**Supplementary Table 1.** Literature review of high-throughput next-generation sequencing experiments showing the impact of human helminth infection on microbiome diversity, composition and differential abundance of key bacterial taxa in response to helminth infection. These data show only bacterial taxa below the family level.

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **Helminth (Group)** | **Study type** | **Country** | **Type of sample** | **Method for microbiome profiling** | **Impact of helminth infection on microbiome** | **Differential abundance of bacterial OTUs in response to helminth infection** | **Reference** |
| **Microbiome diversity** | **Microbiome composition** | **Increasing** **abundance** | **Decreasing** **abundance** |
| Soil-transmitted helminths(Nematode) | Natural infection | India | Faeces | 16S rDNA amplicon sequencing, Illumina with custom bioinformatics workflow | No significant difference | No significant difference | NA | **Actinobacteria:***Bifidobacterium, Olsenella***Firmicutes:**Lachnospiraceae, *Dorea, Lactobacillus* | Huwe et al., 2019 |
| Soil-transmitted helminths(Nematode) | Natural infection | Colombia | Faeces | 16S rDNA amplicon sequencing (V4), Miseq Illumina with MOTHUR analysis platform | Significant increasing | Significant difference | **Bacteroidetes:**Porphyromonadaceae, *Alloprevotella, Prevotella,*  | **Bacteroidetes:***Bacteroides* | Toro-Londono et al., 2019 |
| Soil-transmitted helminths(Nematode) | Natural infection | Indonesia and Liberia | Faeces | 16S rDNA amplicon sequencing (V1-V3), and metagenomic approach, 454 GenomeSequencer FLX Titanium, Miseq and Hiseq Illumina with MOTHUR and Shotgun Metagenomic analysis platforms  | Significant increasing | Significant difference | **Actinobacteria:***Olsenella***Firmicutes:***Allobaculum, Enterococcus, Flavonifractor, Solobacterium***Proteobacteria:** *Desulfovibrio, Succinivibrio,*  | **Actinobacteria:***Rhodococcus***Firmicutes:**Lachnospiraceae, | Rosa et al., 2018 |
| Soil-transmitted helminths(Nematode) | Natural infection | Sri Lanka | Faeces | 16S rDNA amplicon sequencing (V3-V4), Miseq Illumina with QIIME analysis platform | No significant difference | Significant difference | **Firmicutes:***Lactococcus***Verrucomicrobia:**Verrucomicrobiaceae, *Akkermansia muciniphila* | **Bacteroidetes:**Bacteroidaceae,*Bacteroides***Firmicutes:** Leuconostocaceae | Jenkins et al., 2017 |
| Soil-transmitted helminths(Nematode) | Natural infection | Malaysia | Faeces | 16S rDNA amplicon sequencing (V4), Miseq Illumina with QIIME analysis platform | Significant increasing | Significant difference | **Bacteroidetes:**Paraprevotellaceae | **Actinobacteria:***Bifidobacterium* | Lee et al., 2014 |
| Soil-transmitted helminths(Nematode) | Natural infection | Ecuador | Faeces | 16S rDNA amplicon sequencing (V3-V5), 454 GenomeSequencer FLX Titanium with MOTHUR analysis platform | Significant decreasing | Significant difference | **Firmicutes:***Streptococcus* | **Firmicutes:***Clostridium* | Cooper et al., 2013 |
| *Necator americanus*(Nematode) | Experimental infection | UK | Faeces | 16S rDNA amplicon sequencing (V3-V4), Miseq Illumina with QIIME2 analysis platform | Significant increasing | No significant difference | **Firmicutes:**Ruminococcaceae**Proteobacteria:***Haemophilus* | **Firmicutes:** Peptostreptococcaceae,Streptococcaceae, *Agathobacter, Dorea*, *Tyzzerella,**Roseburia faecis, Eubacterium hallii* | Giacomin et al., 2016 |
| *Necator americanus*(Nematode) | Experimental infection | Australia | Faeces | 16S rDNA amplicon sequencing (V1-V3), 454 GenomeSequencer FLX Titanium with QIIME analysis platform | Significant increasing | Significant difference | **Bacteroidetes:***Bacteroides, Bacteroides eggerthii, Parabacteroides distasonis, Prevotella,**Prevotella copri***Verrucomicrobia:** *Akkermansia muciniphila* | NA | Giacomin et al., 2015 |
| *Necator americanus*(Nematode) | Experimental infection | Australia | Faeces | 16S rDNA amplicon sequencing (V1-V3 and V3-V5), 454 GenomeSequencer FLX Titanium with QIIME analysis platform | No significant difference | No significant difference | NA | NA | Cantacessi et al., 2014 |
| *Strongyloides stercolaris* (Nematode) | Natural infection | Italy | Faeces | 16S rDNA amplicon sequencing (V3-V4), Miseq Illumina with QIIME analysis platform  | Significant increasing | Significant difference | **Bacteroidetes:**Paraprevotellaceae**Firmicutes:** Leuconostocaceae, Ruminococcaceae, *Peptococcus* | **Bacteroidetes:***Bacteroides***Proteobacteria:***Pseudomonas*  | Jenkins et al., 2018 |
| *Enterobius vermicularis* (Nematode) | Natural infection | Taiwan | Faeces | 16S rDNA amplicon sequencing (V4), Miseq Illumina with custom bioinformatics workflows | Significant increasing | Significant difference | **Actinobacteria:***Bifidobacterium**longum***Bacteroidetes:***Alistipes, Alistipes putredinis* **Firmicutes:***Faecalibacterium, Faecalibacterium prausnitzii, Oscillospira, Ruminococcus flavefaciens,*  | **Fusobacteria:***Fusobacterium, Fusobacterium varium***Firmicutes:***Acidaminococcus, Acidaminococcus intestine, Megasphaera, Megasphaera**elsdenii, Veillonella, Veillonella dispar*  | Yang et al., 2017 |
| *Clonorchis sinensis* (Trematode) | Natural infection | China | Faeces | 16S rDNA amplicon sequencing (V3-V4), Miseq Illumina with QIIME analysis platform | Significant increasing | Significant difference | **Actinobacteria:** *Microbacterium,***Firmicutes:**Clostridiaceae, Erysipelotrichaceae, *Dorea*, *Epulopiscium, Ruminococcus***Proteobacteria:**Caulobacteraceae, Comamonadaceae, Enterobacteriaceae, *Agrobacterium*, *Nevskia*, *Sphingomonas, Variovorax* **Synergistetes:**Synergistaceae,*Cloacibacillus,*  | **Actinobacteria:** *Bifidobacterium***Firmicutes:***Veillonella***Bacteroidetes:**Porphyromonadaceae, *Bacteroides,* *Parabacteroides, Paraprevotella***Proteobacteria:***Enhydrobacter, Enterobacter* | Xu et al., 2018 |
| *Opisthorchis felineus* (Trematode) | Natural infection | Russia | Bile | 16S rDNA amplicon sequencing (V3-V4), Miseq Illumina with QIIME analysis platform | No significant difference | Significant difference | **Actinobacteria:***Cellulosimicrobium, Phycicoccus***Bacteroidetes:***Parabacteroides distasonis***Firmicutes:***Lactobacillus, Staphylococcus equorum, Veillonella dispar,* **Proteobacteria:***Aggregatibacter, Klebsiella, Haemophilus**parainfluenzae, Paracoccus aminovorans, Sphingomonas**changbaiensis,* **Spirochaetes:***Treponema* | **Actinobacteria:***Streptomyces***Bacteroidetes:***Flectobacillus***Firmicutes:***Jeotgalicoccus psychrophilus* **Proteobacteria:***Burkholderia, Xanthobacter,*  | Saltykova et al., 2016 |
| *Opisthorchis viverini* (Trematode) | Natural infection | Romania, Singapore, Thailand  | Bile duct tissue | 16S rDNA amplicon sequencing (V3-V6), Hiseq Illumina with customized analysis pipeline and QIIME analysis platform | Significant increasing | Significant difference | **Actinobacteria:**Bifidobacteriaceae**Firmicutes:**Enterococcaceae**Proteobacteria:**Enterobacteriaceae | NA | Chng et al., 2016 |
| *Schistosoma mansoni* (Trematode) | Natural infection | Ivory coast | Faeces | 16S rDNA amplicon sequencing (V3-V4), Miseq Illumina with QIIME analysis platform | No significant difference | NA | **Proteobacteria:***Klebsiella, Enterobacter arachidis* | **Firmicutes:**Peptococcaceae, *Fructobacillus***Proteobacteria:**Campylobacteraceae**Tenericutes:**Anaeroplasmataceae**Verrucomicrobia:**Cerasicoccaceae | Schneeberger et al., 2018 |
| *Schistosoma haematobium* (Trematode) | Natural infection | Zimbabwe | Faeces | 16S rDNA amplicon sequencing (V3-V4), Miseq Illumina with QIIME analysis platform | Significant increasing | Significant difference | **Bacteroidetes:***Prevotella* | NA | Kay et al., 2015 |