2016 Sep 30;10(9):1035–41.

992 68. Šlapeta J, Dowd SE, Alanazi AD, Westman ME, Brown GK. Differences in the faecal microbiome
993 of non-diarrhoeic clinically healthy dogs and cats associated with Giardia duodenalis infection:
994 impact of hookworms and coccidia. Int J Parasitol. 2015 Aug 1;45(9):585–94.

995 69. Beatty JK, Akierman SV, Motta J-P, Muise S, Workentine ML, Harrison JJ, et al. Giardia
996 duodenalis induces pathogenic dysbiosis of human intestinal microbiota biofilms. Int J
997 Parasitol. 2017;47(6):311–26.

998 70. Yildiz S, Doğan İ, Doğruman-Al F, Nalbantoğlu U, Üstek D, Sarzhanov F, et al. Association of
999 Enteric Protist Blastocystis spp. and Gut Microbiota with Hepatic Encephalopathy. J
1000 Gastrointest Liver Dis JGLD. 2016 Dec;25(4):489–97.

1001 71. Audebert C, Even G, Cian A, Loywick A, Merlin S, Viscogliosi E, et al. Colonization with the
1002 enteric protozoa Blastocystis is associated with increased diversity of human gut bacterial
1003 microbiota. Sci Rep [Internet]. 2016 Jul [cited 2018 May 7];6(1). Available from:
1004 http://www.nature.com/articles/srep25255

1005 72. Iebba V, Santangelo F, Totino V, Pantanella F, Monsia A, Di Cristanziano V, et al. Gut
1006 microbiota related to Giardia duodenalis, Entamoeba spp. and Blastocystis hominis infections
Morton ER, Lynch J, Froment A, Lafosse S, Heyer E, Przeworski M, et al. Variation in Rural African Gut Microbiota Is Strongly Correlated with Colonization by Entamoeba and Subsistence. PLoS Genet [Internet]. 2015 Nov 30 [cited 2019 Jan 4];11(11). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4664238/.

Kelly PH, Bahr SM, Serafim TD, Ajami NJ, Petrosino JF, Meneses C, et al. The Gut Microbiome of the Vector Lutzomyia longipalpis Is Essential for Survival of Leishmania infantum. mBio. 2017 17(8(1)).

Heimesaat MM, Dunay IR, Alutis M, Fischer A, Möhle L, Göbel UB, et al. Nucleotide-Oligomerization-Domain-2 Affects Commensal Gut Microbiota Composition and Intracerebral Immunopathology in Acute Toxoplasma gondii Induced Murine Ileitis. Blader IJ, editor. PLoS ONE [Internet]. 2014 Aug 20 [cited 2018 May 30];9(8):e105120. Available from: http://dx.plos.org/10.1371/journal.pone.0105120.

Brotman RM, Bradford LL, Conrad M, Gajer P, Ault K, Peralta L, et al. Association between Trichomonas vaginalis and vaginal bacterial community composition among reproductive-age women. Sex Transm Dis [Internet]. 2012 Oct [cited 2018 Jun 9];39(10):807–12. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3458234/.

Villarino NF, LeCleir GR, Denny JE, Dearth SP, Harding CL, Sloan SS, et al. Composition of the gut microbiota modulates the severity of malaria. Proc Natl Acad Sci U S A. 2016 Feb 23;113(8):2235–40.

Barash NR, Maloney JG, Singer SM, Dawson SC. Giardia Alters Commensal Microbial Diversity throughout the Murine Gut. Infect Immun [Internet]. 2017 Jan 6 [cited 2018 Jun 14];85(6):e00948-16. Available from: http://iai.asm.org/cgi/doi/10.1128/AEM.67.11.5037-5042.2001

Oliveira BCM, Widmer G. Probiotic Product Enhances Susceptibility of Mice to Cryptosporidiosis. Appl Environ Microbiol [Internet]. 2018 Oct 17 [cited 2020 Feb 20];84(21). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6193388/.

Hatter JA, Kouche YM, Melchor SJ, Ng K, Bouley DM, Boothroyd JC, et al. Toxoplasma gondii infection triggers chronic cachexia and sustained commensal dysbiosis in mice. PLoS ONE [Internet]. 2018 Oct 31 [cited 2020 Feb 19];13(10). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6209157/
Alamer E, Carpio VH, Ibitokou SA, Kirtley ML, Phoenix IR, Opata MM, et al. Dissemination of non-typhoidal Salmonella during Plasmodium chabaudi infection affects anti-malarial immunity. Parasitol Res. 2019 Jul;118(7):2277–85.

Lappan R, Classon C, Kumar S, Singh OP, de Almeida RV, Chakravarty J, et al. Meta-taxonomic analysis of prokaryotic and eukaryotic gut flora in stool samples from visceral leishmaniasis cases and endemic controls in Bihar State India. PLoS Negl Trop Dis [Internet]. 2019 Sep 6 [cited 2020 Feb 17];13(9). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6750594/

Kodio A, Coulibaly D, Koné AK, Konaté S, Doumbo S, Guindo A, et al. Blastocystis Colonization Is Associated with Increased Diversity and Altered Gut Bacterial Communities in Healthy Malian Children. Microorganisms [Internet]. 2019 Dec 4 [cited 2020 Feb 21];7(12). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6956266/

Morton ER, Lynch J, Froment A, Lafosse S, Heyer E, Przeworski M, et al. Variation in Rural African Gut Microbiota Is Strongly Correlated with Colonization by Entamoeba and Subsistence. PLoS Genet. 2015 Nov;11(11):e1005658.

Wu S, Li RW, Li W, Beshah E, Dawson HD, Urban JF. Worm Burden-Dependent Disruption of the Porcine Colon Microbiota by Trichuris suis Infection. PLoS ONE [Internet]. 2012 Apr 20 [cited 2018 Jun 27];7(4). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3332011/

Li RW, Wu S, Li W, Navarro K, Couch RD, Hill D, et al. Alterations in the Porcine Colon Microbiota Induced by the Gastrointestinal Nematode Trichuris suis. Infect Immun [Internet]. 2012 Jun [cited 2018 Jun 28];80(6):2150–7. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3370577/

Cooper P, Walker AW, Reyes J, Chico M, Salter SJ, Vaca M, et al. Patent Human Infections with the Whipworm, Trichuris trichiura, Are Not Associated with Alterations in the Faecal Microbiota. PLOS ONE. 2013 Oct 4;8(10):e76573.

Lee SC, Tang MS, Lim YAL, Choy SH, Kurtz ZD, Cox LM, et al. Helminth Colonization Is Associated with Increased Diversity of the Gut Microbiota. PLoS Negl Trop Dis. 2014 May 22;8(5):e2880.

Rosa BA, Supali T, Gankpala L, Djuardi Y, Sartono E, Zhou Y, et al. Differential human gut microbiome assemblages during soil-transmitted helminth infections in Indonesia and Liberia. Microbiome. 2018 28;6(1):33.

Houlden A, Hayes KS, Bancroft AJ, Worthington JJ, Wang P, Grenchis RK, et al. Chronic Trichuris muris Infection in C57BL/6 Mice Causes Significant Changes in Host Microbiota and Metabolome: Effects Reversed by Pathogen Clearance. PLOS ONE. 2015 May 4;10(5):e0125945.

Williams AR, Krych L, Ahmad HF, Nejsum P, Skovgaard K, Nielsen DS, et al. A polyphenol-enriched diet and Ascaris suum infection modulate mucosal immune responses and gut microbiota composition in pigs. PLOS ONE. 2017 Oct 13;12(10):e0186546.

Jenkins TP, Rathnayaka Y, Perera PK, Peachey LE, Nolan MJ, Krause L, et al. Infections by human gastrointestinal helminths are associated with changes in faecal microbiota diversity and composition. PLOS ONE. 2017 Sep 11;12(9):e0184719.
95. Giacomini P, Zakrzewski M, Croese J, Su X, Sotillo J, McCann L, et al. Experimental hookworm infection and escalating gluten challenges are associated with increased microbial richness in celiac subjects. Sci Rep [Internet]. 2015 Sep 18 [cited 2018 Jul 12];5. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4585380/

96. Vicente CSL, Ozawa S, Hasegawa K. Composition of the Cockroach Gut Microbiome in the Presence of Parasitic Nematodes. Microbes Environ. 2016 Sep 29;31(3):314–20.

97. El-Ashram S, Suo X. Exploring the microbial community (microflora) associated with ovine Haemonchus contortus (macroflora) field strains. Sci Rep. 2017 06;7(1):70.

98. Kay GL, Millard A, Sergeant MJ, Midzi N, Gwisai R, Mduluza T, et al. Differences in the Faecal Microbiome in Schistosoma haematobium Infected Children vs. Uninfected Children. PLoS Negl Trop Dis [Internet]. 2015 Sep 26 [cited 2018 Sep 30];9(6):e0003861. Available from: https://journals.plos.org/plosntds/article?id=10.1371/journal.pntd.0003861

99. Yang C-A, Liang C, Lin C-L, Hsiao C-T, Peng C-T, Lin H-C, et al. Impact of Enterobius vermicularis infection and mebendazole treatment on intestinal microbiota and host immune response. PLoS Negl Trop Dis. 2017 Sep 25;11(9):e0005963.

100. Walk ST, Blum AM, Ewing SA-S, Weinstock JV, Young VB. Alteration of the murine gut microbiota during infection with the parasitic helminth, Heligmosomoides polygyrus. Inflamm Bowel Dis [Internet]. 2010 Nov [cited 2018 Jun 27];16(11):1841–9. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2959136/

101. Kreisinger J, Bastien G, Hauffe HC, Marchesi J, Perkins SE. Interactions between multiple helminths and the gut microbiota in wild rodents. Philos Trans R Soc Lond B Biol Sci. 2015 Aug 19;370(1675).

102. Rausch S, Held J, Fischer A, Heimesaat MM, Kühl AA, Bereswill S, et al. Small Intestinal Nematode Infection of Mice Is Associated with Increased Enterobacterial Loads alongside the Intestinal Tract. Allen IC, editor. PLoS ONE [Internet]. 2013 Sep 10 [cited 2018 Oct 1];8(9):e74026. Available from: http://dx.plos.org/10.1371/journal.pone.0074026

103. Shimokawa C, Obi S, Shibata M, Olia A, Imai T, Suzue K, et al. Suppression of Obesity by an Intestinal Helminth through Interactions with Intestinal Microbiota. Infect Immun. 2019;87(6).

104. Jenkins TP, Peachele AE, Ajami NJ, MacDonald AS, Hsieh MH, Brindley PJ, et al. Schistosoma mansoni infection is associated with quantitative and qualitative modifications of the mammalian intestinal microbiota. Sci Rep [Internet]. 2018 Aug 13 [cited 2020 Apr 23];8(1):1–10. Available from: http://www.nature.com/articles/s41598-018-30412-x

105. Houlden A, Hayes KS, Bancroft AJ, Worthington JJ, Wang P, Grecnis RK, et al. Chronic Trichuris muris Infection in C57BL/6 Mice Causes Significant Changes in Host Microbiota and Metabolome: Effects Reversed by Pathogen Clearance. Kim CH, editor. PLOS ONE [Internet]. 2015 May 4 [cited 2018 Sep 28];10(5):e0125945. Available from: http://dx.plos.org/10.1371/journal.pone.0125945

106. Williamson LL, McKenney EA, Holzknecht ZE, Belliveau C, Rawls JF, Poulton S, et al. Got worms? Perinatal exposure to helminths prevents persistent immune sensitization and cognitive dysfunction induced by early-life infection. Brain Behav Immun. 2016 Jan;51:14–28.
107. Wegener Parfrey L, Jirků M, Šíma R, Jalovecká M, Sak B, Grigore K, et al. A benign helminth alters the host immune system and the gut microbiota in a rat model system. PloS One. 2017;12(8):e0182205.

108. McKenney EA, Williamson L, Yoder AD, Rawls JF, Bilbo SD, Parker W. Alteration of the rat cecal microbiome during colonization with the helminth Hymenolepis diminuta. Gut Microbes. 2015;6(3):182–93.

109. Cattadori IM, Sebastian A, Hao H, Katani R, Albert I, Eilertson KE, et al. Impact of Helminth Infections and Nutritional Constraints on the Small Intestine Microbiota. Serrano Ferron E, editor. PLOS ONE [Internet]. 2016 Jul 20 [cited 2018 Oct 1];11(7):e0159770. Available from: http://dx.plos.org/10.1371/journal.pone.0159770

110. Duarte AM, Jenkins TP, Latrofa MS, Giannelli A, Papadopoulos E, de Carvalho LM, et al. Helminth infections and gut microbiota - a feline perspective. Parasit Vectors. 2016 Dec 3;9:625.

111. Wang Y, Liu F, Urban JF, Paerewijck O, Geldhof P, Li RW. Ascaris suum infection was associated with a worm-independent reduction in microbial diversity and altered metabolic potential in the porcine gut microbiome. Int J Parasitol. 2019 Mar;49(3–4):247–56.

112. Broadhurst MJ, Ardeshir A, Kanwar B, Mirpuri J, Gundra UM, Leung JM, et al. Therapeutic Helminth Infection of Macaques with Idiopathic Chronic Diarrhea Alters the Inflammatory Signature and Mucosal Microbiota of the Colon. Douek DC, editor. PLoS Pathog [Internet]. 2012 Nov 15 [cited 2018 Jul 11];8(11):e1003000. Available from: http://dx.plos.org/10.1371/journal.ppat.1003000

113. Peachey LE, Molena RA, Jenkins TP, Di Cesare A, Traversa D, Hodgkinson JE, et al. The relationships between faecal egg counts and gut microbial composition in UK Thoroughbreds infected by cyathostomins. Int J Parasitol [Internet]. 2018 May 1 [cited 2020 Feb 21];48(6):403–12. Available from: http://www.sciencedirect.com/science/article/pii/S0020751918300201

114. Cooper P, Walker AW, Reyes J, Chico M, Salter SJ, Vaca M, et al. Patent Human Infections with the Whipworm, Trichuris trichiura, Are Not Associated with Alterations in the Faecal Microbiota. Bereswill S, editor. PLoS ONE [Internet]. 2013 Oct 4 [cited 2018 Jul 11];8(10):e76573. Available from: http://dx.plos.org/10.1371/journal.pone.0076573

115. Lee SC, Tang MS, Lim YAL, Choy SH, Kurtz ZD, Cox LM, et al. Helminth Colonization Is Associated with Increased Diversity of the Gut Microbiota. PLoS Negl Trop Dis [Internet]. 2014 May 22 [cited 2018 Jul 11];8(5). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4031128/

116. Rosa BA, Supali T, Gankpala L, Djuardi Y, Sartono E, Zhou Y, et al. Differential human gut microbiome assemblages during soil-transmitted helminth infections in Indonesia and Liberia. Microbiome. 2018 Feb 28;6:33.

117. Schneeberger PHH, Coulibaly JT, Panic G, Daubenberger C, Gueuning M, Frey JE, et al. Investigations on the interplays between Schistosoma mansoni, praziquantel and the gut microbiome. Parasit Vectors [Internet]. 2018 Mar 12 [cited 2020 Feb 21];11. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5848565/
1171. Li S, Sha Z, Wang X, Bu Z, Wang L, Guan X, et al. Yeast Surface Display of Escherichia coli Enterotoxin and Its Effects of Intestinal Microflora and Mucosal Immunity. Curr Microbiol. 2017 Jul;74(7):854–62.

1174. Pinheiro I, Robinson L, Verhelst A, Marzorati M, Winkens B, den Abbeele PV, et al. A yeast fermentate improves gastrointestinal discomfort and constipation by modulation of the gut microbiome: results from a randomized double-blind placebo-controlled pilot trial. BMC Complement Altern Med. 2017 Sep 4;17(1):441.

1178. Borgo F, Verduci E, Riva A, Lassandro C, Riva E, Morace G, et al. Relative Abundance in Bacterial and Fungal Gut Microbes in Obese Children: A Case Control Study. Child Obes Print. 2017 Feb;13(1):78–84.

1181. Zeber-Lubecka N, Kulecka M, Ambrozkiewicz F, Paziewska A, Lechowicz M, Konopka E, et al. Effect of Saccharomyces boulardii and Mode of Delivery on the Early Development of the Gut Microbial Community in Preterm Infants. PloS One. 2016;11(2):e0150306.

1184. Sokol H, Leducq V, Aschard H, Pham H-P, Jegou S, Landman C, et al. Fungal microbiota dysbiosis in IBD. Gut. 2017;66(6):1039–48.

1186. Frykman PK, Nordenskjöld A, Kawaguchi A, Hui TT, Granström AL, Cheng Z, et al. Characterization of Bacterial and Fungal Microbiome in Children with Hirschsprung Disease with and without a History of Enterocolitis: A Multicenter Study. PloS One. 2015;10(4):e0124172.

1190. Lamendella R, Wright JR, Hackman J, McLimans C, Toole DR, Bernard Rubio W, et al. Antibiotic Treatments for Clostridium difficile Infection Are Associated with Distinct Bacterial and Fungal Community Structures. mSphere [Internet]. 2018 Jan 10 [cited 2018 Dec 25];3(1). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5760750/

1194. Chang C-J, Lin C-S, Lu C-C, Martel J, Ko Y-F, Ojcius DM, et al. Ganoderma lucidum reduces obesity in mice by modulating the composition of the gut microbiota. Nat Commun. 2015 Jun 23;6:7489.

1197. Shelburne SA, Ajami NJ, Chibucos MC, Beird HC, Tarrand J, Galloway-Peña J, et al. Implementation of a Pan-Genomic Approach to Investigate Holobiont-Infecting Microbe Interaction: A Case Report of a Leukemic Patient with Invasive Mucormycosis. PLOS ONE [Internet]. 2015 Nov 10 [cited 2019 Jan 15];10(11):e0139851. Available from: https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0139851

1202. Hoarau G, Mukherjee PK, Gower-Rousseau C, Hager C, Chandra J, Retuerto MA, et al. Bacteriome and Mycobiome Interactions Underscore Microbial Dysbiosis in Familial Crohn’s Disease. mBio [Internet]. 2016 Nov 2 [cited 2018 Dec 26];7(5):e01250-16. Available from: https://mbio.asm.org/content/7/5/e01250-16

1206. Strati F, Cavalieri D, Albanese D, De Felice C, Donati C, Hayek J, et al. Altered gut microbiota in Rett syndrome. Microbiome [Internet]. 2016 Jul 30 [cited 2019 Jan 15];4(1):41. Available from: https://doi.org/10.1186/s40168-016-0185-y

1209. Tan S-Q, Zhang K-Q, Chen H-X, Ge Y, Ji R, Shi W-P. The mechanism for microsporidian parasite suppression of the hindgut bacteria of the migratory locust Locusta migratoria manilensis. Sci Rep. 2015 Nov 27;5:17365.
130. Shao M-W, Lu Y-H, Miao S, Zhang Y, Chen T-T, Zhang Y-L. Diversity, Bacterial Symbionts and Antibacterial Potential of Gut-Associated Fungi Isolated from the Pantala flavescens Larvae in China. PloS One. 2015;10(7):e0134542.

131. van Leeuwen PT, van der Peet JM, Bikker FJ, Hoogenkamp MA, Oliveira Paiva AM, Kostidis S, et al. Interspecies Interactions between Clostridium difficile and Candida albicans. Imperiale MJ, editor. mSphere [Internet]. 2016 Dec 28 [cited 2018 Oct 22];1(6). Available from: http://msphere.asm.org/lookup/doi/10.1128/mSphere.00187-16

132. Valentine M, Benadé E, Mouton M, Khan W, Botha A. Binary interactions between the yeast Candida albicans and two gut-associated Bacteroides species. Microb Pathog [Internet]. 2019 Oct [cited 2020 Feb 17];135:103619. Available from: https://linkinghub.elsevier.com/retrieve/pii/S0882401019301007

133. García G, Dogi C, de Moreno de LeBlanc A, Greco C, Cavaglieri L. Gut-borne Saccharomyces cerevisiae, a promising candidate for the formulation of feed additives, modulates immune system and gut microbiota. Benef Microbes. 2016 Nov 30;7(5):659–68.

134. Sovran B, Plantchais J, Jegou S, Straube M, Lamas B, Natividad JM, et al. Enterobacteriaceae are essential for the modulation of colitis severity by fungi. Microbiome [Internet]. 2018 Sep 1 [cited 2020 Feb 18];6. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6119584/

135. Matsuo K, Haku A, Bi B, Takahashi H, Kamada N, Yaguchi T, et al. Fecal microbiota transplantation prevents Candida albicans from colonizing the gastrointestinal tract. Microbiol Immunol [Internet]. 2019 [cited 2020 Feb 18];63(5):155–63. Available from: http://onlinelibrary.wiley.com/doi/abs/10.1111/1348-0421.12680

136. Panpetch W, Somboonna N, Palasuk M, Hiengrach P, Tumwasorn S, et al. Oral Candida administration in a Clostridium difficile mouse model worsens disease severity but is attenuated by Bifidobacterium. PLoS ONE [Internet]. 2019 Jan 15 [cited 2020 Feb 19];14(1). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6333342/

137. Markey L, Shaban L, Green ER, Lemon KP, Mecsas J, Kumamoto CA. Pre-colonization with the commensal fungus Candida albicans reduces murine susceptibility to Clostridium difficile infection. Gut Microbes [Internet]. 2018 May 30 [cited 2020 Feb 20];9(6):497–509. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6287688/

138. Charlet R, Pruvost Y, Tumba G, Istel F, Poulan D, Kuchler K, et al. Remodeling of the Candida glabrata cell wall in the gastrointestinal tract affects the gut microbiota and the immune response. Sci Rep [Internet]. 2018 Feb 20 [cited 2020 Feb 21];8. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5820338/

139. Ducray HAG, Globa L, Pustovyy O, Morrison E, Vodyanoy V, Sorokulova I. Yeast fermentate prebiotic improves intestinal barrier integrity during heat stress by modulation of the gut microbiota in rats. J Appl Microbiol [Internet]. 2019 Oct [cited 2020 Feb 17];127(4):1192–206. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6852649/

140. Briand F, Sulpice T, Giammarinaro P, Roux X. Saccharomyces boulardii CNCM I-745 changes lipidemic profile and gut microbiota in a hamster hypercholesterolemic model. Benef Microbes [Internet]. 2019 May 28 [cited 2020 Feb 18];10(5):555–67. Available from: https://www.wageningenacademic.com/doi/abs/10.3920/8M2018.0134
254. Wang J, Liu S, Wang H, Xiao S, Li C, Li Y, et al. Xanthophyllomyces dendrorhous-Derived Astaxanthin Regulates Lipid Metabolism and Gut Microbiota in Obese Mice Induced by A High-Fat Diet. Mar Drugs [Internet]. 2019 Jun 5 [cited 2020 Apr 23];17(6). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6627754/

258. Mueller KD, Zhang H, Serrano CR, Billmyre RB, Huh EY, Wiemann P, et al. Gastrointestinal microbiota alteration induced by Mucor circinelloides in a murine model. J Microbiol. 2019 Jun;57(6):509–20.

261. Solano-Aguilar GI, Jang S, Lakshman S, Gupta R, Beshah E, Sikaroodi M, et al. The Effect of Dietary Mushroom Agaricus bisporus on Intestinal Microbiota Composition and Host Immunological Function. Nutrients [Internet]. 2018 Nov 9 [cited 2020 Feb 19];10(11). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6266512/

265. Rouzé R, Moné A, Delbac F, Belzunces L, Blot N. The Honeybee Gut Microbiota Is Altered after Chronic Exposure to Different Families of Insecticides and Infection by Nosema ceranae. Microbes Environ [Internet]. 2019 Sep [cited 2020 Feb 17];34(3):226–33. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6759349/

269. Robino P, Ferrocino I, Rossi G, Dogliero A, Alessandria V, Grosso L, et al. Changes in gut bacterial communities in canaries infected by Macrorhabdus ornithogaster. Avian Pathol J WVPA. 2019 Apr;48(2):111–20.

272. Lamendella R, Wright JR, Hackman J, McLimans C, Toole DR, Rubio WB, et al. Antibiotic Treatments for &ITClostridium difficile&IT Infection Are Associated with Distinct Bacterial and Fungal Community Structures. Msphere. 2018 Feb;3(1):e00572-17.

275. Swidsinski A, Loening-Baucke V, Schulz S, Manowsky J, Verstraelen H, Swidsinski S. Functional anatomy of the colonic bio reactor: Impact of antibiotics and Saccharomyces boulardii on bacterial composition in human fecal cylinders. Syst Appl Microbiol [Internet]. 2016 Feb [cited 2018 Oct 22];39(1):67–75. Available from: https://linkinghub.elsevier.com/retrieve/pii/S0723202015001812

280. Lemoine S, Kemgang A, Belkacem KB, Straube M, Jegou S, Corpechot C, et al. Fungi participate in the dysbiosis of gut microbiota in patients with primary sclerosing cholangitis. Gut [Internet]. 2020 Jan 1 [cited 2020 Feb 18];69(1):92–102. Available from: https://gut.bmj.com/content/69/1/92

284. Strati F, Cavaleri D, Albanese D, De Felice C, Donati C, Hayek J, et al. Altered gut microbiota in Rett syndrome. Microbiome. 2016 30;4(1):41.

286. Sam QH, Chang MW, Chai LYA. The Fungal Mycobiome and Its Interaction with Gut Bacteria in the Host. Int J Mol Sci [Internet]. 2017 Feb 4 [cited 2020 Oct 19];18(2). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5343866/

289. Hoffmann C, Dollive S, Grunberg S, Chen J, Li H, Wu GD, et al. Archaea and Fungi of the Human Gut Microbiome: Correlations with Diet and Bacterial Residents. PLOS ONE. 2013 Jun 17,8(6):e66019.

292. Mwangi W, de Figueiredo P, Criscitiello MF. One Health: Addressing Global Challenges at the Nexus of Human, Animal, and Environmental Health. PLoS Pathog [Internet]. 2016 Sep 15 [cited 2019 Jul 28];12(9). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5025119/
Figure and Table legends

**Figure 1:** Flow diagram of the selection of articles and data extraction

**Table 1:** Impact of protozoa on bacterial community structure. Information on the protozoa in question, host status, types of sampling, sample sites corresponding to the parts of the host sampled, methods used, changes in the abundance and diversity of the bacterial microbiota are discussed.

**Table 2:** Influence of helminths on bacterial community structure. Information on the helminths implicated, host status, types of sampling, sample sites corresponding to the parts of the host sampled, methods used, changes in the abundance and diversity of the bacterial microbiota are discussed.

**Table 3:** Interactions between fungal and bacterial communities. Information on the fungi associated, host status, types of sampling, sample sites corresponding to the parts of the host sampled, methods used, changes/associated in the abundance and diversity of the bacterial microbiota are discussed.
Table 1: Impact of protozoa on bacterial community structure

| Protozoa                       | Host                  | Type of sample | Bacterial microbiota method | Bacterial microbiota change                                                                 | Diversity profile | Reference                  |
|--------------------------------|-----------------------|----------------|-----------------------------|---------------------------------------------------------------------------------------------|-------------------|-----------------------------|
| Blastocystis spp               | Cirrhotic patients    | Faeces         | High-throughput sequencing of 16S rRNA amplicons (Illumina) | Family: *Enterobacteriaceae*↑, *Ruminococaceae*↓  
Genus: *Lactobacillus*↑, *clostridial cluster XIV*↓ | ↓alpha diversity     | Sedat Yildiz *et al.* 2016                       |
|                               | Healthy human         |                | High-throughput sequencing of 16S rRNA amplicons (Ion Torrent) | Class: *Clostridia*↑, *Mollicutes*↑  
Order: *Clostridiales*↑, *Lactobacillales*↓  
Family: *Enterobacteriaceae*↓, *Enterococccaceae*↓, *Streptococccaceae*↓, *Lactobacillaceae*↑, *Ruminococccaceae*↑, *Prevotellaceae*↑  
Genus: *Acetanaerobacterium*↑, *Acetivibrio*↑, *Coprococcus*↑, *Hespellia*↑, *Oscillibacter*↑, *Papillibacter*↑, *Sporobacter*↑, *Ruminococcus*↑, *Prevotella*↑, *Roseburia*↑, *Faecalibacterium*↓ | ↑alpha diversity     | Audebert Christophe *et al.* 2016       |
| Blastocystis spp with or not Dientamoeba fragilis | Healthy human | Faeces | qPCR | Genus: *Bacteroides*↓, *Clostridial cluster XIVa*↓, *Prevotella*↑ |                  | Not evaluated              | O’Brien Andersen L *et al.* 2016 |

Phylum: *Firmicutes*↑, *Elusimicrobia*↑, *Lentisphaerae*↑, *Euryarchaeota*↑, *Actinobacteria*↓, *Proteobacteria*↓, *unassigned bacteria*↓, *Deinococcus–Thermus*↓  
Class: *Clostridia*↑, *IHU_PC_PC_Bacteria*↑, *Elusimicrobia*↑, *Lentisphaerae*↑, *Metanobacteria*↑, *Deituprobacteria*↑, *Planctomycetacia*↑, *Rubrobacteria*↑, *Deinococci*↑, *Gammaproteobacteria*↑, *Actinobacteria*↑, *unassigned bacteria*↓, *Bacilli*↓  
Order: *Clostridiales*↑, *IHU_PO_Bacteria*↑, *Victivallales*↑, *Methanobacterales*↑, *Elusimicrobiales*↑, *Aeromonadales*↑, *Acidaminococcales*↑, *Desulfovibrionales*↑, *Planctomycetales*↓, *Rhodobacterales*↓, *Sphingomonadales*↓, *Rubrobacterales*↓, *Veillonellales*↓, *Pasteurellales*↓, *Micrococciales*↓, *Pseudonocardiales*↓, *Enterobacterales*↓, *Myxococcales*↓, *Bifidobacterales*↓, *unassigned bacteria*↓, *Lactobacillales*↓  
Family: *Clostridiaceae*↑, *Ruminococccaceae*↑, *Lachnospiraceae*↑, *Streptococccaceae*↑, *Bifidobacteriaceae*↑, *Enterobacteraeae*↑, *Leuconostocaceae*↓  
Genus: *Ruminococcus*↑, *Clostridium*↑, *Streptococcus*↓, *Bifidobacterium*↓, *Shigella*↓  
Species: *Clostridiumsaudii*↑, *Methanobrevibactermithii*↑, *Streptococcus sp.*↓, *Bifidobacterium sp.*↓, *Shigella sp.*↓
Table 1: Impact of protozoa on bacterial community structure (continued)

| Protozoa                      | Host/Type of sample | Type of sample | Bacterial microbiota method                  | Bacterial microbiota change                                                                 | Diversity profile | Reference                        |
|-------------------------------|---------------------|----------------|---------------------------------------------|------------------------------------------------------------------------------------------------|-------------------|-----------------------------------|
| Cryptosporidium parvum        | CD-1 mice           | Faeces         | High-throughput sequencing of 16S rRNA amplicons (Illumina) | Phylum: Unclassified Bacteroidetes↑, Family: Porphyromonadaceae↑, Prevotellaceae↑                  | Not change        | R.Ras et al. 2015                |
|                               |                     |                |                                             | Phylum: Proteobacteria↑, Firmicutes↓                                                          |                   | Oliveira BC et al. 2018           |
| Entamoeba histolytica         | Children            | Faeces         | Quantitative polymerase chain reaction (qPCR) | Species: Prevotella copri↑                                                                     | Not evaluated     | Gilchrist et al. 2016            |
| Entamoeba (dispar, histolytica, or both) | Pygmy hunter-gatherers Bantu individuals | Faeces | High-throughput Sequencing of 16S rRNA amplicons (Illumina) | Phylum: Actinobacteria↑, Bacteroidetes↑, Cyanobacteria↑, Elusimicrobia↑, Euryarchaeota↑, Firmicutes↑, Fusobacteria↑, Lentisphaerae↑, Spirochaetes↑, Tenericutes↑, Verrucomicrobia↑ Order: Clostridiales↑, Elusimicrobiales↑, Treponemata↑ Family: Christensenellaceae↑, Elusimicrobiaceae↑, Spirochaetaceae↑ Specie: Prevotella copri↓ | ↑alpha diversity | Elise R. Morton et al. 2015 |
| Giardia Duodenalis, Ancylostoma Caninum, Cystoisospora, Giardia cati | Dog Cat Dog Cat | Faeces | High-throughput sequencing of 16S rRNA amplicons (Ion Torrent) | Dog: giardia Phylum: Firmicutes↑, Bacteroidetes↑, Proteobacteria↑ Family: Erysipelotrichaceae↑, Bacteroidaceae↑, Lachnospiraceae↑, Pseudomonadaceae↑ Genus: Catenibacterium↑, Pseudomonas↑, Howardella↑, Bacteroides↑, Pseudobutyrivibrio↑ | No change         | Jan Slapeta et al. 2015  |
|                               |                     |                |                                             | Cat: cystoisospora Phylum: Actinobacteria↑, Firmicutes↑ Deinococcus-Thermus↑, Proteobacteria↑ Family: Bifidobacteriaceae↑, Coriobacteriaceae↑, Veillonellaceae↑, Bacillaceae↑, Thermaceae↑, Xanthomonadaceae↑, Comamonadaceae↑, Beijerinckiaceae↑, Xanthomonadaceae↑ Genus: Bifidobacterium↑, Olsenella↑, Megamonas↑, Geobacillus↑, Meiothermus↑, Bacillus↑, Thermomonas↑, Schlegelellla↑, Chelatococcus↑, Silanimonas↑ |                   |                                   |
|                               |                     |                |                                             | Cat: giardia Phylum: Firmicutes↑ Family: Lachnospiraceae↑, Ruminococcaceae↓ Genus: Roseburia↑, Subdoligranulum↓ |                   |                                   |
| Protozoa                          | Host                      | Type of sample      | Site of sample                          | Bacterial microbiota method                                                                 | Bacterial microbiota change                                                                 | Diversity profile | Reference                      |
|----------------------------------|---------------------------|---------------------|-----------------------------------------|---------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|------------------|---------------------------------|
| Giardia lamblia                  | C57BL/6J mice             | Mucosal and luminal | Foregut, hindgut                        | High-throughput sequencing of 16S rRNA amplicons (Illumina)                                  | Phylum: Melainabacteria↓ Order: Clostridiales↓ Family: Rhodocyclaceae↑, Moraxellaceae↑         | alpha diversity  | N.R.Barash et al. 2017         |
|                                 |                           | proximal Small     | Distal small intestine, Cecal contents, and colonic contents |                                                                               |                                                                               |                  |                                 |
|                                 |                           | intestine          |                          |                                                                               |                                                                               |                  |                                 |
| Giardia duodenalis               | Healthy human             | Mucosal biopsies    | Colon                     | High-throughput sequencing of 16S rRNA amplicons (Illumina)                                  | Phylum: Firmicutes↑ Order: Clostridales↑ Genus: Phascolarctobacterium↓                          | alpha diversity  | Beatty, J.K et al. 2017        |
|                                 |                           |                    |                          |                                                                               |                                                                               |                  |                                 |
| Giardia spp, Entamoeba spp/ Blastocystis hominis | Human with or without symptoms | Faeces              |                                                                                   | qPCR                                                                         | Genus: Bilfdobacterium↑ Species: Escherichia coli↑ Faecalibacterium prauonizii- Escherichia Coli ratio↑ | Not evaluated    | Lebba et al. 2016              |
|                                 |                           |                    |                          |                                                                               |                                                                               |                  |                                 |
| Leishmania infantum              | Lutzomyia longipalpis    | midguts            | 16Sv4 rRNA gene sequencing          |                                                                               |                                                                               | alpha diversity  | Kelly PH et al. 2016           |
|                                 |                           |                    |                          |                                                                               |                                                                               |                  |                                 |
| Plasmodium yoelii                | BALB/c mice               | Cecum, colon       | Distal small intestine            | High-throughput sequencing of 16S rRNA amplicons (Illumina)                                  | Phylum: Firmicutes↑, Bacteroidetes↓ Order: Clostridiaceae↑, Erysipelotrichaceae↑, Lactobacillaceae↑, Peptostreptococcaceae↑ Bacteroidaceae↓, Prevotellaceae↓, Sutterellaceae↓ Genus: Lactobacillus↑, Bifidobacterium↑ | alpha diversity  | Villarino et al. 2016          |
|                                 | Resistant, C57BL/6 mice   |                    |                          |                                                                               |                                                                               |                  |                                 |
|                                 | susceptible               |                    |                          |                                                                               |                                                                               |                  |                                 |
| Trichomonas vaginalis            | North American women      | Vaginal swabs      | Vaginal swabs                  | High-throughput Sequencing of 16S rRNA amplicons (454 pyrosequencing)                      | Genus: Lactobacillus↑, Mycoplasma↑, Parvimonas↑, Sneathia↑                                   | Not evaluated    | Rebecca M.Brotman et al. 2012  |
|                                 |                           |                    |                          |                                                                               |                                                                               |                  |                                 |
| Toxoplasma gondii                | NOD2/- mice               | Feces              | Real Time-PCR                  | Order: Enterobacteria↑ Genus: Lactobacillus↑, Bifidobacterium↑, Enterococci↑, Bacteroides/Prevotella spp.↑, eubacterial↑ | Not evaluated                                                                                     |                  | Heimesaat MM et al. 2014       |
|                                 |                           |                    |                          |                                                                               |                                                                               |                  |                                 |
|                                 | C57BL/6 mice              |                    | High-throughput sequencing of 16S rRNA amplicons (Illumina)                      | Phylum: Firmicutes↑ Genus: Clostridia↑                                                   |                                                                               |                  | Hatter IA et al. 2018          |
|                                 |                           |                    |                          |                                                                               |                                                                               |                  |                                 |
Table 2: Influence of helminths on bacterial community structure

| Helminths                  | Host                  | Type of sample | Site of sample | Bacterial microbiota method                                           | Bacterial microbiota change                                                   | Diversity profile | Reference                  |
|----------------------------|-----------------------|----------------|----------------|-----------------------------------------------------------------------|-----------------------------------------------------------------------------|--------------------|----------------------------|
| Ascaris, Trichuris, Hookworm | Human volunteers      | fresh stool    |                | High-throughput sequencing of 16S rRNA amplicons (Illumina)           | Class: Verrucomicrobiaceae↑ Order: Verrucomicrobiales↑                        | No change         | Jenkins et al., 2017       |
|                           |                       |                |                |                                                                       | Family: Bacteroidaceae↑, Prevotellaceae↑ Verrucomicrobiaceae↑, Enterobacteriaceae↑, Leucostocaceae↑, Bacteroidaceae↓ |                    |                             |
|                           |                       |                |                |                                                                       | Genus: Lactococcus↑, Akkermansia↑, Enterobacteriaceae↑, Bacteroides↓         |                    |                             |
|                           |                       |                |                |                                                                       | Species: Prevotella copri↑                                                  |                    |                             |
| Ascaris lumbricoides      | Subject cohort        | Feces          |                | High-throughput sequencing of 16S rRNA amplicons (Illumina)           | Phylum: Firmicutes↑, Bacteroidetes↑, Actinobacteria↑                         | ↑alpha diversity   | Rosa et al. 2018           |
| (“Ascaris”), Necator Americanus (“Necator”), Trichuris trichiura (“Tricharis”) |                |                |                |                                                                       | Family: Lachnospiraceae↑, Erysipelotrichaceae↑                              |                    |                             |
|                           |                       |                |                |                                                                       | Genus: Succinivibrio↑, Solobacterium↑, Desulfovibrio↑, Allobaculum↑, Rhodococcus↑, Lachnospiraceae incertae sedis↑, Olsenella↑, Flavonifractor↑, Enterococcus↑. |                    |                             |
| Ascaris suum              | Pigs                  | Digesta        | Proximal Colon | High-throughput Sequencing of 16S rRNA amplicons (Illumina)           | Genus: ↑Prevotella, ↑Faecalibacter, ↑Turicibacter, ↓Ruminicoccus, ↓Lactobacillus, ↑Treponema, ↑Camylobacter | ↑alpha Diversity with Basal diet No change with Grape pomace diet | Williams et al. 2017 |
| Caenorhabditis elegans    | Wild C. elegans       | NA             |                | High-throughput Sequencing of 16S rRNA amplicons (Illumina)           | Phylum: ↑Proteobacteria, ↑Actinobacteria, ↑Firmicutes, ↑Bacteroidetes↑       | Not evaluated      | Zhang et al. 2017          |
|                           |                       |                |                |                                                                       | Family: ↑Enterobacteriace, ↑Pseudomonadaceae, ↑Xanthomonadaceae, ↑Sphingobacteriaceae |                    |                             |
| Cyathostomins spp.        | Equines               | Feces          |                | High-throughput Sequencing of 16S rRNA amplicons (Illumina)           | Class: Methanomicrobiaceae↑, Dehobacterium↓                                 | No difference      | L.E. Peachey et al. 2018   |
| (Eggs high versus low)    |                       |                |                |                                                                       |                                                                            |                    |                             |
| Enterobius vermicularis   | School children       | Feces          |                | High-throughput Sequencing of 16S rRNA amplicons (Illumina)           | Phylum: ↑Fusobacteria, ↑Actinobacteria                                    | ↑alpha diversity   | Yang et al. 2017           |
|                           |                       |                |                |                                                                       | Genus: ↑Bifidobacterium, ↑Alistipes, ↑Faecalibacterium, ↓Fusobacterium, ↓Veillonella, ↓Megasphaera, ↓Acidaminococcus |                    |                             |
|                           |                       |                |                |                                                                       | Species: ↑Faecalibacterium prausnitzii, ↑Ruminococcus flavescens, ↑Alistipesputredinis, ↑Bifidobacterium longum, ↑uncultured Oscillospira, ↑Acidaminococcus intestine, ↓Megasphaera elsdenii, ↓Veillonella dispar, ↓Fusobacterium varium |                    |                             |

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| Helminths                  | Host                          | Type of sample | Site of sample | Bacterial microbiota method                                      | Bacterial microbiota change                                                                 | Diversity profile | Reference                          |
|---------------------------|-------------------------------|----------------|----------------|-----------------------------------------------------------------|-----------------------------------------------------------------------------------------------|------------------|------------------------------------|
| *Haemonchus contortus*    | Sheep (Ovis aries)            | Faeces         | Abomasal, rumen | High-throughput Sequencing of 16S rRNA amplicons (Illumina)     | Abomasal microbiome  
Genus: ↑Flavonifractor, ↑Anaerotruncus, ↓Roseburia, ↓Ruminobacter, ↓Blautia, ↓Mogibacterium, ↑Acetitomaculum, ↑Moryella, ↑Anaerovibrio, ↑Incetae_Sedis, ↑Butyrivibrio, ↑Comamonas, ↓U29-B03, ↑Bacillus, ↑Fibrobacter, ↑Syntrophococcus, ↓Candidatus_Saccharimonas, ↑Saccharofermentans, ↑Citrobacter, ↓Oscillibacter, ↓RC9_gut_group, ↑Victivallis, ↑Lactococcus, ↑Prevotella, ↓probable_genus_10, ↓Selenomonos, ↓Intestiimonas, ↑Succinivibrio, ↑Victivallis, ↑Lactococcus, ↑Prevotella, ↓probable_genus_10, ↑Selenomonos, ↓Intestiimonas, ↓Succinivibrio, ↑Victivallis  
Family: Lactobacillaceae↓ | ↑alpha diversity             | El-Ashram and Suo 2017 |
| *Heligmosomoides Polygyrus* | Inflammatory Bowel Disease (IBD) mouse | Mucosa | Ileum, caecum | Cloned 16S rRNA Sequencing qPCR of total bacteria                 | Family: Lactobacillaceae↓  
Phylum: Proteobacteria↓, unassigned bacteria↑  
Genus: Bacillus↑, Escherichia↑ | Not evaluated | Walk et al. 2010 |
| *Heligmosomoides polygyrus* | C57BL/6J obese mice           | Faeces         |                 | High-throughput Sequencing of 16S rRNA amplicons (Illumina); qPCR | Phylum: Actinobacteria↓, Tenericutes↓, Bacteroidetes↑  
Order: Clostridiales↑ (Escherichia coli) | Not evaluated | Shimokawa C et al. 2019 |
| *Hymenolepsis diminuta*   | Rat model, pups, adults       | Cecum, large bowel |                 | High-throughput Sequencing of 16S rRNA amplicons (Illumina)     | Phylum: Peptostreptococcaceae↑  
Genus: Turibacter↓ | Not evaluated | Williamson et al. 2016 |
| *Hymenolepsis diminuta*   | Rat (Rattus norvegicus)       | Lumen          | Caecum          | High-throughput Sequencing of 16S rRNA amplicons (Illumina)     | Phylum: Peptostreptococcaceae↑  
Genus: Turibacter↓ | Not evaluated | McKenney et al. 2015 |
Table 2: Influence of helminths on bacterial community structure (continued)

| Helminths                        | Host                                    | Type of sample | Site of sample | Bacterial microbiota method | Bacterial microbiota change                                      | Diversity profile | Reference               |
|----------------------------------|-----------------------------------------|----------------|----------------|----------------------------|------------------------------------------------------------------|------------------|--------------------------|
| Heligmosomoides Polygyrus bakeri | IL-4Ra/- mice; C57BL/6 mice              | Lumen          | Caecum; ileum; colon | Culture; Cloned 16S rRNA amplicon; qPCR; Denaturing gradient gel electrophoresis | γ-Proteobacteria, Enterobacteriaceae↑, Bacteroides/Prevotella↑ | Not evaluated | Rausch et al. 2013       |
| Heligmosomoides Polygyrus, Syphacia spp, Hymenolepis spp | Wild mouse (Apodemus flavicollis) | Lumen, mucosa | Stomach, ileum, caecum, colon | High-throughput Sequencing of 16S rRNA amplicons (454) | Hymenolepis spp. Family: Ruminococcaceae↓, Acetobacteraceae↓, Sphingomonadaceae↓, S24–7 family (Bacteroidetes)↑ | No change | Kreisinger et al. 2015 |
| Leidynema appendiculatum; Leidynema appendiculatum; Hammerschmidtia desingi; Thelastoma balhoesi | Periplaneta fuliginosa Periplaneta americana | Faeces | Foregut; Midgut; Hindgut | High-throughput Sequencing of 16S rRNA amplicons (Illumina) | Phylum: Firmicutes↑, Proteobacteria↑, Bacteroidetes↑, Actinobacteria↑ Genus: Bacillales↑, Brevibacterium↓, Gordonia↓, Xylanimicrobium↑, Bacteroides↑ Order: Lactobacillales↓, Enterobacteriales Family: Lachnospiraceae↑, Ruminococcaceae↑, Porphyromonadaceae↑, Desulfovibrionaceae↑, Weeksellaceae↑, Bacteroidaceae↑ Genus: Lactobacillus↑ | ↑alpha diversity | Vicente et al. 2016 |
| Necator americanus | Patients with coeliac disease | Faeces | High-throughput Sequencing of 16S rRNA Amplicons (454) | Phylum: Firmicutes↑, Bacteroides↑, Tenericutes↑, RF39↑ Class: Bacteroidia↑, Erysipelotrichia↑, Clostridia↑ Genus: Ruminococcus↑, Lachnospira↑ | ↑alpha diversity | Giacomin et al. 2015 |
| Trichuris muris | C57BL/6 mice | Faeces, lumen | Caecum | High-throughput Sequencing of 16S rRNA amplicons (Illumina) | Alistipes↑, Odoribacter, and Parasutterella↑, Allobaculum↑, Barnesiella↑ | ↑alpha diversity | Holm et al. 2015 |
|                         | Faeces, Faeces |                      | Denaturing gradient gel electrophoresis; High-throughput sequencing of 16S rRNA amplicons (454) | Phylum: Bacteroidetes↑, Genus: Prevotella↑, Parabacteroides↑ |                      |                      | Houlden et al. 2015 |
### Table 2: Influence of helminths on bacterial community structure (continued)

| Helminths                  | Host                      | Type of sample | Site of sample         | Bacterial microbiota method                        | Bacterial microbiota change                                                                 | Diversity profile | Reference               |
|----------------------------|---------------------------|----------------|------------------------|----------------------------------------------------|---------------------------------------------------------------------------------------------|-------------------|-------------------------|
| *Trichostrongyulus retortaeformis* | Rabbits (Oryctolagus cuniculus) | Mucosa         | Duodenal               | High-throughput Sequencing of 16S rRNA amplicons (Illumina) | Phylum: ↑Proteobacteria, ↑Spirochaetes, ↓Firmicutes Family: Leptospiraceae, ↑Ruminococcaceae, ↑Phyromonadaceae, ↑Desulfbacteraceae, ↑Bacteroidaceae Genus: ↑Leptomena, ↑Desulfoecella, ↓Bacteroides ↓Ruminococcus | ↓alpha diversity | Cattadori et al. 2016 |
| *Toxocara cati*           | Cat (Felis catus)         | Faeces         |                        | High-throughput Sequencing of 16S rRNA amplicons (Illumina) | Phylum: ↑Actinobacteria Class: ↑Coreobacteriia, ↑Gammaproteobacteria Order: ↑Lactobacillales, ↑Coribacteriales Family: ↑Enterococcaceae, ↑Coreobacteriaceae Genus: ↑Collinsella, ↑Enterococcus, ↑Dorea, ↑Lactobacillus, ↑Ruminococcus, ↓Bulleidia, ↓Jeotgalicoccus | No change         | Duarte et al. 2016     |
| Two undescribed thelagnostid species: Pa-nem-L (larger); Pa-nem-S (smaller) | Cockroach (Panesthia angustipennis) | Entire/sections of nematode body surfaces | Hindgut | High-throughput Sequencing of 16S rRNA amplicons (Illumina) | Family: ↑Dysgonomonadaceae (Bacteroidales termite cluster V), ↑Rikenellaceae, ↑Ruminococcaceae. | ↑alpha diversity | Takumi Murakami et al. 2019 |
| *Trichuris suis*          | Pigs (Sus scrofa domestica) | Faeces         | Proximal colon         | Whole metagenome shotgun Sequencing (Illumina) | Phylum: ↑Fibrobacteres, ↓Spirochaetes, ↓Tenericutes, ↓Gemmatimonadetes Genus: ↑Fibrobacter, ↑Campylobacter, ↑Treponema, ↓Dorea, ↓Ruminococcus | Not evaluated | Wu et al. 2012         |
| Pigs (Sus scrofa domestica) | Lumen                     | Proximal colon | Whole metagenome shotgun 454 sequencing High-throughput sequencing of 16S rRNA amplicons (454) | Phylum: ↑Proteobacteria, ↓Deferribacteres, ↑Euryarchaeota Genus: ↑Prevotella, ↓ Succinivibrio, ↓Mucispirillum, ↓Oscillibacter, ↑Paraprevotella, ↑Desulfovibrio, ↑Heliobacter | No change         | Li et al. 2012          |
Table 2: Influence of helminths on bacterial community structure (continued)

| Helminths                  | Host                                      | Type of sample | Bacterial microbiota method | Bacterial microbiota change                                                                 | Diversity profile | Reference                     |
|----------------------------|-------------------------------------------|----------------|----------------------------|-------------------------------------------------------------------------------------------------|-------------------|--------------------------------|
| *Trichuris trichiura,     | School children                          | Faeces         | High-throughput            | Phylum: ↓*Firmicutes*  
Class: ↓*Clostridia*, ↑*streptococi*  
Genus: ↓*Clostridium sensu stricto*,  ↓uncharacterised clostridial cluster IX, ↑*Streptococcus, Roseburia*  
↓alpha diversity                                                               |                   | Cooper et al. 2013               |
| *Ascaris lumbricoides*    |                                           |                | Sequencing of 16S rRNA Amplicons (454) |                                                                                                  |                   |                                |
| *Trichuris spp.,         | Indigenous community                      | Faeces         | High-throughput            | Phylum: ↑*Mollicutes*, ↑*Bacteroidales,  
↑*Alphaproteobacteria*  
Family: ↑*Paraprevotellaceae,  
↑*Lachnospiraceae,  
↑*Prevotellaceae*  
Genus: ↑*Bifidobacterium*  
↓alpha diversity                                                               |                   | Lee et al. 2014                 |
| *Ascaris spp., hookworm* |                                           |                | Sequencing of 16S rRNA Amplicons (Illumina) |                                                                                                  |                   |                                |
| *Schistosoma haematobium*| Children (six months to 13 years old)     | Urine, stool   | High-throughput sequencing of 16S rRNA amplicons (Illumina) | Phylum: *Bacteroidetes*, *Firmicutes*, *Proteobacteria*  
Genus: *Prevotella*  
↑alpha diversity                                                               |                   | Kay et al. 2015                 |
| *Schistosoma mansoni*    | Children from Côte d’Ivoire              | Faeces         | High-throughput sequencing of 16S rRNA amplicons (Illumina) | Phylum: *Proteobacteria*  
Family: *Cerasicoccaceae, Anaeroplasmataceae,  
Campylobacteraceae, Peptococcaceae  
Genus: *Klebsiella*, *Enterobacter arachidis*,  *Fractobacillus*  
↓alpha diversity                                                               |                   | Schneeberger et al. 2018       |
| *Trichuris trichiura*    | Rhesus monkeys                           | Colon mucosa   | High-throughput sequencing of 16S rRNA amplicons (Illumina) | Phylum: ↑*Cyanobacteria,  
↑*Firmicutes,  
↑*Bacteroidetes,  
↑*Tenericutes,  
↓unclassified bacteria taxon ZB2  
Genus: ↓*Streptophyta*  
No change                                                                    |                   | Broadhurst et al. 2012         |
Table 3: Interactions between fungal and bacterial communities

| Fungi                  | Host                      | Type of sample | Bacterial microbiota method                                      | Bacterial microbiota change/association | Diversity profile | Reference              |
|------------------------|---------------------------|----------------|------------------------------------------------------------------|------------------------------------------|-------------------|------------------------|
| Phylum: Ascomycota†,   | Clostridium difficile     | Faeces         | High-throughput sequencing of 16S rRNA amplicons (Illumina)      | Phylum: Planctomycyes↓                   | *α*-diversity     | Lamendella et al. 2018 |
| Family: Pichiaceae↓    | infection patient cohort  |                |                                                                  | Class: Clostridia†, Bacteroidia†         |                   |                        |
| Basidiomycota†,        | Crohn’s disease patients  | Colon, mucosa  | High-throughput sequencing of 16S rRNA amplicons (Illumina; 454) | Phylum: Proteobacteria ↑, Fusobacteria†  | *α*-diversity     | Liguori et al. 2016   |
| Ascomycota↑            |                           |                |                                                                  |                                          |                   |                        |
| Phylum: Basidiomycota†,| Patients with IBD         | Faeces         | High-throughput sequencing of 16S rRNA amplicons (Ion Torrent); qPCR | Genus: Ruminococcus↑, Clostridium↑,     | *α*-diversity     | Sokol et al. 2017      |
| Ascomycota↑            |                           |                |                                                                  | Bacteroidetes↓, Eubacterium↓, Roseburia↓, Faecalibacterium↓, Dorea↓, Blautia↓, Actinobacillus↑ |                   |                        |
| Genus: Saccharomyces↓, |                           |                |                                                                  | Species: Rumunococcus gnanus↑, Streptococcus anginosus↑, Aggregatibacter segnis↑ |                   |                        |
| Candida↑               |                           |                |                                                                  |                                          |                   |                        |
| Species: Malassezia    |                           |                |                                                                  |                                          |                   |                        |
| symподialis↑,          |                           |                |                                                                  |                                          |                   |                        |
| Saccharomyces cerevisiae↓, |                      |                |                                                                  |                                          |                   |                        |
| Candida albicans↑      |                           |                |                                                                  |                                          |                   |                        |
| Genus: Candida↑,       | Rett Syndrome patients    | Faeces         | High-throughput sequencing of 16S rRNA amplicons (454)           | Phylum: Actinobacteria↑, Firmicutes↓,     | *α*-diversity     | Strati et al. 2016    |
| Penicillium↓,          |                           |                |                                                                  | Bacteroidetes↑, Genus: Bifidobacterium↑, Clostridia↑, Erysipelotrichaceae↑, Actinomyces↑, Lactobacillus↑, Eggerthella↑, Enterococcus↑, Enterobacteriaceae↑ |                   |                        |
| Aspergillus↓,          |                           |                |                                                                  |                                          |                   |                        |
| Malassezia↓,           |                           |                |                                                                  |                                          |                   |                        |
| Debaryomyces↓,         |                           |                |                                                                  |                                          |                   |                        |
| Mucor↓,                |                           |                |                                                                  |                                          |                   |                        |
| Eremothecium↓,         |                           |                |                                                                  |                                          |                   |                        |
| Pichia↓,               |                           |                |                                                                  |                                          |                   |                        |
| Cyberlindnera↓,        |                           |                |                                                                  |                                          |                   |                        |
| Trichosporon↑          |                           |                |                                                                  |                                          |                   |                        |
| Candida glabrata       | DSS-induced colitis mouse | Stool          | Culture                                                          | Species: E. coli↑, E. faecalis↑, Bacteroides vulgatus↓, B. thetaiotaomicron↓, Bacteroides sp. TP5↓, Bifidobacterium animalis↓, L. johnsonii↓, Lactobacillus reuteri↑ | Not evaluated     | Rogatien Charlet et al. 2018 |
|                        | model.                   |                |                                                                  |                                          |                   |                        |
| Candida tropicalis↑    | Crohn’s Disease patients  | Stool          | High-throughput sequencing of 16S rRNA amplicons (Ion Torrent)   | Phylum: Bacteroidetes↓, Species: Bifidobacterium adolescentis↑, Ruminococcus gnanus↑, Faecalibacterium prausnitzii↑, Escherichia coli↑, Serratia marcescens↑ | Not evaluated     | Hoarau et al. 2016    |
|                        |                          |                |                                                                  |                                          |                   |                        |
| Fungi | Host | Type of sample | Site of sample | Bacterial microbiota method | Bacterial microbiota change/association | Diversity profile | Reference |
|-------|------|----------------|---------------|----------------------------|------------------------------------------|------------------|-----------|
| Candida albicans | Culture | Clostridium difficile↑ | Not evaluated | Van Leeuwen et al. 2016 |
| | Culture ; qPCR | Family : Enterobacteriaceae↑ | Not evaluated | Bruno Sovran et al. 2018 |
| | Culture | Bacteroides fragilis ↑, Bacteroides vulgatus↑ | Not evaluated | Marisa Valentine et al. 2019 |
| | High-throughput sequencing of 16S rRNA amplicons (Illumina) | Phylum : Verrucomicrobia↑, Proteobacteria↑, Actinobacteria↑, Firmicutes↑, Bacteroidetes↑ Family: Comamonadaceae↑, Erysipelotrichaceae↑, S24-7↑ Genus: Akkermansia sp. ↑, Sutterella sp. ↑, Bifidobacterium sp. ↑, Adlercreutzia sp. ↑ | ↓alpha diversity | Laura Markey et al. 2018 |
| | Mouse model of Clostridium difficile | Faeces | Colon | Culture | Clostridium difficile↑ | Not evaluated | Wimonrat Panpetch et al. 2019 |
| Debaryomyces hansenii↑, Candida spp↓, and Saccharomyces spp↓ | Obese children | Faeces | Denaturing gradient gel electrophoresis (DGGE) qPCR | Species: Akkermansia muciniphyla↓, Faecalibacterium prausnitzii↓ | ↑alpha diversity | Borgo et al. 2017 |
| Ganoderma lucidum mycelium | High-Fat Diet (HFD)-fed Mice Chow mice | Faeces | Caecal | Pyrosequencing of bacterial 16S rRNA | Phylum: Firmicutes-to-Bacteroidetes ratios↓, Proteobacteria↓, Species: Parabacteroides goldsteinii↓, Bacteroides↑, Anaerotruncus colihominis↑, Roseburia hominis↑, Clostridium↑, Clostridium methylpentosum↑, Clostridium XIVa and XVIII↑, Eubacterium coprostanoligenes↑ | ↑alpha diversity | Chang et al. 2015 |
| Fungi                          | Host                                      | Type of sample | Bacterial microbiota method | Bacterial microbiota change/association                                                                 | Diversity profile | Reference                                      |
|-------------------------------|-------------------------------------------|----------------|----------------------------|---------------------------------------------------------------------------------------------------------|-------------------|------------------------------------------------|
| Macrorhabdus ornithogaster    | Canaries (Serinus canaria domestica)      | Faeces         | PCR-DGGE, High-throughput sequencing of 16S rRNA amplicons (Illimuna) | Phylum: Acidobacteria↑, Actinobacteria↑, Cyanobacteria↑, Planctomycetes↑ Family: Lachnospiraceae↑, Enterobacteriaceae↑ Genus: Lactobacillus↑, Streptococcus↑, Clostridium↓, Lactococcus↓, Pseudomonas↓, Acinetobacter↓, Weissella↓, Propionibacterium↓ Species: Candidatus Arthromitus↑ | ↓alpha diversity  | Patrizia Robino et al. 2018                   |
| Mushroom (Agaricus bisporus)  | Pigs                                      | Faeces, Proximal colon contents | High-throughput sequencing of 16S rRNA amplicons (Ion Torrent) | Family: Lachnospiraceae↑, Ruminococcaceae↑ Order: Clostridiales↑ | No change       | GloriaI.S. Aguilar et al. 2018                |
| Mucor circinelloides         | BALB/C mice                               | Faeces         | High-throughput sequencing of 16S rRNA amplicons (Illimuna) | Genus: Bacteroides↑ Species: Akkermansia muciniphila↑ | ↑alpha diversity | Katherine D. Mueller et al. 2019               |
| Mucor velatinosus            | Old man with Onychomycosis and acute myelogenous leukemia | Oral Stool     | High-throughput sequencing of 16S rRNA amplicons (Ion Torrent) | Staphylococci↑ | ↓alpha diversity | Shelburne et al. 2015                        |
| Malassezia↓, Saccharomyces sp↓ | Children with Hirschsprung disease        | Faeces         | High-throughput sequencing of 16S rRNA amplicons (Illimuna) | Phylum: Firmicutes↓, Verrucomicrobia↓, Bacteroidetes↓, Proteobacteria↓ | ↓alpha diversity | Frykman et al. 2015                          |
| Nosema ceranae               | Adult workers Honeybees (Apis mellifera) | Hindguts       | qPCR                        | Lactobacillus spp.↓ and Bifidobacterium spp.↓, Snodgrassella alvi↑, Gilliamella apicola↑ | Not evaluated     | Rouzé et al. 2019                           |
| Pichia kudriavzevii↑, Saccharomycetales↓ | Atopic patient with wheeze                | Faeces         | High-throughput sequencing of 16S rRNA amplicons (Illimuna) | Streptococcus sp.↑, Bacteroides sp.↑, Bifidobacterium sp.↓, Ruminococcus gnava↓ | ↑alpha diversity | Marie-Claire Arrieta et al. 2017             |
### Table 3: Interactions between fungal and bacterial communities (continued)

| Fungi                         | Host                  | Type of sample | Site of sample | Bacterial microbiota method | Bacterial microbiota change/association | Diversity profile | Reference                  |
|-------------------------------|-----------------------|----------------|----------------|----------------------------|------------------------------------------|-------------------|----------------------------|
| *Paranoosema locustae*        | *Locusta migratoria manilensis* | Faeces         | Hindgut        | High-throughput Pyrosequencing of 16S rRNA amplicons (454) | Genus: *Citrobacter*↑, *Lactococcus*↑, *Raoultella*↑  
Species: *Corynebacterium* sp. WA7↓, *Raoultella terrigena*↓ | ↓alpha diversity | Tan Shu-Qian *et al.* 2015 |
| *Sordariomycetes*             | *Pantala flavescens*  | Fresh mycelia  | Larvae         | Culture; High-throughput sequencing of 16S rRNA | Phylum: *Proteobacteria*↑, *Firmicutes*↑  
Genus: *Sphingomonas, Methylobacterium, Burkholderia, Pantoea, Enterobacter*↑,  
*Leclercia, and Serratia, Oceanobacillus*  
Species: *Leclercia* sp., *Oceanobacillus oncorhynchi, Methylobacterium extorquens* | Not evaluated      | Shao *et al.* 2015 |
| *Eurotiomycetes*              |                       |                | Silvatices      | Sequencing of 16S rRNA    | Phylum: *Firmicutes*↓, *Tenericutes*↓, *TM7*↓,  
*Proteobacteria*↑, *Lentisphaeracea*↑, unknown phyla↑  
Genus: *Allobaculum*↑, CF231↑ | ↑alpha diversity    | Zeber-Lubecka *et al.* 2016 |
| *Dothideomycetes*             |                       |                |                |                            |                                          |                   |
| *Leotiomycetes*               |                       |                |                |                            |                                          |                   |
| *Saccharomyces boulardii*      | Premature infants     | Faeces         |                | High-throughput sequencing of 16S rRNA amplicons (Ion Torrent) | Phylum: *Proteobacteria*↓, *Bacteroidetes*↓,  
*Actinobacteria*↓  
Genus: *Escherichia*↑, *Enterococcus*↓, *Veillonella*↑,  
*Clostridium*↑, *Bifidobacterium*↑ | ↑alpha diversity    | Zeber-Lubecka *et al.* 2016 |
| Hamster hypercholesterolemic model |                       |                |                |                            |                                          |                   |
Table 3: Interactions between fungal and bacterial communities (continued)

| Fungi                  | Host                        | Type of sample | Site of sample | Bacterial microbiota method                  | Bacterial microbiota change/association                                      | Diversity profile          | Reference                      |
|------------------------|-----------------------------|----------------|----------------|---------------------------------------------|-----------------------------------------------------------------------------|---------------------------|--------------------------------|
| Saccharomyces cerevisiae | Male BALB/c mice            | Faeces         | Caecum         | Culture                                    | Family: Enterobacteriaceae↓                                                  | Not evaluated             | Garcia et al. 2016             |
|                        | Rats                        | Faeces         | Colon          | Terminal restriction Fragment length Polymorphism (T-RFLP) analysis | Genus: Bacteroides↑, Fusobacterium↑, Bifidobacterium↑, Lactobacillus↑, Enterococcus↑ | ↑alpha diversity          | Li et al. 2017                 |
| EpiCor fermentate      | Healthy volunteers           | Faeces         | Faeces         | High-throughput Sequencing of 16S rRNA amplicons (Illumina) | Genus: Bifidobacterium↓, Allobaculum↓, Acetanaerobacterium↑, Bacteroides↑, Eubacterium↑, Johnsonella↑, Lactococcus↑, Oscillibacter↑, Roseburia↑, Vallitalea↑ | Not evaluated             | H.A.G. Ducray et al. 2019     |
| (dried yeast fermentate made using Saccharomyces cerevisiae) | Sows; piglets              | Faeces         | Rectum         | High-throughput Sequencing of 16S rRNA amplicons (Illumina) | Phylum: Firmicutes↓, Bacteroidetes↑, Family: Bacteroidaceae↑, Porphyromonadaceae↑, Prevotellaceae↑, Genus: Propionibacterium↑, Paraprevotella↑, Oscillibacter↑, Barnesiella↑, Prevotella↑, Akkermansia↑, Odoribacter↑, Anaerostipes↑, Blautia↑, Roseburia↓ | Community evenness↑       | Pinheiro et al. 2017           |
| Yeast derivatives      |                             | Faeces         | Faeces         | High-throughput Sequencing of 16S rRNA amplicons (Illumina) | Sows Phylum: Proteobacteria↓, Genus: Roseburia↑, Paraprevotella↑, Falsiporphyromonas↑, Alkalitalea↑, Eubacterium↑, Turicibacter↑, Papillibacter↑, Desulfovibrio↓, Escherichia/Shigella↑, Helicobacter↓ | No change with sows;       | Shah Hasan et al. 2018         |
| (Saccharomyces cerevisiae) |                             | Faeces         | Faeces         | High-throughput Sequencing of 16S rRNA amplicons (Illumina) | Piglets Phylum: Firmicutes↑, Bacteroidetes↑, Syntrophobacter↑, Synergistetes↑, ofActinobacteria↑, Lentisphaerace↑, Genus: Oscillibacter↑, ClostridiumIV↑, Blautia↑, Gemmiger↑, Anaerobacterium↑, Anaerovibrio↑, Paraprevotella↑ | ↑alpha diversity with Piglets |                                |

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